Linking animal science and animal agriculture:
Meeting the global demands of 2050

July 20–24, Kansas City, Missouri

2014 Joint Annual Meeting ABSTRACT BOOK

Journal of Animal Science, Volume 92, E-Supplement 2
Journal of Dairy Science®, Volume 97, E-Supplement 1

ADSA® ASAS CSAS

JOURNAL OF DAIRY SCIENCE® *SINCE 1917*

1800 S. Oak St., Ste 100, Champaign, IL 61820
Phone 217/356-5146 | Fax 217/378-4083 | adsa@assochq.org | http://www.journalofdairyscience.org

Journal of Dairy Science (ISSN 0022-0302) is published monthly on behalf of the American Dairy Science Association® by the Federation of Animal Science Societies, Champaign, IL, and Elsevier Inc., 360 Park Avenue South, New York, NY 10010-1710. Business and Editorial Office: 1600 John F. Kennedy Blvd., Ste. 1800, Philadelphia, PA 19103-2899. Customer Services Office: 3251 Riverport Lane, Maryland Heights, MO 63043. Periodicals postage paid at New York, NY, and additional mailing offices. The electronic edition of the journal (ISSN 1525-3198) is published online at http://www.journalofdairyscience.org.

JOURNAL OF DAIRY SCIENCE® *SINCE 1917*
1800 S. Oak St., Ste 100, Champaign, IL 61820
Phone 217/356-5146 | Fax 217/378-4083 | adsa@assochq.org | http://www.journalofdairyscience.org

Postmaster: Send address changes to *Journal of Dairy Science*, Elsevier Health Sciences Division, Subscription Customer Service, 3251 Riverport Lane, Maryland Heights, MO 63043.

Customer Service (orders, claims, back volumes, online access, change of address): Elsevier Health Sciences Division, Subscription Customer Service, 3251 Riverport Lane, Maryland Heights, MO 63043. Telephone: 800.654.2452 (US and Canada), 314.447.8871 (outside US and Canada); fax: 314.447.8029; e-mail: journalscustomerservice-usa@elsevier.com (for print support) or journalsonlinesupport-usa@elsevier.com (for online support). Allow 4 to 6 weeks for the change of address to be implemented.

Institutional Subscription Rates: For institutions in the United States and possessions: $949 for print. For institutions in all other countries (prices include airspeed delivery): $1070 for print. Current prices are in effect for back volumes and back issues. Electronic access is additional. Please contact customer service for pricing.

ADSA Membership Rates: For individual membership, contact the ADSA office (adsa@assochq.org) to pay dues and obtain access to the journal. For professional members: $110 per year, graduate student membership: $10, undergraduate student affiliate membership: $5. Membership includes electronic version of the journal; additional $61.50 for paper copy in US, and additional $91.50 for paper copy in all other countries). Membership in the ADSA is on a calendar year basis from January through December.

Advertising Information: To advertise a position announcement in the News and Announcements section of the journal, please use the FASS Job Resource Center (http://www.fass.org/job.asp); e-mail jrc@assochq.org if you have questions.

For display advertising orders and inquiries please contact Ken Senerth at 609.577.0916; by fax at 212.633.3980; or by e-mail at kensenerth@gmail.com. For non-recruitment classified advertising orders and inquiries please contact John Marmero at 212.633.3657; by fax at 212.633.3820; or by e-mail at j.marmero@elsevier.com.

Author Inquiries: For inquiries relating to the submission of articles, complete Instructions for Authors can be found online at http://www.journalofdairyscience.org. Manuscripts submitted for consideration should be submitted electronically at http://mc.manuscriptcentral.com/jds in accordance with the Instructions for Authors. Need help? Contact shaunam@assochq.org.

Offprints. Authors may place orders for offprints when proof corrections are sent to the editorial office (before the journal is sent for printing). For queries about offprints or order status, e-mail vickip@assochq.org; fax 217.378.4083.

Reprints. To order author reprints after the issue has been printed, e-mail authorsupport@elsevier.com. To order 100 or more reprints for educational, commercial, or promotional use, contact the Commercial Reprints Department, Elsevier Inc., 360 Park Avenue South, New York, NY 10010-1710; fax: 212.633.3820; e-mail: reprints@elsevier.com. Access to single articles available online may be obtained by purchasing Pay-Per-View access on the journal website (http://www.journalofdairyscience.org).

Application for membership in the American Society of Animal Science (ASAS) is invited from persons with interest in animal science and livestock production. In 2014, annual dues including access to the electronic version of the Journal of Animal Science are $135 in the United States, Canada, and Mexico and in other countries. For those in the United States, Canada, or Mexico who wish to receive a paper copy of the journal, the additional fee is $200; for those in other countries, the additional fee is $300. Student affiliate membership is granted to those who are certified by a professional member as a regularly enrolled college student who does not hold a full-time position at the time of application for, or annual renewal of, membership. Graduate student memberships ($20 annually) and undergraduate student memberships (free) include access to the electronic version of the Journal of Animal Science. Postdoctoral fellows' membership dues are $65. An institutional subscription ($599 annually) entitles an institution Internet access to e-JAS within appropriate IP addresses. For an additional $125 fee, institutions within the United States, Canada, and Mexico will receive a paper copy of the journal (an additional $150 fee for all other countries). For corporate subscriptions, please contact the ASAS office for pricing. Individual sustaining membership, $375 per year. Applications for membership with remittance should be mailed to the ASAS Business Office.

ASAS Business Office, PO Box 7410, Champaign, IL 61826
Telephone: 217-356-9050; Fax: 217-689-2436; E-mail: asas@asas.org Office hours: 8:00 a.m.–5:00 p.m.

American Society of Animal Science World Wide Web address: http://www.asas.org

Calendar of American Society of Animal Science Upcoming Meetings

Midwestern Section (with ADSA)	March 16–18, 2014	Des Moines, IA
Western Section	June 24–26, 2014	San Angelo, TX
Northeast Section	July 20–24, 2014	Kansas City, MO
National Annual Meeting (with ADSA)	July 20–24, 2014	Kansas City, MO

Manuscript Submission. Information about manuscript submission is given in *Style and Form* published on the journal website (http://jas.fass.org). All manuscripts submitted to the *Journal of Animal Science* must be accompanied by the JAS manuscript submission form certifying that any research that involves animals has followed established standards for the humane care and use of animals. Manuscripts should be submitted online via http://mc.manuscriptcentral.com/jas.

Address Change and Missing Copies. Notice of change in address should be received by the ASAS Business Office 60 days in advance of change. A claim for a missing copy of the *Journal of Animal Science* should be received within 30 days (90 days foreign) after publication date to ensure replacement at no additional charge. The current policy is one replacement per monthly issue of the *Journal of Animal Science*. If additional replacements are requested beyond that, a single-issue price of $60 per issue domestic and $65 per issue foreign shall be charged. These prices reflect the current single issue pricing structure.

Journal of Animal Science (ISSN 0021-8812) is published 12 times per year (monthly) by the American Society of Animal Science. Periodicals postage paid at 201 W. Springfield, Ste 1202, Champaign, IL 61820 and at additional mailing offices. Form 3579 to be returned to the ASAS Business Office. Postmaster: Send change of address to American Society of Animal Science, PO Box 7410, Champaign, IL 61826.

TABLE OF CONTENTS

ORAL SESSIONS

POSTER SESSIONS

ADSA FOUNDATION SYMPOSIUM: MEETING THE PRESENT AND FUTURE DEMAND FOR EMPLOYEES WITH A PhD IN DAIRY SCIENCE

0001 Current problems with funding PhD programs.

L. H. Baumgard* and M. G. Hogberg, *Iowa State University, Ames.*

The dairy industry's need for scientifically trained personnel is increasing, whereas academic output of PhD graduates with a dairy emphasis is decreasing. This enhanced requirement for industry scientists is the obvious result of a maturing, evolving, and increasingly educated global dairy industry. Reasons for the reduction in the number of PhD candidates are less apparent and multifaceted. First, the field of dairy science is becoming more geographically regionalized and thus many U.S. land grant institutions have either de-emphasized or eliminated their dairy curriculum and dairy research capabilities. Second, the means by which graduate students are funded has markedly changed over the last 30 yr. In the past, most faculty members were "allocated" state-appropriated monies that were used to pay graduate student stipends and fund research projects. At most universities, these state "lines" have either experienced severe attrition or, in most cases, have completely been eliminated. Although variable among universities, current graduate student stipends (direct and indirect costs) range between $25,000 and $40,000 annually. Consequently, faculty are required to generate approximately $70,000 or $140,000 in stipend funds for a M.S. or PhD student, respectively, to graduate students in a timely manner. Funds to support research are necessary in addition to the stipend, raising total training costs for a PhD to < $300,000. Federal grants (USDA, NSF, NIH, etc.) are often monetarily large (i.e., $300,000 to $1 million), typically run for 3 to 5 yr, and are generally "focused" on a specific area of biology. However, the likelihood that a PI can continuously fund a research program based on competitive funding is low, as success rates on federal grants are commonly < 10%. This is especially true for applied researchers. Alternate sources of research funding are commodity groups and allied industry. However, relying on industry funding to train a PhD student requires successfully obtaining at least 4 yr' worth of industry grants large enough to complete a student's degree. Further, research revenue from different aspects of the industry will undoubtedly create inconsistencies in the area and type of research that the student conducts. Consequently, the experiments are less likely to "build on each other" and lack biological continuity; circumstances that compromise critical thinking and jeopardize scientific independence. Therefore, untraditional and creative funding strategies are urgently needed to meet the global demand for technically trained dairy scientists. Potential strategies will be provided in the presentation.

Key Words: funding

0002 Current situation for finding qualified people with a PhD; an industry perspective, dairy production.

W. C. Weldon*, *Elanco Animal Health, Greenfield, IN.*

A population growing to 9 billion people and 3 billion people moving to the middle class is projected by 2050. These global trends are increasing milk demand globally. Milk demand is projected to exceed supply, as people drink milk and eat dairy products to improve their nutrition, as their economic status improves. The increased need for milk will drive a significant demand for individuals with a PhD in dairy science. Industry roles for PhD graduates span a significant spectrum, including leading research, providing nutrition, reproduction, health, and management consulting services. There is also significant advancement in the underlying technology being used to produce milk and dairy products, requiring a continual investigation and learning over the course of an entire career. The demand for milk globally is significantly increasing the demand for qualified PhD graduates across the globe, in an effort to develop products, practices, and genetics that can rapidly improve productivity. In our experience, the most successful PhD scientists have a broad view of the industry, coupled with deep technical training. Including real life experiences through industry cooperation can help students develop key industry knowledge that will be critical for their future. These experiences will enhance their career. Our industry is becoming more complex with multiple partnerships. This requires students that are not only good in the lab but are very effective at collaboration and transferring knowledge. Finding PhD scientists with these qualities is difficult. In many cases, it can take a year or more to fill a position with a qualified candidate. The long searches can negatively impact the hiring companies. Significant opportunities exist to increase global milk production by increasing the population of PhD dairy science graduates to help meet the global demand for the nutrition from milk and dairy products. These scientists will be most effective if PhD programs focus on sound scientific training but also expose and train students in interpersonal skills, economics, and dairy industry fundamentals.

Key Words: dairy, PhD

0003 Current situation for finding qualified people with a PhD; an industry perspective, dairy foods. C. Allen*, *Kraft Foods, Glenview, IL*.

The current situation for finding qualified PhD graduates with dairy foods experience is bleak. There are limited experienced people in the industry and an even smaller amount coming out of the universities. The trends in dairy that are continuing to influence the dynamic evolution of employee requirements are: economic shift to the extremes and decline of the middle, continual push to drive for sustainable products, and global shifts in the commodity market. Dairy foods are complex matrices and span a wide range of food systems. The need for dairy talent with deep and varied expertise is urgent, but academic institutions shouldn't lose sight of the need to produce talent with a strong base in fundamental sciences and strong technical rigor. Companies are often recruiting, developing, and retaining their specific talent, but this approach is minimally successful and often leaves gaps in expertise. Suggestions to close this gap are: applied internships within strong fundamental programs or joint university programs (degreed or specialty) that combine strong fundamentals with application.

Key Words: dairy foods, internships

0004 Current situation for finding qualified people with PhDs; an academic perspective. V. V. Mistry*, *South Dakota State University, Brookings.*

The tripartite mission of teaching, research, and extension established 150 yr ago remains at the core of land grant universities today, but numerous structural differences today have an impact on programs. The PhD-holding candidates at universities may find positions, such as post-doctoral research associates, faculty members, and later in their careers, administrative positions, such as department head, associate dean, and dean, that help define academic programs. University programs that were typically funded by state and federal funds in the form of teaching, Hatch, and extension funds have seen a substantial reduction in dependency on these funds due to competition from other local (state) and national needs. Therefore, dependency on other non-appropriated funds has become essential (e.g., competitive grants, tuition and fees, and discretionary funds). Expectations of research output from faculty members have also increased. Thus, dependency on competitive grants for supporting research programs, graduate students, and portions of faculty salaries has become imperative. Simultaneously, non-university research programs, as in industry, have also become more sophisticated and, in many cases, targeted at long-term research efforts. Consequently, only those high quality PhD graduates that have a strong desire to develop a career in academia become candidates for faculty positions. Salaries in industry are usually higher than academic faculty positions. It is essential for universities to fill faculty positions with highly competitive individuals that in today's climate are not just excellent researchers that have an interest in teaching but are also competitive entrepreneurs. Such individuals if provided the right resources through start-up funds, grant writing training, and research resources will be well positioned to develop research programs that will train graduate students. Opportunities provided in a university environment are sometimes not known by prospective faculty members, such as the ability to consult, ability to share royalties from patents and licensed intellectual property they develop, and the general fulfilling nature of training students. It is therefore imperative that industry, universities and state and federal governments jointly develop efforts to help make the academic career attractive for PhD-holding candidates. Further, university graduate programs should be encouraged to design curricula that will help students position themselves for a successful academic career. Examples include courses or training in teaching, grant writing, and publications. Also important is the ability for students and faculty to develop relationships with industry.

Key Words: faculty, recruitment, university

0005 Short-term employment opportunities in industry for people pursuing graduate degrees. C. Johnson*, *Land O'Lakes, Inc., Arden Hills, MN.*

Short-term employment opportunities offer companies seeking to employ people with graduate degrees and people seeking graduate degrees several key benefits. First, short-term employment opportunities allow potential employers to determine what the graduate degree candidate can bring to the table before extending an employment offer. Graduate degree candidates can acquire valuable skills and training in practical, "real world" work settings. Acquired skills and training can complement the candidate's academic education and increase the candidate's market value when pursuing employment. These short-term employment opportunities also allow the graduate candidate to determine if a position and/or company are a right fit for the candidate's career goals, further solidifying career direction and understanding broader applicability of one's education. Another benefit of short-term employment opportunities for graduate degree candidates is the ability to expand their business network, which is not only beneficial in the short term when seeking employment but also throughout one's career. Finally, short-term employment opportunities allow graduate candidates to add depth and breadth to their curriculum vitae, setting themselves apart from other candidates.

Key Words: careers, dairy, graduate degrees

ADSA SOUTHERN SECTION SYMPOSIUM: STRATEGIES FOR HOUSING DAIRY ANIMALS IN THE SOUTHEAST

0006 Photoperiod management of dairy cattle: considerations and applications. G. E. Dahl*, *University of Florida, Gainesville.*

Photoperiod, the duration of light exposure relative to darkness in a day, has significant impact on productivity and health of dairy cattle and other farmed species. A light:dark cycle of 16 h light and 8 h dark (16L:8D) is termed a long day photoperiod, whereas a 8L:16D cycle is termed a short day photoperiod. The physiological basis for the response begins with light perception at the eye and signaling to the hypothalamus and pineal gland to alter secretion of melatonin. Circulating melatonin increases during exposure to darkness from concentrations that are typically undetectable and thus the lighting schedule drives a pattern of melatonin release that allows the animal to track daylength. The most consistent endocrine effects of variable photoperiod are the responses of circulating prolactin and insulin-like growth factor-1, both of which impact growth and mammary gland function throughout the life cycle. Specifically, long day photoperiod increases lean growth in heifers and increases milk yield in lactating cows. In contrast, cows maintained on short days during the dry period subsequently produce more milk than those on long days when dry. Cows on short days when dry and those on long days in lactation have increased dry matter intakes relative to herdmates on the respective opposite treatments. Managing lighting in barns is easily implemented with commonly available fixtures and lamps. Indeed, the choice of light installed is made by combining the highest efficiency lamp available for the effective mounting height of the barn. Typically, with lower ceilings, a compact fluorescent lamp is the most appropriate selection, whereas the higher mounting heights available in freestall barns are better suited to metal halide or similar high efficiency lamps. Recently, LED lamps have been recommended due to their superior energy efficiency, but direct, robust testing of LED lamps has not been reported. Low intensity red lighting can be used in facilities during darkness, as it is not perceived as light by many species, including cattle. Target light intensity is in the range of 150 lux at a level 1 m above the barn's floor and that intensity should be maintained throughout the facility. Photoperiod manipulation is a low cost, high return method to increase a dairy herd's productivity throughout the cow's life cycle.

Key Words: dairy cow, housing, photoperiod

0007 Impacts of heat stress on cow and calf. S. Tao*[1], G. E. Dahl[2], and J. K. Bernard, *[1]University of Georgia, Tifton, [2]University of Florida, Gainesville.*

Heat stress has negative impacts on dairy cattle at different stages of their life cycle. Compared with the lactating dairy cow, the dry cow and neonatal calf have lower upper critical temperature, but their performance is still negatively impacted by heat stress. During the dry period, heat stress elevates cow body temperature and also disrupts several normal physiological functions during late gestation, such as impaired mammary growth and fetal development, which compromise future performance of the cow and calf. Compared with cooled cows, heat-stressed dry cows have lower milk production in the subsequent lactation and altered metabolic and immune function during the transition period. Maternal heat stress of dams during the dry period also has negative effects on their offspring. For example, calves born to heat-stressed cows have lower birth weight and impaired ability to absorb immunoglobulin from colostrum relative to calves from cooled dams. Emerging evidence also suggests that heat stress in utero may have long-term impact on a heifer's future performance, including milk production in the first lactation. Heat stress has direct negative impact on neonatal calf performance, as well. When exposed to heat stress, calves have impaired passive immunity and high mortality rate in the first month of life. Additionally, heat stress lowers a calf's average daily gain, feed efficiency, and overall growth during early life. Thus, proper management tools need to be implemented to cool the dry cow and neonatal calf as a way to alleviate the negative impacts of heat stress on these animals.

Key Words: dairy calves, dry period, heat stress

0008 Implications of overstocking on the behavior, health, and productivity of dairy cows in the Southeast. P. D. Krawczel*, *The University of Tennessee, Knoxville.*

The survivability of dairy farms across the Southeastern United States is being challenged by a variety of factors, such as high costs of production and aging housing and milking facilities. One common response to this is to attempt to increase revenue by increasing herd size, yet keep costs low by not investing in related infrastructure. This approach may be counterproductive to the overall performance of the farm, as there is a growing body of evidence that suggests there are negative consequences on lactating dairy cows that are required to compete for resting and feeding resources. This presentation reviews the current understanding of: 1) the relationships among overstocking, behavior, health, and productivity; 2) the behavioral strategies that dairy cows use to mitigate the effects of overcrowding and potential consequences of these strategies on health and productivity; 3) factors that are spe-

cific to the Southeast that may impact the relationship among stocking density and other considerations of housing management; and 4) current gaps in our knowledge that should be addressed with future research. Overall, the behavioral changes that were evident in overstocked freestall-based housing facilities included a decrease in the number of hours spent lying per day, an alteration of the feeding times and overall time spent feeding, and increased antagonistic behaviors occurring at the freestalls and feed barriers. From a performance perspective, there were indications that both milk production and reproductive success might be altered by overstocking either the freestalls or feed barriers of a housing facility. The hot, humid summers, which typify the region, and the age, design, and management of freestall facilities represent 2 factors with the potential to compound the overall impact of overcrowding in the Southeast. On the other hand, the commonality of pasture access in the overall housing strategy across the region might mitigate some of the negative effects of overstocking on lactating cows. The extent to which these interactions are detrimental or successful when associated with overstocking reflects a major gap in our current understanding of managing dairy housing systems in the Southeast. Beyond freestall-based housing facilities, there is a growing interest in the use of composted bedding pack housing in the region. However, there is little empirical data to support recommendations for the space required per cow within these housing systems.

Key Words: behavior, dairy cow, housing, overstocking

0009 Managing heat stress in dairy calves and heifers: Housing considerations. S. H. Ward*, *Mississippi State University, Mississippi State.*

Dairy calves and heifers are often overlooked when considering not only cooling strategies but housing in general. Providing housing with cooling in the summer for both young calves and older heifers could improve growth, subsequent lactation performance, and profitability for the dairy operation. While hutches for dairy calves have become fairly standard throughout the industry, providing a source of shade over the hutches has been shown to improve respiration rates and reduce skin temperature of calves (Spain and Spiers, 1996). Coleman et al. (1995) found a tendency for improved feed efficiency when calves were housed in shaded hutches, along with lower rectal temperatures. Calves that were housed under metal roofing, with and without cooling, had lower temperatures, increased IgG, and lower mortality rates compared with those housed in hutches (with metal covers). Providing a source of shade over hutches during prolonged heat stress can improve calf performance, but cooling the shaded area may not result in further improvements. Similar trends have been noted in older heifers housed on pasture with different shade sources. Twenty-one yearling, Holstein heifers (n = 7) were assigned to 1 of 3 paddocks, each with a different type of shade: 1) natural shade from trees (T); 2) hutches (H); and 3) shade cloth (SC). All heifers were fed a commercial grain mix and ryegrass hay, and grazed a grass-legume mix pasture. Body weight, frame measures, rectal temperatures, and blood samples were collected once per week. Heifer behavior was observed twice weekly for a total of 24 h. There was a tendency for decreased body weights in heifers housed under SC, but ADG, wither height, or hip height were not affected by shade type. Blood parameters were not affected by shade type. Time spent in the shade vs. not was also not different with shade type, but time spent lying was greater in both T and SC when compared with H ($P < 0.05$). Temperature was also lower in T and SC compared with H, which may have contributed to decreased time lying down.

Key Words: dairy heifers, heat stress, housing

0010 Compost bedded pack barns as a lactating cow housing system for the Southeast. J. M. Bewley*[1], R. A. Black[2], F. A. Damasceno[3], E. A. Eckelkamp[1], G. B. Day[1], and J. L. Taraba[1], *[1]University of Kentucky, Lexington, [2]University of Tennessee, Knoxville, Federal University of Mato Grosso, Campus Rondonópolis, Brazil.*

A compost bedded pack barn is a lactating dairy cow housing system consisting of a large, open resting area, usually bedded with sawdust or dry, fine wood shavings. Bedding material is composted in place, along with manure, when mechanically stirred on a regular basis. Recently, the popularity of compost bedded pack barns has unquestionably increased in the Southeast (at least 80 compost bedded pack barns have been constructed in Kentucky). Because of warm climates, the compost bedded pack barn fits the Southeast particularly well. Galama (2011) suggested that compost bedded pack barns fit within goals of sustainable agriculture because of benefits to the cow (space, rest, exercise, and social interaction), farmer (low investment, labor extensive, reduced manure storage costs), and environment (reduced ammonia and greenhouse gas emissions, odor and dust emissions, reduced energy consumption). Producers report reduced incidence of lameness and improved hoof health, resulting from greater lying times and a softer, drier surface for standing. Cows may be more likely to exhibit signs of estrus because of improved footing on a softer surface, leading to improved heat detection rates. Compost bedded pack barns reduce the need for liquid-based manure storage systems and provide producers with the option to economically transport nutrients in a dry, concentrated form to areas where there is an off-farm demand for nutrients. The initial investment costs of a compost bedded pack barn are lower than for traditional freestall or tiestall barns, because less concrete and fewer internal structures (stall loops, mattresses) are needed. This system represents a viable entry option for smaller, start-up dairies. Proper composting increases the bedding temperature and decreases the bedding moisture by increasing the drying rate. Keeping the top layer of bedding material dry is the most important part of

managing a compost bedded pack barn. The pack should be stirred at least twice daily. Stirring is typically accomplished while the cows are being milked, using various types of cultivators or roto-tillers. Poor management may lead to undesirable compost bed conditions, dirty cows, elevated SCC, and increased clinical mastitis incidence. Proper management of compost bedded pack barns includes facility design, ventilation, timely addition of fresh, dry bedding, frequent and deep stirring, and avoidance of overcrowding.

Key Words: cow comfort, compost bedded pack, housing,

ADSA-ASAS NORTHEAST SECTION SYMPOSIUM: **OPPORTUNITIES TO MEET CHANGING CONSUMER PREFERENCES FOR ANIMAL PRODUCTS**

0011 The science and art of cheesemaking.
K. E. Kaylegian*, *Pennsylvania State University, University Park.*

Without a doubt, the interest in cheese is growing. From a total volume perspective, the increase in the use of cheese in foodservice and fast food is good for the dairy industry. However, the more interesting story is the explosive growth in specialty and artisanal cheeses. The American public is becoming more focused on connecting with the manufacturers of their foods. This is illustrated by the increase in popularity of local farmers' markets and the Buy Fresh Buy Local organization that now has chapters in 24 states. Consumers are adventurous and always looking for new flavors, shapes, and varieties of cheese. The dairy industry is quite responsive to this opportunity, seeing these value-added products as a way to stay viable in an industry that is relatively saturated in the fluid milk market. Artisanal cheeses are produced on levels from large, multi-plant operations to 1-person farmstead operations, making cheese only using their farm's milk. Artisanal cheeses are marketed in many different outlets. Some cheesemakers choose to sell more common types of cheese, like plain and flavored varieties of Cheddar, Colby and Jack for their local markets, whereas others choose to make unique cheeses destined for restaurants or high-end cheese shops. There are legal constraints regarding standards of identity and raw milk cheese aging requirements that must be followed. Beyond these, the world of cheese offers an empty canvas for the cheesemaker's creativity. Cheesemakers have an amazing palette of bacteria, yeasts, and molds to choose from to develop unique cheeses that complement their milk, the seasons, their geographical location, their values, and their passions. Milk from cow, goats, sheep, and water buffalo are used to make cheese, further expanding the varieties of cheese that can be created. Understanding how to combine these variables to make a high quality, consistent cheese requires an understanding of the science behind the cheesemaking process. The growth in cheese varieties is measured by the number of entries in cheese competitions. The first American Cheese Society Competition in 1985 had 89 cheeses in 7 categories; in 2003 there were 762 cheeses; and in 2013 there were > 1700 cheeses entered in ~80 categories. The interest in cheese is definitely growing.

Key Words: artisan cheese, value-added

0012 The 'Greek yogurt effect:' Impact on milk production and the dairy industry in New York.
A. Novakovic*, *Cornell University, Ithaca, NY.*

The production of Greek yogurt has nearly quadrupled from 2008 to 2013 in New York. In the last decade, Greek yogurt has gone from being a relatively obscure product imported from Greece to New York City to an exciting new product that is transforming the retail dairy case, spinning off a host of new products and capturing the imaginations of consumers around the country. Long a significant player in the yogurt category, New York rapidly moved to become the dominant player in the Greek yogurt segment and is now the leading manufacturer of yogurt in the United States. The large farm milk production sector in New York is an important factor in the development of this product segment, but the proximity of this large production area relative to the demographically large, rich, and diverse population centers of the northern Atlantic Coast is even more important. The new Greek yogurt category has strong appeal and should be a durable feature in U.S. dairy markets, but this is not without challenges. New York's role in this burgeoning sector is likely to be durable as well, but it will surely see increased competition as processors expand product lines and develop markets. The development of this new product category has had a positive impact on dairy sector sales and revenue, but the impact is small when measured against the total dairy sector. There are significant impacts for local communities in which new plants are located and meaningful benefits to nearby farmers who are able to supply those plants instead of more distant customers.

Key Words: dairy demand, dairy products, Greek yogurt, milk markets, milk prices, milk production, New York, yogurt

0013 New approaches to low-fat meat products to better meet consumer demands.
E. W. Mills*, *Penn State University, University Park.*

Reduced fat meat products have received a great deal of consumer interest for several years. Livestock producers and meat processors work together to provide products that satisfy consumers' desire for products with low fat, low saturated fat, and low trans-fat, among others. The techniques for fat reduction in meat products are more important now than ever. The biggest challenge has always been maintaining desirable texture, flavor, and juiciness in reduced fat meat products. Options available for ensuring palatability of reduced fat products focus mostly on replacement of fat with 1 or more ingredients that mimic the actions of fat. Water is commonly utilized for fat replacement because it imparts juiciness at a very low cost. Various ingredients may be included to bind water in the product or provide a more oil-like mouth feel. Whole muscle cuts pose different challenges than comminuted products when fat is reduced. In whole muscle cuts, water containing

a small amount of salt, water binding agent, and flavorings is often injected to improve juiciness of the cooked product. In this context, the ingredients should be fully soluble or easily suspended, and generally must not impart detectable color to the product. Processors and suppliers are constantly trying new label-friendly ingredients that may provide the functions of water binding, texture modification, or flavoring. Natural plant extracts, including hydrocolloids, carbohydrates, and proteins, may be used. Comminuted products offer a different set of challenges and opportunities. Ingredients utilized in these products need not be soluble because they will be incorporated by mixing. Also, their visible presence may make a desirable contribution to the product's appearance. This is especially true in situations where products are made to suit a particular ethnic or regional consumer preference. A coarse texture or distinctive particles of seasoning are often used to establish the character of a niche product. One of the biggest challenges in formulating reduced fat meat products is flavor delivery. In conventional products, fat serves as a carrier for hydrophobic flavor compounds. In low fat products, the absence of a hydrophobic delivery system means that some flavor compounds are not detected. It may be necessary to use different forms of seasonings to improve seasoning flavor. With continued consumer interest in lower fat foods, it is imperative that meat producers and processors use the best technology available to provide those products.

Key Words: fat replacer, low fat, meat

ADSA-SAD UNDERGRADUATE STUDENT PAPER COMPETITION: ADSA-SAD UNDERGRADUATE PRESENTATIONS—DAIRY FOODS

014 Dairy Fats: The good, the bad, and the ugly. H. Potts*, B. A. Corl, and D. R. Winston, *Virginia Tech, Blacksburg.*

Consumers have a misinformed, negative perspective of dairy products because of their fat content, specifically the "bad" saturated fats and "ugly" trans fatty acids. However, dairy fats also contain a valuable "good" fat that does not show up on a nutrient label: conjugated linoleic acids (CLA). Conjugated linoleic acids are biologically active isomers of linoleic acids, a type of trans fatty acid, which have been studied for their possible health benefits. The 2 most abundant CLA isomers are the cis-9, trans-11 isomer and trans-10, cis-12 isomer, and are found in significant concentrations in high fat dairy products, such as full-fat milk, cheese, and butter. Research began when the anti-carcinogenic properties of CLA were discovered. Then, it was looked at as a possible weight loss mechanism and more recently the research has focused on CLA's possible effects in preventing cardiovascular disease. Animal and human studies on CLA's effects related to major components of cardiovascular health, including heart disease, cholesterol levels, and high blood pressure, have shown that consumption of high levels of CLA can lead to a decrease in many cardiovascular risk factors. Pintus et al. showed that a dietary intervention of CLA-enriched cheese lowered LDL cholesterol by 7% in 42 adult volunteers. Further studies demonstrated that CLA consumption was nearly as effective in humans as taking certain hypertension drugs. However, current CLA intake in different countries shows that consumers are only eating minor amounts of CLA. Current negative consumer perspectives on dairy fats need to be changed so consumers will include these beneficial dairy fats in their diets at levels high enough to receive cardiovascular health benefits. The main way to accomplish this is through educating the American consumer on where to find these "good" dairy fats and how to get their associated health benefits. The best consumer education will be accomplished through media advertisements and including information regarding CLA on dairy product labels and packaging.

Key Words: cardiovascular health, conjugated linoleic acid, fats

0015 Differences in bovine and caprine cheese production. K. Wolf* and J. M. Bewley, *University of Kentucky, Lexington.*

The dairy goat cheese market is the primary milk-based income source for dairy goat producers. Efficient cheese production is more challenging with goat milk than cow milk. These challenges arise from structural and molecular characteristics unique to goat milk. Goat milk has a lower pH than cow milk, which results in differences in the acidification process for initializing curd formation. Another factor is the smaller fat globules of goat milk, which result in a natural homogenization effect and greater difficulty in separating smaller particles. Less particle separation results in lower cheese yields. Possibly the most significant difference is seen in the α S1-casein frequencies across the goat population when compared with the cow population. Casein is the major protein in milk and is essential for cheese production. The primary casein subclasses are α and β caseins. In cow milk, the α caseins are more prevalent than any others, whereas in goat milk β caseins are more typically observed. Alpha S1-casein, in particular, is associated with higher solids non-fat content than any other casein class, but it is among the least common goat milk proteins. This means lower cheese yield because the most important cheese protein is not the most prevalent in goat milk. Presence and frequency of α S1-casein is primarily genetic with 17 alleles identified. Further variation in α S1-casein expression exists among dairy goat breeds, with the Swiss breeds expressing the weakest α S1-casein alleles compared with African and American breeds, which have a higher α S1-casein frequency. The breed relationships to cheese proteins suggest that the first step in achieving good cheese yields is selecting goats of the correct breeds. Additional problems to be combatted are the higher SCC seen in goats compared with cows, reducing curd formation ability, and a greater variation in diet with most goat herds compared with cow herds, which can cause inconsistent yields, textures, and flavors. Cheese recipes can be modified to optimize yield from goat milk by adding more rennet, using less starter, and maintaining a lower temperature during the cheesemaking process.

Key Words: α S1-casein, cheese, goat

0016 Do current regulations for raw milk cheeses ensure consumer safety? C. T. Redding*, K. H. Ingawa, and S. P. Washburn, *North Carolina State University, Raleigh.*

Raw milk cheeses are made from milk that is not pasteurized nor homogenized, and it is currently legal in the United States to sell raw milk cheeses that have been aged for at least 60 d. In some studies, raw milk cheeses have been documented to have more intense flavor than pasteurized cheeses and variations in diets with various pasture species can also affect flavor. In a preference study, 890 consumers sampled Cheddar and Gouda cheeses made from either raw milk or pasteurized milk. A majority of the consumers preferred raw milk cheese, even though many of them either were not sure or had considered raw milk cheeses to be less safe. However, there can be situations in which pathogenic organisms or resulting toxins could survive the aging process. One study investigated 8

pathogens that were intentionally injected into raw milk that was then used to make Swiss hard or semi-hard cheeses. The study showed hard cheeses to be free of inoculated pathogens 1 wk after production. The semi-hard cheeses were free of most pathogens and toxic metabolites, except for *Listeria monocytogenes*, which had survived the manufacturing and ripening processes. A recent study that used milk spiked with various strains of *E. coli* resulted in detection of *E. coli* in almost all cheeses at the end of the 16-wk ripening period, which could be a food safety issue. In contrast to studies in which pathogens were injected into milk, most raw milk produced for small scale artisan cheesemaking in Vermont was of high microbiological quality with no detectable target pathogens in the cheese. Aging for 60 d seems effective for eliminating or reducing most pathogens, but frequent testing to ensure milk is pathogen free before making cheese is recommended.

Key Words: food safety, pathogens, raw milk cheese

0017 Applications for functional dairy starter cultures.

G. G. FitzPatrick* and D. R. Olver, *Pennsylvania State University, University Park.*

Bacteria starter cultures are large numbers of cells of microorganisms that are used to initiate a fermentation process in certain foods, such as cheese, yogurt, butter, sourdough, and fermented meats. Certain bacterial strains can be selected or genetically modified to exhibit functional properties that enhance the foods they help produce. For instance, specific strains of bacteria can be used to combat the growth of *Listeria monocytogenes* and other pathogenic microbes. Maisnier-Patin et al. demonstrated that starter cultures containing nisin-producing subspecies of *Lactococcus lactis* were able to control growth of *Listeria monocytogenes* while maintaining suitable pH for Camembert cheese development. This may have importance in raw milk cheese production. Consumers often prefer the interesting flavors offered by these cheeses but have concerns about the health risks of consuming raw milk products. Additional types of functional bacteria starters have the potential to improve the sensory qualities of cheese. Guldfeldt et al. used genetically modified strains of *Lactococcus lactis* to improve flavor and reduce bitterness in Cheddar cheese. Other functional starters have been used to speed up the maturation process of cheese aging and prevent over acidification in yogurt. Functional starter cultures offer the opportunity to produce wholesome, safe products with enhanced sensory properties and probiotic qualities desired by consumers.

Key Words: cheese, functional starter culture

ADSA-SAD UNDERGRADUATE STUDENT PAPER COMPETITION: ADSA-SAD UNDERGRADUATE PRESENTATIONS—DAIRY PRODUCTION

0018 Dairy cow welfare: Bridging the gap.
E. A. Morabito* and J. M. Bewley, *University of Kentucky, Lexington.*

Most consumers are unaware of dairy production practices and generally rely on information from print, television, and social media to obtain information. Animal welfare is 1 consumer concern that often creates a gap between consumers and dairy producers. Differing values and ethics increase the complexity of animal welfare as an ethical issue. Current dairy welfare research includes objective physiological, behavioral, preference, and motivational research. Objective research observes measureable variables to determine whether the welfare of a dairy cow is compromised. These measures may not be useful indicators of psychology or natural behaviors, but are helpful in other types of welfare research. Cow comfort research examines cow behavior with different facilities and management practices. This research demonstrates how cow comfort is beneficial for welfare and production. Preference research includes observing dairy cow choices among alternative situations. This indicates cow inclinations and helps redefine natural behaviors. Motivational research is similar to preference research where an obstacle is used to get to 1 of the situations. An obstacle could include a physical barrier or longer walk to get to the destination. This demonstrates how motivated a cow is to choose 1 situation over another. All of these current research areas are allowing scientists to understand more about animal behavior and psychology. Knowledge of dairy cow emotions is still lacking and difficult to measure. Animal welfare models have been created to understand the broader definition of welfare. These models go beyond the traditional measures of welfare and include less measureable traits, such as emotions and an animal's need for a natural environment. Before applying these models to improve the definition of animal welfare, research must be conducted to understand more about emotion, psychology, physiology, and natural behavior. Some studies on both lab and livestock species have been conducted to measure emotions. Translating these studies into dairy research may be beneficial in the future. Publicizing information about current and future research is important for public education. Education, along with the implementation of welfare models, may help bridge the gap between consumers and dairy producers. Improving animal welfare will improve dairy cow well-being, public perception, and overall dairy production.

Key Words: dairy, ethics, welfare

0019 The effects of overcrowding on the behavior of lactating dairy cows in freestall housing systems.
S. F. Templeton*, R. A. Black, and P. D. Krawczel, *University of Tennessee, Knoxville.*

Overcrowding is commonly seen among freestall dairy operations to increase herd size without altering facilities. Overcrowding occurs at stocking densities > 100%. Overcrowding at the feedbunk is defined as > 1 cow per headlock or < 0.6 m of linear feedbunk space per cow. Overcrowding at the resting space is defined as providing < 1 stall per cow. At maximum capacity, 48.5% of freestall farms in the United States provided < 1 stall and 67.9% provided < 0.6 m of feedbunk space per animal (USDA, 2010). These crowded environments interfere with time budgets of cows by disrupting lying and feeding behaviors. A normal behavior time budget for a lactating dairy cow includes 3 to 5 h of eating per day (Grant & Albright, 2001). As stocking density increased, time cows spent feeding decreased, whereas feeding rate increased. This may alter intake during these feeding bouts. Increased feeding rate may increase the risk for ruminal acidosis and displaced abomasums after calving. Aggressive interactions among animals resulting in displacements from the feedbunk also occur more frequently in overcrowded pens (DeVries et al., 2004). Providing 0.5 m of feeding space as opposed to 0.1 m of feeding space resulted in 60% less space between animals and 57% more aggressive interactions while feeding. Subordinate animals are most affected, as they will often be displaced from the bunk by a dominant animal. Feed quality tends to decline throughout the day as TMR is sorted and submissive cows will ultimately consume a poorer quality diet after waiting for feedbunk access. A typical lactating dairy cow will rest for 12 to 14 h/d to meet her daily time budget (Grant & Albright, 2001). Cows prioritize rest and will choose to rest rather than eat when both lying time and feeding time are limited (Munksgaard et al., 2005). At stocking densities of 150%, cows spent 1.7 h/d less lying relative to those housed at 100% (Fregonosi et al., 2007). These data may help explain the positive relationship between milk production and freestall availability described by Bach et al. (2008). Krawczel et al. (2008) reported average time standing idly in the alley also increases at stocking densities > 110%, which is associated with an increased risk for lameness.

Key Words: freestalls, overcrowding, stocking density

0020 A Polled Future.
M. Richard*[1] and C. C. Williams[2], *[1]Louisiana State University, Baton Rouge, [2]Louisiana State University AgCenter, Baton Rouge.*

The horn is an adaptation of the skin, characterized by hardened keratin in the epidermis. Dairy cattle have used their horns as a defense mechanism since the beginning of their existence. However, since dairy cattle no longer need to ward off predators in the wild, their horns do not serve a purpose. Addi-

tionally, horns can cause injury to handlers and other cows in the herd. Thus, disbudding or dehorning is necessary to lower risk associated with the horns of dairy cattle. Disbudding and dehorning techniques differ; however, they both have disadvantages associated with the procedure relating to cost, health, and animal welfare. The solution presents itself in polled genetics. Animals born without horns carry 1 or 2 polled alleles. German researchers found that this genetic marker was associated with certain mutations, such as a hairy eyelid. Since the polled gene is dominant, genetic selection can improve rapidly. An animal with 2 polled alleles will produce 100% polled offspring, whereas an animal with only 1 polled allele will still have 50% of its offspring polled. Polled genetics are also more cost efficient than dehorning, as a farmer can spend an additional $7.50 for polled genetics. Other advantages of polled genetics include eliminating the risk of infection and reduced labor required. However, limited genetic selection is a major reason dairy farmers are hesitant to embrace polled genetics. Although still a minority, polled dairy cattle are increasing in generic merit and polled bulls are beginning to rank in the top of genetic evaluations. In conclusion, using polled genetics provided a more cost efficient and less labor intensive alternative to traditional dehorning methods.

Key Words: dairy cattle, polled genetics

0021 The future role of metabolomics in dairy science.
A. E. Kraus*, K. J. Harvatine, and D. R. Olver, *Pennsylvania State University, University Park.*

Metabolomics is an emerging field used to investigate chemical fingerprints left behind by biological and pathological processes. Although research in this discipline far predates its modern name, metabolomics studies are now conducted in a more global, non-targeted manner because of technological advancements. Metabolites in tissues and biofluids are identified using chromatography coupled with mass spectrometry platforms. Metabolites can then be identified by matching their unique masses and fragmentation patterns with standards in metabolome databases. Changes in metabolite fingerprints can differentiate between healthy cows and those with subacute diseases. For example, the metabolites in rumen fluid and milk can be used to gain insight into the mechanisms behind subacute diseases such as acidosis, ketosis, and mastitis. By examining these global changes in metabolite expression, researchers can investigate perturbations to biochemical pathways and eventually use these novel biomarkers to develop metabolite monitoring systems. An increasing number of metabolomics studies are being conducted to better understand the health-disease continuum in humans and model organisms. However, the potential for this tool in dairy science research remains largely unrealized as endogenous and exogenous metabolites continue to be characterized. Recent investigations published in the *Journal of Dairy Science* demonstrate the potential for metabolomics to help increase feed efficiency and reduce production losses in the dairy industry. In the future, metabolomics will be influential in revealing the complex mechanisms behind costly subacute metabolic disorders and pathogen-induced diseases in dairy cattle.

Key Words: mass spectrometry, metabolomics, subacute disease

0022 Polled genetics: Benefits, detriments, and identification of polled dairy cattle.
A. L. Patch*, R. R. Cockrum, and D. R. Winston, *Virginia Polytechnic Institute, State University, Blacksburg.*

The polled trait demonstrates autosomal complete dominance that results in horn growth suppression. Selection for polled cattle has become increasingly popular and can be identified phenotypically by observation and/or genotypically through genomic testing. Dairy cattle are classified with 3 identifiers: observed polled (PO), heterozygous polled (P), and homozygous polled (PP). Observed polled cattle are visually identified by the producer, whereas genomic testing requires analysis of the DNA. Animals identified through genotyping can be determined with a high density SNP chip. A genome-wide association analysis in beef and dairy cattle revealed a 1 Mb region within chromosome 1 associated ($P \leq 0.002$) with P and PP. Further analyses determined a SNP (AC000158:G1390292G > A) located within intron 3 of Interferon γ receptor 2 gene (IFNGR2) and an immune gene was co-segregated with polled in Holsteins. The SNP, AC000158:G1390292G > A, can be used as a genetic marker when testing for polled in dairy cattle. The benefits of polled cattle include: increased docility, decreased labor requirements, improved public perception, and eliminating the necessity of dehorning the animal. Polled genetics allow the producer to realize a profit of $7.50/animal. Conversely, the disadvantages of selecting for polled genetics include: decreased genomic total production index (GTPI), reduced net merit value (NM$), and an increased risk of inbreeding, due to a smaller available gene pool. One possible solution to incorporate polled genetics into the herd is to breed for heterozygous polled cattle by crossing genetically superior cows with polled bulls or breeding polled cows with superior bulls.

Key Words: dairy cattle, polled, single nucleotide polymorphism

---

0023 Crossbreeding—Is it a good option?
R. J. Yarbrough* and S. Washburn, *North Carolina State University, Raleigh.*

Long-term selection of dairy cattle for increased production has resulted in a decline in various functional traits, including reduced fertility, as well as concerns about soundness of feet and legs, resistance to disease, and overall shorter productive life. Some of those effects may be related to increased inbreeding and others due to unfavorable correlations of production traits to fitness traits. Crossbreeding is 1 way to

eliminate inbreeding and bring heterosis into a herd, which could result in improved functional traits in that herd. There has been renewed interest in crossbreeding worldwide with use of both traditional and non-traditional dairy breeds. Some studies have documented up to a 10% economic gain in the F_1 crosses. Holstein and Jersey crosses are popular, due to the commonality of these 2 breeds. Those crosses generally have advantages in fertility, calving ease, neonatal survival, maintenance of body condition score, and are still competitive for milk yield and milk components. Holsteins have a higher milk yield, but Holstein × Jersey crosses produce milk with higher fat and protein content. Across time, 2-breed crosses maintain 67% of the heterosis of the original F_1, whereas 3-breed crosses maintain ~86% of the initial heterosis. Cows that have lower fertility or lack functionality otherwise lead to lost revenue, greater cow turnover, and simply do not last long term on a farm. Selection for improved fitness within breed is a good approach, but crossbreeding may also be a strategy to improve the bottom line in some herds.

Key Words: functionality, heterosis, inbreeding

ADSA-SAD UNDERGRADUATE STUDENT PAPER COMPETITION: ADSA-SAD UNDERGRADUATE PRESENTATIONS—ORIGINAL RESEARCH

0024 Weaning age impacts growth, feed intake, and behavioral indicators of stress in Holstein calves fed a high plane of nutrition. H. E. Brown*[1], E. C. Eckert[1], K. E. Leslie[1], T. J. DeVries[1], and M. A. Steele[2], [1]*University of Guelph, ON, Canada,* [2]*Nutreco Canada, Guelph, ON.*

Recent research has revealed the short- and long-term advantages of feeding more nutrients preweaning. Unfortunately, calves that are fed more nutrients preweaning may be more susceptible to depressed growth and weaning stress during the transition from liquid to solid feed. The objective of this study was to investigate the relationship between age of weaning and feed intake, growth, and behavioral indicators in dairy calves fed higher planes of nutrition. To meet this objective, 20 Holstein female calves were randomly assigned at birth to be weaned at 6 or 8 wk. Milk replacer (mixed at 150 g/L) was offered at 1.2kg/calf/d in 2 meals until a 1-wk stepdown, where meals were reduced by 50% 1 wk before weaning. Measurements included daily starter, chopped straw, and water intake, as well as weekly body weight until d 70 of life. Behavioral indicators, including ruminating, lying/standing, vocalizing and non-nutritive oral behavior, were measured by visual observation each minute for 3 h/wk before the second feeding of the day. Data were analyzed using a repeated measures general linear mixed model; comparisons were made by week relative to weaning and week of life. The calves weaned at 8 wk compared with 6 wk had higher ($P < 0.01$) ADG for the week preweaning (0.79 ± 0.09 vs. 0.34 ± 0.10 kg/d) and post weaning (1.05 ± 0.09 vs. 0.35 ± 0.11 kg/day), and were heavier ($P < 0.01$) at the end of the experiment (99.92 ± 1.81 vs. 91.01 ± 2.26 kg). Starter, straw, and water intake were delayed in calves weaned at 8 wk of age. However, their overall starter intakes and growth rates were not different during the last week of the experiment. Furthermore, calves weaned at 8 wk compared with 6 wk had higher ($P < 0.01$) starter intake for the week preweaning (1.36 ± 0.13 vs. 0.40 ± 0.08 kg/d) and post weaning (2.51 ± 0.20 vs. 1.16 ± 0.15 kg/day). Treatment × week relative to weaning interactions indicated that several behaviors varied between early- and later-weaned calves during the week before weaning; 6-wk calves tended ($P = 0.07$) to exhibit 75% more non-nutritive oral behavior, spent 55% less ($P < 0.01$) time ruminating, and 36% less ($P = 0.01$) time lying than 8-wk calves. These results suggest that calves fed higher planes of nutrition preweaning benefit from extending weaning age from 6 to 8 wk of age.

Key Words: age, calves, weaning

0025 Effects of AICAR, rapamycin, and non-essential amino acids on cell signaling in bovine mammary tissue. A. Felock*, S. I. Arriola Apelo, R. L. Garnett, and M. D. Hanigan, *Virginia Polytechnic Institute and State University, Blacksburg.*

Studies in animal and cell culture models have revealed that essential amino acids play a role in regulating protein synthesis not only as substrates but also through direct signaling to the protein synthetic machinery. Essential AA affect the mammalian target of rapamycin- (mTOR) signaling pathway in bovine mammary cells, which is associated with increased milk protein synthesis. Three experiments were conducted to study the effect of AICAR, an activator of AMP kinase, rapamycin, a mTOR complex 1 inhibitor, and non-essential AA on mTOR signaling in mammary tissue. Three Holstein cows in late lactation were slaughtered and mammary tissue was collected from uninfected rear quarters. Tissue slices (120 ± 30 mg) were incubated for 4 h in the respective treatment medium. In the first experiment, treatments consisted of complete Dulbeco Modified Eagle Medium (DMEM) or DMEM with essential AA (EAA) at 5% of regular concentrations, and AICAR at 0, 0.4, or 4.0 mM. The second experiment consisted of the same EAA treatments supplemented with rapamycin at 0, 0.5, and 10 μM. In the third experiment, tissue slices from 2 cows were incubated in minimum essential medium supplemented with 4.5 g glucose,10 μg insulin, and per liter of media. The AA examined were Ala, Asx, Glx, Gly, Pro, and Ser, where Asx represented Asn plus Asp, and Glx represented Glu plus Gln. Phosphorylated and total forms of mTOR, eukaryotic elongation factor 2, and ribosomal protein S6 were determined by Western blotting and the ratio of phosphorylated to total ratio was calculated. Essential AA had no effect on signaling proteins in either experiment. The AICAR significantly reduced mTOR phosphorylation but had no effect on phosphorylation of eEF2 or rpS6. Rapamycin did not affect phosphorylation of mTOR or eEF2. However, rapamycin significantly reduced rpS6 phosphorylation. Non-essential AA had no effect on phosphorylation of signaling proteins in the mTOR pathway. There was no effect of EAA on protein synthesis rates, implying that there are other causes regulating synthesis rates besides cell signaling.

Key Words: AICAR, mTOR, rapamycin

0026 Within day alteration of ration starch fermentability had no effect on feed intake, total tract NDF digestibility, and milk fat concentration of cows in late lactation. B. C. Oglesby* and M. S. Allen, *Michigan State University, East Lansing.*

The objective of this experiment was to evaluate the effects of feeding lactating cows diets differing in starch fermentability twice per day on DMI, total tract NDF digestibility, and milk fat concentration. Feeding highly fermentable starch sources

to ruminants is expected to increase short-chain fatty acid production by rumen microbes, increase the flux of propionate to the liver during meals, and potentially decrease ruminal pH, NDF digestibility, and milk fat concentration. Diurnal variation in feeding results in lower digesta mass and rumen buffering, and increased plasma NEFA and hepatic acetyl CoA concentrations before the morning feeding. We previously reported that propionic acid is more hypophagic when hepatic acetyl CoA concentration is elevated. Therefore, we hypothesized that the negative effects of greater starch fermentability would be more pronounced following the morning feeding compared with the evening feeding. Sixteen multiparous cows (291 ± 68 DIM; mean ± SD) were used in a crossover design experiment with 14-d periods, including 10 d for diet adjustment and 4 d for sample collection. Cows were offered diets containing either dry corn grain (DC, less fermentable) or high (33%) moisture corn grain (HM, more fermentable), at 0900 h and 1700 h each day in opposite sequences: 1) HM at 0900 h, DC at 1700 h, and 2) DC at 0900 h, HM at 1700 h. Sequence DC:HM tended to increase the amount of DMI following the morning feeding (10.6 vs. 9.7 kg, $P = 0.07$) and decrease DMI following the afternoon feeding (14.4 vs. 15.4 kg, $P = 0.08$), compared with HM:DC, resulting in no overall effect of treatment ($P > 0.15$). Treatment did not affect digestibility of NDF or DM, or yields of milk, fat, protein, lactose, or milk composition. Sequence DC:HM tended to decrease BW (776 vs. 771 kg, $P < 0.10$) but not BCS compared with HM:DC. Lack of treatment effects on digestibility of NDF and concentration of milk fat indicate that the buffering capacity of rumen contents was likely adequate to maintain ruminal pH during the morning when digesta mass is normally lowest. Opposite effects of treatment on DMI following the morning and afternoon feedings suggest that HM tended to decrease DMI compared with DC similarly at each feeding. These results indicate that potential advantages to altering ruminal starch fermentability within a day are minimal for late lactation cows.

Key Words: diurnal variation, feeding management, starch fermentability

---

0027 Growth of periruminant Holstein bull calves fed a fermentation extract of *Aspergillus oryzae*.

E. M. Dudash*, T. T. Yohe, R. M. Townsley, Y. Roman Garcia, A. R. Gibson, K. M. O'Diam, and K. M. Daniels, *Department of Animal Sciences, The Ohio State University, Wooster.*

A fermentation extract of the fungus *Aspergillus oryzae* can be used as a direct fed microbial. The objective was to determine if dietary inclusion of an extract of *A. oryzae* would improve the growth of Holstein bull calves from birth through 1 wk postweaning; it was hypothesized that it would. Bull calves ($n = 52$) were used in this experiment. Calves were randomly assigned to a slaughter age, 4 wk ($n = 16$) or 8 wk ($n = 36$), and treatment, control (CON; $n = 27$) or direct fed microbial (DFM; $n = 25$). Calves averaged 43.2 ± 1.0 kg BW and 2.8 ± 0.3 d of age at the beginning of the experiment. Calves were housed and fed individually; no bedding was used. Calves assigned to DFM were fed 2 g of DFM daily. Liquid DFM was delivered in milk replacer for the first 4 wk of the trial; solid DFM was top dressed on texturized grain thereafter. Calves were fed non-medicated milk replacer twice daily (22.0% CP, 20.0% fat DM basis; 680 g/d) and were weaned on consumption of 0.91 kg of grain (20% CP, 2.0% fat; medicated with decoquinate) for 3 consecutive days or on d 45 of the study, whichever came first. Calves had ad libitum access to grain and water throughout the trial. Feed intake was recorded daily. Body weight was recorded weekly. There was no effect of treatment on BW; 8 wk BW was 74.5 ± 1.9 kg for CON and 74.6 ± 1.9 kg for DFM. Total DMI per calf did not differ: from 0 through 4 wk (19.48 ± 0.67 kg of DM), 5 through 8 wk (39.44 ± 2.05 kg of DM), or for the whole trial (58.70 ± 3.30 kg of DM). Lastly, the gain to feed ratio did not differ by treatment: from 0 through 4 wk (0.59 ± 0.05), 5 through 8 wk (0.53 ± 0.03), or for the whole trial (0.56 ± 0.04). Here, dietary inclusion (2 g/d) of an extract of *A. oryzae* did not result in improved calf growth when supplemented animals were compared with cohorts not fed the direct fed microbial. It is possible that the dose used here was not high enough to elicit treatment effects. Given that effects have been noted in other species, a follow-up dose titration study with similar diets as used here seems warranted.

Key Words: dairy calf, direct fed microbial, growth, nutrition

---

0028 [Withdrawn]

0029 Case study: Effect of alley floor scraping frequency on environmental mastitis-causing pathogen counts.

J. L. Lowe*, K. A. Akers, A. E. Sterrett, J. D. Clark, and J. M. Bewley, *University of Kentucky, Lexington.*

The objective of this case study, conducted at the University of Kentucky Coldstream Dairy from 21 August 2013 to 29 September 2013, was to determine if increased alley scraping frequency decreased teat end and milk environmental mastitis-causing pathogen counts (EMC). Sixteen Holstein cows were monitored during two, 3-wk treatments; removing manure from the alley floors once (1X) or twice (2X) daily. Milk and teat end swab samples were collected twice weekly to observe changes in EMC and somatic cell score (SCS). The GLM procedure of SAS (SAS Institute, Inc., Cary, NC) was used to evaluate fixed effects of treatment, parity group (1 or ≥ 2), and days in milk group (≤ 150 or > 150), and their interactions on teat end and milk *Escherichia coli*, total coliform, *Klebsiella* spp., and streptococci counts, with cow as subject. Stepwise backward elimination was used to remove

nonsignificant interactions ($P \geq 0.05$) and all main effects were kept in each model, regardless of significance level. The CORR procedure of SAS was used to evaluate the correlations between all study variables. The least squares means (± SE) indicated increased scraping frequency decreased milk sample total coliform count from 0.30 to 0.05 ± 0.09 $\log_{10}$ cfu/g ($P < 0.05$). Likewise, teat end total coliform, *E. coli*, and streptococci counts decreased between 1X and 2X; 2.11 to 1.56 ± 0.14 $\log_{10}$ cfu/g, 1.86 to 1.30 ± 0.14 $\log_{10}$ cfu/g, and 5.06 to 4.10 ± 0.19 $\log_{10}$ cfu/g, respectively ($P < 0.01$). Increased scraping frequency did not significantly affect SCS, milk *E. coli,* streptococci, and *Klebsiella* spp. counts, or teat end *Klebsiella* spp. counts ($P > 0.05$). Teat end total coliform and streptococci counts were moderately correlated with the same bacteria counts within the milk ($r = 0.53$, $P < 0.01$ for both species). Milk streptococci counts were moderately correlated with SCS ($r = 0.40$, $P < 0.05$). Because increased scraping frequency decreased EMC, which could reduce intramammary infection risk, this practice could reduce mastitis caused by environmental mastitis-causing pathogens.

Key Words: environmental mastitis, pathogen counts, scraping frequency

---

0030 Dry matter intake and efficiency in lactating Holstein cows grouped by direct genomic values for feed utilization.

I. W. Haagen* and C. D. Dechow, *Pennsylvania State University, University Park.*

Feed costs represent the largest expense for lactating dairy cows, yet the dairy industry does not currently select directly for feed efficiency. The purpose of this study was to observe how accurately genomic predictions of feed utilization developed from a small reference population could predict feed utilization in lactating Holsteins. Feed intake data were collected from 970 Holstein cows across 11 commercial Pennsylvania herds. Genetic evaluations of 4 feed utilization traits were conducted: DMI, dry matter efficiency (DME; energy corrected milk/DMI), crude protein efficiency (CPE; protein yield protein intake), and residual feed intake (RFI). A genome-wide association study was performed using 45,138 SNP genotypes from 340 cows with the e-BIGS program (http://bigs.ansci.iastate.edu) and SNP associations were used to generate direct genomic values (DGV) of feed utilization. Cows were subsequently separated into feed utilization groups, with pen milk yield and feed intake monitored for 2 wk. High and low DGV groups of 20 cows for each of the 4 feed utilization traits were observed at Penn State, whereas cows from a commercial dairy farm were divided into high, medium, and low DGV groups of 51 cows for DMI and 68 cows for DME. Mixed models were used to evaluate differences in feed utilization between high, medium (commercial herd only), and low DGV groups, and included DGV group, a random effect for date, and random error. The high DMI group consumed 10.8 kg more dry matter per day ($P < 0.01$) than the low DMI group at Penn State. Likewise, the high CPE group produced 0.04 kg more protein per kilogram of protein intake ($P < 0.05$). The high DME group tended ($P < 0.10$) to produce more milk (+0.17 kg) per kilogram of intake than the low group. Differences among high and low RFI groups were opposite of expectations, with the low group consuming significantly more dry matter than predicted ($P < 0.01$), based on milk yield and body weight, compared with the high group. Differences in DMI ($P = 0.36$) and DME ($P = 0.14$) were not significant among groups on the commercial dairy farm. This research demonstrated that it is feasible to apply genomic predictions of feed utilization developed from a reference population to select for improved efficiency in commercial dairy herds. However, not all the predictions were as expected and a larger reference population is required to increase prediction accuracy.

Key Words: feed efficiency, genomics

0031 Can prior subjection to pre-heating enhance the heat tolerance of mesophilic bacterial cultures?

R. E. Brown*[1] and K. J. Aryana[2], [1]*Louisiana State University, Baton Rouge,* [2]*Louisiana State University Agricultural Center, Baton Rouge.*

The enhancement of heat tolerance of mesophilic bacterial cultures is important for withstanding the elevated temperatures in the development of probiotic processed cheeses. The objective was to determine whether prior subjection to preheating would enhance heat tolerance of mesophilic cultures. *Lactococcus lactis* ssp. *lactis* and *Lactococcus lactis* ssp. *cremoris* were suspended in a 0.1% peptone and exposed to the preheat temperatures of 30°C, 40°C, 50°C, 60°C, 70°C, or 80°C for 1, 5, or 10 min. The cultures were then grown in M17 broth at 32°C for 72 h. After the first generation of growth, the cultures were then subjected to the same preheat temperature and time, and then grown in M17 broth at 32°C for 72 h. The second generation was also subjected to the same preheat temperature and time, and grown in M17 broth at 32°C for 72 h. After 3 generations of growth, the cultures were then subjected to the challenge conditions of 95°C for 5 min. The control cultures were exposed to the challenge conditions without the subjection to any of the preheat temperatures and times. The cultures were plated in M17 agar and allowed to incubate aerobically at 32°C for 72 h. Three replications were conducted. No growth was obtained when any of the pre heat treated cultures were subjected to the challenge temperature and time conditions. Heat tolerances of mesophilic cultures studied were not enhanced under these conditions.

Key Words: cheese, heat tolerance, mesophilic cultures

ANIMAL BEHAVIOR AND WELL-BEING I

0032 Associations between bovine respiratory disease complex and the probability and latency of group-reared neonatal dairy calves to approach a novel object or stationary person. M. C. Cramer* and A. L. Stanton, *University of Wisconsin-Madison, Madison.*

Bovine respiratory disease complex (BRD) is an important disease that impacts the welfare and performance of dairy calves. With group housing of calves becoming more common, it is imperative to identify behaviors indicative of illness in a socially competitive environment. The objective of this study was to determine associations between BRD status of group-housed dairy calves and their latency to approach a novel object or stationary person. On a commercial dairy in Wisconsin, 75 Holstein preweaned, group-housed heifer calves were tested once a week for 6 wk. The average age of calves on enrollment was 4.1 ± 1.9 d. Calves were housed in 8 pens with an average of 9 ± 1 calves per pen. Each week, all calves in the study were tested for their willingness to approach a novel object (OBJ) and a stationary person (SP) within 60 s. Approach was defined as 1 step in the direction of SP. or OBJ. Pen and test order were randomized. After both OBJ and SP. tests were complete, a standardized health assessment was conducted. The behaviors of calves with clinical signs of BRD were compared with calves with no clinical signs of BRD. All models were controlled for week, pen, pen order, and test order. Associations between probability of approach and BRD status were analyzed, using a linear mixed model with a logit transform (PROC GLIMMIX), controlling for calf as a random effect. Calves without BRD were 2.5 (95% CL: 1.4 to 4.6) and 2.6 times (95% CL: 1.4 to 4.8) as likely to approach than calves without BRD for the SP. ($P < 0.005$) and OBJ tests ($P < 0.005$), respectively. The latency of calves that approached the SP. or OBJ was analyzed using a Cox proportional hazards regression (PROC PHREG). The BRD status did not significantly impact the latency to approach in either test. The median latency to approach was 18 and 9 s for SP. and OBJ tests, respectively. Clinical signs of BRD impacted the probability of approach but did not impact the latency to approach, which indicates that BRD influences the willingness to approach but not the rapidity at which a calf approaches. These findings suggest that approach tests may be used to identify calves with BRD in group housing.

Key Words: behavior, BRD, calves

0033 Effect of concentrate feeder design on feeding behavior in Holstein bulls fed high-concentrate diets. M. Verdu*[1], A. Bach[2], and M. Devant[1], *[1]IRTA-Department Ruminant Production, Caldes Montbui-Barcelona, Spain, [2]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain*

A total of 240 Holstein bulls (121 ± 2.0 kg BW and 99 ± 1.0 d of age), in a replicated factorial study, were randomly allocated in 1 of 6 pens and assigned to 1 of the 3 treatments, according to the feeder design: conventional feeder with 4 feeding spaces (CF), conventional feeder with less concentrate capacity (CFL), and a single-space feeder with lateral protections (SF). Also, each pen had 1 straw feeder and 1 drinker. Each feeder was suspended on 4 load cells that registered continuously contained concentrate weight. Feeding pattern was video recorded for 24 h on d 7, 119 to 120, and 215 to 216 of the study, and was analyzed by continuous scan sampling. Only 12 h (from 0600 to 0018 h) were analyzed as the greatest activity was observed during that time window. Data were analyzed using a mixed-effects model with repeated measures. The percentage of concentrate bunk attendance was greater ($P < 0.01$) in SF (79.3% ± 0.75%) compared with CF and CFL (70.2% ± 0.75%). The number of visits in SF (44.3 ± 17.36) was less ($P < 0.05$) compared with CF and CFL (118.6 ± 17.36). Obviously, the number of bulls at the SF feeder was ($P < 0.01$) 1 and constant throughout the study in contrast with CF and CFL (1.7 ± 0.02), where the number of bulls at the feeder was > 1.5 and decreased with age. No displacements at SF were observed ($P < 0.01$), whereas in the other feeders some displacements at feeder were registered (CF: 2.3 ± 0.51, CFL: 3.4 ± 0.51 displacements/1 h). The percentage of waiting time at the feeder was greater ($P < 0.01$) in SF (13.3 ± 2.18%) than CF and CFL (0.53 ± 2.18%). However, the waiting time at the feeder in SF was reduced ($P < 0.05$) with age. The eating rate increased ($P < 0.05$) with age in all treatments, being greater in CF (205.7 ± 7.84 g/min) than CFL (177.4 ± 7.84 g/min) and SF (151.2 ± 7.84 g/min). In conclusion, the design of the SF, 1 feeding space with lateral barriers, distributes feeder visits throughout the day, decreases displacements at the feeder, and decreases eating rate compared with the conventional feeders. The reduction of concentrate capacity at the feeder increases displacements and decreases concentrate eating rate at the feeder.

Key Words: beef, feeder, feeding behavior

0034 The effect of respiratory disease on lying behavior in Holstein dairy calves. T. L. Ollivett[1], K. E. Leslie[*1], D. V. Nydam[2], T. F. Duffield[1], G. Zobel[3], J. Hewson[1], and D. F. Kelton[4], *[1]University of Guelph, ON, Canada, [2] Department of Population Medicine and Diagnostic Sciences, Cornell University, Ithaca, NY, [3]University of British Columbia, Vancouver, Canada, [4]Department of Population Medicine, Ontario Veterinary College, University of Guelph, Canada.*

The objective of this cohort study was to determine the effect of naturally occurring bovine respiratory disease (BRD) on lying behavior in preweaned Holstein dairy calves. This study was performed on 1 commercial dairy in southwestern Ontario, Canada, during November and December 2012. Calves were enrolled at 10 d of age and were grouped according to vaccination status ($n = 19$ vaccinated and $n = 20$ unvaccinated). Each calf was examined at weekly intervals for signs of BRD before and during the peak 4-wk period when calves are at risk for developing disease. Respiratory scoring (RS) and thoracic ultrasonography (US) were performed at each of the 5 visits. Individual electronic accelerometers recorded lying behavior throughout the 4-wk period. Descriptive statistics and repeated measures linear models were developed using commercially available software. Fever, sickness, and lung consolidation increased from 11%, 3%, and 0%, respectively, at the first examination to 33%, 33%, and 58%, respectively, at the last examination ($P < 0.05$). Overall, calves spent 20.6 ± 0.7 h/d (mean ± SE) or 86% of the day lying down when all variables were set to the referent. Lying time (LT) decreased by 4 ± 1 min/d for each successive day of age. Fever was associated with 44 ± 14 min/d additional LT. Calves housed in group pens had lower but not statistically significant LT than those housed in single pens. Also, housing type confounded the LT estimate for age. Ultrasonographic lung consolidation and health status (RS > 4) were not significantly associated with LT. Lying bout duration (BD) was 72 (61 to 85) min/d (median; IQR) and lying bout frequency (BF) was 16 (13 to 18) bouts per day (median; IQR). Health status and lung consolidation were not significantly associated with BD or BF. Fever numerically increased BD but was not associated with BF. Monitoring LT in preweaned dairy calves might have a place in identifying febrile animals requiring individual examination and possible intervention. Further studies are needed to determine if early identification and treatment of animals experiencing fever improves future health and performance, as compared with traditional methods of disease detection. Lastly, researchers should consider monitoring rectal temperature during behavioral studies to assess for bias due to undetected fevers.

Key Words: accelerometer, dairy calf pneumonia, ultrasonography

0035 Freestall housing during the dry period altered lying time but did not affect milk quality or energy balance compared with pasture. R. A. Black[*1], H. M. Dann[2], and P. D. Krawczel[1], *[1]University of Tennessee, Knoxville, [2]William H. Miner Agricultural Research Institute, Chazy, NY.*

The objective was to determine changes in behavior and performance of cows housed in freestalls or pasture during a 60-d dry period. Non-lactating Holstein cows were assigned to either deep-bedded, sand freestalls ($n = 14$) and grassy pasture ($n = 14$) at stocking densities below industry recommendations using rolling enrollment. At dry off, cows were equipped with an accelerometer to determine daily lying time (h/d), lying bouts (bouts/d), and steps (steps/d). Data were divided into 4 periods relative to calving: FO (d −60 to -15), CU (d -14 to -1), CA (d 0), and PP (d 1 to 14). Cows were scored for BCS (1 = thin, 5 = obese), hygiene (1 = clean, 5 = dirty), locomotion (1 = normal, 5 = severely lame), and weighed 1 wk before dry off, at dry off, at calving, and on d 7 and 14 postpartum. All cows commingled following calving in a pen identical to the freestall housing treatment. Blood samples were analyzed cow side for β-hydroxybutyrate (BHBA) on d 0, 2, 5, 8, 11, and 14. Milk samples collected at the morning milking on d 0, 1, 2, 7, and 14 were analyzed for somatic cell count (SCC), fat, and protein. On d 0, colostrum volume and quality were assessed. Data were analyzed with the MIXED procedure of SAS with model effects for day, treatment, and the interaction of day and treatment. Cows housed in freestalls lay down longer during FO (11.9 ± 0.3 vs. 10.2 ± 0.3 h/d; $P < 0.01$) and CU (12.6 ± 0.3 vs. 10.3 ± 0.3 h/d; $P < 0.01$) periods. Freestall cows had fewer lying bouts during the CA (11.6 ± 0.8 vs. 15.8 ± 0.8 bouts/d; $P < 0.01$) period with no other periods differing. Freestall cows took fewer steps during FO (1844.5 ± 165.1 vs. 2909.4 ± 202.0 steps/d; $P < 0.01$), CU (1714.6 ± 177.0 vs. 2648.8 ± 214.9 steps/d; $P < 0.01$), and CA (2015.8 ± 204.2 vs. 2874.3 ± 245.6 steps/d; $P < 0.01$) periods. Overall, milk fat was greater for freestall cows (4.9% ± 0.2 vs. 4.1% ± 0.2, respectively; $P < 0.01$). Lower locomotion scores tended to be associated with freestall housing compared with pasture (1.4 ± 0.1 vs. 1.8 ± 0.1, respectively; $P = 0.06$). No differences in BHBA, colostrum amount and quality, hygiene, SCC, milk protein, BCS, or weight existed between housing treatments ($P > 0.22$). Freestall-housed cows were less active (fewer steps and greater lying times) throughout the dry period; however, this did not affect colostrum or energy balance postpartum. The more important factor (lying time vs. moderate exercise) needs to be established for improved management of dry cows.

Key Words: behavior, dairy cattle, dry cow housing

0036 Health of dairy calves when using automated feeders in the Midwest United States.
M. Jorgensen*[1], A. Adams Progar[1], S. Godden[1], H. Chester-Jones[2], J. Rushen[3], A. M. de Passille[3], and M. I. Endres[1], *[1]University of Minnesota, St. Paul, [2]University of Minnesota Southern Research and Outreach Center, Waseca, [3]University of British Columbia, Agassiz, Canada.*

Research is limited regarding best housing and management practices for automated calf feeding systems, particularly in terms of how these factors influence animal health and welfare. This ongoing study is characterizing health scores, morbidity, and mortality of group-housed calves on U.S. farms and relating these to housing and management practices. Thirty-eight dairy farms in the Midwest United States were visited every 60 d. During each visit, calves (n = 7779) were scored for health using 4 categories: attitude (0 to 4), ears (0 to 4), nose (0 to 3), eyes (0 to3), and cleanliness (an indicator of diarrhea, 0 to 2), with 0 representing a normal, healthy calf. In addition, blood was drawn from any calves 1- to 5-d old (n = 711) and serum protein concentration was used to assess passive immunity transfer. During each season, milk samples were collected from the mixing container inside the feeder and the tube leading to the nipple for measurement of standard plate count (SPC) and coliform count. Pearson's correlation coefficient was used to analyze the relationship between mean SPC and health scores. There was a large variation among farms in calf health. On the 10 farms with the best health scores, a mean of 9.7% (range of 2.9 to 12.9) of animals displayed abnormal scores for attitude, 3.7% (1.7 to 5.1) for ears, 12.2% (7.8 to 14.8) for nose, 7.2% (2.0 to 11.9) for eyes, and 26.4% (20.1 to 32.6) for cleanliness. On the 10 farms with the worst health scores, a mean of 22.8% (15.7 to 30.3) of animals displayed abnormal scores for attitude, 14.4% (10.0 to 22.5) for ears, 27.2% (22.8 to 30.6) for nose, 30.3% (22.5 to 36.4) for eyes, and 54.9% (50.6 to 60.3) for cleanliness. Mean serum protein across all samples was 5.40 ± 0.74 mg/dl. Mean serum protein by farm was 5.34 mg/dl (minimum = 4.27, maximum = 6.5). The highest overall bacterial counts were recorded in feeder tube samples (median, coliform = 2550 CFU/ml; SPC = 330,000 CFU/ml; Q3 = 3350,000). No relationship was observed between tube SPC and attitude, ears, nose, or eyes scores; however, SPC was correlated with calf cleanliness scores (r = 0.26, P = 0.002). The variation in health scores among farms shows that welfare in automated feeder systems can be improved. In addition, results indicate that the cleanliness of automated feeder equipment may influence calf health; however, further data collection and analyses of calf morbidity and mortality should provide a more complete understanding of risk factors. This project is supported by Agriculture and Food Research Initiative competitive grant no. 2012–67021–19280 from the USDA National Institute of Food and Agriculture.

Key Words: automated calf feeders, calf health

0037 Effect of heat retaining covers on calf hutch temperature during cold weather.
J. A. Haberman*, T. H. Friend, and W. Binion, *Texas A&M University, College Station.*

Previous studies have demonstrated that reflective hutch covers reduce temperatures inside calf hutches, but the efficacy of reflective covers during cold weather has yet to be determined. This study determined the effect of heat-retaining covers on the internal air temperature of polyethylene calf hutches. Treatments on farm 1 included an aluminized 3.0-ml, black, low-density polyethylene (LDPE; reflective) and a 4.0-ml, LDPE (non-reflective) cover. Farm 2 included only the reflective cover. The covers fit over the top of the hutch, overlaying the top, sides, and back, leaving the front of the hutch exposed. The study was conducted for a 29-d period from December to January at 2 dairy farms located near Plainview, TX. At both farms, 5 uncovered (control) hutches and 5 hutches from each treatment were fitted with duplicate temperature loggers that recorded temperature every 30 min for the duration of the study. At the start of the study, hutches housed calves 2 to 4 d of age. The coldest 2-h period was identified and treatment effects were determined with ANOVA and LSD. At farm 1, the reflective covers were warmer than control hutches by 1.5°C (P < 0.01) and the non-reflective covers were warmer than the control by 1.2°C (P < 0.01). At farm 2, the reflective covers were warmer than the control by 1.5°C (P < 0.05). This period was also characterized by very little wind. When the coldest ambient temperature each day throughout the study was identified, covers were not significantly different than the control (P > 0.05) on both farms. This emphasizes the importance of wind influencing air temperature in the hutch. However, there was still a consistent trend on both farms in which the reflective cover was warmer by 1.16°C on farm 1 and 1.5°C on farm 2. In conclusion, the reflective cover was more effective and the hutch covers had the greatest effect on internal air temperature in low wind. The heat-retaining covers in this study can be expected to improve the comfort of calves in cold temperatures; however, the biological significance of these covers is currently being investigated.

Key Words: cold stress, dairy calf, hutch

0038 Modeling the effect of reflective film calf hutch covers on reducing heat loss.
W. Binion* and T. H. Friend, *Texas A&M University, College Station.*

Many dairy operations are located in environments subject to periods of cold weather and calf hutches are a popular method of protecting calves from environmental extremes. This study determined if a reflective film could be useful in moderating the rate of heat loss from calves housed in polyethylene hutches during cold weather. An engineering approach was

used in which rate of heat loss was modeled, using 38-l, water-filled, steel drums covered by a yearling cow hide. Hides were collected the day before and cut to fit the drums so no metal was exposed. Duplicate loggers mounted in the center of each drum recorded temperature at 5-min intervals during each experiment. Two agitators circulated the water inside each drum. The reflective film (cover) consisted of aluminized 2.5-ml, low-density polyethylene, full metal on olive color, with flat black spray paint covering the olive. The covers were 1.8- × 3-m finished size with the aluminized side facing the hutch and paint facing outward. Two of 4 hutches were either uncovered or had covers across the top and sides of the hutch, leaving the front and back exposed. Water temperature ranged from 43.3°C to 32.2°C and there was an average 24 data points per experiment. Data loggers in each drum were averaged at each 5-min interval and averaged within treatments, and quadratic regression was used to predict rate of heat loss. During the cold night experiment, when ambient temperature was declining (mean temperature -13.6°C), the mean rate of temperature loss was -0.21°C per 5-min interval in the covered and -0.25°C in the uncovered ($R^2 = 0.99$). During the daytime trial when the sun was shining and ambient temperature was rising (mean 14.3°C), mean rate of heat loss was -0.15°C per 5-min interval in the covered and -0.11°C in the uncovered ($r^2 = 0.99$). Reflective film does appear to have potential to reduce the rate of heat loss when calves would be most at risk, cold nights. When the sun was shining on the hutches during mid-day, the uncovered warmed up more and hence, reduced the rate of heat loss when compared with the covered. Even with a black surface toward the sun, the covers did inhibit heating of the hutches, but calves would be able to move into the sun during those periods. Improved materials and designs for hutch covers are presently being developed.

Key Words: cold stress, dairy calf, hutch

ANIMAL BEHAVIOR AND WELL-BEING II

0039 Evaluation of hair cortisol as a biomarker of chronic stress in beef cattle. D. Moya*, M. He, Y. Wang, T. A. McAllister, and K. S. Schwartzkopf-Genswein, *Agriculture and Agri-Food Canada, Lethbridge, AB.*

Three experiments were conducted to assess hair cortisol concentration as a biomarker of chronic stress in beef cattle. In Exp. 1, 24 calves (230.4 ± 13.0 kg BW) were randomly split into 2 groups immediately after weaning. Half of them remained at the ranch of origin (OR), whereas the other half were transported to a feedlot (TF). Weight and hair samples were collected from all calves at the time of weaning and for a period of 30 d postweaning to determine performance and cortisol concentration. In Exp. 2, 24 calves (299.1 ± 28.2 kg BW) were randomly split in 2 treatments: no castration (CT) or band castration (BA). Weight and hair samples were collected from all calves at d 0, 35, and 63 after castration to determine performance and cortisol concentration. In Exp. 3, 160 crossbred steers (538 ± 36 kg BW) were used in a 84-d experiment, with a randomized block design, to study the effects of wheat- (WH; 88.4% DM) or barley- (BA; 89% DM) based diets, or processing index (PI) of either 75% (PI75) or 85% (PI85) of their original volume-weight, on growth performance, stress, and behavior of finishing beef cattle. Cattle were allocated to 16 feedlot pens (10 animals per pen, 4 pens per treatment), 8 of which were equipped with an automatic feed monitoring system. Flight speed and hair and saliva samples were collected on d 1, 28, 56, and 84 to determine behavior and acute and chronic stress. The TF group had a greater ADG ($P < 0.01$) and hair cortisol concentration ($P = 0.05$) than OR. There was a castration × time interaction ($P < 0.05$), where BA calves had greater hair cortisol and lower ADG than CT only at d 35 after castration. The PI75 treatment reduced ($P = 0.05$) DMI and increased ($P = 0.04$) feed efficiency. Cattle fed WH had greater hair cortisol ($P = 0.01$) and flight speed ($P < 0.01$) than those fed BA. There was a trend ($P = 0.07$) for a grain × PI interaction, where heifers fed WH-PI85 had lower salivary cortisol than those fed other treatments. Results indicate that hair cortisol can be used to assess chronic stress in beef cattle related to conditions associated with calf management at weaning, band castration, or feeding management.

Key Words: feedlot, stress, welfare

0040 Maternal behavior in sheep production: Effects on lamb performance and economic indicators. C. Raineri[*1,2], B. C. Nunes[3], T. B. Bovo[4], E. A. Titto[4], E. R. Afonso[1], and A. H. Gameiro[1], *[1]Department of Animal Nutrition and Production, University of São Paulo School of Veterinary Science and Animal Science, Pirassununga, Brazil, [2]Federal University of Uberlândia. School of Veterinary Medicine, Uberlândia, Brazil, [3]Ministry of Science, Technology and Innovation, Brasilia, Brazil, [4]University of São Paulo. School of Animal Science and Food Engineering, Pirassununga, Brazil.*

This study assessed the economic impact of inadequate maternal behavior of sheep between birth and first suckle of lambs in a commercial flock of meat sheep. We observed 222 pregnant Santa Ines ewes and their 327 lambs. Behavioral observations were performed, by direct method with focal samplings every 5 min. Maternal activities considered negative were preventing suckling, withdrawing, and butting. Statistical analyses were conducted by multiple linear and logistic regression models, using functions PROC REG and PROG LOGISTIC of the software SAS 9.3. In economic analysis, we simulated the ratios for production costs and revenues in case of manifestation or not of negative maternal activities. We investigated connections between maternal behavior, incidence of dystocia, need for artificial rearing, birth weight, preweaning mortality, prolificacy rate, and weaning weight. Negative maternal behaviors were displayed by 19.37% of the ewes. Lamb weaning weight was influenced by birth weight ($P < 0.001$) and litter size ($P < 0.01$), but not by maternal behavior, artificial rearing, or dystocia. Preweaning mortality was probably affected by maternal behavior ($P = 0.10$) and litter size ($P < 0.05$), but not by artificial rearing. Lambs from dams that did not display negative behavior had 82% higher chances of surviving until weaning. Probability of surviving until weaning fell 50% with the increase of each additional lamb in the litter. Maternal behavior was significantly influenced by birth weight ($P < 0.01$) and dystocia ($P < 0.05$), but not by litter size. The chance of ewes not displaying negative maternal behavior increased 105% for each 1-kg increase on birth weight of lambs. On the other hand, dystocia incidence increased in 79% the chances of negative behavior to occur. In the studied flock, dystocia incidence was not related to lamb birth weight. Economic analysis demonstrated that production cost would be higher for lambs whose mothers displayed negative behaviors, mainly due to greater need for artificial rearing, whereas sale income would be similar between groups. Negative maternal behavior was related to increases in preweaning mortality rate and need of artificial rearing. Thus, negative maternal behavior resulted in economic impact, represented by the increase of production cost and the decrease in 7% of revenues. These results are important to guide viability evaluation of investments that aim to improve maternal-offspring relation in

sheep. Reasons for displays of negative behavior by important portions of that flock are not clearly elucidated, although data suggest relations with higher prolificacy and dystocia.

Key Words: economic evaluation, ewe, production cost

0041 Effect of rest-stop duration during long-distance transport on indicators of animal welfare in weaned beef calves. S. Marti* and K. S. Schwartzkopf-Genswein, *Agriculture and Agri-Food Canada, Lethbridge, AB.*

Forty newly weaned Angus beef calves (260 ± 32.6 kg) were transported 15 h in a livestock trailer (7.3 × 2.1 m) on 2 separate days (20 calves per day) to evaluate the effect of rest-stop duration on indicators of calf welfare. Immediately following the 15-h journey, all calves were unloaded at a feedlot and randomly assigned to 1 of the 4 treatments. Treatments included: 0- (Control; C), 5- (RS5), 10- (RS10), or 15- (RS15) h rest periods in pens containing ad libitum access to water and long-stem hay. Following each rest period, calves were reloaded onto the same trailer and taken on another 5-h journey for a total transport event lasting 20 h. Control calves did not have access to feed or water until the end of the 20-h transit event. Behavioral measurements included: loading and unloading scores (fall, aggression, mount, slip, trip, balk and walk, trot, or run), animal condition (non-ambulatory, lame, injured, fatigued, wet coat, and dirty), number of steps (steps per day), feeding behavior (minutes per day), standing and lying frequency (number per day), and duration (minutes per day) during rest periods and at the end of the 20-h transport event. Physiological measurements included: saliva and hair cortisol, total blood cell count, and substance P concentrations. All measurements were taken immediately before loading and after unloading at the rest stop and the end of the 20-h event. Salivary cortisol was greater ($P < 0.01$) in C and RS15 than in RS5 and RS10 calves at the end of each rest stop period and the 20-h event. The RS15 calves had greater ($P = 0.02$) salivary cortisol concentrations before and after the last 5 h of transport compared with RS5 and RS10 calves. The RS10 calves spent more ($P < 0.01$) time lying than any other treatment. No treatment differences ($P = 0.14$) were observed for feeding duration, although it was numerically less in RS10 calves. Meal duration following 20 h of transport was less ($P = 0.05$) in C calves than all other treatments. The results of this study indicate that provision of a rest stop < 10 h reduces stress in weaned calves as witnessed by reduced salivary cortisol concentration and less time spent lying.

Key Words: calves, resting stop, transport, welfare

0042 Monitoring stress behavior in grazing beef cows with a long range pedometric system. R. Gabrieli*, *Ministry of Agriculture and Rural Development, Extension Service, Beit Dagan, Israel, Beit Dagan.*

Beef breeding is an extensive operation performed in vast pastures. Hierarchy within the herd is an important factor that determines priority of access to limited resources and level of feed intake, resulting in stress to the subordinate animals. Hierarchy is mainly passive, thus difficult to detect in conventional breeding systems. Most of the cows that are culled due to low production are subordinate cows. Identifying subordinate cows may enable the breeder to improve grouping management and thereby minimize stress. This will lead to improved production and lower replacement costs. A newly developed long range pedometric system, based on RF transmission, providing online activity monitoring, was installed in a crossbred Simmental beef herd of 250 cows, grazing in a 300-ha pasture in the Upper Galilee, Israel. The hypothesis was that the average cow will maintain a daily activity routine, whereas stress will result in deviations of activity expressed in the graph. Thirty transmitting tags were mounted on front legs of randomly selected cows. Analysis of data showed 17 cows with regular activity graphs (i.e., lower than average values of activity with lower values of standard deviation, 161 + 105 steps per hour) and 13 expressed irregular activity graphs (higher than average values of activity with higher values of standard deviation, 209 + 128 steps per hour). Observations near the food trough were conducted during feeding time to rank cows according to their social status. A cow that reached the trough and wasn't rejected was ranked "dominant." Order was established thereafter by number of rejections from the trough each cow received. The lowest ranking cows did not approach the trough during feeding at all. Comparison between activity graphs and observations showed that dominant cows expressed regular activity graphs and subordinate cows expressed irregular activity graphs. Cortisol levels in hair samples were taken to validate activity results (0.1975 + 0.039 and 0.2862 + 0.0423 μg/dL for dominant and subordinate, respectively; $P = 0.018$). Cortisol level in hair reflects the stress status over a fortnight, thus the effect of sampling-related stress is minimal. The activity pattern expressed while measuring hourly activity online, we believe, reflects the measure of freedom each cow has to choose for her ongoing activity within the herd. Assuming that establishing an individual routine is beneficial for cows, detecting those that are unable to do so and grouping them by social order will minimize stress and improve production.

Key Words: beef breeding, stress

0043 Effect of 4 different reflective barriers on black-globe temperatures in calf hutches and on calf ADG. T. H. Friend*, W. Binion, and J. Haberman, *Texas A&M University, College Station.*

Polyethylene hutches are a popular method of housing dairy calves from birth to ± 60 d of age, although these hutches get hot when in full sun. Shading the hutches and yard has been effective, but shade increases concerns about increased pathogens and moisture from the lack of sunlight. This study characterized the relative differences in the ability of 4 different types of radiant barriers to reduce black globe (BG) temperature within these hutches during hot weather and reports the results from some field trials. Treatments for the BG trials included 3 different types of covers [2 types of reflective laminates (Cadpak P and Cadpak ESD) and an aluminized 3.0-mL white low-density polyethylene (LDPE)], and a reflective paint (LO/MIT-1). The reflective covers were 1.8- × 3-m finished size and covered the top and sides of the hutch down to 0.15 m above the ground, leaving the front and back exposed. The LO/MIT-1 paint covered the entire sides and roof of the hutch. Two 24-h trials, 1 wk apart, were conducted during relatively hot and clear days in early August. Black globe temperatures were recorded at 20-min intervals in duplicate, using blackened table tennis balls mounted 0.3 m above the floor in the center of each hutch. Ambient temperature (shade) during the hottest 2-h period for both trials averaged 39.9°C, whereas the uncovered control averaged 41.1°C and LO/MIT-1 39.9°C, both of which were significantly higher (ANOVA followed by LSD, $P < 0.01$) than the Cadpak P (38.9), Cadpak ESD (38.6), and aluminized LDPE (38.7°C). Twelve to 24 of the covers were field tested on 3 collaborating dairy farms in the Panhandle Region of Texas from June to September 2013. Despite having a relatively cool summer, the farms reported increased ADG ranging from 0.018 to 0.045 kg/d. A statistical analysis was not possible because the calves in each treatment were weighed as a group on the farms ($n = 3$). Both the Cadpak P and Cadpak ESD were starting to delaminate at the end of the trails. The reflective covers evaluated in this study can be expected to improve calf comfort and most likely gain, but additional field testing is needed to refine the design and determine cost effectiveness of the covers.

Key Words: calf, hutch heat stress

0044 Effects of 3 tail painting formulations on behavior of dairy heifers. C. S. Skenandore* and F. C. Cardoso, *University of Illinois, Urbana.*

Studies have shown that the correct use of tail paint can identify almost 90% of cows in standing heat. To investigate the potential relationship among the use of different formulations of commercially available tail paint and their effectiveness in heifers, 18 Holstein heifers at breeding age were selected, balanced by age (13.7 ± 1.2 mo), body weight (394 ± 32 kg), and BCS (3.43 ± 0.1 on a 1 to 5 scale), and randomly assigned to 1 of 3 treatment groups. Experimental treatments were: Control (CON), orange color, tail chalk, commercial formulation; Treatment A (TRTA), orange color, tail chalk, new formulation; and Treatment B (SPRAY), orange color, spray formulation. Experimental design was a replicated 3 × 3 Latin square design with 6 total squares, 3 animals per square. Each period was 14 d. Visual observations were performed for tail paint licking (LICK; being licked at the tail paint), social licking (SOCLICK; being licked at the head, neck, or leg areas), rump licking (RUMPLICK; being licked at the rump area), and product disappearance (TPREMOVED; score from 0 to 2, according to the degree of tail paint removal) in 30-min segments every 2 h from 0600 to 1800 h. Video recordings were used to confirm observations. The outcome variables of interest, LICK, SOCLICK, and RUMPLICK, were summarized to daily counts of interactions. Assessment of TPREMOVED was done once daily before subsequent treatment application. A synchronization protocol (Ovsynch: 100 mg GnRH, then 25 mg $PGF2_{\alpha}$ 7d later, and 100 mg GnRH 2d after $PGF2_{\alpha}$) was used to stimulate high and low social interactions. Statistical analyses were performed using the GLIMMIX procedure of SAS (SAS v9.3 Institute Inc., Cary, NC, USA). Half of the heifers (51.4%) received at least 1 SOCLICK, but only 10.1% of the heifers received a RUMPLICK. There were no treatment differences for SOCLICK ($P > 0.88$) or RUMPLICK ($P > 0.42$). The majority (75.3%) of heifers did not receive LICK and < 2% of the heifers received < 1 LICK. Heifers receiving SPRAY had a lower number of LICK per day ($P = 0.005$) when compared with CON or TRTA. Heifers that received SPRAY had less TPREMOVED ($P = 0.0001$) when compared with CON or TRTA, and TRTA heifers had less TPREMOVED ($P = 0.01$) when compared with CON. In conclusion, SPRAY had a lower number of LICK and lower TPREMOVED. Licking behavior seen on commercial dairy farms may be primarily from social licking rather than tail paint licking.

Key Words: dairy heifers, licking behavior, tail paint

0045 Balking behavior incidence in cattle at the processing plant and carcass implications. M. L. Thomas*[1], Y. V. Thaxton[2], A. H. Brown, Jr.[1], K. E. Pfalzgraf[1], K. D. Christensen[3], K. Anschutz[1], and C. F. Rosenkrans[4], *[1]Department of Animal Science, University of Arkansas Division of Agriculture, Fayetteville, [2]Center for Food Animal Wellbeing, University of Arkansas, Fayetteville, [3]Center of Excellence for Poultry Science, University of Arkansas, Fayetteville, [4]University of Arkansas, Fayetteville.*

Balking behavior in the cattle processing line can pose welfare issues as electric prod use to coerce forward movement is implemented. Temperament differences have been shown among breed-type categories, within breed-type categories,

among crossbreds, and between genders. Objectives in this study were to determine if breed-type predominance, based on coat color or gender, had an effect on balking behavior and if that behavior affects carcass economics. A total of 6510 balking observations over 7 random dates in 1 yr were recorded at the entrance to the restrainer in a high-capacity processing plant. Balking scores were assigned on a scale of 1 to 5 by a trained, consistent observer. Thirteen color combinations and 16 feedlot sources were represented at random collection dates and times. Holstein cattle balked more ($P < 0.0001$) than all other colors, which were similar. Gender differed in balking incidence with heifers balking more ($P = 0.05$) than steers and pens containing both steers and heifers balked intermediately. The feedlot source affected ($P < 0.0001$) balking behavior, with balking score means ranging from the lowest at 1.1 to 2.3 as the highest mean. Balking behavior was negatively correlated (r = -0.18, $P < 0.0001$) with dressing percentage. Mean pen weight and dressing percentage were also affected ($P < 0.0001$) by feedlot source. Mean pen weight was affected by color. Holstein cattle had greater ($P < 0.0001$) pen weights than all other colors, which were similar. Steers had heavier ($P < 0.0001$) pen weights than mixed pens, with heifers having the lowest pen weight (602.8 ± 15.4, 546.1 ± 0.59, and 541.1 ± 0.36kg, respectively). Dressing percentage was affected ($P < 0.0001$) by coat color and gender ($P = 0.01$). Steers had the greatest ($P = 0.01$) dressing percentage at 64.8 ± 0.1 vs. heifers at 64.3 ± 0.3, with mixed pens being intermediate at 63.4 ± 0.5. Our results suggest an association with dressing percentage and balking behavior, and dressing percentage is affected by coat color and gender.

Key Words: balking, behavior, welfare

0046 Effects of ractopamine or zilpaterol on physiologic and metabolic parameters in feedlot steers.

A. L. Fuller*[1,2], T. L. Covey[2], T. E. Lawrence[1], and J. T. Richeson[1], *[1]West Texas A&M University, Canyon, [2]OT Feedyard and Research Center, Hereford, TX.*

The feeding of β adrenergic agonists has recently been implicated as a potential animal welfare concern. The objective of this study was to determine the effects of ractopamine hydrochloride or zilpaterol hydrochloride on physiologic and metabolic blood parameters indicative of stress. Thirty crossbred steers (BW = 573 ± 27.4 kg) were used in a randomized complete block design. Steers were grouped into 2 blocks based on harvest date, stratified by BW within block, assigned randomly to treatment, and then placed into individual pens. A basal finishing ration was delivered to each steer twice daily. Treatments were applied via premix containing 20 g ground corn at each feeding and consisted of: 1) no β agonist (CON), 2) 300 mg/d ractopamine hydrochloride (RH), or 3) 90 mg/d zilpaterol hydrochloride (ZH). Blood samples were collected via jugular venipuncture on d −7, -1, 0, 0.25, 0.5, 1, 3, 7, 14, and 21, relative to initial delivery of treatment. Whole blood (excluding d 21) was analyzed for complete blood count using an automated hemocytometer. Serum was analyzed for cortisol and haptoglobin via ELISA, and an array of blood metabolites were evaluated using an automated analyzer. Overall, the total leukocyte concentration was greater ($P = 0.01$) in steers that received RH compared with CON; whereas ZH did not differ ($P \geq 0.43$). On d 1, total leukocytes were greater for both RH and ZH vs. CON (treatment × d; $P \leq 0.046$). Overall, neutrophil concentration was greater in RH ($P = 0.01$) and ZH ($P < 0.01$) compared with CON. Neutrophils were greater for ZH on d 1 and 3, and RH on d 7 compared with CON (treatment × d; $P \leq 0.045$). Although RH did not alter ($P = 0.36$) the neutrophil to lymphocyte ratio (NLR), NLR was greater ($P = 0.03$) in steers fed ZH vs. CON. Treatment did not affect any other complete blood count variables ($P \geq 0.10$) and cortisol and haptoglobin were not different ($P \geq 0.19$). Serum urea nitrogen was decreased ($P < 0.02$) and potassium and chloride were increased ($P < 0.01$) for both RH and ZH. Creatine kinase was increased for ZH on d 14 and 21 ($P \leq 0.017$). Serum albumin, globulins, NEFA, creatinine, calcium, phosphorus, and magnesium were not different ($P \geq 0.57$). Under conditions of this study, feeding of either β-agonist did not clearly affect blood parameters indicative of physiological stress.

Key Words: β-agonists, stress

ANIMAL BEHAVIOR AND WELL-BEING III

0047 Breeding may simultaneously reduce pig aggressiveness at regrouping and in stable social groups, but management may not.
S. P. Turner*[1], S. Desire[1], R. B. D'Eath[1], L. Canario[2], and R. Roehe[1], *[1]SRUC, Edinburgh, United Kingdom, [2]INRA UMR1388, F-31326 Castanet-Tolosan, France.*

Aggression between pigs compromises welfare and productivity. Individual sow stalls are now banned in the European Union after wk 4 of gestation and are being phased out in some parts of North America. Better control of both acute regrouping aggression and chronic aggression in stable social groups is required at all ages. This paper examines whether efforts to control these 2 forms of aggression may be complementary or antagonistic, and whether optimal aggression phenotypes can be identified to target in management or breeding. Acute regrouping and subsequent chronic aggressiveness are stable traits of the individual but highly variable among animals and groups. Delivery of aggressive behavior at regrouping is heritable (h^2 > 0.31 SE 0.04) as is the number of skin lesions from regrouping or chronic aggression (h^2 = 0.19 SE 0.02 to 0.43 SE 0.04). The lesion count is genetically correlated to reciprocal fighting or receipt of non-reciprocal bullying, and is therefore an indicator of aggressive propensity (e.g., r_g between reciprocal fighting duration at regrouping and lesions to the anterior of the body = 0.67 SE 0.04). The lesion count shows a low but positive genetic correlation between 24-h and 3-wk post-regrouping (r_g 0.28 SE 0.07 to 0.50 SE 0.09), suggesting that breeding to reduce regrouping lesions would also reduce lesions from chronic aggression. However, at the phenotypic level, individual pigs or entire social groups that fight greatly at regrouping, even if this is often unsuccessful, show few injuries from chronic aggression (group level, r = -0.28 to -0.38, $P < 0.05$). Furthermore, pigs with a beneficial effect on the growth of penmates can be more aggressive at regrouping but receive fewer lesions 3 wk later. Acute aggression may therefore reduce the costs of chronic aggression at the phenotypic level. Fight quantity appears to primarily drive this association as fight outcome at regrouping had less impact on later lesions. However, some pigs show few injuries from both acute and chronic aggression. The behavior of these pigs will be discussed to highlight whether optimal phenotypes can be targeted in management or breeding. Currently, breeding for reduced regrouping aggressiveness is likely to simultaneously reduce subsequent chronic aggression, but phenotypically reducing regrouping aggression through management change may lead to long-term increases in aggression unless controlled.

Key Words: aggression, breeding, pig

0048 Effect of concentrate feeder design on performance, animal behavior, and ruminal health in Holstein bulls fed high-concentrate diets.
M. Verdu*, A. Bach, and M. Devant, *IRTA-Department Ruminant Production, Caldes Montbui-Barcelona, Spain*

A total of 240 Holstein bulls (121 ± 2.0 kg BW and 99 ± 1.0 d of age), in a replicated factorial study, were randomly allocated in 1 of 6 pens and assigned to 1 of 3 treatments, according to the feeder design: conventional feeder with 4 feeding spaces (CF), conventional feeder with less concentrate capacity (CFL), and a single space feeder with lateral protections (SF) forming a chute (1.4 × 0.8 m). Also, each pen had 1 straw feeder and 1 drinker. Concentrate intake was recorded daily, straw consumption weekly, and BW every 14 d. On d 7, 119 to 120, and 215 to 216, rumen fluid and blood samples were collected to determine rumen pH and VFA, and serum NEFA. Animal behavior was registered on d 1, 3, 5, 8, 14 and every 28 d by scan sampling. Animals were slaughtered after 221 d and HCW, rumen wall, and liver lesions were recorded. Data were analyzed using a mixed-effects model with repeated measures. Bulls on CF tended (P = 0.07) to have greater ADG than CFL and SF bulls (1.54, 1.50, and 1.49 ± 0.017 kg/d, respectively). However, no differences among treatments were observed in concentrate intake (7.6 ± 0.16 kg/d), straw intake (0.8 ± 0.03 kg/d), FE (0.2 ± 0.01 kg/kg), HCW (247.2 ± 2.09 kg), dressing percentage (53.6 ± 0.23%), and rumen and liver lesions. Mean rumen pH was always > 5.6; at 7 and 215 to 216 d, SF bulls had greater ($P < 0.05$) rumen pH compared with CF and CFL bulls. Acetate to propionate ratio was greater ($P < 0.05$) in SF compared with CFL and CF. At d7, NEFA of SF was greater ($P < 0.05$) compared with CF and CFL, although at 119 to 120 d in SF bulls serum NEFA concentration was less ($P < 0.01$) than in CF and CFL bulls. Bulls on SF spent more time ($P < 0.05$) eating straw, exhibited fewer ($P < 0.05$) displacements at feeders and drinker, and expressed more oral behaviors ($P < 0.05$) than CF and CFL bulls. The CFL bulls tended (P = 0.10) to perform more mounts than SF and CF. In conclusion, the different feeder designs evaluated did not affect overall performance, although some behavior traits differed among them. Serum NEFA concentrations at the beginning suggest that animals at the SF may have adaptation problems and SF does not negatively affect rumen wall health and pH.

Key Words: beef, feeder, performance

0049 Impact of using an electrified crowd gate on milk yield and milk flow. I. Guasch[1], A. Pinto[2], and A. Bach[*3,4], *[1]Blanca, Hostalets de Tost, Spain, [2]Department of Ruminant Production, IRTA, Barcelona, Spain, [3]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [4]ICREA, Barcelona, Spain.*

Many dairy enterprises use automatic crowd gates in the milking parlor's waiting area to assist and expedite the entrance of cows into the parlor. Some of these systems include electrified gates. We hypothesized that the use of an electrified crowd gate may impose an alert response in the cows, which in turn may negatively affect milk let down and production. One hundred fifty dairy cows (71 primiparous, 79 multiparous; days in milk = 225 ± 109 d) were split into 2 groups and milked in a 32-stall rotary parlor, using a crowd gate that was either not electrified (NEG) or electrified (EG). The experiment followed a 2 × 2 Latin square design with 2 periods of 9 d each. The waiting area was 200 m^2 and equipped with rubber flooring. The crowd gate was 13 m long. Cows were milked at 0600 and 1800 h. At each milking, milk production, milk fat content, milk protein content, average milk flow, maximum milk flow, and time to peak milk flow were recorded on an individual basis. The first 4 d of each period were discarded and data from the last 5 d were averaged by cow and analyzed using a 2-level mixed-effects model that accounted for the random effect of cow and period, and the fixed effects of type of crowd gate, parity, their 2-way interaction, and days in milk as a covariate. Time elapsed between the initiation of milking and peak milk flow (1.61 ± 0.05 min). Peak milk flow did not differ ($P = 0.67$) between treatments. However, peak milk flow tended to be greater ($P = 0.10$) in NEG (5.8 ± 0.16 kg/min) than in EG (5.6 ± 0.16 kg/min) cows. Similarly, average milk flow tended to be greater ($P = 0.06$) in NEG (3.00 ± 0.07 kg/min) than in EG (2.96 ± 0.07 kg/min) cows. Milk yield was greater ($P < 0.01$) when cows were milked with NEG (14.0 ± 0.25 kg/milking) than when milked with EG (13.6 ± 0.25 kg/milking). Treatment had no effect on milk protein ($P = 0.33$) or fat ($P = 0.77$) content. It is concluded that using an electrified crowd gate may compromise milk flow and results in decreased milk yield.

Key Words: let down, parlor, stress

0050 Using designer diets to reduce aggression in pregnant sows. A. Sapkota[*1], J. N. Marchant-Forde[2], B. T. Richert[1], and D. C. Lay Jr.[2], *[1]Purdue University, West Lafayette, IN, [2]USDA-ARS, West Lafayette, IN.*

The U.S. Swine industry is under pressure to switch from individual to group housing for pregnant sows. The study objective was to evaluate effects of increased dietary fibrous ingredients to reduce aggression during mixing by increasing satiety. Five isocaloric (NE basis) treatment diets (CONTROL, Resistant-STARCH, BEET pulp, soy hulls INCREASED INTAKE, and SOY Hulls + FAT diets) were fed to 5 sows (parity 1 to 6) per treatment per replicate. One hundred fifty sows (25 sows/replication × 6 replications) were used for the study. Sows were bred and moved into individual crates (0.61 × 2.13 m) on d 7 to 14 post-breeding. Sows remained in crates for 21 d while fed assigned diets. Data on weight, backfat, and BCS for each sow were collected on first and last days in crates. On d 22, sows were moved into mixing pens (2.13 × 3.05 m mixing area and five 0.61 × 2.13 m crates). As a measure of aggressiveness, lesions on left and right in front, mid, and rear parts of each sow were counted before mixing, and on d 1, 2, and 3 of mixing. After 72 h of mixing, sows were switched to regular diets and management. Production data (piglets born, percent alive, average birth weight, average wean weight, percent weaned, farrowing rate) were collected from 75 sows (3 replications). The effects of diets on skin lesions, backfat, weight, BCS, and production data were compared using PROC GLM and least squares means in SAS 9.3. Chi-square test was performed to compare farrowing rates. Skin lesions in the front left portion of sows were 6.7 ± 0.9^{ab}, 6.8 ± 0.9^{a}, 7.4 ± 1.0^{ac}, 4.0 ± 1.0^{b} and 9.9 ± 1.0^{c} for CONTROL, Resistant-STARCH, BEET, INCREASED INTAKE, and SOY Hulls + FAT diets, respectively, on d 1 ($P = 0.002$). Skin lesions in the front left portion of sows were 11.2 ± 1.6^{a}, 11.5 ± 1.6^{a}, 10.3 ± 1.6^{a}, 9.7 ± 1.6^{a}, and 16.5 ± 1.7^{b} for CONTROL, Resistant-STARCH, BEET, INCREASED INTAKE and SOY + FAT diets, respectively, on d 3 ($P = 0.038$). Diets did not affect ($P > 0.05$) other skin lesion scores, number of piglets born, percent alive, average birth weight, average wean weight, percent weaned, and farrowing rate. Change in weight, backfat, and BCS did not differ with treatments ($P > 0.05$). There were fewer skin lesions in INCREASED INTAKE treatment on d 1 indicating less aggression and higher skin lesions in left front parts of the sows fed SOY Hulls + FAT diet, indicating more aggression compared with other diets.

Key Words: aggression, group housing, sow

0051 Selection and breeding for improved feed efficiency alter gilt behavioral responsiveness to a novel object. J. D. Colpoys[*1], N. K. Gabler[1], C. E. Abell[2], A. F. Keating[1], S. T. Millman[1], J. M. Siegford[3], and A. K. Johnson[1], *[1]Iowa State University, Ames, [2]DNA Genetics, Columbus, NE, [3]Michigan State University, East Lansing.*

As feed efficiency is becoming more of a priority, our objective was to determine if divergent selection for residual feed intake (RFI) altered gilt approach and fear behavior. Twenty low-RFI (more feed efficient) and 20 high-RFI (less feed efficient) gilts (36 ± 5.7 kg BW) from the ninth generation Iowa State University Yorkshire RFI selection lines were randomly selected. Gilts were evaluated once over a 2-wk period, using a

novel object test (NOT). Individual gilts were moved from the home pen into a weigh scale for 1 min. Gilts then entered the NOT arena (4.9 long × 2.4 m wide with black corrugated plastic walls 1.2 m high) and their behavior was video recorded for 10 min. All testing occurred between 1300 and 1900 h. The video was watched continuously by 1 trained observer for latency, frequency, and duration of novel object touches (defined as oral, nasal, and/or facial interaction with the novel object, an orange traffic cone), frequency of escape attempts (defined as 2 front legs off the ground, possibly including a jump), and frequency and duration of freezing postures (defined as the whole body remaining still for $\geq$ 3 sec). Data were analyzed using the GLIMMIX procedure of SAS and the model included the fixed effect of genetic line, covariate of gilt age, and pig as the experimental unit. Compared with high-RFI gilts, low-RFI gilts tended to take longer to first touch the object ($P = 0.06$) and touched the object fewer times ($P = 0.0001$); however, there was no observed differences between lines in duration of time spent touching the object ($P = 0.14$). Low-RFI gilts attempted to escape fewer total times compared with high-RFI gilts ($P = 0.001$). No difference was observed in frequency or duration of freezing ($P \geq 0.14$). In conclusion, low-RFI gilts interacted with the novel object fewer times but engaged in fewer total escape attempts compared with high-RFI gilts. These data suggest that while there are differences in approach behaviors to a novel object between low- and high-RFI selection lines, selecting for improved feed efficiency (low-RFI) may have resulted in calmer, less fearful gilts.

Key Words: approach, fear, residual feed intake

ANIMAL BEHAVIOR AND WELL-BEING IV

0052 Sprinkler flow rate affects dairy cattle physiological and behavioral responses.
J. M. Chen*[1], K. E. Schütz[2], and C. B. Tucker[1], [1]*University of California, Davis,* [2]*AgResearch, Hamilton, New Zealand.*

The accumulation of heat load can be problematic for dairy cow welfare and productivity. Sprinklers effectively reduce heat load, but little is known about the optimal amount of water needed for cooling or about cattle behavioral responses to this resource. Two studies assessed how flow rate affected: 1) the effectiveness of sprinklers and 2) cattle preferences. In Exp. 1, 19 lactating cows were restrained at the feedbunk for 1 h/d and received 1 of 4 treatments in a crossover design: Control (0 L/min; 3X total) or sprinkler (0.4, 1.3, and ≥ 4.5 L/min, 6X each). Spray was delivered in 4 cycles (3 min on 12 min off). Cooling effectiveness was evaluated using body temperature (BT) and respiratory rate (RR), by taking the differences between measurements recorded before the first spray cycle (-2 min) and after the final cycle (49 min). In Exp. 2, 18 lactating cows were tested in a shaded Y-maze, with 3 pairwise comparisons between either the Control (0 L/min) and/or 0.4 or 4.5 L/min sprinklers. For each pairing, cows chose once daily (12 min/d) for 8 consecutive days. In Exp. 1, BT and RR differed among all 4 treatments: as flow rate increased, so did cooling effectiveness ($P < 0.01$, GLMM). However, for BT, there was an interaction with weather [volume × air temperature (AirT), $P < 0.004$]. At AirT < 28°C, both sprinklers ≥ 1.3 L/min kept BT from rising ($P \leq 0.003$), whereas at AirT ≥ 32°C, only the ≥ 4.5 L/min sprinkler did ($P \leq 0.001$). In Exp. 2, cows choose 0.4 L/min over Control 69% of the time (SE: 9.3%, $P = 0.096$, Wilcoxon signed-rank test) and showed no preferences in the other comparisons (4.5 L/min: 58% vs. Control, SE: 9.4%; 42% vs. 0.4 L/min, SE: 9.6%; $P \geq 0.552$). However, preferences for 4.5 L/min over Control tended to depend on weather ($P = 0.065$, GLMM): at AirT ≤ 24.9°C, the probability of choosing 4.5 L/min was 0.40, whereas at AirT ≥ 30.0°C, this increased to 0.74. In conclusion, sprinkler flow rate influenced both cooling effectiveness and cattle preferences. In warmer weather, sprinklers ≥ 4.5 L/min were most effective and were preferred over shade alone. However, more work is needed to fully understand how cattle choose to use cooling resources throughout the day.

Key Words: heat load, preference, sprinklers

0053 Short-term increases in stocking density did not alter feeding behavior of lactating Holstein dairy cattle.
R. A. Black*[1], R. J. Grant[2], and P. D. Krawczel[1], [1]*University of Tennessee, Knoxville,* [2]*William H. Miner Agricultural Research Institute, Chazy, NY.*

Increasing stocking density at key resources may have negative effects on the feeding pattern of dairy cattle. The objective of this study was to determine the impact of short-term increases in stocking density on meal duration and frequency of lactating Holstein dairy cattle. Cows ($n = 136$) were allocated to 1 of 4 groups ($n = 34$), balanced for parity, days in milk (DIM), and milk production. Four stocking density treatments of 100% (1 cow per freestall and headlock), 113%, 131%, and 142% were assigned using a 4 × 4 Latin Square, with treatments imposed for 14-d periods. Twelve cows from each pen were selected to form focal groups, balanced by milk production (50.2 ± 1.1 kg), parity (2.2 ± 0.2), DIM (162.2 ± 7.0 d), BW (700.1 ± 11.0 kg), and BCS (3.09 ± 0.05). On d 11 of each period, feeding behavior was recorded at 10-min intervals for 24 h. Meals were defined as repeated observations of eating with a maximum 20 min of not eating between observations. To evaluate diurnal effects, 24 h of data was divided into BLOCK1 (0400 to 1200 h), BLOCK2 (1200 to 2000 h), and BLOCK3 (2000 to 0400 h), based on milking time. The MIXED procedure of SAS (SAS 9.3, SAS Inst., Cary, NC) was used to determine the effect of stocking density on meals per day, meals per hour, meal duration, time between meals, and meal duration 2 h before and after milking. Stocking density did not affect the number of meals per day ($P = 0.25$), time between meals ($P = 0.93$), number of meals per hour ($P = 0.71$), or meal duration ($P = 0.33$). However, meals were longer during BLOCK1 (38.8 ± 1.2 min) and BLOCK2 (39.7 ± 1.2 min), compared with BLOCK3 (33.8 ± 1.3 min; $P < 0.01$). Feed delivery occurred daily at 0430 h, with feed pushed up throughout the day. This suggests meal length decreases relative to time of feed delivery. However, meal duration increased after milking compared with before milking (29.5 ± 1.0 vs. 21.0 ± 1.0 min, respectively; $P < 0.01$), regardless of stocking density ($P = 0.98$). Short-term increases in stocking density did not impact the feeding pattern of lactating dairy cows. Future studies should investigate ways cattle compensate for increased stocking density while avoiding changes in feeding pattern.

Key Words: dairy cattle, feeding behavior, stocking density

0054 Evaluation of prepartum lying behavior as an indicator of health disorders in transition dairy cows. K. Lobeck-Luchterhand*[1], P. Basso Silva[1], R. C. Chebel[2], and M. I. Endres[1], [1]*University of Minnesota, St. Paul,* [2]*Department of Veterinary Population Medicine, University of Minnesota, St. Paul.*

The objective of this study was to determine if prepartum lying behavior (lying time, lying bouts, or lying bout duration) could be used as an indicator of health disorders in transition dairy cows. Lying behavior of 281 prepartum Jersey cows enrolled 4 wk before expected calving date was recorded using HOBO Pendant G data loggers attached to the cow's rear leg 1 d after entrance into the close-up pen, left on for 12 d, removed for 7 d, and reattached for 12 d or until the cow calved. Blood samples were taken on days in milk (DIM) 3, 10, 17, and 24 for determination of BHBA concentrations. All cows were examined on DIM 1, 4, 7, 10, and 13 for metritis and retained fetal membrane. Locomotion (1 to 5 scale) was evaluated on DIM -28, 0, and 35; cows with locomotion score $\geq$ 3 were considered lame. Data were analyzed using PROC MIXED of SAS. Increased daily lying time was associated with displaced abomasum (Difference, LSMEANS ± SE, min/d; 54.0 ± 13.2; $P < 0.01$), retained fetal membrane (20.4 ± 6.6; $P < 0.01$), twin pregnancies (59.4 ± 14.4; $P < 0.01$), and lameness at DIM 0 (163.2 ± 21.0; $P < 0.01$). Decreased daily lying time was associated with subclinical ketosis (50.4 ± 13.8; $P < 0.01$) and mastitis (34.2 ± 8.4; $P < 0.01$). An increase in the number of daily lying bouts was associated with lameness at DIM 0 (2.28 ± 0.61; $P < 0.01$) and first AI pregnancy (0.24 ± 0.12; $P = 0.04$). A decrease in the number of lying bouts was associated with displaced abomasum (1.45 ± 0.36; $P < 0.01$), retained fetal membrane (0.68 ± 0.22; $P < 0.01$), mastitis (1.21 ± 0.26; $P < 0.01$), and pregnancy loss from first AI (1.46 ± 0.27; $P < 0.01$). Decreases in lying bout duration (min) were associated with subclinical ketosis (14.4 ± 3.0; $P < 0.01$) and first AI pregnancy (2.4 ± 0.6; $P = 0.01$). Displaced abomasum (18.0 ± 3.0; $P < 0.01$) and pregnancy loss from first AI (7.8 ± 2.4; $P < 0.01$) were associated with increased lying bout duration. In conclusion, changes in lying behavior may be an indicator of cows at risk for transition disorders; however, the behavioral relationships were not consistent among the health disorders evaluated in this study.

Key Words: lying behavior, transition cow

0055 Effect of stocking density on social and feeding behavior of prepartum dairy cows. K. Lobeck-Luchterhand*[1], P. Basso Silva[1], R. C. Chebel[2], and M. I. Endres[1], [1]*University of Minnesota, St. Paul,* [2]*Department of Veterinary Population Medicine, University of Minnesota, St. Paul.*

The objective of this study was to investigate the effect of 2 feedbunk stocking densities on prepartum social and feeding behavior of dairy cows. Seven hundred fifty-seven Jersey cows at 4 wk before expected calving date were assigned randomly to 1 of 2 treatments. Treatments were 80% (38 cows/48 headlocks; 80D) or 100% (48 cows/48 headlocks; 100D) feedbunk stocking density. Four pens with sand-bedded freestalls were used: 2 nulliparous and 2 mixed primiparous and multiparous, referred to as "parous" pens over 4 repetitions (total of 350 nulliparous and 407 parous cows were used). Cows were balanced for BCS and cows with a locomotion score > 2 were excluded from the study. Pens were stocked twice a week to maintain the desired stocking density. Displacements from the feedbunk were measured using video recordings during 3 h following fresh feed delivery on d 2, 5, and 7 of each week of the 5-wk rep. Feeding times were measured using 10-min video scan sampling on d 2, 5, and 7 of the first week of the rep and d 2 and 5 for the final 4 wk of the rep. Displacements and feeding behavior data were analyzed using PROC MIXED of SAS with observation day (rep) as repeated measures. The random statement cow ID (pen) was included for the feeding behavior model. The 80D cows had fewer displacements from the feedbunk than 100D cows (15.2 ± 0.7 and 21.3 ± 0.7, respectively; $P < 0.001$). There was a treatment × parity interaction for daily feeding time ($P = 0.014$). Parous 80D cows had a tendency for longer feeding times than parous 100D cows (296.9 ± 3.3 and 289.3 ± 2.9 min, respectively; $P = 0.081$), whereas there was a tendency for longer feeding times for nulliparous 100D than nulliparous 80D cows (251.2 ± 3.2 and 242.8 ± 3.6, respectively; $P = 0.079$). In conclusion, stocking cows at 80% of headlocks reduced displacements from the feedbunk and had a tendency to increase daily feeding time for parous cows but not nulliparous cows.

Key Words: stocking density, transition cows

0056 Using prepartum feeding behavior to identify dairy cows at risk for transition health disorders. K. Lobeck-Luchterhand*[1], P. Basso Silva[1], R. C. Chebel[2], and M. I. Endres[1], [1]*University of Minnesota, St. Paul,* [2]*Department of Veterinary Population Medicine, University of Minnesota, St Paul.*

The objective of this study was to investigate whether changes in prepartum feeding behavior could be used as an indicator of health disorders in postpartum transition cows. Retrospective daily feeding times for 925 Jersey dairy cows within 21 d prepartum were used. Data were from 2 studies: study 1, 209 prepartum cows enrolled in either a stable group of 44 cows moved to a pen with no new cows added during a 5-wk rep or conventional group with cows added once weekly to maintain a desired pen stocking density of 44 cows; or study 2, 716 prepartum cows housed at either 80% (38 cow/48 headlocks) or 100% (48 cows/48 headlocks) feedbunk stocking density with twice weekly entrance of new animals. Prepartum feeding behavior was measured using 10-min video scan sampling for

24-h periods (4 d/wk for study 1 and 2d/wk for study 2). Blood samples were taken on days in milk (DIM) 3, 10, 17, and 24 for measuring BHBA concentrations. Cows were classified with subclinical ketosis when BHBA levels were $\geq$ 1400 μmol/L. All cows were examined on DIM 1, 4, 7, 10, and 13 for metritis and retained fetal membrane. Lameness was evaluated on DIM -28, 0, and 35; cows with locomotion score $\geq$ 3 (1 to 5 scale) were classified as lame. Cows with a health disorder were excluded from the lameness analysis. Other health events were obtained from on-farm records. The MIXED procedure of SAS was used to determine if feeding times were associated with transition health disorders. There was a reduction in daily prepartum feeding time for cows with metritis (Difference, LSMEANS ± SE min/d; 7.4 ± 2.7; $P < 0.01$), ketosis (15.4 ± 7.2; $P = 0.03$), retained fetal membrane (8.8 ± 3.9; $P = 0.02$), mastitis (9.2 ± 4.3; $P = 0.03$), lameness at DIM 0 (56.2 ± 10.0; $P < 0.01$), and lameness at DIM 35 (25.0 ± 6.2; $P < 0.01$), compared with cows without the respective disorder. There was a tendency for a reduction in feeding time for cows with displaced abomasum ($P = 0.09$) and cows carrying twins ($P = 0.08$). In conclusion, prepartum feeding behavior appears to be a useful indicator of cows at risk for transition disorders.

Key Words: feeding behavior, prepartum behavior, transition cows

---

0057 Eating and drinking behavior prediction by use of Tri-axial accelerometers in dairy cattle.
K. J. Haerr* and F. C. Cardoso, *University of Illinois, Urbana.*

Tri-axial accelerometers are often used to measure behavior in cows (e.g., estrus, standing, and lying). However, there may be other practical uses for accelerometers on dairy farms. Our objective was to determine if accelerometers placed on a collar around the cow's neck can be used to monitor feeding and drinking behaviors. For this study, 12 lactating Holsteins (DIM 76 ± 35) were housed in stanchion stalls and continuously recorded for 6 d (Swann Pro-530 night/day cameras, DVR). Cows were fitted with Onset Pendant G accelerometers on the collar and sampling intervals set at 6 s. Video data were watched and evaluated by the same person. Daily video duration (Video) of each behavior was summarized and compared with daily duration predicted by accelerometers. Three methods were created to evaluate behavior prediction by accelerometers. For method 1 (MET1), data set was constructed based on the mean for the 3 axes recorded. For method 2 (MET2), data set was constructed based on the mean plus the standard error for the 3 axes recorded. For method 3 (MET3), data set was constructed based on the mean minus the standard error for the 3 axes recorded. Four behaviors analyzed were standing and eating with head up (SEHU), standing and eating with head down (SEHD), standing and eating (EAT = SEHU + SEHD), and drinking (DRK). Statistical analysis was performed using the MIXED procedure in SAS. For SEHU, there was difference ($P < 0.001$) between Video (119.0 min) and MET1, MET2, and MET3, and tendency ($P > 0.06$) for differences among MET1, MET2, and MET3. For SEHD, there was a difference ($P < 0.001$) between Video (141.7) and MET1, MET2, and MET3, and tendency ($P > 0.09$) for differences among MET1, MET2, and MET3. For EAT, there was a difference ($P < 0.001$) between Video (260.7 min) and MET1, MET2, and MET3, however, there was no difference ($P > 0.48$) among MET1, MET2, MET3, and EAT. For DRK, there was no difference ($P = 0.89$) between Video (315.3 min) and MET1, MET2, and MET3. The accelerometer under predicted SEHU by 42.6%, 35.4%, and 49.2%; SEHD by 72.0%, 65.3%, and 71.8%; EAT by 57.6%, 51.6%, and 61.05% for MET1, MET2, and MET3, respectively. The accelerometer accurately predicted DRK by 100%, 103%, and 99% for MET1, MET2, and MET3, respectively. In conclusion, accelerometers were successful in predicting drinking behavior.

Key Words: accelerometer, intake, prediction

0058 Herding cows with a robot: The behavioral response of dairy cows to an unmanned ground vehicle.
C. E. Clark, S. C. Garcia*, K. L. Kerrisk, J. P. Underwood, J. I. Nieto, M. S. Calleija, S. Sukkarieh, and G. M. Cronin, *University of Sydney, Australia.*

Advances in technology could reduce time farmers spend on repetitive tasks. In pasture-based systems, herding cows from grazing areas to the milking parlor is a repetitive task ideally suited to automation. We conducted a field study at Sydney University's dairy farm to determine the behavioral response of dairy cows to a remotely operated unmanned ground vehicle (UGV) across time. Twenty milking cows were separated from the main herd at 0830 h and offered 0.5 ha of an ad libitum kikuyu pasture allocation (50 kg DM/cow to ground level). A pre-defined Fig. 8 route was determined for the UGV within this area. The UGV entered the pasture allocation at 0900 h and traversed this route at a target speed of 2.5 km/h, with the whole procedure repeated 6 times at 15-min intervals. The 0.5 ha was virtually split into 4 sectors. Four observers monitored cows exiting or entering each sector. Data were analyzed by REML, where Cows out = Fixed [Robot (presence/absence) × Traverse number] + Random (Cow). Alongside human observations, 3D LiDAR data from the UGV determined the velocity of cow movement for each traverse. There was a significant effect of Robot ($P = 0.02$) and Traverse ($P < 0.01$) on the number of cows (% of total cows) exiting a sector; however, there was no interaction between these fixed effects. Twice as many cows exited a sector when the robot was present (8%) as compared with absent (4%). More cows exited a sector in traverse 1 (14%) as compared with all other traverses (mean = 4%). The 3D LiDAR data showed a reduction in cow velocity moving away from the UGV for the first 3 traverses (Table 0058). These results show that dairy cows

habituated quickly to an UGV. The greater number of cows exiting a sector in the first traverse was likely associated with an initial period of increased cow movement as cows foraged. Future work will aim to fully automate the process of herding and integrate this process with the monitoring of animal health, ground cover, and soil moisture levels.

Key Words: cow behavior, herding, unmanned ground vehicle

Table 0058. Average (SD) velocity of cows away from the unmanned ground vehicle (UGV; m/s) for traverse 1 to 5

Traverse	Average (SD) velocity of cows moving away from UGV (m/s)
1	0.06 (0.27)
2	0.04 (0.27)
3	0.02 (0.21)
4	0.01 (0.17)
5	0.01 (0.19)

0059 Responses to rectal and uterine palpation for assessment of visceral pain associated with metritis in dairy cows.

J. Stojkov[*1], D. M. Weary[1], and M. A. G. von Keyserlingk[2], *[1]Animal Welfare Program, Faculty of Land and Food Systems, The University of British Columbia, Vancouver, Canada, [2]University of British Columbia, Vancouver, Canada.*

Metritis is a common disease in dairy cattle following calving, but to our knowledge no work has assessed the associated pain. A common method of assessing pain in human and veterinary medicine is through responses during tissue palpation. The objective of this study was to evaluate visceral pain responses in cows with clinical signs of metritis during rectal and uterine palpation. A total of 62 Holstein dairy cows (mean ± SD parity 3 ± 1.5) were subjected to systematic health checks starting d 3 after parturition and continuing every third day for 21 d. Cows were scored for vaginal discharge (0 to 4); 13 cows showed a discharge score ≥ 2 during at least 1 health check; these cows were classified as metritic. A matched (by parity and days in milk at diagnosis) sample of 13 cows was classified as "healthy." Cows showing any other signs of disease (including mastitis, ketosis, and lameness) were not included in the study. Behavioral and physiological responses during palpation were recorded using video and heart rate monitors. The effects of health status (healthy vs. metritic) and exam method (rectal vs. uterine palpation) were tested using the MIXED model. Back arch (cm^2) on the day of diagnosis was higher for metritic cows than healthy cows ($P < 0.01$), with no significant effect of palpation method or interaction. During rectal palpation, back arch averaged (± SE) 28 ± 2.3cm^2 for metritic vs. 18 ± 2.3cm^2 for healthy cows. During uterine palpation, back arch averaged 31 ± 2.3 vs. 19 ± 2.3cm^2, respectively. Standard deviation between normal to normal inter beat intervals (SDNN) and root of the mean square of successive differences (RMSSD) were log transformed before analysis. Both measures varied in response to exam method ($P < 0.05$) but not health status or interaction. The SDNN during rectal palpation averaged (± SE) 2.7 ± 0.16 compared with the uterine palpation 2.1 ± 0.16. Similarly, RMSSD was 1.8 ± 0.14 during the rectal palpation but decreased in the uterine palpation to 1.4 ± 0.14. The heart rate variation measures indicate that both healthy and metritic cows found uterine palpation more stressful than rectal palpation. The back arch results indicate that metritic cows are more sensitive to palpation (both methods) than healthy cows. These results also suggest that these types of veterinary exams may be used to identify cows that are experiencing pain associated with metritis and thus may be useful in deciding which animals will benefit from treatment with analgesics.

Key Words: metritis, pain response, visceral pain

ANIMAL HEALTH SYMPOSIUM I: ANIMAL HEALTH RESEARCH FROM THE PERSPECTIVE OF INFORMATION GAPS

0060 Animal health—From systems biology to translational research. C. Gay*, *USDA-ARS Office of National Programs, Beltsville, MD.*

Genome-enabled technologies are driving fundamental changes in the approaches used to understand mechanisms of disease, selection of animals for beneficial health traits, and discovery of tools to control and mitigate animal diseases. New research strategies using high-throughput gene expression analysis are providing novel platforms for more comprehensive understanding of host–pathogen interactions. In particular regard to application of the findings that result from these new technical capabilities, a systems biology approach has begun, is evolving in focus, and rapidly revolutionizing the analysis of whole genome responses of host and pathogens, which will ultimately lead to a better understanding of disease processes in affected animals. Concurrently, the capabilities facilitate new insights into the mechanisms through which pathogens evade host immunity, the genetic basis of host–pathogen interactions, and ultimately the discovery of novel and highly effective vaccines, drugs, biotherapeutics, and integrated management strategies that ensure the abundance and safety of the food supply while maintaining its economic affordability to all.

Key Words: animal, disease, intervention

0061 Respiratory disease management in livestock—New challenges and knowledge gaps. What is critical on the horizon? A. W. Confer*, *Oklahoma State University, Stillwater.*

Despite availability and use of numerous bovine respiratory pathogen vaccines and new antimicrobial drugs as well as a greater understanding of the pathogenesis of bovine respiratory disease (BRD), pneumonia ranging from subclinical to fatal remains a major cause of morbidity, mortality, and economic loss to the beef and dairy cattle industries. Gaps in our BRD knowledge that could greatly enhance our clinical management schemes mainly fall into 4 general questions. The objective of this presentation is to address briefly each question from the standpoint of general current knowledge and what we need to know to improve management and control of BRD. First, various environmental factors and stressors stimulate potential pathogens that are quiescent in the nasopharynx to replicate and be inhaled, resulting in disease. Can a better understanding of this process translate into improved disease management? Second, currently published studies indicate low heritability for BRD resistance. Can BRD morbidity and mortality be reduced through genomic studies and breeding for genetic resistance. Third, numerous antibiotics are currently available and in use to control and treat BRD. Does in vitro antibiotic resistance and susceptibility of BRD pathogens correctly predict in vivo antimicrobial efficacy? Fourth, in the last 20 yr, we have greatly increased our knowledge base about immunity against BRD pathogens. What has been and can be translated from the research laboratory into improved commercial vaccines?

Key Words: cattle, disease, management

0062 Metabolic and health consequences of heat stress: Knowledge gaps and opportunities. L. H. Baumgard*[1], J. W. Ross[1], N. K. Gabler[1], S. M. Lonergan[1], A. F. Keating[1], J. T. Selsby[1], and R. P. Rhoads[2], [1]*Iowa State University, Ames,* [2]*Virginia Tech, Blacksburg.*

Environmental-induced hyperthermia compromises efficient animal production and jeopardizes animal welfare. Reduced animal agriculture productive output during heat stress was traditionally thought to result from decreased nutrient intake. Our results in ruminants and monogastrics challenge this dogma and indicate heat-stressed animals use homeorhetic strategies to modify metabolic and fuel selection priorities independently of nutrient and energy intake. Systemic shifts in bioenergetics are characterized by increased basal and stimulated circulating insulin. Hepatocyte and myocyte metabolism also show clear differences in glucose production and oxidation during heat stress. Perhaps most intriguing given the energetic shortfall of the heat-stressed animal is the apparent lack of basal adipose tissue mobilization coupled with reduced responsiveness to lipolytic stimuli. The origin of the aforementioned metabolic changes may lie at the gastrointestinal track. For a variety of reasons, heat stress compromises intestinal integrity. Increased permeability to luminal contents results in local and systemic inflammatory responses. Bacterial components might be additional signals influencing insulin secretion during heat stress. For example, in vivo lipopolysaccharide (LPS) IV infusion acutely increases circulating insulin in pigs and cattle, which is paradoxical as endotoxemia is a potent catabolic condition accompanied by severe pyrexia and marked hypophagia. Understanding how and why LPS induces hyperinsulinemia remains to be elucidated, but the practical implications of this phenomenon to animal agriculture are numerous. Consequently, heat-stressed animals are simultaneously confronted with life-threatening hyperthermia and endotoxemia. However, the fields of both environmental metabolism and intestinal integrity are essentially in their infancies (especially in animal agriculture). As a result, there are numerous knowledge gaps that exist and need attention before mitigation strategies can be developed. Of particular relevance to animal agriculture are the tissue- and organ-specific consequences of heat stress. For example, how the liver, muscle, adipose, mammary, and

ovarian systems respond to elevated temperatures, endotoxemia, and LPS-induced inflammation is of obvious interest. Further, determining how these systems are homeostatically and homeorhetically coordinated to prioritize acclimation and survival vs. agriculturally productive purposes would presumably enlighten mechanisms amenable to manipulation. In summary, heat stress is 1 of the primary hurdles to efficient animal production. Defining the physiology and mechanisms that underlie how heat stress jeopardizes animal performance is critical for developing approaches to ameliorate current production issues and a prerequisite for generating future strategies (genetic, managerial, nutritional, and pharmaceutical) to improve animal well-being and performance.

Key Words: heat stress, insulin, intestinal integrity

0063 Ensuring good health and well-being in the aging equine population. K. Malinowski*, R. C. Avenatti, and K. H. McKeever, *Rutgers Equine Science Center, New Brunswick, NJ.*

One of the largest industries in the United States involves horses, a $39.2 billion business associated with 9.2 million animals. The horse industry's contribution to the U.S. gross domestic product is $102 billion, generating more than 1.4 million full-time equivalent jobs across the country. More than 15% of the equine population is > 20 yr old and many of these animals continue to participate in athletic activities. Partly responsible for the increased lifespan of horses is the fact that equine nutritionists have advanced the development of "senior feeds," and that the animal pharmaceutical industry has developed effective anthelmentics for parasite control. However, advancing age in horses is often associated with declining body condition, muscle tone, aerobic capacity, thermoregulatory ability in response to acute exercise, and general well-being. While aging and obesity-related loss of function and diseases have many factors, understanding the underlying imbalance of molecular signaling mediators in metabolically important tissues, such as muscle, to preserve functionality of physiological systems, needs to be addressed. Advanced age in horses is associated with a decline in immune response and is characterized by increased production of pro-inflammatory cytokines, termed inflammageing, which has been linked to obesity. Horses > 20 yr old can improve aerobic performance, reduce body fat, and partially restore changes that occur in the hypothalamic-pituitary-adrenal axis, in response to acute exercise and insulin sensitivity with regular exercise training. Physiological similarities between humans and horses allow for broad implications of equine exercise physiology research in relation to aging and performance. Understanding the molecular mechanisms behind the adaptive response to exercise will aid in the development of exercise conditioning and nutritional strategies meant to preserve the health and well-being of this socioeconomically important species.

Key Words: aging, exercise, horses

ANIMAL HEALTH I: **MODELS OF DISEASE AND STRESS**

0064 Heat stress as a model to study the effect of a gut health concept (Presan-Fx) on the intestinal barrier function of weanling piglets. P. J. Roubos* and Y. M. Han, *Nutreco Research and Development, Boxmeer, Netherlands.*

An acute heat stress model is used to study effects on the intestinal barrier function. During heat stress, the animal redistributes the blood supply to the periphery, leading to increased gut permeability. To mitigate the impairment on barrier function, a mixture of Presan-Fx (synergistic blend of organic acids, medium chain fatty acids, butyrates, and a phenolic compound) was used in this model with weanling piglets. The objective of this study was to evaluate the effect of a heat stress challenge on intestinal barrier function and the role of gut health concept in it. Twenty-four piglets were distributed over 4 treatments in a 2 × 2 factorial design, with a control diet with or without Presan-Fx (2 kg/ton), under the condition with or without heat challenge. After a 6-d adaptation period, animals in the heat stress groups were given an acute heat stress of 40°C for 10 h followed by 28°C for 24 h. Animals were monitored for growth performance and the barrier function was evaluated by morphological assessment, tight junction proteins, and cytokine production. Heat stress decreased ADG, but the impact was reversed significantly in animals fed Presan-Fx (see Table 0064). For the animals fed Presan-Fx, villus height was higher and the crypt depth was lower after heat stress compared with the control, suggesting that enterocytes had fewer damaged villi and higher cell production. Heat stress decreased the overall expression of the tight junction proteins Claudin-4, Claudin-7, and Occludin had no effect on E-cadherin. The dietary treatments did not influence the expression of tight junction proteins. However, the expression of 5 inflammatory cytokines (Il-1α, IL-8, IL-10, IL-17, and IL-23) was decreased by the Presan-Fx as measured by Q-PCR. In conclusion, an acute heat stress impaired intestinal barrier function. Adding Presan-Fx supported the animals with a better resistance to a heat stress challenge.

Key Words: gut health, heat stress, intestinal barrier function

Table 0064. Average daily growth and histology data

	No stress		Heat stress		
	Control	Presan-Fx	Control	Presan-Fx	P-value
ADG 0 to 6, g	411.0	455.5	456.6	416.7	0.98
ADG 6 to 8, g			90.0[a]	341.7[b]	0.05
ADG 6 to 11, g	550.0	503.3			
Villus height, µm	ND	ND	327.3[a]	421.2[b]	0.07
Crypt depth, µm	ND	ND	74.5[a]	119.3[b]	0.08

ND = not determined.

0065 A dual challenge of corticotropin-releasing hormone and vasopressin alters immune cell profiles in beef heifers. J. A. Carroll*[1], N. C. Burdick Sanchez[1], J. O. Buntyn[2], S. E. Sieren[3], S. J. Jones[3], and T. B. Schmidt[3], *[1]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [2] Department of Animal Science, University of Nebraska, Lincoln, [3]University of Nebraska, Lincoln.*

The duration and magnitude of cortisol release can have different effects on the immune response. Over the last decade, studies have suggested that acute stress, when cortisol is elevated for a short duration of time, can be immuno-stimulatory rather than immuno-suppressive. This study was designed to determine the effect of an induced cortisol release, via a dual corticotropin-releasing hormone (CRH) and vasopressin (VP) challenge, on changes in immune cell profiles of beef heifers. Four days before the challenge, 10 heifers (605 ± 13 kg) were fitted with indwelling jugular cannulas and indwelling vaginal temperature (VT) recording devices that measured VT continuously at 5-min intervals. On d 0, heifers were challenged IV with 0.3 µg/kg BW bovine CRH and 1.0 µg/kg BW bovine VP concurrently. Two whole blood samples were collected at 30-min intervals from -2 to 8 h relative to the challenge at 0 h. One vacutainer containing EDTA was collected for complete blood cell count (CBC) analysis and the second was collected in a 9-mL monovette serum tube. After collection, serum was isolated and stored at −80°C until analyzed for cortisol concentrations by ELISA. There was a time effect ($P < 0.001$) for VT, cortisol, and CBC variables. A multiphasic response was observed for VT, with VT initially increasing ($P = 0.05$; relative to 0 h) within 15 min post challenge. Serum cortisol concentrations increased ($P < 0.001$) immediately after the challenge, reaching maximum concentrations between 0.5 and 2 h post challenge, and then continuously decreasing until reaching baseline concentrations at 6 h post challenge ($P = 0.17$; 0 vs. 6 h). Total white blood cell and lymphocyte concentrations increased ($P < 0.001$) 2 h after CRH/VP challenge and remained elevated for the duration of the blood collection period. Monocyte concentrations initially decreased 1 h post challenge ($P < 0.001$), and returned to baseline concentrations by 2 h post challenge ($P = 0.08$; 0 vs. 2 h). In contrast, neutrophil concentrations decreased ($P = 0.02$) 3 h post challenge and remained decreased throughout the duration of the blood collection period. These data demonstrate that immune cell populations are influenced by an acute activation of the hypothalamic-pituitary-adrenal axis. Additionally, the increase in circulating concentrations of lymphocytes and decrease in circulating concentrations of neutrophils observed in this study are indicative of an immunological priming event that could be beneficial to the animal.

Key Words: acute stress, cortisol, immune response

0066 Investigating innate immune response differences between Angus and Holstein cattle with the dermal fibroblast model. A. L. Benjamin[*1], W. J. Weber[2], S. D. McKay[1], B. A. Crooker[2], and D. E. Kerr[1], *[1]University of Vermont, Burlington, [2]University of Minnesota, St. Paul.*

Individual immune responses to pathogens can be variable, depending on environmental, genetic, and possibly epigenetic influences. Holstein and Angus cattle are selectively bred and managed for different traits, which could impact disease susceptibility between these breeds. A dermal fibroblast model was used to investigate potential genetic and epigenetic influences on the innate immune response in each breed. Skin biopsies were collected from the shoulder area of 5 Holstein and 12 Angus 19-mo-old heifers. Fibroblasts were isolated by collagenase digestion and cryopreserved. Revived cells were challenged with LPS (100ng/ml; 24h) and levels of secreted IL-8 were determined. The Holstein cultures produced ~3 times more ($P < 0.01$; unpaired t test) IL-8 then the Angus cultures (2190 ± 600 vs. 650 ± 370 pg/ml, respectively). Total RNA was collected from 4 Angus and 4 Holstein cultures that were cultured in parallel and challenged with LPS for 0, 2, and 8 h. Whole transcriptome analysis was performed by RNA-seq with an average of 46 million reads per sample aligned to the UMD 3.1 reference genome by NextGENe software. Breed differences in gene expression were determined with the edgeR statistical package. Between breeds, there were 849, 1014, and 751 genes differentially expressed genes (FDR < 0.05, fold change > 2) at h 0, 2, and 8 post-LPS, respectively. Immune response genes, such as TNF-a at 2,h and IL-8 and CCL20 at 8 h, were induced 6.9-, 4.5-, and 8.6-fold more in Holsteins compared with Angus, whereas expression at 2 h of CXCL12 and TRAIP, an inhibitor of TRAF2-mediated NF-kB activation, were 7.4- and 2.7-fold higher in Angus. Additionally, a semi-quantitative assessment of global DNA methylation was performed by methylated CpG island recovery assay (MIRA-seq) on genomic DNA extracted from these cultures. Read alignment (44 million reads per sample) and differential methylation region (DMR) analysis were performed similarly to RNA-seq. The genome was analyzed in consecutive 3 kb regions and revealed 51 DMR (FDR < 0.1, fold change > 2). Of these, 35 were more methylated in Angus and 16 were more methylated in Holsteins. Relationships among these DMR and the differential gene expression are not readily apparent, but are being further investigated. Our results reveal breed differences in the LPS response of dermal fibroblasts isolated from Angus and Holstein heifers. Given that the cells were cultured side by side in controlled environmental conditions, the observed differences are likely due to a combination of genetic and epigenetic factors.

Key Words: epigenetics, variation

0067 Predictive models of lameness in dairy cows achieve high sensitivity and specificity with force measurements in 3 dimensions. J. T. Dunthorn[*1], R. M. Dyer[2], U. Tasch[3], N. Neerchal[3], P. Rajkondawar[4], and G. Steingraber[4], *[1]Step Analysis, Baltimore, MD, [2]University of Delaware, Newark, [3]University of Maryland, Baltimore County, Baltimore, [4]BouMatic, Madison, WI.*

Lameness remains a significant cause of production losses and a growing welfare concern across the dairy industry. Metabolic, nutritional, and housing factors interact to sustain a steady increase in the prevalence of lameness, driving a growing need for automated and continuous methods of lameness detection. A force-plate system restricted to the vertical (z) dimension yielded a high specificity but low sensitivity of detection. The objective of this study was to determine the effect of supplementing the vertical dimension with the transverse (x) and longitudinal (y) dimensions on detection accuracy. We used a parallel, force-plate system to measure the ground reaction forces (GRF) across 3 orthogonal directions (3D). The GRF for randomly selected cows ($n = 83$) were recorded and a clinical diagnosis of lameness was generated using locomotion score, lesion diagnosis, lesion score, and claw and interdigital integument pain score. Logistic regression was used to characterize the relationship between the clinical characteristics and GRF across all 3 orthogonal dimensions to generate a statistical algorithm for the probability of lameness. Misclassification error was estimated using a modification of the Leave-One-Out (LOO) method of cross validation. The LOO

Table 0067. Model performance using various combinations of measurement directions (1-degree, 4-knot spline transformation). Results have been ordered by increasing AUC

Measurement direction (including stance time)	TN	FP	FN	TP	Sensitivity	Specificity	AUC
x	213	44	94	45	0.32	0.83	0.59
z	212	45	87	52	0.37	0.82	0.62
x, z	210	47	61	78	0.56	0.82	0.73
y	218	39	77	62	0.45	0.85	0.75
y, z	222	35	53	86	0.62	0.86	0.79
x, y	221	36	50	89	0.64	0.86	0.83
x, y, z	239	18	14	125	0.90	0.93	0.98

x = transverse (medial-lateral) direction; y = longitudinal (cranial-caudal) direction; z = vertical (weight) direction.

cross validation trains the model using all but a single run. We modified LOO to leave out all runs except for those from a single cow, Leave-One-Cow-Out (LOCO), to use as the training data and tested the resulting model using the runs of the cow not used in model development. This preliminary study determined that 76 variables across all 3 dimensions resulted in a model with 90% sensitivity, 93% specificity, and 98% area under the receiver operating curve (AUC). Furthermore, all 3 dimensions were both necessary and sufficient to accurately establish the probability of lameness (Table 0067).

Key Words: animal welfare, lameness, 3-dimensional ground reaction forces

---

0068 Performance trends in commercial livestock populations in the United States before and subsequent to the inclusion of genetically modified feed in livestock diets. A. L. Van Eenennaam*, *University of California-Davis, Davis.*

The first genetically modified (GM) crops were planted in the United S in 1996; by 2000, GM soy and cotton comprised > 50% of U.S. land devoted to these crops. Adoption increased steadily thereafter and in 2013 a total of 93% of soy, 90% of cotton, and 90% of all corn grown in the United States were GM varieties. It is estimated that 70 to 90% of harvested GM biomass is fed to food-producing animals, making the world's livestock populations the largest consumers of the current generation of GM crops. It has been purported by some that GM feed has deleterious effects on underlying animal health. The United States feeds billions of livestock each year, providing a very large uncontrolled GM feeding field data set. Considering that animal health is critical to optimizing production performance and animal production systems are managed to minimize disease, it would be reasonable to hypothesize that if animal feed derived from GM crops had deleterious effects on the billions of animals that have been fed on diets containing predominantly GM feed, then animal performance and health attributes in these large populations would have been negatively impacted. To test this hypothesis, data on livestock productivity and health (somatic cell count, percent mortality, percent postmortem carcass condemnation) were collated from publicly available sources for 2 time periods: 1983–1994, before the introduction of GM crops in 1996, and 2000–2011, a period with high levels of GM feed based on high rates of U.S. adoption and international trade of GM crops. These data on broilers, dairy and beef cattle, and swine revealed improving productivity and animal health trends. Productivity improvements in all livestock species continued in the positive direction they were trending before the introduction of GE feed, often at an accelerated rate ($P < 0.05$), and health parameters also improved over time. Available mortality and carcass condemnation data suggest that these rates actually decreased during the 2000–2011 time period when high levels of GM ingredients would be expected to be present in livestock feed. Field data sets representing billions of observations do not reveal disturbing trends in U.S. livestock health and productivity data. These data are in agreement with the many peer-reviewed, controlled animal feeding studies that have reported no biologically relevant difference between the nutritional attributes and safety of feed from GM plants, as compared with feed derived from conventional crop varieties.

Key Words: animal health, feed, genetically modified, GMO

0069 Evaluation of a Brix refractometer to estimate serum immunoglobulin G concentration in neonatal dairy calves. S. M. Deelen[1], T. L. Ollivett[1], D. M. Haines[2], and K. E. Leslie*[1], *[1]University of Guelph, ON, Canada, [2]University of Saskatchewan, Saskatoon, Canada.*

The objective of this study was to evaluate the utility of a digital Brix refractometer for the assessment of success of passive transfer of maternal immunoglobulin, as compared with the measurement of serum total protein (STP) by refractometry. Blood samples (n = 400) were collected from calves 3 to 6 d of age. Serum IgG concentration was determined by radial immune-diffusion (RID) and STP and percent Brix (%Brix) using a digital refractometer. The mean (± SD) IgG concentration was 24.1 ± 10.0 g/L, with a range from 2.1 to 59.1 g/L. The mean STP concentration was 6.0 ± 0.8 g/dL, with a range from 4.4 to 8.8 g/dL. The mean %Brix concentration was 9.2 ± 0.9%, with a range of 7.3 to 12.4%. Brix percentage was highly correlated with IgG [correlation coefficient (r) = 0.93]. Test characteristics were calculated for the assessment of failure of passive transfer (FPT; serum IgG < 10 g/L). The sensitivity and specificity of STP at 5.5 g/dL were 76.3% and 94.4%, respectively. However, it is noteworthy that relatively few samples had IgG levels < 10 g/L. As such, further evaluations of different populations are warranted. A receiver operating characteristic curve was created to plot the true positive rate against the false positive rate for consecutive %Brix values. The optimal combination of sensitivity (88.9%) and specificity (88.9%) was at 8.4% Brix. Serum total protein was also positively correlated with %Brix (r = 1.00) and IgG (r = 0.93). The results of the current project suggest that dairy producers can successfully monitor their colostrum management and the overall success of passive transfer using a digital Brix refractometer to estimate IgG concentration of colostrum and calf serum.

Key Words: calf, passive transfer, refractometer

0070 Associations of serum haptoglobin in newborn dairy calves with future health, growth, and mortality up to 4 mo old. C. F. Murray[1], C. Windeyer[2], T. F. Duffield[1], K. M. Waalderbos[1], and K. E. Leslie[*1], *[1]University of Guelph, ON, Canada, [2]University of Calgary, AB, Canada.*

The objective of this research was to investigate factors associated with serum haptoglobin (Hp) levels in newborn calves. In addition, the associations between serum Hp levels in newborn calves with future growth, morbidity, and mortality in calves up to 4 mo of age were investigated. A total of 1365 Holstein heifer calves from 15 dairy farms were enrolled in this study during 2008. Following calving, a birth record was completed, including information on the calving event, colostrum administration, and other details. During weekly farm visits, each calf was assessed at 1 to 8, 15 to 21, 36 to 42, and 90 to 120 d of age. At these times, each calf was assessed using a standardized clinical score for general health and height and weight were measured. At the first sampling event, a blood sample was collected for the determination of serum total protein and Hp. Treatment events and death loss were recorded by the farm staff throughout the study. Data analysis was conducted using a multivariable linear regression model to evaluate associations of explanatory variables with serum Hp. Separate multivariable logistic models were used to determine associations of various factors with treatment for disease and mortality. Serum Hp concentration in the first week of life was not significantly associated with the degree of calving difficulty. However, serum Hp was higher in calves with a higher rectal temperature and depressed attitude at the first sampling event. Calves with higher Hp in their first week of life had a significantly higher total health score throughout the entire sampling period. Haptoglobin was not significantly associated with ADG or treatment for bovine respiratory disease. Yet, for every 1 g/L increase in serum Hp in the first week of life, the odds of being treated for any other disease during the study period increased by 7.6 times. In addition, Hp concentration in the first week of life was associated with mortality in calves up to 4 mo of age. The optimal cut point for Hp was determined to be 0.13 g/L for the prediction of disease and death, although the sensitivity of Hp concentration as a diagnostic test for individual calves was low. Monitoring serum Hp in the first week of life shows considerable promise at the group level for overall assessment of calving management and the impact of calving events on future health and mortality.

Key Words: haptoglobin, health, mortality

0071 Dynamics of culling for Jersey, Holstein, and crossbred cows in large multi-breed herds. P. J. Pinedo[*1], A. Daniels[2], J. Shumaker[3], and A. De Vries[4], *[1]Texas A&M AgriLife Research, Amarillo, [2]Circle H Headquarters LLC, Dalhart, TX, [3]Magnolia Veterinary Services, Amarillo, TX, [4]University of Florida, Gainesville.*

The objective of this observational study was to describe and compare the dynamics of reason-specific culling risk for the genetic groups Jerseys (JE), Holsteins (HO), and Jersey × Holstein crossbreds (JH), considering parity, stage of lactation, and milk yield, among other variables, in large multi-breed dairy herds in Texas. The secondary objective was to analyze the association between survival and management factors, such as breeding and replacement policies, type of facilities, and use of cooling systems. After edits, available data included 202,384 lactations in 16 herds, ranging from 407 to 8773 cows calving per year during the study period from 2007 to 2011. The distribution of lactation records by genetic group was 58%, 36%, and 6% for HO, JE, and JH, respectively. Overall culling rates across breeds were 30.1%, 32.1%, and 35.0% for JH, JE, and HO, respectively. The dynamics of reason-specific culling were dependent on genetic group, parity, stage of lactation, milk yield, and herd characteristics. Early lactation was a critical period for "died," and "injury-sick" culling. The risk increased with days after calving for "breeding" and, in the case of HO, "low production" culling. Open cows had a 3.5 to 4.6 times greater risk for overall culling compared with pregnant cows ($P < 0.01$). The odds of culling with reason "died" within the first 60 d in milk (DIM) were not significantly associated with genetic group. However, both JE and JH had lower odds of live culling within the first 60 DIM compared with HO cows [OR = 0.72 ($P < 0.001$) and 0.82 ($P = 0.002$), respectively]. Other cow variables significantly associated with the risk of dying within the first 60 DIM were cow relative 305 mature equivalent (MEQ) milk yield, parity, and season of calving. Significant herd-related variables for death included herd size and origin of replacements. In addition to genetic group, the risk of live culling within 60 DIM was associated with cow relative 305 MEQ milk yield, parity, and season of calving. Significant herd-related variables for live culling included herd relative 305 MEQ milk yield, herd size, type of facility, origin of replacement, and type of maternity. Overall, reason-specific culling followed similar patterns across DIM in the 3 genetic groups.

Key Words: culling, death, Holstein, Jersey

0072 Relationship of ocular and rectal temperatures to indicators of stress in mature horses.

M. J. Anderson*, J. L. Lucia, K. J. Stutts, M. M. Beverly, and S. F. Kelley, *Sam Houston State University, Huntsville, TX.*

Rectal temperature has commonly been used as an indicator of health in many species of livestock, including horses. However, collection of a rectal temperature can be difficult and stressful on the animal. New technology, such as thermal imaging cameras, have recently become more prevalent and have been used to collect the body temperature of animals at other, less-invasive sites, including the ocular globe. The objective of this research was to determine the relationship between rectal temperature and ocular temperature, and to evaluate the efficacy of these measurements as indicators of the stress level of horses. To accomplish this, ocular temperature (OT), rectal temperature (RT), neutrophil count, lymphocyte count, heart rate (HR), and respiration rate (RR) were recorded before and during an immune challenge, using a novel vaccination of 30 mature horses (413 to 551 kg and 5 to 10 yr). Neutrophil to lymphocyte ratio (N:L) has been shown to be a good indicator of systemic inflammation and overall stress in an animal, and was used as the primary indicator of stress in this study. To determine the relationship between temperatures and among indicators of stress, the PROC CORR procedure of SAS was used. The relationship between OT and RT was found to have a weak correlation ($r = 0.37$; $P < 0.01$), illustrating that OT is not a good substitute for traditional RT measurements. Additionally, OT had very little relationship with N:L ($r = -0.01$; $P = 0.94$), HR ($r = 0.19$; $P = 0.31$), or RR ($r = 0.17$; $P = 0.38$). While still very weak, RT had stronger relationships than OT with N:L ($r = -0.11$; $P = 0.40$) and RR ($r = 0.26$; $P = 0.17$) and a similar correlation to HR ($r = 0.19$; $P = 0.31$). Of all the non-invasive measurements (OT, HR, and RR), RR had the strongest correlation to N:L as an indicator of systemic stress, ($r = -0.24$; $P = 0.21$). While OT is less invasive than RT, a direct measurement of OT is not a reliable predictor of RT in an animal. Still, it may hold some value to livestock and wildlife producers due to its ease of measurement, but without further investigation into the relationship of OT and indicators of stress, its utility remains limited.

Key Words: ocular temperature, rectal temperature, stress

0073 Enhancement of the acute phase response to lipopolysaccharide in feedlot steers supplemented with OmniGen-AF.

N. C. Burdick Sanchez*[1], J. O. Buntyn[2], J. A. Carroll[1], T. Wistuba[3], K. DeHaan[3], S. E. Sieren[4], S. J. Jones[4], and T. B. Schmidt[4], *[1]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [2]Department of Animal Science, University of Nebraska, Lincoln, [3]Prince AgriProducts Inc., Quincy, IL, [4]University of Nebraska, Lincoln.*

This study was designed to determine the effect of supplementing feedlot steers with OmniGen-AF on the acute phase response to a lipopolysaccharide (LPS) challenge. Steers ($n = 18$; 270 ± 5 kg BW) were separated into 2 treatment groups ($n = 9$/treatment): 1 group was fed a standard receiving diet (Control, Cont) and the other group was fed the same receiving diet supplemented with OmniGen-AF at 4 g/45.4 kg BW for 29 d (OmniGen-AF). On d 27, steers were fitted with indwelling jugular cannulas and rectal temperature (RT) monitoring devices, and placed in individual stalls. On d 28, steers were challenged IV with LPS (0.5 μg/kg BW at 0 h). Sickness behavior scores (SBS) and 2 whole blood samples were collected at 30-min intervals from -2 to 8 h relative to the challenge at 0 h. One vacutainer containing EDTA was collected for complete blood cell count (CBC) analysis and the second was collected in a 9-mL monovette serum tube; after collection, serum was isolated and stored at −80°C until analyzed for cortisol and cytokine concentrations. Rectal temperature, SBS, and cortisol were affected by time ($P < 0.001$). Before the challenge, RT was greater ($P < 0.001$) in Cont steers (39.31 ± 0.03°C) than OmniGen-AF steers (39.14 ± 0.03°C). Therefore, post-challenge RT was analyzed as the change in response from baseline values. The change in RT relative to baseline values increased ($P < 0.001$) in both groups in response to LPS challenge but was not affected by treatment ($P = 0.49$). Sickness behavior scores increased ($P < 0.001$) after LPS challenge and tended ($P = 0.09$) to be greater in Control (1.57 ± 0.02) than OmniGen-AF steers (1.51 ± 0.02). Cortisol concentrations were affected by treatment ($P = 0.005$) and time ($P < 0.001$). For both groups, cortisol increased ($P < 0.001$) in response to LPS challenge. Cortisol was greater in Cont (29.2 ± 0.9 ng/mL) than OmniGen-AF steers (25.5 ± 0.9 ng/mL). White blood cell and lymphocyte concentrations were greater ($P \leq 0.004$) in Cont than OmniGen-AF steers throughout the study. Neutrophils were decreased ($P = 0.04$) in Cont steers (0.7 ± 0.2 K/uL) compared with OmniGen-AF steers (1.3 ± 0.2 K/uL) before the LPS challenge. There was a treatment ($P \leq 0.02$) and time ($P < 0.001$) effect for tumor necrosis factor-α (TNFα) and interferon-γ (IFNγ). Specifically, TNFα and IFNγ concentrations increased ($P < 0.001$) in response to LPS challenge. Furthermore, concentrations of TNFα and IFNγ were decreased in ($P \leq 0.02$) in Cont steers compared with OmniGen-AF steers. These data suggest that OmniGen-AF supplementation served to prime the immune

system before the LPS challenge, allowing for an enhanced response to LPS challenge.

Key Words: cattle, immune response, OmniGen-AF

0074 Age-dependent changes in heifer fibroblast DNA methylation and LPS-induced gene expression.

B. B. Green*, S. D. McKay, and D. E. Kerr, *University of Vermont, Burlington.*

To determine how the innate immune response develops in dairy calves, dermal fibroblasts were isolated from 15 heifers at 3 stages of development (5, 11, and 16 mo of age) and challenged with 100 ng/ml of lipopolysaccharide (LPS) for 36 h. The secretion of interleukin- (IL) 8 protein into media in response to LPS increased significantly ($P < 0.01$) at each age as measured by a paired 1-way ANOVA with average IL-8 levels of 300 ± 220, 1340 ± 530, and 1750 ± 560 pg/ml at 5, 11, and 16 mo, respectively. To investigate a potential involvement of DNA methylation in this differential responsiveness, cultures from 3 of these animals obtained when they were young (5 mo) and older (16 mo), underwent DNA de-methylation through exposure to 10mM 5-aza-2'-deoxycytidine (AZA) for 4 d before 24-h LPS exposure ($n = 3$/group). The AZA treatment abolished the differential IL-8 response to LPS seen under control conditions ($P < 0.01$), primarily due to an increase in production by the young cultures (control young vs. old 240 ± 20 vs. 1350 ± 290 pg/ml, respectively; AZA Young vs. Old 1580 ± 50 vs. 1690 ± 70 pg/ml, respectively). The role of DNA-methylation in the gene expression response to LPS was further investigated by comparing the findings of methylated -CpG island recovery assay (MIRA-seq) on DNA from 3 pairs of young and older cultures to RNA-seq findings on the same cultures at 0, 2, and 8 h post-LPS exposure. The resulting libraries averaged 71 and 49 million reads per sample for RNA-seq and MIRA-seq, respectively. Sequence reads were aligned to the UMD3.1 reference genome using NextGENe software and expression and methylation analysis were performed with EdgeR. The overall response to LPS was robust with 617 and 414 genes displaying differential expression (> twofold difference; FDR < 0.05) at h 2 and 8, respectively, as compared with h 0. Older cultures had greater expression than younger cultures of many immune-associated genes, such as IL-8, IL-6, TNF-a, and CCL20 at 2 h post-LPS exposure (5.8-, 10.5-, 10.4-, and 18.1-fold, respectively). In addition, whole genome MIRA-seq analysis of consecutive 3 kb regions identified 20 differentially methylated regions between young and older cultures (> twofold difference; FDR < 0.1). Further analysis of these candidate regions is being conducted to determine how DNA methylation changes within animals over time and its potential role in development of the innate immune response.

Key Words: epigenetics, innate immunity, methylation

0075 Effect of trace mineral supplementation on clinical signs, immune response variables, and mineral balance of calves following exposure to bovine viral diarrhea virus and subsequent *Mannheima haemolytica* infection.

B. K. Wilson*[1], G. I. Zanton[2], D. L. Step[1], R. W. Fulton[1], A. W. Confer[1], C. L. Maxwell[1], C. A. Gifford[1], C. R. Krehbiel[1], and C. J. Richards[1], *[1]Oklahoma State University, Stillwater, [2]Novus International, Inc., St. Charles, MO.*

The objective was to determine the influence of copper, manganese, and zinc supplementation on the clinical signs, immune response variables, and mineral balance of calves, following a bovine viral diarrhea virus (BVDV) and *Mannheima haemolytica* (MH) immune challenge. Steers ($n = 16$; BW = 225 ± 20 kg) from a single ranch were processed, weaned, and randomly pairwise assigned to either the mineral supplemented (MIN) or control (CON) experimental treatments. The MIN calves received 150 mg of Cu, 130 mg of Mn, and 360 mg of Zn daily, whereas CON calves received the basal diet with no additional Cu, Mn, or Zn supplementation. The basal diet contained sufficient Mn and Zn, but inadequate Cu based on published nutrient requirements. After 46 d on the experimental treatments, all calves were naturally exposed to BVDV type 1b for 4 d and subsequently infected with *MH*. Data were analyzed using the GLM procedure of SAS with sampling time serving as a repeated measure. Calf served as the experimental unit. The immune challenge was validated via increased ($P < 0.001$) BVDV antibody titers, MH whole cell (WC) and leukotoxin (LKT) antibody titers, rectal temperatures (TEMP), and subjective clinical scores (CS). A time by treatment interaction was observed for BVDV and MHWC antibody titers ($P \leq 0.04$). Calves receiving MIN had reduced ($P = 0.03$) BVDV antibody titers but increased ($P = 0.02$) MHWC antibody titers compared with CON calves. Mineral supplementation did not impact CS, TEMP, or MHLKT antibody titers ($P \geq 0.48$). There was a significant ($P < 0.001$) time by treatment interaction observed for liver Cu levels. Time significantly impacted the concentrations of Cu, Mn, Fe, and Zn within the liver and Cu, Zn, and Fe within the muscle and serum ($P \leq 0.03$). Calves receiving MIN had greater liver Cu ($P < 0.001$) and Mn ($P = 0.04$) concentrations compared with CON calves. In contrast, serum Cu concentrations were increased ($P = 0.02$) in CON calves compared with MIN calves. Mineral supplementation did not impact mineral levels within the muscle samples ($P \geq 0.20$). The supplementation of Cu, Mn, and Zn may potentially impact the antibody response to a BVDV and MH immune challenge in calves. When Cu is supplemented to calves receiving a marginally Cu deficient diet, Cu status within the body can be altered.

Key Words: bovine respiratory disease, mineral supplementation, immune challenge

ANIMAL HEALTH SYMPOSIUM II: OPTIMIZING DISEASE RESPONSE MODELING

0076 Understanding animal-to-animal variation in disease management. D. E. Kerr*, *University of Vermont, Burlington.*

A long-term goal of animal health research is to understand causes of animal-to animal variation in innate immune function, such that this knowledge can be applied to breeding, selection, management, or other strategies to generate animals with enhanced disease resistance. Key to this research is an accurate determination of phenotype. However, variation in expression of the phenotype due to differing environmental conditions, including differing physiological states of the animal, confound the ability to accurately compare animal-to animal responses, except under well-defined experimental conditions. The range of infection responsive phenotypes is quite likely dependent on underlying genetic variation that gives much promise to finding genetic markers for use in breeding programs. However, the evolving field of epigenetics suggests that in utero and early life environments can have significant effects on gene expression. Model systems to evaluate variation in the innate immune response may assist in more accurate determination of phenotype to enable detection of genetic or epigenetic biomarkers. These model systems may also be of use in testing immature animals for a prediction of adult performance. An example of a model system is the in vivo endotoxin (LPS) challenge that has been used to identify hyper responder animals. Another approach is the dermal fibroblast model in which substantial animal-to-animal variation has been revealed by how their fibroblasts respond to an in vitro LPS challenge. In this model, the cells are cultured under controlled conditions for several passages to limit environmental effects in an attempt to reveal underlying genetic or epigenetic causes for animal variation. Future studies using these and other model systems, combined with well-controlled disease challenges of extreme phenotypes, will lead to a greater understanding of factors contributing to variation in disease resistance.

Key Words: epigenetics, innate immunity, LPS

0077 Can the genetic selection for improved immune response be tailored to expand the efficacy of disease management interventions. B. Mallard*, *Department of Pathobiology, OVC, University of Guelph, ON, Canada.*

Infectious diseases are costly to all aspects of domestic animal management, care, and well-being across all aspects of husbandry, including companion, food, and sport animals. One aspect of animal health, however, serves as both an intriguing puzzle and an opportunity to exploit the basis for the puzzle. That aspect encompasses the underlying cause for some animals to be devastated by an infecting organism that another might only be minimally affected by. Observations of cattle resistant to natural infections have implied the feasibility of breeding livestock for disease resistance. Studies of pigs selected for antibody- (AMIR) and cell- (CMIR) mediated immune responses have demonstrated increased immune responsiveness, suggesting enhanced protection by both type 2 and type 1 responses, respectively. Additionally, natural or artificial infections of cattle suggest that the production of particular IgM, IgG1, and IgG2 isotypes are important for protecting against pathogens. In fact, IgG1/IgG2 ratios are often used to establish whether type 1 (CMIR) or type 2 (AMIR) responses predominate following immunization or infection. With this in mind, this presentation will address novel aspects of animal-to-animal variability in adaptive immune response, as well as some newer findings in the rapidly expanding area of epigenetics and chromatin modifications, and present both new findings, as well as suggestions for promising areas of research out of which may result better strategies toward maintaining animal health.

Key Words: cattle, immunity, phenotype

0078 Selecting pharmacological interventions through rapid screening motifs and proper cell models. E. Zudaire*, *NIH-NCI, Bethesda, MD.*

There is no doubt that the magnitude and complexity of challenges to pharmacological intervention in disease processes are increasing exponentially. These challenges span all facets of intervention from countering antimicrobial resistance to expanding the pharmacogenomic capacity toward individualizing therapy and prevention. While the drug development landscape is rapidly evolving, current pipelines to approval and applied medicine often rely on well-established compartmentalized research models. In this rubric, targets are first identified in laboratories, frequently on the basis of the now discredited philosophy of "disease-causing" targets. More appropriately, target-specific therapeutics are capable of being designed with the goal of increasing efficacy while better managing undesirable toxicities. However, it has recently been proposed that target-based approaches often fail under clinical trials due in part to the robust nature of networks that control biological processes. The issue is 1 of having the needed target specificity as screenable with high throughput cell-based assessment models, where those models accurately reflect the complexity of in vivo cell-cell interactions and associated gene expression patterns, largely now in evidence in traditional 2D monoculture conditions. The goal is then to connect diseases with underlying pharmacologically tractable targets and drugs that can be translated for their clinical management. To this aim, I will present the case for increasing research into novel technological approaches based on the hypothesis that the most effective therapies for a given disease

would target a complex set of interactions among different components of the system, rather than the activity of a single component. I will expand on how the discovery of effective disease therapeutic modulators requires the development of novel kinds of in vitro assays, which recapitulate the complexity of disease-specific tissue microenvironments.

Key Words: disease, intervention, pharmacogenomics

0079 Managing animal health from an aquaculture perspective. C. A. Shoemaker*, B. R. LaFrentz, D. Xu, and D. Zhang, *USDA-ARS, Aquatic Animal Health Research Unit, Auburn, AL.*

Aquaculture is the production of aquatic animals for food. The aquaculture industry is a rapidly expanding segment of U. S. agriculture and NOAA estimated the industry was worth $1.2 billion in 2011. Disease-related losses in aquaculture either by decreased performance and/or mortality is estimated by the World Bank to be around $3 billion globally. In 1974, Snieszko proposed the host-pathogen-environment relationship theory as applied to fish with regard to development of disease. Age, species, strain(s), nutritional, and immunological status of the host are relevant to disease induction. The pathogen, including exposing dose, virulence, and genetic type (strain), is also pertinent to disease in aquatic animals. For aquatic animals, the environment is probably the most important factor in relation to disease development. Fish are produced in all types of water (i.e., fresh, brackish, and salt water) and fish must rely on water for temperature regulation, oxygen, waste removal, etc., for optimal performance and health. Aquatic animal health management is unique due to the fact that animals are reared in water. Disease can be difficult to discover in water. Once disease is identified, treatment can be problematic because of the size of ponds and/or volume of water. Also, limited treatment options are available due to the fact that few medicines are FDA approved. In some aquaculture operations (e.g., catfish production), all sizes of fish may be raised together in a multi-batch culture. Therefore, separation of healthy and sick animals is challenging. Prevention is the key to successful health management of fish and should include good husbandry practices to limit stress, providing adequate balanced nutrition, use of vaccines, and prudent use of medicines. This presentation will highlight the unique aspects of aquatic animal health management and outline areas where further work may improve our understanding of animal health.

Key Words: aquaculture, fish, health management

ANIMAL HEALTH II: HOST–MICROBIAL INTERACTIONS: DETECTION AND INTERVENTION

0080 Alterations in the response of pigs to *Salmonella typhimurium* when provided *Enterobacter cloacae*. J. R. Donaldson*[1], J. A. Carroll[2], N. C. Burdick Sanchez[2], J. W. Dailey[2], T. B. Schmidt[3], T. R. Callaway[4], and J. G. Wilson[1], *[1]Mississippi State University, Mississippi State, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]University of Nebraska, Lincoln, [4]USDA-ARS, College Station, TX.*

Weanling pigs are at risk of succumbing to illness due to an immature immune system and insufficient supply of available energy at the time of weaning. Recent evidence has suggested that providing pigs with *Enterobacter cloacae* can increase the concentration of circulating triglycerides (TAG) and thus available energy. To determine if this increase in TAG improved the response of pigs to an infection, 36 weaned pigs 30 d of age (6.7 ± 0.1 kg BW) were individually housed and randomly assigned to 3 treatment groups: 1) *Enterobacter cloacae* (JD6301; 1×10^{10} CFU); 2) an alternate form of this bacterium (JD8715; 1×10^{10} CFU) that secretes TAG into the surrounding environment; or a control of PBS. For each treatment, bacteria were supplemented to the water daily using a medicator water system (~1×10^6 CFU/mL). Pigs were provided water supplemented with *E. cloacae* for 5 d before and 3 d after in relation to being challenged with lipopolysaccharide (LPS) from *Escherichia coli* (25 ug/kg BW, time 0 h) and *Salmonella typhimurium* (1×10^9 CFU, time 6 h). Serum samples were collected every 6 h for a period of 72 h and analyzed for NEFA, TAG, and whole blood cell counts. At 24, 48, and 72 h post-challenge, gastrointestinal contents were collected and analyzed for the presence of *E. cloacae* and *S. typhimurium*. Circulating TAG increased ($P = 0.05$) in pigs provided JD6301 in comparison with PBS controls within 5 d of supplementation but did not increase ($P = 0.33$) in pigs provided JD8715. Within 18 h post-challenge with LPS (and 12 h post-challenge with *S. typhimurium*), an increase in NEFA ($P < 0.05$) and TAG ($P < 0.04$) was observed in pigs provided PBS in comparison with pigs provided either form of *E. cloacae*. Pigs provided JD6301 had a reduction ($P = 0.05$) in *S. typhimurium* populations between 24 and 72 h post-challenge. However, *S. typhimurium* populations in pigs provided either JD8715 or PBS did not decrease ($P = 0.18$) during this time period. Pigs provided JD8715 did have an increase ($P = 0.05$) in neutrophil concentrations within 6 h post-exposure to the endoxotin. These data suggest that the oleaginous bacteria JD6301 may improve clearance of *S. typhimurium* from the gastrointestinal tract. Further research is needed to determine whether this decrease is due to an improved immune response or competitive inhibition.

Key Words: pigs, probiotics, triglycerides

0081 Adhesion of *Escherichia coli* in piglets and association of phenotypes to known candidate genes in South African breeds. N. S. Chaora*, *Agricultural Research Council, Pretoria, South Africa.*

Enterotoxigenic *Escherichia coli* is a major pathogenic bacterium that causes diarrhea in preweaned and postweaned piglets. The adhesion of *E. coli* to the brush borders of the epithelial cells of piglets is a prerequisite for effective colonization leading to diarrhea. Successful adhesion occurs in the presence of *E. coli* receptors that are found on the brush borders of epithelial cells. The study's objective was to compare the susceptibility of South African breeds to enterotoxigenic *E. coli* strains. An in vitro adhesion experiment was performed for F4, PAA, and EAST-1 *E. coli* strains, using intestinal brush borders from 109 pigs of 3 South African pig breeds. Large White, indigenous, and crossbred pigs that were 3- to 12-wk old were used. The results showed significant differences ($P < 0.05$) in adhesion frequencies of receptors among the 3 breeds. Adhesion phenotypes, adhesive, weakly adhesive, and non-adhesive were found in all breeds. The F4 and PAA strains adhered in all 3 breeds. The indigenous pigs had the highest frequency of non-adhesive intestines and > 70% of the Large White pigs were adhesive to all strains. Indigenous and crossbred pigs' adhesion was higher in suckling piglets than weaners. The *TFRC*, *MUC13*, *MUC4*, and *MUC20* genotypes were not associated with adhesion phenotypes. The South African population studied carried receptors for all strains measured. If there is an outbreak of *E. coli* carrying the above strains, the South African population is most likely to be affected. The indigenous pigs of the South African population studied were more resistant to F4, PAA, and EAST-1 *E. coli* strains, compared with Large White and crossbred pigs.

Key Words: adhesion, *E. coli* strains, piglets, susceptibility

0082 Effect of metaphylaxis on production responses and antimicrobial usage in high-risk steers. A. B. Word*[1], T. A. Wickersham[1], G. Mays[1], L. A. Trubenbach[1], and J. E. Sawyer[2], *[1]Texas A&M University, College Station, [2]Texas AgriLife Research, College Station.*

A trial was conducted to determine the effects of on-arrival metaphylaxis in beef cattle for controlling bovine respiratory disease (BRD) and determining subsequent effects on health and performance. Male calves in a randomized complete block design ($n = 198$, arrival weight = 231 kg ± 2.43) received either 3.3 mL/100 kg (6.6 mg/kg) ceftiofur crystal-

line free acid (EXC), 4.4 mL/100 kg (13.2 mg/kg) tilmicosin phosphate (MIC), or were not treated (CON). These products are commonly used in production settings. Cattle receiving metaphylaxis had 25.2% lower morbidity rates than CON (P = 0.01; 51.5% vs. 76.7%). Significant differences were not observed in morbidity rates (P = 0.14) between cattle on the MIC (46.4% ± 4.32%) or EXC treatments (56.5% ± 4.32%). Of cattle requiring BRD therapy, the CON group displayed symptoms ~5 d earlier than cattle in the metaphylaxis group (P = 0.01). Cattle displaying BRD symptoms in the MIC group required treatment 3 d earlier than those in the EXC group (P = 0.02, 8 vs. 11 d, respectively). Metaphylaxis improved ADG (1.63 vs. 1.28 kg/d; P = 0.06) and G:F (0.29 vs. 0.22, P = 0.01) during the first 14 d compared with CON, but differences between EXC and MIC were not significant (P > 0.40) during the first 14 d. Despite differences at 14 d, no differences were observed in ADG (P = 0.20) or G:F (P = 0.18) between CON and treatment groups across the 42-d trial. Total antimicrobial usage was 6.03 vs. 6.16 g active ingredient per animal for CON vs. metaphylaxis (P = 0.88), and 5.99 vs. 6.33 for MIC vs. EXC (P = 0.74). These results suggest that both tilmicosin phosphate and ceftiofur crystalline free acid effectively reduce overall morbidity and delay onset of clinical illness in newly received beef cattle. Furthermore, this reduction in overall morbidity was achieved with minimal increase in total antimicrobial use. While overall performance outcomes were not different, animal health was improved with metaphylaxis.

Key Words: bovine respiratory disease, metaphylaxis

0083 PR-39 ameliorates *Salmonella typhimurium*-induced intestinal epithelial barrier dysfunction.

X. Xi*, *Institute of Feed Science, Zhejiang University, Hangzhou, China.*

Salmonella enterica Serovar typhimurium infection is a primary enteric pathogenic disease affecting both human and animals. PR-39 is a porcine antimicrobial peptide that shows strong antibacterial effects toward *Salmonella typhimurium* in vitro and multiple immunomodulation functions. Here we investigated the potential mechanisms of PR-39 in preventing *Salmonella typhimurium*-induced gut barrier dysfunction in mouse infection model and in polarized intestinal porcine epithelial cell line IPEC-J2. The intestinal permeability, the expression of tight junction proteins, and biodistribution of PR-39 were determined by using chamber, immunofluorescence, qRT-PCR, and in vivo fluorescence imaging technology, respectively. One-way ANOVAs were performed using a 95% confidence interval. The results revealed that PR-39 attenuated the altered ileum architecture and reduced the increased intestinal permeability in *Salmonella*-infected mice. These protective effects were not attributed to the antibacterial activity of PR-39 because PR-39 showed no antimicrobial activity against *Salmonella typhimurium* in simulated intestinal liquids or serum. Moreover, pre-treatment with PR-39 significantly reduced the adhesion and invasion of *Salmonella typhimurium* toward polarized IPEC-J2 monolayer, and attenuated the decreased ZO-1 and claudin-1 expression caused by *Salmonella* infection. Collectively, these findings provide evidence that PR-39 could prevent *Salmonella typhimurium*-induced intestinal epithelial barrier dysfunction through an antimicrobial-independent mechanism.

Key Words: intestinal epithelial barrier function, PR-39, *Salmonella typhimurium*

0084 Quantification of microbial populations in organic and inorganic dairy cattle bedding materials.

R. F. Rowbotham*[1,2], T. L. Peters[2], T. M. Walker[2], and P. L. Ruegg[2], *[1]Grande Cheese Company, Brownsville, WI, [2]Department of Dairy Science, University of Wisconsin-Madison, Madison.*

The objective of this study was to quantify differences in microbial populations of 4 different bedding types used in dairy barns: 1) deep-bedded, new sand (NS), 2) deep-bedded, recycled sand (RS), 3) deep-bedded organic solids (DBOS), and 4) shallow-bedded organic solids on top of mattresses with foam cores (SBOS). Weekly composite bedding samples were systematically collected from selected locations within randomly selected stalls in each of 4 identical pens containing 32 freestalls and ~28 lactating cows during the 49-wk study period. Microbial populations were determined by plating 10-µL inoculations of duplicate sets of serial dilutions (10^{-1} to 10^{-5}) on 3 selective media. Bacterial groups were quantified as: Gram-negative (total growth on MacConkey's agar), coliforms (lactose-positive colonies on MacConkey's agar), *Klebsiella* (red to pink colonies on MacConkey inositol-carbenicillin agar), and Streptococci spp. (total growth on Edward's modified medium agar). The relationship between bacterial populations and bedding type was analyzed in a repeated measures model using PROC MIXED (SAS 9.3). The model included effects of bedding type with sampling date repeated. $Y_i = \alpha + \beta_1 X_{i1} + \beta_2 X_{i2} + e_i$ where Y_i is the $\log_{10}$ CFU count for bedding sample i from pen X_{i1} and date X_{i2}. Bacterial counts differed among bedding materials. Fewer bacteria were isolated from NS as compared with other bedding materials, with the exception of *Klebsiella* in SBOS and Streptococci spp. in DBOS. More bacteria were isolated from DBOS compared with other bedding materials, except for Streptococci spp. in sand bedding. Distribution of bacteria varied among bedding types. In general, NS had the fewest bacteria, whereas DBOS contained the most bacteria.

Key Words: bacteria, bedding, dairy

Table 0084. Bacteria isolated from different dairy cattle bedding types (Log_{10}CFU/g)

Bedding material	Gram-negative	Coliform	*Klebsiella*	Streptococci spp.
NS	4.72[a]	3.59[a]	2.41[a]	6.88[a]
RS	5.25[b]	4.10[b]	3.19[b]	7.21[b]
SBOS	5.81[c]	4.08[b]	2.74[ab]	8.16[c]
DBOS	6.83[d]	5.70[c]	5.05[c]	7.08[ab]

[a,b,c,d]Values with different letters in the same column differ significantly ($P \leq 0.02$).

0085 Prevalence of bovine mastitis pathogens in bulk tank milk. Y.-L. Bi[*1], Z. J. Cao[1], W. Sun[2], Y. Qin[2], and S. L. Li[1], *[1]State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, [2]Laboratorios Hipra, Gerona, Spain.*

Bovine mastitis is the most significant disease of dairy herds that can cause huge economic losses in the world. The objective of this study was to assess the bacteriological quality of bulk tank milk at herd level. Bulk tank milk samples collected from 894 dairy herds in Inner Mongolia (375), Heilongjiang (242), and Hebei Province (277) of China were examined for the presence of mastitis pathogens from March 2012 to May 2013. Each sample was tested using a previously validated Multiplex PCR assay for the detection of 12 pathogens at a time. In addition, a maximum of 21 samples were examined simultaneously using the Multiplex PCR assay. Contagious pathogens, including *Streptococcus agalactiae* (90.16%), Coagulase negative staphylococci (89.17%), *Streptococcus dysgalactiae* (71.14%), *Arcanobacterium pyogenes* (60.51%), *Staphylococcus aureus* (44.85%), and environmental pathogens, consisting of Coliforms (63.26%) and *Escherichia coli* (31.66%), were detected in the milk samples. Of the 894 bulk tank milk samples, 743 (83.11%) contained 4 or more species of bacterial pathogens. It was also observed that an increase in the frequency of isolation of bacterial pathogens was significantly associated with an increased bulk tank bacterial and somatic cell counts. Bulk tank milk with lower bulk tank bacterial and somatic cell counts had fewer species of bacteria. Herd size and farm management practices had considerable influence on the species of bacteria and bacterial and somatic cell counts in bulk tank milk. The percentage of small herds (< 50 cows) with 4 or more types of bacterial pathogens detected in milk samples was higher than that of big herds (> 500 cows), which was 86.45% and 71.79%, respectively. Of the bulk tank milk samples, 85.20% (501/588) had 4 or more types of bacterial pathogens in winter, whereas the percentage was 88.89% (272/306) in winter. There were no differences in the species of bacteria in bulk tank milk between summer and winter. In conclusion, species of bacteria and bacterial and somatic cell counts could serve as indicators of bulk tank milk quality and we should formulate strategies to improve milk quality and reduce the incidence of mastitis in dairy herds.

Key Words: bulk tank milk, bovine, mastitis pathogens

0086 Modulation of the acute phase response in feedlot steers supplemented with *Saccharomyces cerevisiae*. J. O. Buntyn[*1], N. C. Burdick Sanchez[2], J. A. Carroll[2], E. Chevaux[3], K. Barling[4], S. E. Sieren[5], S. J. Jones[5], and T. B. Schmidt[5], *[1]Department of Animal Science, University of Nebraska, Lincoln, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]Lallemand Animal Nutrition, Milwaukee, WI, [4]Lallemand Animal Nutrition, Iola, TX, [5]University of Nebraska, Lincoln.*

This study was designed to determine the effect of supplementing feedlot steers with *Saccharomyces cerevisiae* CNCM I-1079 (SC) on the acute phase response to a lipopolysaccharide (LPS) challenge. Steers (n = 18; 266 ± 4 kg BW) were separated into 3 treatment groups (n = 6/treatment). One group was fed a standard receiving diet (Control, Cont); 1 group was fed the standard receiving diet supplemented with SC (Lallemand, Inc.) at 0.5 g/steer/d (SC-0.5), and the final group was fed the standard receiving diet supplemented with SC at 5.0 g per steer day (SC-5.0) for 29 d. On d 27, steers were fitted with indwelling jugular cannulas and rectal temperature (RT) probes that measured RT continuously at 5-min intervals, and were placed in individual stalls. On d 28, steers were challenged IV with LPS (0.5 μg/kg BW at 0 h) and blood samples were collected at 30-min intervals from -2 to 8 h and 24-h post-challenge. Serum was isolated and stored at −80°C until analyzed for cortisol and cytokine concentrations. Before the challenge, there was an effect of treatment ($P < 0.001$) on RT; SC-0.5 steers (39.50 ± 0.03°C) had greater RT than Cont (39.06 ± 0.04°C) and SC-5.0 (39.27 ± 0.04°C) steers. Also, Cont steers had greater ($P < 0.001$) RT than SC-5.0 steers. Therefore, RT was further analyzed as the change from baseline. In response to LPS challenge, the change in RT was affected by treatment ($P < 0.001$); Cont steers had the greatest change in RT (0.434 ± 0.0510°C) compared with SC-0.5 (-0.059 ± 0.039°C) and SC-5.0 (-0.007 ± 0.045°C) steers. There was a tendency ($P = 0.06$) for baseline cortisol concentrations to be affected by treatment; SC-5.0 steers having greater (7.8 ± 0.8 ng/mL) cortisol than Cont (4.9 ± 0.8 ng/mL) steers. Post-LPS challenge, there was a treatment × time interaction ($P = 0.005$); SC-5.0 steers had decreased ($P < 0.02$) cortisol concentrations than Cont steers from 4.5 to 7 h post-challenge. There was a treatment effect ($P \leq 0.05$) for all cytokines (tumor necrosis factor-α, interleukin-6, and interferon-γ). Cytokines were decreased in SC-0.5 and SC-5.0 steers compared with Cont steers following LPS challenge. While these data demonstrate that *Saccharomyces cerevisiae* supplementation can reduce the inflammatory response to a LPS challenge, further research is needed to determine

whether or not *Saccharomyces cerevisiae* supplementation is beneficial when animals are exposed to a live pathogen.

Key Words: cattle, immune response, live yeast

0087 Performance evaluation of calves with diarrhea in different systems supplemented with yeast culture plus enzymatically hydrolyzed yeast cell wall.

V. R. Rabassa*[1], B. Scherer[1], F. B. Del Pino[2], C. C. Brauner[2], F. M. Gonçalves[1], R. F. S. Raimondo[1], E. G. Xavier[3], C. C. Elrod[4], and M. Nunes Corrêa[2], [1]*Universidade Federal de Pelotas, Pelotas, Brazil,* [2]*Federal University of Pelotas, Brazil,* [3]*Granjas 4 Irmãos, Rio Grande, Brazil,* [4]*Vi-COR, Inc., Mason City, IA.*

The aim of this study was to evaluate the performance of calves with diarrhea in different systems supplemented with yeast culture plus enzymatically hydrolyzed yeast cell wall during the neonatal period. Seventy-eight female Holstein calves were divided into 2 groups: yeast group (Celmanax, Vi-COR, Mason City, IA), $n = 38$, which were supplemented with 8mL/d during the first 42 d of age and a control group, $n = 40$, which received no supplementation. The yeast was administered daily as an oral drench and measurements of weight, heart girth, wither height, rump width, and ADG were performed weekly. The animals were also divided into 2 systems based on the types of facilities: houses (confined) and stakes (outdoor), and monitored daily for the occurrence of diarrhea. Data were analyzed by MIXED PROCEDURES of SAS. There was no difference ($P > 0.05$) in calf performance between groups and group × collection. However, there was an interaction ($P < 0.05$) between groups and system. Control calves maintained in the stakes system had greater ($P < 0.05$) heart girth than the yeast group (83.69 ± 0.58 cm and 81.65 ± 0.68 cm, respectively) and higher ($P < 0.05$) ADG (0.44 ± 0.02 kg and 0.33 ± 0.03 kg, respectively). Calves from the yeast group kept in houses had higher averages ($P < 0.05$) than the control group in the parameters wither height (81.43 ± 0.64 cm and 79.61 ± 0.54 cm), rump width (29.44 ± 0.32 cm and 28.23 ± 0.29 cm), and ADG (0.32 ± 0.04 kg and 0.21 ± 0.02 kg), respectively. In conclusion, supplementation with yeast culture plus enzymatically hydrolyzed yeast cell wall can improve the growth performance of animals showing diarrhea housed in confined environments.

Key Words: dairy, health, system

0088 Variations in the survival of *Listeria monocytogenes* to grow in bile from porcine gallbladders.

J. G. Wilson*, S. J. White, and J. R. Donaldson, *Mississippi State University, Mississippi State.*

Listeria monocytogenes is a facultative intracellular, Gram-positive bacterium that can cause disease, including abortion, in sheep, goats, cattle, pigs, and poultry. These animals are also known reservoirs for this pathogen and it is primarily acquired through ingestion of contaminated silage or soil. This bacterium's ability to survive within the gastrointestinal tract and cross the intestinal lining is directly related to the ability of the pathogen to cause disease. However, it is not clear whether there are variations in the ability of this pathogen to survive. The purpose of this study was to determine whether variations exist in the ability of different serotypes of *L. monocytogenes* to survive within porcine gallbladder bile and if survival affected the ability of these bacteria to invade epithelial cells in vitro. Avirulent strain HCC23 (serotype 4a) and virulent strain 10403S (serotype 1/2a) were cultured in brain-heart-infusion (BHI) broth media to mid-logarithmic ($OD_{600} = 0.5$), then transferred to bile collected from pigs 30 d of age (6.7 ± 0.1 kg BW). Anaerobic growth was monitored by viable plate counts on BHI agar. The influence of bile on invasion potential of *L. monocytogenes* was tested in colon epithelial cells (GPC-16) cultured in Eagle's Minimal Essential Media with 20% fetal bovine serum. Cell culture media was supplemented with 10% bile and HCC23 or 10403S was inoculated at a multiplicity of infection of 100:1. Cultures were incubated at 37°C, 5% CO2. At 1 h and 2 h post infection, cells were washed to remove extracellular bacteria then lysed to release intracellular bacteria. Lysates were serially diluted and plated onto BHI agar. Survival of HCC23 in bile did not change ($P = 0.3$), though a decrease ($P = 0.05$) in survival of 10403S was observed 24 h after bile exposure. Virulent strain 10403S also had a decrease ($P = 0.05$) in invasion potential in the presence of bile. In contrast, avirulent strain HCC23 did not decrease ($P = 0.08$) in invasion potential in the presence of bile. Together with previous reports of variations in the intracellular presence of *L. monocytogenes* in the gallbladder, these results suggest that avirulent and virulent strains respond differently to the gastrointestinal environment and this difference may influence the outcome of the infectious process.

Key Words: gallbladders, *Listeria monocytogenes*, pig

0089 Yeast probiotics vary in their potential to bind to Gram-positive or Gram-negative bacteria.

G. Posadas*[1], J. A. Carroll[2], J. R. Corley[3], A. Lawrence[1], and J. R. Donaldson[1], [1]*Mississippi State University, Mississippi State,* [2]*USDA-ARS, Livestock Issues Research Unit, Lubbock, TX,* [3]*Lesaffre Feed Additives, Milwaukee, WI.*

Probiotics are widely used in the livestock industry to improve health and overall productivity. Despite the extensive amount of research performed on examining the mechanisms by which probiotics confer positive effects on hosts, their use is still highly debated and are undoubtedly under characterized. The hypothesis for this study was that variations exist in the binding potential of probiotics to Gram-negative and Gram-positive bacteria. To test this hypothesis, the binding capability of 5 different types of live yeasts or yeast cell wall products to 2 Gram-negative bacteria (*Salmonella typhimu-*

rium and *Escherichia coli* O157:H7) and 3 Gram-positive bacteria (*Listeria monocytogenes, Clostridium perfringens*, and *Bifidobacterium bifidum*) was determined using an adhesion assay and subsequent analysis by scanning electron microscope. The probiotics were incubated on cover slips and then challenged with the array of different pathogens. To assess each probiotic's propensity toward adhesion, extensive washings of the cover slips were done. This removal of unbound bacteria determined that any bacteria remaining resulted from direct interactions between the pathogens and probiotics, inferring antagonistic behavior of adhesion displayed by the probiotics. Though *S. typhimurium* bound well to all probiotics tested (> 90%, $P = 0.3$), *E. coli* O157:H7 had a preference ($P = 0.003$) to bind to the yeast cell wall products in comparison to live yeast. The opposite was observed for the Gram-positive bacteria tested, which exhibited an improved binding potential to live yeast ($P = 0.01$). A sample size of > 20 yeast cells or cell wall products was analyzed. These data suggest that combining both live yeast probiotic and yeast cell product probiotic will allow for an increase in binding to different enteric bacteria. To test the binding capability of this combination mixture to colon epithelial cells, another adhesion assay was performed and prepared for analysis by fluorescent microscope (1 fluorochrome-labeling epithelial DNA and another staining yeast actin filaments). A sample size of > 30 epithelial cells was analyzed. The data determined that no variations were observed in the ability of these probiotics to bind to epithelial cells, indicating that the antagonist activity observed is specific to the pathogen tested and not a general defect of the product. Together, these data suggest that mechanisms of action of the yeast-based probiotics are dictated by variations of direct adhesion to pathogens. Further research is warranted to determine how these variations in binding potential influence the activity of these yeast-based probiotics in vivo.

Key Words: bacteria, probiotics, yeast

0090 An analysis of *Giardia lamblia* and *Cryptosporidium parvum* in bucket calves at the University of Findlay's animal science barn. S. M. Waibel*, F. D. McCarthy, R. M. Wood, and B. Henderson-Dean, *The University of Findlay, OH.*

Giardia lamblia and *Cryptosporidium parvum* are protozoal parasites that can cause gastroenteritis in dairy calves and are zoonotic diseases that cause intestinal enteritis in humans. The initial objective of this study was to determine the presence of *G. lamblia* or *C. parvum*, and if environmental stressors promote shedding of *G. lamblia* cysts or *C. parvum* oocysts in male dairy calves ($n = 35$). The environmental stressors considered were arrival to the facility, transfer from isolation to the main barn, and processing (castration, dehorning, vaccination). Fecal samples were analyzed using rapid immunochromatographic assay. Data analysis of Group 1 ($n = 17$) suggested environmental stressors failed to influence shedding and isolation may not be effective at preventing the spread of disease. Subsequently, the objective of the study on Group 2 ($n = 18$) was to determine the effectiveness of isolation and if the same environmental stressors promote shedding of *G. lamblia* cysts or *C. parvum* oocysts. For both groups, fecal samples were collected within 24 h of arrival (IN), 24 h before isolation removal (BIR), 36 to 60 h after isolation removal (AIR), 24 h before processing (BP), and 36 to 60 h after processing (AP). Group 2 had additional fecal samples collected at the end of wk 1 (W1) and 2 (W2) in isolation. Results indicated there was no degree of significance between environmental stressors and shedding of *G. lamblia* or *C. parvum*. Isolation appeared ineffective at preventing *G. lamblia* or *C. parvum* from spreading. Results did not detect *G. lamblia* or *C. parvum* in Group 1 calves at IN. However, at BIR, calves showed an increase in measured incidence of 27%. Fecal samples from calves in Group 2 tested positive for *G. lamblia* or *C. parvum* at IN of 22% and BIR of 56%. The average for both groups was 12% at IN and 42% at BIR. Overall, 11% of calves were positive for *G. lamblia* and *C. parvum* simultaneously; 31% tested positive for *C. parvum*, 72% tested positive for *G. lamblia*, and 86% tested positive for either parasite at least once. Given the potential for infection, increased hygiene measures are recommended. The isolation procedure should be examined for plausible breeches. Potential source of infection for calves needs to be investigated.

Key Words: *Cryptosporidium parvum, Giardia lamblia*

ANIMAL HEALTH III: **PERIPARTURIENT AND LACTATION HEALTH**

0091 Milk quality and milk components in lactating dairy goats fed OmniGen-AF from dry-off through the entire lactation. A. D. Rowson*, T. J. Boyle, D. J. McLean, S. A. Armstrong, and S. B. Puntenney, *Prince Agri Products, Inc., Quincy, IL.*

In the United States, the legal somatic cell count (SCC) limit for dairy goat milk is 1500,000 mL^{-1}. However, it is common for SCC to be much higher than this. Production of milk with a SCC higher than the legal limit results in farms being unable to ship their milk and lost income. The objective of this study was to evaluate the supplementation of OmniGen-AF to dry and lactating dairy goats on milk quality and milk components over an entire lactation. Thirty-five, 2-yr-old does housed on a commercial goat dairy located in south central Wisconsin were randomly assigned to 1 of 2 groups: 1) Control-fed (n = 18) and 2) OmniGen-AF-fed (n = 17). Animals in Group 1 were fed a complete feed pellet twice a day and ad libitum alfalfa hay. Animals in Group 2 were fed the same diet but with 6 g/h/d of OmniGen-AF added to the pellet. The project started at dry-off (~40 to 60 d before kidding) and continued for the full lactation. Breeds of does were Alpine, Saanen, Nubian, and La Mancha, and all breeds were equally represented in both groups. Monthly Dairy Herd Improvement Association (DHIA) milk testing was performed on all animals for 9 mo. The SCC, percent milk fat, percent milk protein, and milk production data were collected at each test. The mean SCC for OmniGen-AF-supplemented does was 585,000 mL^{-1}, which was significantly lower ($P < 0.05$) than the mean SCC for control-fed does, which was 894,600 mL^{-1}. These differences were more pronounced as does approached the end of lactation where the mean SCC was 1669,000 mL^{-1} less in OmniGen-AF-fed does compared with controls (2094,000 mL^{-1} vs. 3763,000 mL^{-1}, respectively). Milk percent fat ($P < 0.01$) and percent protein ($P < 0.05$) were different between the OmniGen-AF-fed and control-fed does. Specifically, mean milk percent fat was 3.21% from control-fed does and 3.45% from OmniGen-AF-fed does. Mean milk percent protein was 2.93 and 3.08% from control and OmniGen-AF-fed does, respectively. There was no difference in milk production between groups. Data from this trial demonstrate that OmniGen-AF fed goats experienced benefits in milk components and attenuation of the dramatic increase in SCC that normally occurs late in lactation, both of which are indicative of improved mammary gland health.

Key Words: goats, OmniGen-AF, SCC

0092 Modulation of innate immune function and phenotype in bred dairy heifers during the periparturient period induced by feeding an immunostimulant 60 d before delivery. E. L. Nace, S. C. Nickerson*, F. M. Kautz, S. Breidling, D. Wochele, L. O. Ely, and D. J. Hurley, *University of Georgia, Athens.*

The purpose of this study was to evaluate the effect of an immunostimulating feed additive on innate immunity and health events during the periparturient period in dairy heifers when mammary immunity is suppressed. From 60 d prepartum through day of calving, supplemented heifers (n = 20) received OmniGen-AF daily and were compared with unsupplemented controls (n = 20). Blood leukocyte innate immune activity [phenotypic markers, phagocytic activity, and reactive oxygen species (ROS) production] was measured before feeding (60 d prepartum), 30 d later, and on d 1, 7, 14, and 30 postpartum. Health parameters and milk production were measured at calving and early lactation. Expression of CD62L among leukocytes from supplemented heifers was greater during the periparturient period than controls. Specifically, on d 1 postpartum, mean percentage of neutrophils exhibiting CD62L surface markers was 95.3% for OmniGen-AF treated heifers vs. 91.4% for controls ($P < 0.10$), and the percentage decreased from 98.3% 30 d prepartum to 91.4% on d 1 postpartum among controls ($P < 0.05$); values for supplemented heifers did not decrease. Likewise, leukocyte phagocytic activity against *Escherichia coli* and *Staphylococcus aureus* was greater in heifers supplemented with OmniGen-AF; e.g., on d 30 prepartum and d 7 postpartum, mean percentage of monocytes from supplemented heifers exhibiting phagocytic activity against *E. coli* were 11.7 and 11.3%, respectively, whereas values for controls were 7.3 and 7.4% ($P < 0.10$), respectively. In controls, phagocytosis decreased from 13.7% 60 d prepartum to 7.3 and 7.5% on d 30 prepartum and d 7 postpartum ($P < 0.05$), respectively, but values for supplemented heifers did not decrease over time. Conversely, ROS production in response to PMA and killed *S. aureus* stimulation was greater among control heifers compared with supplemented animals; e.g., the quantities of ROS generated in response to *S. aureus* lysate on d 1 and 7 postpartum were 68.8 vs. 51.9 and 56.1 vs. 41.3 units ($P < 0.05$), respectively. Supplemented heifers exhibited fewer deleterious health events (retained placenta, displaced abomasum, ketosis, udder edema, death) than controls (1.25 vs. 1.93/heifer) and a lower rate of new cases of mastitis (9.6% vs. 23.2%); however, no significant differences were observed in overall prevalence of mastitis, milk SCC, or milk production. Results demonstrated a positive role of OmniGen-AF in amplifying leukocyte antibacterial activity during the periparturient period and support the continued study of dietary supplementation to enhance mammary gland health in dairy cattle.

Key Words: dairy heifer, innate immunity, periparturient period

0093 Restriction in energy or protein affects differentially behavior of lactating dairy cows.

V. Fischer*[1], E. Forgiarini Vizzotto[1], F. André Schmidt[2], D. Werncke[1], A. Susenbach de Abreu[1], and A. Thaler Neto[2], [1]*Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil,* [2]*Universidade Estadual de Lages, Brazil.*

Feed restriction adversely affects feeding and social behavior in cattle. However, data on the effects of nutrient composition on these characteristics are limited. The objective was to quantify the effects of dietary energy and protein restriction on feeding and behavior in lactating Holstein and Jersey cows. Twelve cows in mid-lactation balanced for breed and days in milking were used in a Latin square design: 3 cows × 3 periods. Each experimental period lasted 3 wk and consisted of: 1) adaptation, where all animals were fully fed according to their requirements, 2) restriction, where animals were fed to provide 50% of their daily energy (E) and protein (P) requirements, and 3) treatment, where animals were fed with 1 of the following diets: 100E + P, 50E + 100P, and 100E + 50P, to provide 100% of energy + protein requirement, 50% of energy requirement, 50% of protein requirements, respectively. On the last day of the treatment period, cows were visually observed from 0600 to 2100 h. The behavioral attributes were recorded as time spent in feeding behavior and number of social and adaptation events. Data were logarithmic transformed and submitted to analysis of variance, considering main effects of diet, cow, and period. Nutrient restriction did not change feeding and ruminating times or aggressive interactions. Energy restriction reduced time spent lying but increased tongue curling and licking events. Protein restriction reduced idling time, number of low intensity vocalizations, and tended to reduce standing time. The data are consistent with the concept that cows react differently to limitations in energy or protein in the diet.

Key Words: behavior, nutrient, restriction

Table 0093.

	Diet				
Attribute	100% E+P	50%E + 100%P	50%P + 100%E	$P > F_{diet}$	RSD (%)
Eating (min)	276.1	254.1	278.7	NS	2.2
Ruminating (min)	116.6	129.1	145.2	NS	6.7
Idling (min)	243.1[a]	243.7[a]	182.6[b]	0.0094	4.3
Lying (min)	203.7[ab]	176.6[b]	243.7[a]	0.0381	5.1
Standing (min)	169.8[d]	130.0[de]	87.7[e]	0.0615	12.6
Aggressing (n°)	0.9	1.6	2.9	NS	300.6
Being aggressed (n°)	1.9	1.2	1.6	NS	257.7
Vocalizing (n°)	0.5 a	0.3[ab]	0.1[b]	0.0440	93.5
Licking the floor (n°)	0.1 b	1.7[a]	0.5[ab]	0.0271	217.0
Curling the tongue (n°)	0.1 b	0.2[a]	0.1[b]	0.0279	15.6

[a,b] Means in the same row are different (least squares means, DMS test, $P < 0.05$).
[d,e] Means in the same row tend to be different (least squares means, DMS test, $P < 0.10$).
RSD = relative standard deviation; NS = not significant

0094 Dynamics of culling for Jersey, Holstein, and crossbred cows in large multi-breed dairy herds.

P. J. Pinedo*[1], A. M. Daniels[2], J. Shumaker[3], and A. De Vries[4], [1]*Texas A&M AgriLife Research, Amarillo,* [2]*Circle H Headquarters LLC, Dalhart, TX,* [3]*Magnolia Veterinary Services, Amarillo, TX,* [4]*University of Florida, Gainesville.*

The objective of this observational study was to describe and compare the dynamics of reason-specific culling risk for the genetic groups Jerseys (JE), Holsteins (HO), and Jersey × Holstein crossbreds (JH), considering parity, stage of lactation, and milk yield, among other variables, in large multi-breed dairy herds in Texas. The secondary objective was to analyze the association between survival and management factors, such as breeding and replacement policies, type of facilities, and use of cooling systems. After edits, available data included 202,384 lactations in 16 herds, ranging from 407 to 8773 cows calving per year during the study period from 2007 to 2011. The statistical analyses were performed through logistic regression (PROC GLIMMIX, SAS) and by estimation of hazard functions (PROC LIFETEST, SAS). The distribution of lactation records by genetic group was 58%, 36%, and 6% for HO, JE, and JH, respectively. Overall culling rates across breeds were 30.1%, 32.1%, and 35.0% for JH, JE, and HO, respectively. The dynamics of reason-specific culling were dependent on genetic group, parity, stage of lactation, milk yield, and herd characteristics. Early lactation was a critical period for "died" and "injury-sick" culling. The risk increased with days after calving for "breeding" and, in the case of HO, "low production" culling. Open cows had a 3.5 to 4.6 times greater risk for overall culling compared with pregnant cows ($P \leq 0.01$). The odds of culling with reason "died" within the first 60 d in milk (DIM) were not significantly associated with genetic group. However, both JE and JH had lower odds of live culling within the first 60 DIM compared with HO cows [OR = 0.72 ($P \leq 0.001$) and 0.82 ($P \leq 0.002$), respectively]. Other cow variables significantly associated with the risk of dying within the first 60 DIM were cow relative 305 mature equivalent (MEQ) milk yield, parity, and season of calving. Significant herd-related variables for death included herd size and origin of replacements. In addition to genetic group, the risk of live culling within 60 DIM was associated with cow relative 305 MEQ milk yield, parity, and season of calving. Significant herd-related variables for live culling included herd relative 305 MEQ milk yield, herd size, type of facility, origin of replacement, and type of maternity. Overall, reason-specific culling followed similar patterns across DIM in the 3 genetic groups.

Key Words: culling, death, Holstein, Jersey

0095 Effect of an organic-certified treatment (Optimum UterFlush) for toxic puerperal metritis on cure and reproductive performance of dairy cows. P. J. Pinedo[*1], J. S. Velez[2], H. Bothe[3], D. Merchan[3], J. M. Piñeiro[3], and C. A. Risco[4], *[1]Texas A&M AgriLife Research, Amarillo, [2]Aurora Organic Farms, Boulder, CO, [3]Aurora Organic Dairy, Boulder, CO, [4]College of Veterinary Medicine, University of Florida, Gainesville.*

The objective was to evaluate the efficacy of an organic-certified product (Optimum UterFlush, Van Beek Natural Science) on the treatment of toxic puerperal metritis (TPM) in cows in an organic dairy farm. Evaluation included clinical cure, survival, and reproductive performance. The TPM was defined as an abnormally enlarged uterus and fetid watery red-brown vaginal discharge, associated with systemic illness and fever (rectal temperature > 39.5°C), within 12 d postpartum. Cows diagnosed with TPM (n = 220) were randomly assigned to 2 intrauterine treatments (every other day for a total of 3 treatments): 1) Control (CON) = 200 mL of Povidone iodine diluted in 2 L of distilled water (n = 113) and 2) UterFlush (UF) = 15 mL diluted in 105 mL of distilled water (n = 107). All treated cows received hypertonic solution (500 mL of 25% calcium borogluconate IV) and oral aspirin (5 boluses/d). Outcome variables for treatment efficacy included fever and presence of fetid vaginal discharge at d 6 and 14 after diagnosis, survival at d 6, 14, and 30, and reproductive performance. Control variables were parity, BCS at enrollment, and calving season. Logistic regression and ANOVA were used for the analyses (PROC GLIMMIX and PROC GLM, SAS). The odds of surviving at d 6, 14, and 30 for cows in the UF treatment were 4.7 (95%, CI = 1.4 to 15.8), 2.8 (95%, CI = 1.3 to 6.1), and 3.6 (95%, CI = 1.7 to 7.7) times the odds of cows in the CON treatment. Occurrence of fever at d 6 and 14 was not different between the 2 treatments. Presence of a fetid vaginal discharge at d 6 and 14 was lower in cows treated with UF compared with cows in the CON group [11% vs. 28% (P < 0.001) and 1% vs. 8% (P = 0.017)]. The odds of breeding until 150 d in milk (DIM) and the time to first breeding were not different for the 2 treatments. The odds of pregnancy at the first breeding and at 300 DIM for cows treated with UF were 2.2 (95%, CI = 1.1 to 4.4) and 2.0 (95%, CI = 1.1 to 3.5) times the odds of cows in the CON group. Days to pregnancy were similar in both treatments. The number of breedings per pregnancy was 1.96 vs. 2.58 for cows in the UF and CON treatments (P = 0.01), respectively. Results indicated that cows with TPM treated with Optimum UterFlush had higher odds of recovering and improved reproductive performance, compared with cows treated with Povidone iodine.

Key Words: puerperal-metritis, organic, UterFlush

0096 Effects of yeast product supplementation on immunity and uterine inflammation in transition dairy cows. K. Yuan[*1], L. Mendonca[1], L. Hulbert[1], L. Mamedova[1], M. Muckey[1], Y. Shen[1], C. C. Elrod[2], and B. Bradford[1], *[1]Kansas State University, Manhattan, [2]Vi-COR, Inc., Mason City, IA.*

The objective of this study was to assess the effects of supplementing a yeast product derived from *Saccharomyces cerevisiae* on immunity and uterine inflammation in transition cows. Forty multiparous Holstein transition cows were blocked by expected calving date and randomly assigned within block to 1 of 4 treatments (n = 10) from 21 d before expected calving to 42 d postpartum. Rations were top dressed with yeast culture plus enzymatically hydrolyzed yeast (Celmanax, Vi-COR, Mason City, IA) at the rate of 0, 30, 60, or 90 g/d throughout the experiment. Blood samples collected on -21, −7, 1, 4, 7, 14, 21, and 35 d relative to calving were incubated with *E. coli* (# 51813) to assess the ability of blood to kill bacteria. Uterine samples were collected on d 7 and 42 postpartum by cytobrush technique to determine neutrophil populations and relative abundance of transcripts involved in inflammation. Fecal samples were collected on d 7 and 21 for analysis of immunoglobulin A (IgA) concentration. Data were analyzed using mixed models with repeated measures over time. The percentage of *E. coli* killed by whole blood was not affected by yeast treatments (P = 0.28). Uterine neutrophil populations were much greater in samples collected on d 7 compared with those on d 42 (32.0% vs. 7.6% ± 3.7 of cells, P < 0.01), indicating greater neutrophil infiltration immediately after calving, but no treatment (P = 0.53) effect was detected. There were significant ($P \leq 0.01$) day effects for IL-6, IL-8, neutrophil myeloperoxidase, and neutrophil elastase, reflecting greater abundance of these transcripts in uterine tissues collected on d 7 compared with d 42. Interestingly, there was a quadratic dose effect (P = 0.02) for IL-6, indicating that 30 and 60 g/d decreased uterine IL-6 mRNA. The mRNA abundance of neutrophil myeloperoxidase and elastase was increased (P < 0.05) by yeast product. Yeast product quadratically increased fecal IgA concentrations (P = 0.03), suggesting that 30 and 60 g/d doses enhanced mucosal immunity. Yeast product supplementation did not affect whole blood bacterial killing ability but modulated uterine inflammatory signals and mucosal immunity in transition dairy cows.

Key Words: immunity, transition cow, yeast

0097 Hyperketonemia in early lactation dairy cattle: Component and total cost per case.

J. A. A. McArt[*1], D. V. Nydam[2], and M. W. Overton[3], *[1]Colorado State University, Fort Collins, [2]Department of Population Medicine and Diagnostic Sciences, Cornell University Ithaca, NY, [3]Elanco Animal Health-Dairy, Athens, GA.*

The purpose was to develop deterministic economic models to estimate the costs associated with: 1) the component cost per case of hyperketonemia (HYK) and 2) the total cost per case of HYK when accounting for costs related to HYK-attributed diseases in dairy cows. Data from current literature were used to model the incidence and risks of HYK, displaced abomasa (DA), and metritis, disease associations, and milk production, culling, and reproductive outcomes. The component cost of HYK was estimated based on 1000 calvings per year, incidence of HYK in primiparous and multiparous animals, percentage of animals receiving clinical treatment, costs associated with diagnostics, therapeutics, labor, and death loss, and costs of future milk production losses, future culling losses, and reproduction losses. Costs attributable to DA and metritis were estimated based on the incidence of each disease in the first 30 d in milk, number of cases of each disease attributable to HYK, costs associated with diagnostics, therapeutics, discarded milk during treatment and withdrawal period, veterinary service (DA only), death loss, and costs of future milk production loses, future culling losses, and reproduction losses. The component cost per case of HYK was estimated at $127 and $106 for primiparous and multiparous animals, respectively; the average component cost per case of HYK was estimated at $112. Thirty-one percent of the average component cost of HYK was due to future reproductive losses, 28% to death loss, 22% to future milk production losses, 13% to future culling losses, 3% to therapeutics, 2% to labor, and 1% to diagnostics. The total cost per case of HYK was estimated at $361 and $247 for primiparous and multiparous animals, respectively; the average total cost per case of HYK was $279. Forty percent of the average total cost of HYK was due to the component cost of HYK, 32% to the cost attributable to metritis, and 28% to the cost attributable to DA. The high total cost of HYK at reported incidences of 40 to 60% highlights the importance of appropriate transition cow nutrition and management to decrease the impact of HYK on both a disease and economic basis. In addition, these estimates can be used to model the cost benefit of various preventative and treatment interventions.

Key Words: component cost, dairy cow, hyperketonemia, total cost

0098 The effects of grain-induced subacute ruminal acidosis on interleukin-6 and acute phase response in dairy cows.

S. C. Li[*1], A. M. Danscher[2], P. H. Andersen[3], E. Khafipour[1], N. B. Kristensen[4], and J. C. Plaizier[1], *[1]Department of Animal Science, University of Manitoba, Winnipeg, Canada, [2]Department of Large Animal Sciences, University of Copenhagen, Denmark, [3]Department of Clinical Sciences, Swedish University of Agricultural Sciences, Uppsala, [4]Danish Agricultural Advisory Service, Aarhus.*

Subacute ruminal acidosis (SARA) resulting from excessive grain feeding to dairy cows is accompanied by an acute phase response. Interleukin 6 (IL-6) has been proposed as a mediator of this response. We tested if the acute phase response associated with grain-induced SARA is mediated by IL-6. Six lactating Danish Holstein cows were used in an incomplete block design study that included 2 periods with 2 cows in a SARA-challenge treatment and 2 cows in a control treatment, and a third period with 2 cows in a SARA-challenge treatment. In the first 2 wk of each experimental period, all cows received a control diet (17.4% CP, 19.2% starch, 6.28 MJ NEL/kg DM). In the third week, the diet for control cows remained unchanged. For the SARA-challenge cows, 40% of the control diet was gradually substituted with grain pellets (50:50 wheat:barley) within 3 d to induce SARA. This SARA-challenge diet was fed for another 4 d. Jugular vein blood was sampled at 7 h post-feeding on Tuesday and Thursday of the second week and during the first 2 and last day of the SARA-challenge diet feeding. The ELISA kits were used for measurement of IL-6 and acute phase proteins haptoglobin (Hp), LPS binding protein (LBP), and serum amyloid A (SAA). For data analysis, a mixed model was used, in which cow was treated as a random factor, whereas treatment (SARA challenge vs. control), period, day within period, as well as the interaction between day within period and treatment, were treated as fixed factors. Compared with control cows, the SARA challenge tended to increase LBP (7.54 vs. 10.23 mg/L, $P = 0.10$) and increased SAA (4.24 vs. 11.60 mg/L, $P = 0.04$) and Hp (3.57 vs. 22.09 mg/L, $P = 0.04$) in blood, confirming that the SARA challenge caused an acute phase response. Concentrations of IL-6 were not affected by the SARA challenge and averaged 5.06 ng/mL across treatments. Our data do not confirm that IL-6 mediates the acute phase response during grain-induced SARA. This confirmation may require more frequent blood sampling around the time of the SARA challenge.

Key Words: acute phase proteins, dairy cow, IL-6

0099 Evaluation of propylene glycol and glycerol infusions as potential treatments for ketosis in dairy cows. P. Piantoni* and M. S. Allen, *Michigan State University, East Lansing.*

Our objective was to evaluate propylene glycol (PG) and glycerol (G) as treatments for ketosis. Two experiments lasting 4 d each were conducted in which cows received 1 bolus infusion per day. All data were analyzed by ANOVA. Experiment 1 used 6 ruminally cannulated cows [28 ± 7 d in milk (DIM)] randomly assigned to 300-mL infusions of PG or G (both ≥ 99.5% pure) in a crossover design experiment. Within each period, cows were randomly assigned to sequence in a crossover for site of infusion in the abomasum (A) or reticulorumen (*R*). Treatments were infused in the cranial reticulorumen (R-PG and R-G) to simulate drenching and abomasum (A-PG and A-G) to prevent metabolism by ruminal microbes. Treatment did not affect DMI or milk yield. Glycerol infused abomasally increased plasma glucose concentration the most (15.2 mg/dL; interaction $P < 0.05$), followed by R-PG (12.0 mg/dL), A-PG (9.7 mg/dL), and R-G (7.9 mg/dL). Glucose area under the curve (AUC) was also highest for A-G (1480 min × mg/dL; interaction $P < 0.10$), followed by A-PG (1167 min × mg/dL), R-PG (1009 min × mg/dL), and R-G (302 min × mg/dL). Abomasal infusions increased glucose AUC compared with ruminal infusions (1324 vs. 656 min × mg/dL; $P < 0.05$). Experiment 2 used 4 ruminally cannulated cows (23 ± 5 DIM) randomly assigned to treatment sequence in a Latin square design experiment balanced for carry-over effects. Treatments were: 300 mL PG, 300mL G, 600 mL G (2G), and 300 mL PG + 300 mL G (GPG), all infused into the cranial reticulorumen. Infusions did not affect DMI or milk yield, but affected time to reach plasma glucose baseline after maximum and glucose AUC (both $P < 0.05$). Treatment contrasts compared PG with G, 2G, and GPG. Propylene glycol increased plasma glucose concentration and glucose AUC compared with G (16.4 vs. 6.6 mg/dL and 1768 vs. 213 min × mg/dL; both $P < 0.05$), but not compared with 2G or GPG. Abomasal infusion of G elicited the best plasma glucose response followed by infusion of PG into the rumen or abomasum. Plasma glucose response to ruminal infusion of PG was better than G, likely because of greater ruminal metabolism of G, and no benefit was detected for doubling the dose of G or infusing G in combination with PG. A 300-mL dose of propylene glycol is as effective a treatment as twice the amount of glycerol when administered in the reticulorumen.

Key Words: fresh cows, glucose precursors, ketosis

0100 Integrating metabolomics and transcriptomics of liver to study susceptibility to ketosis in response to prepartal nutritional management. K. Shahzad*[1], J. S. Osorio[1], D. N. Luchini[2], and J. J. Loor[1], *[1]University of Illinois, Urbana-Champaign, Urbana, [2]Adisseo S.A.S., Alpharetta, GA.*

Postpartal ketosis is associated with body fat mobilization postpartum. Subclinical and clinical ketosis arise more frequently in cows that are overfed energy during the entire dry period or during the close-up period (i.e., last 21 d before parturition). Metabolomics (GC–MS, LC-MS; Metabolon Inc.) and transcriptomics (45K-whole-transcriptome microarray; Agilent) analyses were performed in liver tissue harvested at -10 d relative to parturition from cows that were healthy (H) on 7 d postpartum or diagnosed with clinical ketosis (Ke). Cows in Ke consumed a higher-energy diet (OVE) from -21 d to calving. Cows in H consumed OVE ($n = 8$) or a high-straw, lower-energy diet (CON; $n = 8$) from -21 d to calving. Out of 313 biochemical compounds identified, statistical analysis ($P \leq 0.10$) of metabolomics data for Ke vs. CON, OVE vs. CON, and Ke vs. OVE revealed 34, 33, and 25 affected compounds, respectively. The top-5 affected and up regulated biochemical compounds in Ke vs. CON were taurocholate, adenine, hypotaurine, γ-glutamylcysteine, and taurochenodeoxycholate. In OVE vs. CON cysteine, methylphosphate, cysteinylglycine, and taurocholate were up regulated and γ-glutamylthreonine was downregulated. In Ke vs. OVE, the top-5 affected compounds were all downregulated: xylitol, 1-palmitoylglycerophosphoglycerol, leucylaspartate, sphinganine, and glycylvaline. Bioinformatics analysis revealed that primary bile acid production through cysteine and taurine precursors, and oxidative stress-like activities were affected in both Ke and OVE vs. CON groups. In contrast, in Ke vs. OVE, ketone body production was up regulated and cell signaling pathways were inhibited. Bioinformatics analysis of 2908 differentially expressed genes (DEG; $P \leq 0.05$), using the Dynamic Impact Approach (DIA), revealed that the top-5 impacted pathways in Ke vs. OVE were "hedgehog signaling," "glycosphingolipid biosynthesis-globo series," "renin-angiotensin system," and "other glycan degradation," all of which were inhibited. The "circadian rhythm" pathway was among the most induced pathways. Furthermore, there was marked inhibition in Ke vs. OVE of pathways associated with cellular growth, communication, signal transduction, fatty acid biosynthesis, and immune-related responses. These results suggest that prepartal diet alters hepatic metabolome and transcriptome. Liver from cows developing ketosis postpartum appears to exhibit unique alterations in the transcriptome and metabolome.

Key Words: ketosis, metabolomics, systems biology, transition cows

0101 A competitive and unpredictable feeding environment pre-calving increases inflammation and endometritis in Holstein dairy cows.

K. Proudfoot*[1], S. J. LeBlanc[2], D. Weary[3], B. Bradford[4], L. Mamedova[4], and N. von Keyserlingk[3], *[1]The Ohio State University, Columbus, [2]University of Guelph, ON, Canada, [3]The University of British Columbia, Vancouver, Canada, [4]Kansas State University, Manhattan.*

Pre-calving management may influence the risk of disease after calving. Our objective was to determine the effects of a competitive and unpredictable feeding environment on inflammation and uterine health in dairy cows. Sixty-four animals were randomly assigned to a treatment (n = 4 animals × 8 groups) or control group (n = 4 animals × 8 groups). Each group consisted of 3 multiparous cows and 1 primiparous heifer. During a 1-wk baseline period (5 wk before calving), all groups had free access to 4 electronic feed bins (Insentec, Marknesse, Holland). From 4 wk before calving until calving, control cows were given ad libitum access to 6 feed bins. For treatment groups, 4 non-experimental cows were added to the pen; after 2 wk, treatment groups were moved into a pen with 4 new cows. Throughout the treatment period, morning feeding times were delayed at random 0, 1, or 2 h on alternate days. Cows were excluded if they calved twins, aborted, or calved > 2 wk early. Blood samples were taken at baseline and weekly thereafter until 1 wk after calving. Serum was analyzed for TNF-a using ELISA. A uterine cytology smear was taken 3 to 5 wk post-calving. Smears were stained and examined under 400X magnification for presence of neutrophils and uterine epithelial cells; cows were considered to have endometritis if > 5% neutrophils were identified. Preliminary analysis revealed treatment × parity × week interactions so data were analyzed separately by parity. The percentage of endometritis cases per group was compared among treatments using a Mann–Whitney U test in SAS. Log-transformed TNF-a data were analyzed using a mixed model, including baseline data as a covariate, treatment as a main effect, week as a repeated measure (wk -2, -1, 0, 1 relative to calving), and group as a random effect. There was no difference in the number of cases of endometritis or differences in TNF-a between control and treatment first-calf heifers. For cows, treatment groups had a higher percentage of endometritis cases (64% vs. 17% cases/group; P = 0.02) and higher TNF-a (2.1 vs. 1.8 ± 0.06 log pg/ml; P = 0.02), compared with controls. These results indicate that management practices that create a competitive and unpredictable feeding environment, such as regrouping, overstocking, and variable feeding times, can disrupt immune function and increase disease risk in cows but not first-calf heifers.

Key Words: endometritis, parturition, stress

ARPAS SYMPOSIUM: CUSTOMER/ CONSUMER CONFIDENCE IN THE LIVESTOCK INDUSTRY—ETHICS

0102 Perspectives on business ethics in a new-age feed industry. L. D. Bunting*, *ADM Alliance Nutrition, Lubbock, TX.*

The business of providing animal feed and nutritional services is becoming increasingly sophisticated and global in nature. As the complexity of the feed industry has increased, both livestock producers and feed suppliers alike perceive that the occurrence of unethical behavior in sales and marketing of feed products is on the rise. This perception likely originates not only from some actual decline in ethical standards but perhaps also from an increasing lack of clarity relative to what actually constitutes ethical practice. This paper will discuss the interpretation of ethical practice in the context of the rapidly evolving field of animal nutrition and the great many new feed technologies and suppliers entering the market, from both domestic and international sources. The potential ramifications of a feed industry work force that is becoming less experienced (youthful) and increasingly foreign trained will also be discussed in the context of company training programs that probably fall short in both technical depth and ethical mentoring relative to customer relationships. Feed specialists with less professional experience are more susceptible to ethical creep or ethical blindness, as they may have less appreciation for how seemingly trivial corner cutting leads to cycles of behavior rationalization that slowly progress to practices that are more egregiously unethical. A large proportion of the incidences of unethical practices that are anecdotally reported in the feed industry relate to the selling and use of feed additives, micronutrients, and other higher-cost applications. Some of the problematic practices that are more prevalent include customer confidentiality breaches, unapproved or erroneous product claims, misrepresentation of effective doses or tag dressing, undisclosed substitution of branded products, and undisclosed product commissions for parties in fiduciary roles with livestock producers. This paper will emphasize the need for greater focus on training and mentoring of feed industry employees relative to what constitutes fair business practices and how to sell feed products and programs such that they are honestly represented, both for the benefits they can potentially provide and relative to any competitive products and programs. Ethical behavior must be understood to be of collective importance to the feed industry. Unethical practices can have consequences that cause collateral damage to customer bases well beyond that of the offending sales organization. Unethical practices also undermine the trust of suppliers and other key parties that are business critical to the success of a sales organization.

Key Words: ethics, feed industry, nutrition

0103 Customer/consumer confidence in the livestock industry—ethics: University perspective. M. L. Galyean*, *Texas Tech University, Lubbock.*

Animal science researchers, particularly those working with industry-sponsored research, are under increasing scrutiny with respect to bias and conflict of interest. Following the lead of the federal government, virtually all research universities have well-defined procedures to delineate and record potential bias and conflict of interest issues for faculty members who conduct research. Faculty committees to review and recommend remediation of potential conflicts are a common feature of university procedures. Primary concerns include conflicts of interest associated with financial, professional, and personal relationships. Financial limits vary somewhat among institutions, but an aggregate interest of > $5,000 is typically the threshold for disclosure. Once the threshold is met, faculty members are typically required to list and describe potential conflicts and subsequently inform all members of their research team of business and financial interests, consultancies, and any other potential issues that might influence their objectivity in conducting research. Issues that fall below reporting guidelines can nonetheless constitute potential conflicts. For example, more subtle conflicts of interest and bias might occur as a result of associations that a faculty member might have with companies providing discretionary funding and products to support research activities, regular consultancies that fall below reporting limits, honoraria to faculty members on advisory boards or to those who give technical presentations to clients groups, and all-expense paid trips to company-sponsored activities of various types. Similar conflicts can occur through connections to commodity organizations or even professional societies that have public stands on issues related to the faculty member's research. To ensure public trust in animal science research, animal scientists must adhere fully to applicable university regulations. In addition, they should conduct rigorous self-evaluations of their professional relationships, be transparent with respect to their activities via written disclosures to colleagues and research team members, and provide clear statements of potential conflicts in publications. Peer evaluations of relationships to ascertain real or perceived bias and conflict of interest issues could be useful, particularly in cases where the issues do not meet university or federal guidelines for reporting.

Key Words: bias, conflict of interest, industry-sponsored research

0104 [Withdrawn]

0105 Regulatory definitions, processes, and functionality assessment for animal food.

M. G. Alewynse*[1] and S. A. Benz[2], [1]*Center for Veterinary Medicine, Olney, MD,* [2]*Center for Veterinary Medicine, FDA, Woodbine, MD.*

The Federal Food, Drug, and Cosmetic Act (Act) defines food as "articles used for food or drink for man or other animals." The Act defines drugs as substances intended for diagnosis, cure, mitigation, treatment, or prevention of disease, or that affect the structure or function of the body. However, the Act recognizes that food may affect the body and excludes "food" from the drug definition. The U.S. courts have determined that food provides "aroma, taste, or nutritive value." The Center for Veterinary Medicine (CVM) in the Food and Drug Administration (FDA) regulates both animal food and drugs. Animal food includes both livestock feed and companion animal food. Food and substances added to food must be safe and achieve their intended purpose. The CVM administers 2 regulatory processes for animal food. The food additive petition process is described in regulation 571 in Title 21 of the Code of Federal Regulations (21 CFR 571). The safety of the additive at the intended use rate must be addressed for the animal, environment, and food-producing animals; safety of human food products obtained from animals fed the additive must also be addressed. The second process is similar to the first, except that the information concerning the safety of the substance for the intended use and its functionality are in the public domain, i.e., published in scientific literature. When the safety and functionality of a substance's use in animal food is generally available and recognized, qualified experts may determine that this use is exempt from the premarket requirements of the Act because the use is generally recognized as safe (GRAS). A GRAS determination generally requires the same quantity and quality of information needed for a food additive petition with the added burden that the information be public. Firms cannotify CVM about a GRAS determination through the animal food GRAS notification program. Also, for substances that raise no safety concerns when used in animal food, firms can request the Association of American Feed Control Officials (AAFCO) to publish an ingredient definition in the AAFCO Official Publication. For all these processes, firms must establish what the substance does and determine how their intended use fits under the definition of food in the Act. Firms must also demonstrate that the substance achieves the intended effect.

Key Words: animal food, functionality, intended use, regulation

ASAS CELL BIOLOGY SYMPOSIUM: LONG-TERM CONSEQUENCES OF MATERNAL AND NEONATAL NUTRITION FOR PREGNANCY AND POSTNATAL OUTCOMES

0106 Lactocrine programming of postnatal reproductive tract development. F. F. Bartol[*1] and C. A. Bagnell[2], [1]*Auburn University, AL,* [2]*Rutgers University, New Brunswick, NJ.*

Lactocrine signaling occurs when bioactive factors are communicated from mother to offspring as a consequence of nursing. In the pig (*Sus scrofa*), relaxin was identified as a prototypical lactocrine-active factor in colostrum. Administration of exogenous relaxin from birth [postnatal day (PND) = 0] increased neonatal uterine estrogen receptor-α (ESR1) expression. Using multispectral immunofluorescence imaging, expression of ESR1 is detectable in nascent endometrial glandular epithelium and stroma within 2 d of birth, and supports uterine gland genesis. Imposition of a lactocrine-null condition for 2 d from birth by substitution of porcine milk replacer for colostrum retarded endometrial development and uterine gland genesis. Compared with nursed gilts, replacer feeding from birth reduced stromal ESR1 expression and endometrial cell proliferation, and increased endometrial relaxin receptor expression by PND 2. Effects of transient imposition (48 h) of the lactocrine-null state on endometrial morphology were pronounced by PND 14, when cell proliferation, reflected by patterns of proliferating cell nuclear antigen immunostaining, and development of nascent endometrial glands were markedly reduced. Collectively, the observations suggested a lactocrine-driven mechanism regulating establishment of the uterine developmental program and endometrial adenogenesis in the neonatal pig. The lactocrine hypothesis for maternal programming of reproductive tract development predicts that neonates deprived of colostrum will have reduced uterine capacity to support conceptus development as adults due to disruption of the uterine developmental program shortly after birth. Results of a retrospective study involving 381 gilts indicated that lifetime fecundity (number of piglets born alive over ~4 parities per gilt) was reduced in animals that consumed minimal amounts of colostrum as indicated by low serum immunocrit values on PND 0. To the extent that the first 2 d of neonatal life constitute a critical period for establishment of the uterine developmental program, effects of replacer feeding for 2 d from birth on global patterns of uterine gene expression were evaluated using whole uterine transcriptome analysis via RNA sequencing (RNA-seq). Analyses were performed on uteri (n = 4/group) obtained on PND 2 from gilts that were either nursed (PND 2N) or fed porcine milk replacer from birth (PND 2R). Using RNA-seq, 896 genes were determined to be differentially expressed (> twofold) between the PND 2N and PND 2R groups. Thus, disruption of lactocrine signaling has profound effects on neonatal uterine gene expression. The results indicate that lactocrine support is required to establish a normal uterine developmental program in the neonatal pig.

Key Words: development, lactocrine programming, neonate

0107 Long-term consequences of maternal and neonatal nutrition for pregnancy and postnatal outcomes. D. G. Burrin[*1] and B. Stoll[2], [1]*USDA-ARS Children's Nutrition Research Center, Houston, TX,* [2]*Baylor College of Medicine, Houston, TX.*

The nutritional environment during fetal and neonatal life is a key determinant affecting the risk for adult-onset diseases, such as diabetes and obesity. Studies show that preterm infants experience increased risk for glucose intolerance as adolescents and young adults. Preterm infants often receive parenteral nutrition for several days or weeks after birth as a lifesaving form of clinical support. Considerable evidence shows that the normal and dysfunctional secretion of gut hormones play a key role in metabolic health and diseases, including diabetes and obesity. We have used the model of parenterally fed neonatal pig to test whether the modality of nutritional support (enteral vs. parenteral) significantly impacts both the pattern of gut hormone secretion and metabolic function. We first showed (J. Nutr.140:2193) that chronic parenteral (PN) compared with enteral (EN) nutrition in neonatal pigs for 2 wk leads to an adverse metabolic phenotype marked by increased glucose intolerance, insulin resistance, body fat deposition, and reduced pancreatic β-cell proliferation. We also showed (JPEN.36:538) that the pattern of enteral nutrition (intermittent vs. continuous) is a stronger determinant than modality of nutrition to optimize glucose utilization and insulin sensitivity. We also showed that the secretion of gut incretin hormones, glucose-dependent insulinotropic polypeptide (GIP), and glucagon-like peptide 1 (GLP-1) correlated closely with glucose utilization and insulin sensitivity. An important question is whether the adverse metabolic phenotype that results from that chronic PN during the first 2 wk of neonatal life persists into late infancy and adolescence. We recently tested this in newborn pigs by feeding either PN or EN for 2 wk, followed by ad lib feeding of a high-fat (30%) and sucrose (20%) diet for 5 mo. We measured body composition by dual-emission X-ray absorptiometry at 2 and 8 wk, and 5 mo, and performed an IVGTT at 5 mo. Our results showed that PN during the neonatal period increased adiposity transiently into early infancy, but PN-induced glucose intolerance, adiposity, pancreatic β cell number, and hepatic steatosis were not sustained into adolescence, even when challenged with an obesogenic diet. This presentation will highlight the link between enteral nutrition as a key trigger for gut hormone secretion and function, and how these hormone-signaling pathways may be relevant to domestic animal growth.

Key Words: nutrition, pregnancy, signaling pathways

0108 The epigenetic landscape of the β-cell in IUGR rats. S. Pinney and R. A. Simmons*, *Perelman School of Medicine, University of Pennsylvania, Philadelphia.*

The abnormal intrauterine milieu of intrauterine growth retardation (IUGR) permanently alters gene expression and function of pancreatic b-cells, leading to the development of diabetes in adulthood. Expression of the pancreatic transcription factor Pdx1 is permanently reduced in IUGR and epigenetic modifications are responsible for this decrease. The Pdx1 encodes a homeobox transcription factor, critically important for β-cell function and development. The fetal IUGR state is characterized by loss of USF-1 binding at the proximal promoter of Pdx1, with deacetylation of histones H3 and H4, due to recruitment of the histone deacetylase (HDAC1) and the co-repressor Sin3A. After birth, H3K4 is demethylated and H3K9 is methylated. During the neonatal period, the reduction in Pdx1 expression and these epigenetic changes can be reversed by HDAC inhibition. Finally, once diabetes occurs, DNA methylation of the CpG-island in the proximal promoter ensues, resulting in permanent silencing of the Pdx1 locus. Exendin-4 (Ex-4), a long-acting glucagon-like peptide 1 (GLP-1) analog, given on d 1 to 6 of life increases Pdx1 expression and prevents the development of diabetes in the IUGR rat. The Ex-4 increases USF-1 and PCAF association at the proximal promoter of Pdx1, thereby increasing histone acetyl transferase (HAT) activity, which leads to a permanent increase in histone H3 acetylation and H3K4 methylation. Normalization of these histone modifications precludes DNA methylation, thereby preventing silencing of Pdx1 in islets of IUGR animals. These studies demonstrate a novel mechanism whereby a short treatment course of Ex-4 in the newborn period prevents diabetes in adulthood by restoring Pdx1 promoter chromatin structure, thus preserving Pdx1 transcription. Finally, using the HELP assay, we generated the first DNA methylation map of the rat genome in normal and IUGR β-cells. We validated candidate dysregulated loci with quantitative assays of cytosine methylation and gene expression. The IUGR changes cytosine methylation at 1400 loci in male rats at 7 wk of age, preceding the development of diabetes and thus representing candidate loci for mediating the pathogenesis of metabolic disease that occurs later in life. Epigenetic dysregulation occurred preferentially at conserved intergenic sequences, frequently near genes regulating processes known to be abnormal in IUGR islets, such as vascularization, β-cell proliferation, insulin secretion, and cell death, associated with concordant changes in mRNA expression. These results demonstrate that epigenetic dysregulation is a strong candidate for propagating the cellular memory of intrauterine events, causing changes in expression of nearby genes and long-term susceptibility to type 2 diabetes.

Key Words: diabetes, epigenetic, programming

ASAS GRADUATE STUDENT SYMPOSIUM: RESEARCH ETHICS: WHAT ARE THEY AND WHY ARE THEY NEEDED?

0109 What are research ethics? M. S. Calvo-Lorenzo*, *Oklahoma State University, Stillwater.*

Due to the diversified nature of research, there is no universal manner in which scientific investigations are conducted. Thus, the responsible conduct of research will vary from discipline to discipline, and from laboratory to laboratory. Society's expectations for research responsibility are complex and guidelines for conducting responsible research are not always clearly defined. Some responsible practices are defined and mandated at the professional, institutional, and/or governmental level, whereas other non-binding guidelines and best practices are informally defined and executed through the mentor/trainee relationship. The culmination of these various practices, including responsible behaviors and attention to conducting the best research by scientists, has established that research ethics must be built on a commitment to the essential values of honesty, accuracy, precision, efficiency, and objectivity. These values represent research integrity and are the basis for ethical decisions and actions, regarding data management, mentor and trainee responsibilities, collaborative research, use of humans and animals in experimentation, authorship and publication, public accountability, and the peer review process. "Ethics" is often defined as the study of moral values and ethical decision-making aids us in the critical consideration of such values to make decisions we consider to be "right." However, "ethics" is often used interchangeably with the term "morals" and our ability to ethically analyze our actions should not be confused with the ability of our conscience to differentiate right from wrong. Moreover, ethical behavior implies adherence to principles that underlie a specific context or profession, whereas the use of morals in the work place or research setting implies conformity with a behavioral code generally accepted in some defined setting or culture. This distinction is important in understanding what research ethics are, especially as research enters the realm of moral reasoning. One must determine what is ethically (vs. legally) right and wrong. Ultimately, making well-reasoned ethical and moral responses to dilemmas in the conduct of science should consider: 1) all issues and points of conflict, 2) the interests and expectations of all parties, 3) recognition of possible consequences that may arise from proposed actions, and 4) identification of the professional and moral obligations of scientists. Researchers and trainees can gain more insight and knowledge by using case studies to discuss the elements of critical thinking, ethical decision making, and moral reasoning as it pertains to situations that scientists encounter during the course of a research career.

Key Words: research ethics

0110 Why are research ethics important and how do they affect academia? M. L. Galyean*, *Texas Tech University, Lubbock.*

Animal welfare and associated animal care and use issues have been at the forefront of ethical concerns for animal science researchers for many years. More recently, animal science researchers, particularly those working with industry-sponsored research, have come under increasing scrutiny with respect to bias and conflict of interest in their research programs. Universities and most corporate research units have well-defined procedures that must be followed when vertebrate animals are used in research. Similarly, most universities have established policies for assessing, reporting, and remediating conflicts of interest of a personal, financial, or professional nature. In terms of financial conflicts, a collective interest of > $5,000 is typically the threshold for disclosure of potential conflicts to colleagues and research team members. More subtle conflicts of interest and bias that do not require reporting might affect faculty members who receive discretionary funding and products to support research, consulting activities, honoraria for work on advisory boards or for giving technical presentations to industry clients groups, and trips to company-sponsored activities of various types. In terms of animal research, responsible conduct that will instill public confidence requires more than following minimum guidelines. Faculty researchers, graduate students, and research staff should work together to provide the highest possible standards of animal care; however, ultimately the principal investigator must be responsible and devote appropriate time to oversight of research projects and animal care. Delegating oversight of research activities and animal care to graduate students or staff members without proper training and instruction is unwise and inappropriate. All members of research teams should be dedicated to optimal experimental design and methods of collection, analysis, and interpretation of data. To do otherwise is an unethical defiance of public trust. Busyness is never an appropriate excuse for principal investigators to shirk their responsibilities to research team members in terms of providing proper oversight of research activities. Research teams should conduct regular, transparent self-evaluations of whether they are providing the highest standards of animal care and also assess potential conflicts of interest and bias for all team members. Including peers outside the research team to help evaluate real or perceived bias and conflict of interest issues might be useful. Graduate students and research staff can play a key role in ensuring ethical conduct of research by asking for training and instruction, and questioning potential bias and conflict of interest issues.

Key Words: animal care, bias, conflict of interest, research integrity

0111 Importance and impact of research ethics on industry. M. Brown[*1] and D. Smith[2], [1]*Global Animal Products, Inc., Amarillo, TX,* [2]*Performance Plus Liquids, Inc., Sterling, CO.*

Ethics is commonly defined as the rules of behavior or norms of conduct that differentiate between acceptable and unacceptable practices. Guidance of scientists by an appropriate ethical compass is paramount in research because scientists occupy a unique position of trust with the readers/users of their data. One end of the research ethics spectrum is typified by descriptors, such as error-free, accurate, precise, repeatable, well-documented, transparent, objective, and unbiased, whereas the opposite end of the spectrum involves misconduct in some form. A wealth of resources is available that illuminate the principles of ethics in the context of responsible conduct in research. Full awareness and evolution of one's own understanding of ethics arises from daily use of these principles and periodic reflection. In the scope of this presentation, the impact of research ethics of a given applied research program on industry is a function of the quality of the data generated and conveyed, and on the cultivation of skills and attributes of graduate students from that program that will be carried into future careers. Herein, industry refers to beef cattle production and the professionals that provide service to this sector of agriculture. Discussion will encompass quality assurance considerations in the execution of applied studies and generalized examples that illustrate the potential impact of low-quality data on certain aspects of industry. A comprehensive survey of employers of master's and doctoral graduates in the cattle feeding sector from 20 states in the United States and 1 Canadian province indicates that the area of greatest discrepancy between employer desires and employee preparation involved elements of character, followed by interpersonal and communication skills. Efforts to conduct and report high-quality data garner the highest value and appreciation by industry. Greater emphasis on fostering good character and communication skills of developing scientists will be beneficial to industry, academia, and society.

Key Words: applied science, ethics, quality assurance

BEEF CATTLE REPRODUCTION SYMPOSIUM: **REBUILDING THE U.S. COW HERD: RETHINKING THE WAY INDUSTRY SELECTS AND DEVELOPS REPLACEMENTS**

0112 Rebuilding the U.S. cow herd: Rethinking the way industry selects and develops replacements. D. S. Brown* and D. J. Patterson, *University of Missouri, Columbia.*

The U.S. beef industry is confronted with a significant long-term decline in cattle numbers driven in part by record input costs and severe drought conditions in many major cattle-producing states. These recent challenges only add to the long-term issues the industry has faced, which include an aging producer population, increased global competition, increased competition from other meat proteins, weak domestic demand for beef, and a perceived lack of economic incentives to expand the cattle herd. The weakness in beef demand provided impetus for the industry to begin the Beef Quality Assurance program. Although the industry has experienced more consistency in beef products over the last 3 decades, there are major strides left when today < 5% of cattle grade Prime. In comparison with other domestic livestock sectors in the United States, tradition and segmentation within the U.S. cattle industry has hindered the adoption of newer production and marketing strategies. Coordinating the various industry segments (cow-calf, stocker, feedyard, processor) with allied industry (AI companies, seed stock suppliers, feed and pharmaceutical industries) offers the potential to enhance technology adoption and contribute to increases in production efficiency. As the U.S. cattle industry moves to rebuild its declining numbers, the focus of much of the industry will turn to heifer retention and appropriate practices related to beef heifer development. The industry has provided better beef quality signal transmission through available marketing grids in the industry today. Yet, these grids generally require cow-calf producers to maintain some ownership stake in the cattle through the feedyard. Producers who have invested in developing higher quality cattle and beef in the past often found genetic improvement to be slow and inconsistent, which oftentimes reduced economic incentives of quality focus. The technologies that have come online over the past few years and new genomic advances on the horizon appear poised to rapidly increase genetic improvement and consistency. The combination of better market incentives for higher quality beef coupled with technologies that allow producers to more easily invest in genetics focused on quality provide the industry a unique opportunity to increase the cow herd with a more refined focus on the genetic potential of the herd as it relates to efficiency and higher quality. It would appear these technologies have the added value of reducing producer risk by providing more consistency in the beef produced.

Key Words: economic, quality, technologies

0113 Physiology and endocrinology of puberty in heifers. J. Atkins*[1], K. G. Pohler[2], and M. F. Smith[2], [1]*American Simmental Association, Bozeman, MT,* [2]*University of Missouri, Columbia.*

Most beef producers expect their heifers to be able to calve for the first time at 2 yr of age. Frequently, the breeding season for heifers begins 2 to 3 wk before the beginning of the breeding season for cows. Furthermore, the fertility associated with the first pubertal cycle is reportedly lower than subsequent cycles. Therefore, having heifers that reach puberty 6 to 9 wk before the start of the breeding season can have a positive impact on conception rates and ultimately profit for producers. Additionally, heifers that conceive earlier in the breeding season, calve earlier in the calving season and have a better chance of conceiving the following breeding season. Early-calving heifers produce more calves in their lifetime and remain in production longer than later-calving heifers. Understanding the physiology and endocrine maturation leading to onset of puberty is critical to maximizing heifer development. Puberty, defined as the first ovulatory estrus, is preceded by progressive growth and development of the uterus, ovaries, and hypothalamic-pituitary-ovarian axis. Follicle waves endure longer, dominant follicles become larger, and oocyte competence improves as heifers approach puberty. The CL formed after the first ovulation and luteinization is short lived due to a premature release of $PGF2_{\alpha}$. This short exposure of progesterone followed by a rise in estradiol is important in establishing the appropriate timing of $PGF2_{\alpha}$ release and can be mimicked using a progestin in estrous synchronization protocols. Estradiol shifts from having a strong negative feedback on the hypothalamus and pituitary to a reduced negative feedback, and finally a positive feedback, causing the gonadotropin surge and ovulation (gonadostat hypothesis). The switch in the hypothalamic response to estradiol may be due to a drop in estradiol receptors, coupled with increased concentrations of kisspeptin and increased sensitivity to existing kisspeptin molecules by GnRH neurons. Producers can use reproductive tract scoring (RTS), a subjective measurement of the uterus and ovaries, to assess heifers' sexual maturity before the breeding season (4 to 6 wk, ideally). This gives producers enough time to make management decisions based on the RTS assessment. In summary, this paper/presentation provides a review of the research into the physiological and endocrine maturation leading up to puberty in beef heifers.

Key Words: beef, heifer, puberty

0114 Beef heifer replacement considerations related to breed and biological type. A. L. Van Eenennaam*, *University of California-Davis, Davis.*

The reproductive fitness of females is a major driver of profitability and fertility considerations should be given high priority when selecting the best replacement heifers. Selection for replacement heifers is based on their readiness and ability to conceive in the proposed breeding season, which places indirect selection on dam fertility, as fertile cows tend to conceive early and generate early-born heifers that are more likely to be selected as replacements. Age at puberty is variable among breeds and biological types (British < Continental < *Bos indicus* influenced), and is moderately heritable. The choice of breed(s) and breeding system play an important role in overall ranch profitability and before making a commitment to any breed or breeding system, the logistics, costs (including opportunity costs), benefits, and feasibility should be objectively evaluated for a given set of environmental, resource, management, and marketing constraints. Expected progeny difference (EPD) genetic merit estimates for heifer pregnancy (HP), stayability (STAY), and scrotal circumference (SC) are available for some breeds, and have all been positively associated with female fertility. Heterosis (also known as hybrid vigor) occurs when the performance of the crossbred progeny for a specific trait is greater than the average of their parents. Heterosis effects are significant and important for low heritability fitness and survival traits, such as longevity, lifetime production, and reproduction rate. Improvements in cow-calf production due to heterosis result from both the improved maternal performance of the crossbred cow and individual performance of the crossbred calf. Complementarity results from crossing breeds of different but complementary biological types. This occurs when specialized sire and dam breeds are used in terminal systems to optimize performance levels. Properly designed crossbreeding systems, based on heterosis and complementarity, will generally out produce those based on straight breeding in productivity, but the challenge is to manage the program to produce progeny that meet market specifications and acceptance. The combination of AI and gender-selected, or "sexed" semen, offers the opportunity to rethink the logistics and economics associated with different breeding systems. Gender-selected semen provides the opportunity to develop novel breeding scenarios and avoid some of the logistical problems associated with the various crossbreeding systems. Emerging reproductive and genomic technologies offer exciting possibilities for innovative approaches to heifer selection and breeding program design; but as with all new technologies, enthusiasm needs to be tempered with a realistic evaluation of the costs and expected benefits.

Key Words: breed, complementarity, heterosis

0115 Nutritional development and the target weight debate. J. B. Hall*, *University of Idaho, Carmen.*

Postnatal nutrition has a profound effect on reproductive efficiency and lifetime productivity of beef heifers. A nutritional management strategy that focuses on allowing a high percentage of heifers to achieve puberty before the breeding season while reducing feed costs is the goal of most operations. Both preweaning and postweaning nutrition affect age at puberty. Preweaning nutrition may have a greater effect than postweaning nutrition on the onset of puberty, but the impact of management is limited preweaning. Creep feeding or creep grazing may increase the incidence of precocious puberty in heifers. Similarly, exposure to high concentrate diets during early weaning may increase precocious puberty, but early weaning has variable effects on pregnancy rates in heifers. To some extent, postweaning gain can overcome preweaning nutrient deficiencies. However, it is currently unknown if postweaning nutrition can alleviate negative prenatal nutritional effects on reproduction. Energy is the primary limiting nutrient in beef heifer diets; however, protein must be adequate and may be the limiting nutrient in certain circumstances. A few studies indicate that heifers may benefit from supplementation with rumen undegradable protein. In general, the source of nutrients does not appear to be important as long as animal requirements are met. The nutritional requirements listed in the Beef NRC appear to be adequate for heifer development, but more studies validating the Beef NRC requirements for growing heifers are needed. Altering pattern of growth during the postweaning developmental period may offer opportunities for decreased development costs and perhaps enhanced cow longevity. The most practical benchmark for proper heifer development at the ranch level has been the target weight method. Recently, the traditional target weight of 65% of mature weight at breeding has been challenged. Achieving a target weight of 65% of mature weight by the beginning of the breeding season ensures nutrition does not limit reproductive success of heifers; however, it appears a target weight of 55% has application for some operations and may have positive effects on heifer longevity. At present, multiple nutritional tools are available to design systems or respond to environmental factors (i.e., drought) for developing replacement beef heifers. Proper analyses of the impact of these systems need to include long-term effects on cow reproduction and longevity.

Key Words: heifer, nutrition, reproduction

0116 Management strategies for adding value to replacement beef heifers: A working model—The Missouri Show-Me-Select Replacement Heifer Program. D. J. Patterson*[1], J. M. Thomas[1], D. S. Brown[1], J. E. Decker[1], W. J. Sexten[1], and S. E. Poock[2], [1]*University of Missouri, Columbia,* [2]*University of Missouri-College of Veterinary Medicine, Columbia.*

Utilization of existing and emerging management technologies enable beef producers to improve breeding performance of heifers during the first breeding season and during subsequent calving and rebreeding periods as 2-yr-olds. These practices ensure that heifers that enter herds as raised or purchased replacements contribute to the general performance and productivity of an entire cow herd immediately, and cumulatively long term. In 1996, extension specialists, veterinarians, beef producers, and allied industry in Missouri linked arms to develop and implement a plan that would impact long-term sustainability of beef herds across the state. This plan was focused on the cyclical reproductive process in beef cattle and involves 5 basic steps: 1) create an understanding of the importance of heifer development based on reproductive outcomes; 2) implement changes in heifer development that eventually spill over into the cow herd; 3) emphasize the importance of reproductive management, which becomes apparent as changes are implemented; 4) expand producer focus to genetic improvement; and 5) emphasize to participating herds that creation of a value-added product requires a re-evaluation of marketing strategies. These 5 steps have built equity in herds that embraced the plan; 17 yr later the Missouri Show-Me-Select Replacement Heifer Program has impacted the cattle industry statewide. The program objectives include: 1) a total quality management approach for health and management of heifers from weaning to late gestation; 2) increased marketing opportunities for and added value from Missouri-raised heifers; and 3) creation of reliable sources of quality commercial and purebred replacement heifers. The program incorporates all available tools to support long-term health, reproduction, and genetic improvement of replacement beef heifers and includes provisions for ownership, health and vaccination schedules, parasite control, implant use, weight, pelvic measurement, reproductive tract score, estrous synchronization, AI, service-sire requirements for BW- or CE-EPD, early pregnancy diagnosis, fetal aging, fetal sexing, and BCS. In a state that ranks second in total number of beef cows in production, the Missouri Show-Me-Select Replacement Heifer Program is a working model that integrates improvements in selection, management, health, and genetics into a total development, management, and marketing program through emphasis on reproductive outcomes. Impact in Missouri stemming from the Show-Me-Select program and the proof of concept it demonstrates raises the question as to whether it is time to standardize requirements used in the program to broaden its scope to other major beef cattle-producing states.

Key Words: Missouri, replacement beef heifer, Show-Me-Select

BEEF SPECIES: MAKING MORE BUT USING LESS: THE FUTURE OF THE U.S. BEEF INDUSTRY WITH A REDUCED COW HERD AND THE CHALLENGE TO FEED THE UNITED STATES AND WORLD. *SESSION 1:* THE U.S. STOCKER AND FEEDLOT INDUSTRIES

0117 Nutritional strategies to improve efficiency in the stocker and feedlot industries in a consumer-conscious market. M. S. Kerley*, W. J. Sexten, and A. M. Meyer, *University of Missouri, Columbia.*

Biological efficiency potential and nutrient supply synchrony are primary determinants of feed efficiency when converting feed to beef carcass yield. Feedlot diets have historically been formulated to have a minimum roughage inclusion to maintain rumen health and a minimum protein level (crude, metabolizable, or degradable protein) for targeted growth rates. While historically effective, we have asked if poorly digested and increasingly expensive roughage could be eliminated. We have also asked why diets are formulated for protein when calves have specific requirements for AA. When no-roughage diets were formulated to match absorbable AA supply to diet effective energy density (AAEE), net energy equations were found to overestimate energy required for gain and feed efficiency was improved in growing cattle. Recently developed, commercially available, in-pen weighing technology offers further opportunity to improve feed efficiency and reduce diet costs by formulating diets to supply absorbable AA equal to requirements, based on animal growth rate. Further improvement in efficiency has been demonstrated via selection for efficiency, based on residual feed intake (RFI). Our research to date has led us to conclude that nutrient requirement is influenced by RFI phenotype. More accurate estimates of biological energy requirement, real-time growth performance measurement capability, and increased biological efficiency selection can improve postweaning feed efficiency of cattle to a greater magnitude than generally thought possible, but full potential will not be realized if diet formulations do not support the potential for improvement.

Key Words: beef, efficiency, nutrition

0118 What is the future of genetic selection and cattle sorting technologies in the stocker and feedlot industries? R. L. Weaber*, *Kansas State University, Manhattan.*

The U.S. beef industry has experienced dramatic change over the past several years. The persistent drought throughout much of the United States has resulted in a reduction in cow inventory. The USDA reported that the 1 January 2014 all cattle and calves inventory was down 2% from 2013, now totaling 87.7 million head, the lowest since 1951. In the same report, USDA inventory of cows and heifers that calved totaled 38.3 million, the smallest since 1941. Contraction of cow inventory and resulting calf crop have created challenges all along the beef value chain. Large vacant capacity exists in the U.S. feedlot and packing sectors. As a result of tight inventories, whole sale beef and fed and feeder cattle prices have reached record highs. High prices are shrinking per capita beef consumption to an expected 24 kg in 2014, decreasing 4.5 kg in the last decade. An estimated 60% of domestic beef consumption is ground product. Consumers continue to be value driven, choosing more ground beef in the marketplace for price and convenience. The U.S. all steak price to ground beef price ratio has trended downward over the last decade from 2.5 in early 2004 to < 1.7 in late 2013, indicating that all steak price hasn't kept pace with the price increase in ground beef. Some suggest whole muscle beef cuts are becoming luxury items. While consumers continue to seek lower cost protein sources and lower cost beef, the industry's production model remains unchanged. Most cattle are fed and marketed to maximize the value captured from middle meats, which comprise roughly 20% of the beef carcass, targeted to grade Choice average or better. This leads to substantial inefficiencies in the feeding and packing sector through overfeeding of cattle. In some cases, the additional fat decreases the red meat yield and value of end meats, which comprises the remaining 80% of the carcass. The beef industry's current issues in product demand, high retail prices, and lack of market-targeted products call for substantial changes in the beef value chain in terms of cattle sourcing, genetics, management, pricing, and marketing. Early targeting of cattle to an appropriate end use, based on genetic potential to efficiently meet a specified market target, could substantially change the way cattle are managed in terms of backgrounding and feedlot nutrition, growth-promoting technologies, and sorting for optimal marketing to maximize individual animal profitability.

Key Words: beef cattle, genetics, selection

0119 Beef quality vs. quantity in today's market. B. J. Johnson*, *Texas Tech University, Lubbock.*

Exogenous growth-enhancing compounds, such as steroidal implants and β-adrenergic agonists (βAA), have been used to improve growth rate and efficiency in meat animals for more than a half century. In cattle, these compounds enhance efficiency of growth by preferentially stimulating skeletal muscle growth at the expense of adipose tissue accretion. These compounds have additive effects on carcass gain. Combined use of both these technologies have been shown to increase carcass gain > 35 kg during a typical feeding period. Consequently, these growth-enhancing compounds have been shown to reduce intramuscular fat (marbling) in beef cattle compared with non-treated cattle. This reduction in marbling score has been

associated with lower beef quality. These cellular events may in part be responsible for the negative effects observed with the use of these compounds in terms of marbling development in beef cattle. Markers of adipogenic differentiation were also affected by TBA/E_2. In adipose tissue, an enzyme important for energy balance, AMPKα, may also be affected by anabolic steroids and βAA. These data indicate that in adipose tissue compared with skeletal muscle, anabolic steroids and βAA may have opposite effects on cellular growth and differentiation. This inverse relationship may contribute to changes in beef quality. Balance is needed to maintain beef quality in light of demands to increase beef production, globally.

Key Words: adipose tissue, beef quality, skeletal muscle

0120 Economic considerations related to rebuilding the U.S. cow herd. G. T. Tonsor*[1] and L. L. Schulz[2], *[1]Kansas State University, Manhattan, [2]Iowa State University, Ames.*

The entire U.S. cattle industry is in the middle of several structural changes with pending (or perhaps ongoing) herd expansion at the heart of each current and possible industry adjustment. These changes coupled with issues more external to the industry are effectively increasing the overall uncertainty of profitability for not only cow-calf producers but stakeholders throughout the industry. This increased uncertainty will be welcomed by some producers, who in turn may choose to expand their herds in coming years. Conversely, other producers uncomfortable with this uncertainty or facing favorable alternatives to cow-calf production will stabilize or further reduce their herds. The net impacts of these adjustments will dictate the collective make-up of the U.S. cattle industry for years to come. The ability of cattle producers to grasp the profitability and overall risk situation of their operations and broader industry trends is critical for long-term business success. Farmers and ranchers considering expansion need to make sound decisions to make sure their operations are economically sustainable and well positioned to succeed. In addition, opportunities exist for integration of young producers and future generations into cattle production, but these individuals need knowledge and tools to help them thrive in the industry. These expansion and entry into the industry decisions are best made when working with current and accurate understanding of broader economic trends. This presentation will discuss the broad economic situation motivating growing interest in herd expansion and subsequently outline key trends that are likely to influence realized national herd expansion. Throughout the presentation, a host of decision aides and related educational resources will be highlighted, enabling attendees to act on information they receive and apply it to their own operations and situations.

Key Words: beef cattle herd expansion, cow-calf production, economics, management

BEEF SPECIES: MAKING MORE BUT USING LESS: THE FUTURE OF THE U.S. BEEF INDUSTRY WITH A REDUCED COW HERD AND THE CHALLENGE TO FEED THE UNITED STATES AND WORLD. *SESSION 2:* THE COW-CALF INDUSTRY

0121 Where can we support more cows? Overview of the beef cow herd and land use. J. A. Paterson*, *National Cattlemen's Beef Association, Centennial, CO.*

The U.S. cow herd population has declined from 45 million in 1975 to 29 million in 2014. Record-setting drought in the Southern United States caused beef cow herd liquidation, fewer calves on cereal grain pastures, and more cattle in feedlots. All cattle and calves in the United States totaled 90.8 million head (2012) and was the lowest inventory since 1952. The recent drought caused cow numbers to decline by 13% in Texas, 14% in Oklahoma, and 11% in New Mexico. The consequence of low supply has been the closure of packing plants in Texas and California. When there is a return to normal pasture conditions, there will be more of a willingness to increase heifer retention and increase the nation's cow herd inventory. How many beef cows does the beef industry need to remain sustainable? It has been predicted that the cattle industry may not grow beyond 32 million cows because of the availability of growth-promoting technologies, improved cattle genetics, nutritional and health management practices, and new generation antibiotics and anthelmintics. The reasons for future expansion include better pasture conditions in most areas of cow-calf country, higher feeder calf prices, record high beef prices, lower corn prices, and lower debt in mature ranching operations. The reasons for not increasing cow numbers include advancing age of ranchers, EPA regulations in the Eastern United States, Forest Service and BLM regulations on public lands in the West, and continued fear of drought. A significant increase in the beef cow herd is not expected until 2016 or 2017. With expansion likely underway, it will be 2017 or 2018 before a trend of larger fed cattle supplies will be measured. As a percentage of the nation's cow herd population, the Great Plains increased from 27 to 34.2% and the Corn Belt increased slightly from 13.3 to 14%, whereas the Southern Plains (-3% units), West (-1.2% units), Southern Plains (-3% units), and Southeast (−4.4% units) have all decreased. A decrease in cow numbers is predicted to be more pronounced in the states of Illinois, Indiana, Iowa, Minnesota, Missouri, Kentucky, and Tennessee, where competition with crops is greater. As a result, it is projected that an increasing share of the total beef cow herd will be located in the Great Plains, with a smaller increase in the Western Corn Belt.

Key Words: cattle, drought, retention

0122 How can we improve replacement heifers as we rebuild the cow herd? S. L. Lake*, *University of Wyoming, Laramie.*

The beef industry is currently experiencing a climate that few, if any, generations have ever encountered. Beef demand is soaring, both nationally and internationally, cattle prices continue to break all-time highs, and environmental conditions in many regions of the United States have put a premium on calves and replacement females. One of the areas of greatest potential to increase profitability and sustainability in livestock operations is to capitalize on the heifer enterprise. However, to rebuild the national cow herd in the current economic climate, producers and scientists are going to have to increase the use of technology and outside-the-box thinking to remain competitive in the global market. Applicable research is needed to answer relevant production questions that will enable the U.S. cow herd to grow and remain competitive in global markets.

Key Words: heifers

0123 Can we improve cow efficiency or manipulate feeding strategies to reduce inputs? H. C. Freetly*, *USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

In most temporal environments, nutrient availability does not match the nutrient requirement of the cow; and for part of the year, nutrient availability is less than what is required to keep a cow at maintenance. Intensively managed agriculture production systems use mechanically harvested feed to fill the deficit between nutrient availability and nutrients required to maintain cow weight. These harvested feeds are often expensive. In open and pregnant cows, the energetic efficiency of allowing cows to lose and gain body energy does not differ from holding cows at constant body energy. This common energetic efficiency allows for the development of management strategies that allow cows to decrease BW during periods of low nutrient availability and subsequently gain BW when grazed forages are available. However, these strategies do not decrease the total energy required by a cow in a production cycle. Production efficiency does not differ between cows that lose BW in the second trimester and regain BW in the third trimester, and cows managed to maintain maternal BW throughout pregnancy. The nutrient management strategy chosen for the pregnant cow may influence productivity of the subsequent generation through developmental programing. The timing of nutrient restriction during pregnancy may be a trigger that alters lifetime productivity of heifers that have experienced a restricted nutrient environment in utero. Nutrient restriction in early pregnancy has been associated with reduced fertility in daughters; however, heifers born to cows that receive elevated nutrients in the third trimester breed earlier than heifers born to cows fed to maintain maternal BW. Recent emphasis on the development of tools to select for

feed efficiency in the growing animal may impact subsequent performance of the cow. Residual feed intake (RFI) is a popular measure of feed efficiency in growing and lactating cattle, and EPD are being developed to allow for its selection. One of the outcomes of selecting for lower RFI is a decrease in feed intake. The consequence of selecting for low RFI in growing cattle in the cow herd needs to be explored. The USDA is an equal opportunity provider and employer.

Key Words: beef, cow, nutrition

0124 Can we build the cow herd by increasing longevity of females? A. Roberts*[1], M. Petersen[1], and R. N. Funston[2], *[1]USDA-ARS Fort Keogh Livestock and Range Research Laboratory, Miles City, MT, [2]University of Nebraska, West Central Research and Extension Center, North Platte.*

Increasing longevity of beef cows by decreasing proportion culled due to reproductive failure reduces the number of replacements needed to sustain a constant herd size. Rate of reproductive failure varies with cow age, where failure in cows younger than 4 yr of age can be twofold greater than in cows 4 yr and older. In addition, BW of cow and calf at weaning also increase as cows advance from 2 to 5 yr of age. Cumulative effect of improving retention in young cows is greater production efficiency through decreased replacement rate and a consequent change in age structure of the herd toward a greater proportion of cows at their maximal production potential for calf BW at weaning and cow BW at time of culling. Calculations from cow age-specific culling and BW data from commercial and research herds indicate that reducing replacement rate from 20 to 15% can result in annual increases of 20% of total calf crop weight and 10% in cull cow BW. Although improving longevity can foster increases in efficiency, genetic advancement in longevity is challenging, as it is the sequential culmination of the annual repetition of numerous discrete physiological processes, each ending in a qualitative response, including puberty, ovulation, transport of male and female gametes, fertilization, implantation, pregnancy maintenance, parturition, and calf survival. Successful completion of 1 process is the prerequisite to evaluate subsequent processes. Comparisons among different biological types of cattle maintained under varying levels of nutritional inputs provide evidence for genetic variation in prioritization of nutritional partitioning among production traits (i.e., milk, growth, and reproduction) and the apparent nutritional threshold required for initiation of reproductive processes indicating genetic-by-nutrition interactions. This is in contrast to traits for which EPD exist, where genetic-by-environmental interactions are not substantial. The impact of nutrition on reproduction has been extensively studied. Results for this research led to recommendations that heifers and cows be fed to a threshold BW or BCS to ensure reproductive success. This is a process that basically overrides nutritional interactions, resulting in reproductive failure, thereby minimizing selection of animals better suited for sustained reproductive function under limited nutrition. Rearing and managing cows under nutritionally limited environments can result in adaptation leading to relatively high levels of reproduction with lower levels of input. These management strategies may result in fetal programing that improve chances for longer retention in their offspring.

Key Words: beef cow, efficiency, longevity

0125 Can we develop a cowless cow herd? Beef production without mature cows. G. E. Seidel*, *Colorado State University, Fort Collins.*

A beef production system is being studied that eliminates the mature cow herd. Nulliparous heifers are bred with sexed semen enriched to > 90% X-sperm, so most heifers replace themselves with a heifer calf. Weaning will occur at about 100 d of age, after which the dam is fattened for ~2 mo and slaughtered at 28 to 30 mo of age. Research objectives are: 1) determine profitability by evaluating capital requirements, expenses, and income; 2) evaluate ways of initiating such a program, e.g., starting with weaned heifer calves, open heifers, or bred heifers; and 3) determine if carcasses produced are of a quality that avoids market discounts. There is no cow herd to feed year round and all cattle are growing. In traditional cow-calf systems, ~50% of consumed feed energy goes to metabolic maintenance of mature cows with no accretion in meat. The other ~50% is for calf replacement-heifer maintenance, growth, and fattening, and for cow pregnancy and lactation. In the new system, all cattle are growing, so a high percentage of feed energy goes to growth. The net result is a significant decrease in feed required per pound of beef produced, manure, greenhouse gas production, and excretion of nitrogen and phosphorus. Fringe benefits include: eliminating low pregnancy rates in first-calf heifers that are lactating and still growing; minimizing health problems, such as cancer eye, foot and leg ailments, mastitis, etc., which are more prevalent in older cows; almost eliminating bull calves needing castration; and decreased generation interval. Fringe costs include: increase in dystocia if all calvings are from heifers, which is expected to be minor, because heifer calves average 2 kg lighter than bull calves at birth, and calving ease AI sires will be used. Early weaning requires increased management and heifers gain weight less efficiently than steers, which can be compensated by using anabolic implants. This system is not entirely self-sustaining because of: imperfect gender-selected semen, inevitable deaths, and non -pregnancy or late pregnancy of some heifers. Thus, to maintain herd numbers, 25 to 30% of heifers need to be replaced annually from outside of the system. Fringe benefits appear to outweigh fringe costs, but the main advantage is that more beef can be produced with given feed resources.

Key Words: efficiency, heifer beef, sexed semen

BEEF SPECIES: **COW-CALF**

0126 Changes in body composition during winter gestation of mature beef cows grazing different herbage allowances of native pastures.

A. Casal[*1], A. L. Astessiano Dickson[1], A. I. Trujillo[1], P. Soca[2], A. C. Espasandin[2], and M. Carriquiry[1], *[1]Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay, [2]Departamento de Producción Animal y Pasturas-Facultad de Agronomía-UdelaR, Paysandú, Uruguay*.

The aim of this study was to evaluate the effect of controlling the intensity of grazing native pasture (*Campos biome*), through control of herbage allowance (HA), on body composition (water, protein, and fat) of beef cows of different genotype during the winter gestation period. Mature beef cows (n = 32) were used in a complete randomized block design with a factorial arrangement of HA (2.5 vs. 4 kg DM/d; LO vs. HI) of native pastures (52% DM, 8.4% CP, 39.7% ADF) and cow genotype (CG; Angus-Hereford vs. F1 reciprocal crosses; PU vs. CR). The experiment was conducted during 3 yr and at the end of the third year at 150, 210, and 240 ± 10 d of gestation (during winter) and 190 ± 10 d postpartum (fall). Body composition was estimated using the urea dilution technique. In addition, at 192 ± 10 d postpartum, cows were slaughtered and weight and samples of all tissues and organs were collected for chemical composition analyses. Multiple regressions, using urea space volume and other animal characteristics as predictors, were adjusted by the regression procedure (SAS Institute Inc.), using data obtained at slaughter to estimate body components (kg) during the winter gestation period. Data of body composition during gestation were assessed using a mixed model repeated measures analysis. During the winter gestation period, maternal live weight (LW) and BCS tended (P = 0.09) or were greater (P = 0.02) in HI than LO cows and in CR than PU cows. Maternal LW and BCS decreased (P < 0.05) 18 ± 5 kg and 0.5 ± 0.1 unit from 150 to 210 d of gestation. Total body water and fat and protein mass were greater ($P \leq 0.05$) in CR than PU cows. Body fat and protein mass tended ($P \leq 0.10$) to be greater in HI than LO cows. Total body water and protein mass decreased (P < 0.01) from 150 to 210 d of gestation. Body water was affected (P = 0.03) and body fat tended (P = 0.07) to be affected by the interaction between CG and days of gestation, as they were greater (P < 0.05) in CR than PU cows only at 150 d of gestation and decreased from 150 to 210 d of gestation only in the former ones. Body composition during winter gestation depended on both HA and CG. Changes in the composition of body weight lost or retained would influence energy maintenance requirements and could provide metabolic advantages under periods of negative energy balance.

Key Words: cattle, fat, protein, rangelands

0127 Prepartum supplement level and age of weaning: I. Effects on prepartum and postpartum beef cow performance and calf performance through weaning.

L. M. Shoup[*1], A. C. Kloth[2], D. Gonzalez-Peña Fundora[2], F. A. Ireland[1], S. L. Rodriguez Zas[1], T. L. Felix[2], and D. W. Shike[1], *[1]University of Illinois, Urbana, [2]University of Illinois at Urbana-Champaign, Urbana.*

Objectives were to determine the effects of prepartum supplement level and age of weaning on BW, BCS, milk production, reproduction, and calf performance up to weaning in a fall-calving system over 2 yr. Mature multiparous Angus × Simmental cows (yr 1, n = 326; yr 2, n = 383) were used in a split-plot design that included 3 supplement levels: no supplement (NS), 2.16 kg/d per animal (LS), or 8.61 kg/d per animal (HS). (The supplement = 70% dried distillers grains plus solubles and 30% soybean hulls; fed 103 ± 11 d prepartum to 3 ± 11 d postpartum.) The 2 ages of weaning were: early at 80 ± 11 d of age (EW) and normal at 188 ± 11 d of age (NW). Cow BW for cows fed HS was greater ($P \leq 0.04$) at pre-calving (55 ± 11 d prepartum), post-calving (27 ± 11 d postpartum), and post-breeding (81 d post-breeding), compared with NS and LS cows. Cows fed HS had increased ($P \leq 0.02$) pre-calving, post-calving, and post-breeding BCS, relative to cows fed NS, with no effects ($P \geq 0.60$) on calf birth weight or calving ease. Prepartum supplementation tended (P = 0.09) to improve AI conception. Early weaning resulted in increased ($P \leq 0.05$) AI conception and post-breeding BW and BCS, relative to normal weaning. A significant supplement level × weaning interaction existed (P = 0.03) for overall pregnancy. For cows fed HS, EW improved (P = 0.02) overall pregnancy; however, weaning age did not affect ($P \geq 0.10$) overall pregnancy for NS and LS cows. At time of early weaning, BW increased (P = 0.02) for steers from LS cows compared with steers from NS cows. Steer BW at time of normal weaning and ADG between early and normal weaning was greater (P < 0.01) for EW steers, compared with NW steers. A year × weaning interaction (P < 0.01) occurred for ultrasound marbling score at time of normal weaning. In yr 1, marbling decreased (P = 0.04) in EW steers compared with NW steers; however, in yr 2, marbling increased (P < 0.01) in EW steers compared with NW steers. These data suggest prepartum supplementation and early weaning improved cow BW, BCS, and reproduction. There were minimal effects of dam prepartum supplement on calf performance up to weaning. Early weaning improved calf growth but had inconsistent effects across years on ultrasound measurements.

Key Words: beef cattle, early weaning, prepartum supplementation

0128 Prepartum supplement level and age of weaning: II. Effects of developmental programming on performance and carcass composition of steer progeny. L. M. Shoup*, D. Gonzalez-Peña Fundora, F. A. Ireland, S. L. Rodriguez Zas, T. L. Felix, and D. W. Shike, *University of Illinois, Urbana.*

Objectives were to determine the effects of prepartum cow supplement level and age of weaning on growth performance, feed efficiency, glucose and insulin concentrations, and carcass characteristics of steers (yr 1, n = 134; yr 2, n = 147). Mature multiparous Angus × Simmental cows were used in a split-plot design that included 3 supplement levels: no supplement (NS), 2.16 kg/d per animal (LS), or 8.61 kg/d per animal (HS). (The supplement = 70% dried distillers grains plus solubles and 30% soybean hulls; fed 103 ± 11 d prepartum to 3 ± 11 d postpartum.) The 2 ages of weaning were: early at 80 ± 11 d of age (EW) and normal at 188 ± 11 d of age (NW). Dam prepartum supplement level did not affect ($P \geq 0.15$) growth performance, respiratory health, or carcass traits, with the exception of percentage ≥ Average Choice. A greater ($P = 0.03$) percentage of steers from cows fed HS graded ≥ Average Choice when compared with steers from cows fed NS. Early weaning increased ($P < 0.01$) initial BW and final BW, and reduced ($P < 0.01$) G:F compared with normal weaning. A year × weaning interaction ($P = 0.02$) occurred for ADG; early weaning resulted in reduced ($P < 0.01$) ADG compared with normal weaning in yr 2. Although EW steers were younger ($P < 0.01$) at harvest, they had greater ($P \leq 0.02$) HCW, yield grade, backfat, and marbling scores, compared with NW steers. A year × weaning interaction ($P \leq 0.04$) occurred for quality grade distribution; carcasses from EW steers had increased ($P < 0.01$) proportions ≥ Low Choice and ≥ Average Choice than carcasses from NW in yr 2. The EW steers had greater ($P \leq 0.04$) occurrence of single medical treatments and death due to respiratory disease than NW steers. A year × weaning interaction ($P = 0.03$) occurred for insulin concentration and insulin:glucose; EW steers had greater ($P < 0.01$) insulin concentrations and insulin:glucose than NW steers in yr 1. These data suggest overfeeding supplement to the dam did not affect feedlot performance but did improve steer quality grades. Although EW steers had increased respiratory illness, they were younger at harvest and had greater HCW and marbling scores, compared with NW steers. The absence of supplement level × weaning interactions indicates that these effects may have an additive effect on developmental programming.

Key Words: developmental programming, early weaning, maternal nutrition

0129 Efficiency and performance of primiparous Angus cows raised in a range system. J. S. Lemes*, C. C. Brauner, R. Z. Vaz, and M. A. Pimentel, *Universidade Federal de Pelotas, Brazil.*

The aim of this study was to evaluate the efficiency and performance from calving to weaning of primiparous beef cows in 3 different biotypes in a range system. Forty-two primiparous Angus cows (3 yr of age) with BCS 3 (on a 1 to 5 scale) were classified into 3 groups according to body weight at calving: heavy (431 kg on average, ranging from 405 to 485 kg); medium (388 kg on average, ranging from 373 to 403 kg); and light (348 kg on average, ranging from 293 to 369 kg). Milk production was estimated by weight-suckle-weight method. Calf production efficiency was determined by the adjustment of calf weaning weight (CWW) and pregnancy rate (PR) of cows, resulting in calf production index (CPI) = kg of weaning calves per cow (CWW × PR/100). Data were analyzed using GLM procedures in SAS software. Total weight gained from calving to weaning was affected ($P < 0.05$) by biotype. Once, light and medium cows had 51 and 25 kg gain, respectively, whereas the heavy group had a 3 kg loss during the same period. Calves from heavy and medium groups were heavier ($P < 0.05$) at weaning as compared with light cow calves, being 166.5 ± 4.0; 166.0 ± 3.7, and 151.9 ± 4.3 kg, respectively. The CPI evaluation demonstrated that light and medium cow groups were able to produce more ($P < 0.05$) calf kilograms (16.0 ± 0.4; 15.1 ± 0.4 kg, respectively) than the heavy group (14.0 ± 0.4 kg). There was no difference ($P > 0.05$) in calf production efficiency among groups, being 63.4% ± 1.6; 62.2% ± 1.4; and 59.6% ± 1.5, respectively, for light, medium, and heavy cows. However, light cows had lower ($P < 0.05$) milk production and, as a result, lighter ($P < 0.05$) calves at weaning (151.9 ± 4.3 kg) than medium and heavy groups, 166.0 ± 3.7, 166.5 ± 4.0 kg, respectively. In conclusion, cows in small and moderate biotypes are more efficient, as compared with larger frames in graze production systems.

Key Words: milk production, reproduction, weaning weight

0130 Effect of an injectable trace mineral on reproductive performance of beef cows grazing irrigated pasture. C. J. Brasche*[1], J. B. Hall[2], and M. E. Drewnoski[1], [1]*University of Idaho, Moscow,* [2]*University of Idaho, Carmen.*

Injectable trace minerals can be used to increase trace mineral status of cows and may result in improved reproductive performance. Beef cows (n = 174) were blocked by age and expected calving date, and randomly assigned to treatment in a 2 × 2 factorial of either an injectable trace mineral containing copper, manganese, selenium, and zinc (TMI), or no injection (CON), and timed AI at either 72 or 80 h post controlled-internal-drug-release device (CIDR) removal.

Thirty-8 d before the start of the calving season and again 23 d before AI, cows in the TMI group were injected with Multimin 90 (0.68 mL/68 kg of BW). Liver biopsies were taken before pre-calving injection, before pre-breeding injection, and again 15 d after pre-breeding injection to assess mineral status. All cows were estrous synchronized, using a 5-d CoSynch plus CIDR protocol, in which cows were given an injection of GnRH and inserted with a CIDR 8 d before AI. The CIDR was removed 5 d later and a shot of PG was given, followed by a second PG injection 5.6 h later. Cows were given an injection of GnRH and inseminated either 72 or 80 h after CIDR removal with gender-selected semen. Cows were exposed to fertile bulls for natural service breeding 17 d after AI and remained with the bulls for 45 d. Pregnancy was determined by rectal palpation at 105 d post AI. For the responses measured, there was no interaction ($P \geq 0.19$) between TMI and AI timing; therefore, only the effect of injection will be reported. At 15 d post pre-breeding injection, TMI had no effect on liver concentration of manganese ($P = 0.26$), zinc ($P = 0.22$), or copper ($P = 0.11$); however, TMI cows had elevated concentrations of selenium ($P = 0.01$) when compared with CON. Liver concentrations of the trace minerals measured in both treatments were considered adequate at all time points. There was no difference between CON and TMI in the number of days post calving ($P = 0.21$) or BCS ($P = 0.95$) at AI. Trace mineral injection did not affect reproductive performance of cows as both conception to AI ($P = 0.41$) and overall pregnancy rate did not differ ($P = 0.19$) due to TMI treatment. These data suggest that the use of an injectable trace mineral may not improve reproductive performance of cows that have adequate trace mineral status before injection.

Key Words: cows, injectable trace mineral, reproduction

0131 Effect of injectable trace mineral supplementation in yearling bulls on serum and semen trace mineral levels and reproductive parameters.

A. A. Kirchhoff* and K. E. Fike, *Kansas State University, Manhattan.*

We hypothesized that administration of an injectable trace mineral would cause a short-term increase in circulating trace mineral concentrations but not alter semen quality nor ability to pass a breeding soundness exam (BSE). Sixteen Hereford, 52 Angus, and 22 Simmental bulls were blocked by breed and stratified by age (277 ± 20 d) and weight (377 ± 42 kg), and administered subcutaneously, either a commercially available trace mineral supplement (TM; $n = 45$; 15 mg Cu/mL, 60 mg Zn/mL, 10 mg Mn/mL, and 5 mg Se/mL; Multimin 90, Multimin USA, Inc., Ft. Collins, CO) or sterilized saline (Control; $n = 45$) at 1mL/45 kg BW. Bulls were maintained in a drylot and fed a grower ration that included trace minerals at NRC-recommended levels. Blood was collected via jugular venipuncture immediately before treatment (h 0) and at 8 and 24 h. The BW and scrotal circumferences were measured on the day of treatment (d 0) and d 20, 42, 59, and 91. Semen was collected via electroejaculation on d 42 and 91, and a BSE conducted on d 91. Serum samples from h 0, 8, and 24, and semen samples d 42 and 91, on a subset of 26 bulls per group, were analyzed using inductively coupled mass spectroscopy for concentration of Cu, Zn, Mn, and Se. Data were analyzed using PROC MIXED, PROC GLIMMIX, and PROC FREQ in SAS, with fixed effects of treatment, breed, and time of sampling, and interactions with bull as experimental unit. The TM and Control bulls had similar scrotal circumferences and BW throughout the trial ($P \geq 0.10$). Time and treatment interacted ($P < 0.01$) to affect serum trace mineral concentrations with TM bulls having greater ($P < 0.01$) trace mineral concentrations at 8 h post-treatment than Control bulls. Semen trace mineral concentrations on d 42 and 91 were similar ($P \geq 0.05$) between TM and Control bulls. Sperm motility, percent normal morphology, concentration, and percentage proximal droplets improved ($P < 0.05$) from d 42 to 91, but did not differ between TM and Control ($P \geq 0.05$). A similar ($P \geq 0.05$) percentage of TM (51%) and Control (49%) bulls passed their BSE 91 d post-treatment. A supplemental trace mineral injection is successful at raising circulating trace mineral levels but does not alter semen trace mineral levels nor improve semen quality.

Key Words: bull, semen, trace mineral

0132 Effect of an injection of a fat-soluble vitamin mix (E, A, and D) to newborn beef calves on markers of cell oxidative damage and calf performance.

W. A. Sutton* and M. E. Drewnoski, *University of Idaho, Moscow, ID.*

Early calf death is 1 of the major contributors to economic loss. Muscle lesions not related to white muscle disease may contribute to reduced vigor of calves suffering from weak calf syndrome. The objective of the current study was to determine the effects of a vitamin E, A and D injection on calves exposed to cold temperature. Thirty-two newborn calves from spring calving multiparous Charolais cows (age 3 to 10 yr) were blocked within gender by date of birth and assigned to treatment in a 2 × 2 factorial design. At birth, calves were administered an injection of 4 mL of saline (SAL) or 4 mL VITAL E-A+D (EAD; 300 IU/mL vitamin E as D-α-tocopherol, 100,000 IU/mL vitamin A as retinyl-palmitate, and 10,000 IU/mL vitamin D as cholecalciferol). At 5 h of age, calves were placed in a chamber at 0 or 25°C for 90 min and rectal temperature was recorded every 10 min. At 24 h of age, an injection of Bo-Se (2 mg of selenium as sodium selenite and 136 IU of Vitamin E as D-α-tocopheryl acetate) was administered to all calves. Plasma samples were collected at birth, 5, 6.5, 24, and 48 h, and 45 d. Plasma creatine kinase and 8-isoprostane concentrations at 24 h were not affected ($P > 0.48$) by injection or environmental treatment, showing no effect of treatment on markers of cell damage. Regardless of temperature treatment,

calves receiving the EAD had greater rectal temperatures (P = 0.04) than those calves receiving SAL (38.85 vs. 38.75 ± 0.03°C, respectively) at birth. Calves subjected to cold temperature had greater (P = 0.05) rectal temperatures than calves subjected to thermo-neutral conditions. Calves receiving EAD had lower (P = 0.02) ADG during the first 5.5 wk of life than those receiving SAL (0.93 vs. 1.14 ± 0.06 kg/d). However, 205-d adjusted weaning weights were not different (P = 0.58) between injection treatments (254 vs. 260 ± 8.2 kg for EAD and SAL, respectively). Calves receiving EAD had greater rectal temperatures and lower ADG than calves receiving SAL. There was no detectable difference in markers of cell damage due to treatments. Calves receiving EAD may have had increased metabolic rates, which could have contributed to the increase in rectal temperature and decreased ADG. Injection of EAD at birth may be beneficial to calf health in terms of body heat production.

Key Words: calf, injectable vitamin

0133 Relationships between maintenance energy EPD and performance measures of progeny from Red Angus sires divergent for maintenance energy EPD.

C. M. Welch*[1], S. E. Speidel[2], D. H. Crews[3], J. K. Ahola[3], J. B. Hall[4], W. Price[1], and R. A. Hill[1], *[1]University of Idaho, Moscow, [2]Department of Animal Sciences, Colorado State University, Fort Collins, [3]Colorado State University, Fort Collins [4]University of Idaho, Carmen.*

The Red Angus Association of America (RAAA) developed the maintenance energy (ME_M) EPD as an estimator of maintenance requirements, in an attempt to lower cow maintenance costs within the breeding herd. However, no studies have evaluated the selection and incorporation of ME_M EPD into breeding programs, and the resulting effects on progeny postweaning performance. Conducted as part of a larger study, postweaning performance measures were recorded in 3 birth year contemporary groups from the progeny (n = 222) of sires (n = 12) divergent for ME_M EPD. The objective was to evaluate relationships between various phenotypic performance measurements and EPD of progeny and sires. Sires were partitioned into high and low ME_M EPD groups, based on the RAAA breed average for ME_M EPD. Sire ME_M EPD was found to be positively correlated (P < 0.05) with progeny phenotypic performance measurements, including ADG (r = 0.32), DMI (r = 0.21), and metabolic BW (MBW; r = 0.22). Sire ME_M EPD was negatively correlated with progeny feed-to-gain ratio (r = -0.21). In addition, sire ME_M EPD was also positively correlated (P < 0.05) with progeny ADG EPD (r = 0.43) and MBW EPD (r = 0.24). No association (P > 0.05) was observed between sire ME_M EPD and progeny DMI EPD. Therefore, our data analyses indicate that sire ME_M EPD is associated with growth and BW in Red Angus-sired cattle.

Key Words: maintenance energy, performance, Red Angus

0134 Effects of breeding system of origin (natural service or AI) on growth, attainment of puberty, and pregnancy rates in crossbred beef heifers.

M. R. Schook*[1], P. L. Steichen[1], V. R. G. Mercadante[2], G. C. Lamb[2], B. W. Neville[3], and C. R. Dahlen[1], *[1]North Dakota State University, Fargo, [2]University of Florida, Marianna, [3]North Dakota State University, Streeter.*

The objective of this study was to compare growth, attainment of puberty, and pregnancy rates in beef heifers, originating from 2 different breeding systems. One hundred ninety crossbred Angus heifers were born to dams that were exposed to 1 of 2 treatments: 1) natural service (NS, cows were only exposed to herd bulls for the duration of the breeding season), or 2) fixed-time AI (TAI, cows exposed to ovulation synchronization and AI followed by natural service bulls). Body weights were taken on d 0 and 189, with a mean age of 209 ± 1.2 d at the initiation of the trial (d 0). Blood samples were collected at d 0, 10, 112, 122, 219, and 229, and progesterone concentrations were used to determine the proportion of females that had attained puberty during the development period. On d 229, synchronization of ovulation was initiated: 7-d CO-Synch + controlled-internal-drug-release device (CIDR) and all heifers were inseminated with a single TAI at 54 h after CIDR removal. Clean-up bulls were placed in breeding pastures 10 d after AI and remained with heifers until 56 d after AI. Pregnancy rates were determined via transrectal ultrasonography on d 27 and 91 after AI. Body weight at initiation of the experiment was greater (P = 0.01) for heifers in the TAI treatment (239.9 ± 2.8 kg) compared with heifers in the NS treatment (229.6 ± 2.8 kg). However, no differences ($P \geq 0.14$) between treatments were observed in weights of heifers taken at the time of pasture turnout (d 189; 345.1 ± 3.4 and 338.0 ± 3.4 kg for TAI and NS, respectively) or ADG (0.56 ± 0.01 and 0.58 ± 0.01 kg/d for AI and NS, respectively). At the initiation of the experiment, a greater proportion of the NS heifers (11.6%) tended (P = 0.06) to be cyclic compared with TAI heifers (4.2%). However, no differences ($P \geq 0.40$) were observed between treatments in the proportion of heifers cyclic at the interim evaluation (d 112 and 122, 27.5% cyclic) or at the initiation of the breeding season (d 219 and 229, 85.5% cyclic). No differences ($P \geq 0.81$) were present between treatments in either pregnancy rates to AI (32.9%) or season-ending pregnancy rates (91.1%). Breeding system of origin did not influence growth rate during the development phase, attainment of puberty, or pregnancy rates in crossbred beef heifers.

Key Words: artificial insemination, heifer development, natural service

0135 Simulation and economic analysis of beef cattle natural service and induced twinning via embryo transfer, following AI breeding and 2 calf management systems. D. G. Aherin*, P. J. Ebert, J. R. Shearer, R. L. Weaber, J. M. Bormann, D. W. Moser, and M. D. MacNeil, *Kansas State University, Manhattan.*

The objective of this project was to compare operation profitability, through simulation, of alternate breeding and calf management strategies. Mating systems considered included: 1) 60-d natural bull service and 2) fixed-timed AI program with implanted embryos 7 d following AI to create twins. A 42-d natural service followed embryo transfer (ET). The effect of a preweaning calf nutrient supplementation system that excludes cows (creep feeding) was also of interest. The combination of mating system and calf nutritional management system yielded different management systems for comparison, including: 1) induced twin calving system with calf creep feeding, 2) induced twin calving system without calf creep feeding, 3) natural service (single calving) system with calf creep feeding, and 4) natural service (single calving) system without calf creep feeding. Microsoft Excel was used to develop a spreadsheet that processed input cost and revenue projections, and predicted profitability of each management system. Equations to predict breeding and calf performance allowed entry of different parameters for fertility rates, input costs, and price expectations, which vary across different cattle operations, management, and economic environments. Assumptions incorporated into the simulation included: 1) all natural service cows have single births; 2) no change in stocking rate/pasture usage; 3) simulation in second year of twin production; 4) no heifers involved; 5) if a calf dies, it died the day it was born; and 6) no difference in genetic potential between AI/ET calves and natural service calves. Sensitivity analysis of the simulation model suggests that variation in labor, creep feeding, and reproductive costs between twin and single calving had the greatest impact on profitability. Creep feeding had a substantially greater positive effect on the performance of twin calves compared with single-born calves; thus creating a much greater impact on overall profitability of that management system. Through simulation using common production input costs, creep feed at $220/ton, it was found that management system 1 (induced twinning with creep feed) was the most profitable, if reproductive costs could be held to < $170 per head.

Key Words: beef cattle, management systems, twinning

0136 The indirect effects of horn flies and sire breed on calf preweaning and postweaning performance traits. A. R. Mays*[1], M. A. Brown[2], and C. F. Rosenkrans[3], *[1]Department of Animal Science, University of Arkansas Division of Agriculture, Fayetteville, [2]ARS-USDA, Grazinglands Research Laboratory, El Reno, OK, [3]University of Arkansas, Fayetteville.*

Horn flies negatively impact weaning weight and ADG of beef cattle, but the indirect effect of horn flies on preweaning and postweaning performance traits is less understood. Therefore, the objective of this study was to assess the indirect effects of horn flies on calf performance traits. Angus-sired calves (n = 51) from crossbred cows (n = 53) from Brangus dams sired by either Bonsmara (BONS; n = 7), Brangus (BRAN; n = 13), Charolais (CHAR; n = 8), Gelbvieh (GELV; n = 5), Hereford (HERF; n = 12), or Romosinuano (ROMO; n = 8) bulls were evaluated. Total horn fly counts were recorded on individual cows while in pasture from 0700 to 0900 h, beginning in May and ending in October. Horn fly counts were transformed to natural log horn fly counts before data analysis. Data for preweaning ADG, postweaning ADG, 365-d adjusted yearling weight (YWT), and birth to yearling ADG were analyzed by mixed model least squares. The linear model included sire breed, calf gender, and sire breed × calf gender. Effects of horn fly count on these traits were estimated by including a linear covariate of log horn fly count and log horn fly count × sire breed. Preweaning ADG was affected ($P < 0.002$) by sire breed of dam. Romosinuano, BONS, and CHAR calves had greater preweaning ADG (1.00 ± 0.05, 0.99 ± 0.04, 0.99 ± 0.04 kg/d; respectively), compared with BRAN and HERF calves (0.88 ± 0.03 and 0.81 ± 0.03 kg/d), with GELV calves intermediate to ROMO, BONS, CHAR, and BRAN (0.98 ± 0.05 kg/day). Preweaning ADG was dependent on an interaction of cow sire breed and log horn fly count ($P < 0.10$), with results indicating preweaning ADG being reduced 0.19 kg/d per unit increase in log horn fly count in BONS calves ($P < 0.05$). A 1 unit increase in log horn fly count resulted in 0.07 kg/d ($P < 0.10$) increase in postweaning ADG, 19.52 kg increase ($P < 0.10$) in 365-d adjusted YWT, and 0.05 kg/d ($P < 0.02$) increase in birth to yearling ADG. Horn flies indirectly had a negative impact on preweaning performance of calves from certain cow sire breeds. However, a positive indirect effect on postweaning calf performance was documented in this study. Postweaning management and compensatory gains may explain the results reported, but continued research of indirect effects of horn flies on calf performance traits is needed.

Key Words: average daily gain, calf performance, horn fly

BEEF SPECIES: STOCKER AND FEEDLOT

0137 Effect of crude protein levels and metaphylaxis on growth and performance of newly received stocker calves. T. J. Braud*[1], B. B. Karisch[1], D. R. Smith[1], C. L. Huston[1], R. Vann[2], and S. G. Genova[1], *[1]Mississippi State University, Mississippi State, [2]MAFES-Brown Loam, Mississippi State University, Raymond.*

Newly received stocker calves may have low feed intake and are at risk for bovine respiratory disease (BRD) and other causes of morbidity and mortality. The objectives of this study were to evaluate the effects of: 1) metaphylactic antibiotic administration (none or Excede on arrival); and 2) receiving diet CP levels (12% or 18%) on respiratory disease incidence, mortality, and growth performance of beef calves received into a stocker calf system. Steer calves (n = 244) were stratified by weight and randomly assigned to 20 pens. Treatments were randomly assigned to pen in a 2 × 2 factorial study design. Cattle were examined daily for signs of BRD and fed once daily (NEg = 0.94 MCal/kg). Cattle receiving metaphylactic treatment were not treated for BRD during the first 7 d; otherwise, BRD was diagnosed at the first clinical signs and body temperature > 40°C. Calves were weighed at arrival and every 14 d through d 55 of the 60-d trial. Days at risk for BRD was the number of days from arrival until a calf: 1) first diagnosed with BRD, 2) died, or 3) finished the trial. Overall, 176 calves were treated for BRD over 6410 d at risk (BRD incidence density = 27.4/10^{3}calf-days). The effects of metaphylaxis and diet on BRD incidence density were tested by Poisson regression, accounting for clustering by pen. Cattle receiving metaphylaxis were 60% less likely to be diagnosed with BRD (RR = 0.4, $P < 0.0001$) and every additional 45 kg at arrival reduced incidence of BRD 45% (RR = 0.54, $P = 0.004$). Neither diet nor the interaction between diet and metaphylaxis were significantly associated with BRD incidence. The effects of metaphylaxis, diet, and incoming BW on mortality from all causes were tested in a log-binomial model, accounting for clustering by pen. Mortality totaled 32 calves (13%). Neither diet, metaphylaxis, nor incoming BW were significantly associated with risk for mortality. The effects of metaphylaxis and diet on ADG were tested in a generalized estimating equations model, accounting for clustering by pen. Overall, for the 212 cattle finishing the trial, ADG was 0.72 kg/d. Accounting for metaphylaxis, cattle receiving 18% protein gained an additional 0.19 kg/d ($P = 0.008$). Metaphylaxis did not affect ADG ($P = 0.10$). Metaphylactic treatment reduced the incidence of BRD and increasing CP in the receiving ration to 18% resulted in higher ADG.

Key Words: beef cattle, BRD, metaphylaxis

0138 Effect of growth rate and placement weight of stocker-feeder cattle on subsequent finishing performance and carcass characteristics: A meta-analysis. P. A. Lancaster*, C. R. Krehbiel, and G. W. Horn, *Oklahoma State University, Stillwater.*

Many studies have been conducted evaluating the effect of forage species, stocking rate, supplementation strategies, and length of grazing on subsequent finishing performance and carcass characteristics; however, it is still difficult to ascertain the impact of stocker programs on subsequent finishing performance. The objective of this study was to use meta-analysis methods to determine the effect of 2 important factors of stocker programs, ADG, and placement BW on subsequent finishing performance and carcass characteristics. Following a literature search, a data set was compiled of 24 studies comprising 29 research trials, where stocker treatments differed significantly in rate of gain by ≥ 0.10 kg/d during the stocker phase. Regression analyses were conducted using a mixed model (PROC MIXED of SAS) that included ADG or placement BW as fixed effects, and intercept by ADG or placement BW cross product terms, when slopes differed among trials, as random effects and trial as the subject. The squared standard error for the dependent variable was used as a weighting factor to compute regression coefficients. Stocker ADG and placement BW had a negative relationship ($P < 0.10$) with finishing G:F; but when both ADG and placement BW were included in the model, neither were significant ($P > 0.10$). Stocker ADG and placement BW had positive relationships ($P < 0.05$) with LM area but not 12th-rib fat thickness or yield grade. When both ADG and placement BW were included in the model for rib fat-adjusted marbling score, neither were significant ($P > 0.10$). However, addition of HCW to the model indicated that HCW had a positive relationship ($P < 0.05$) with rib fat-adjusted marbling score, even though ADG and placement BW were included. Stocker ADG had a negative relationship ($P < 0.05$) with rib fat-adjusted HCW, whereas placement BW had a positive relationship ($P < 0.05$). These data suggest that slower rates of gain during the stocker phase, but with longer grazing periods to increase placement BW, can increase rib fat-adjusted HCW and marbling score.

Key Words: carcass characteristics, finishing performance, stocker-feeder cattle

0139 Performance impacts of feeding bermudagrass (*Cynodon dactylon*) or ryegrass (*Lolium multiflorum*), plus rye (*Secale cereale*) baleage to weaned crossbred beef calves. R. M. Martin[*1,2], R. Walker[3], B. Buttrey[3], and C. C. Williams[4], [1]*Louisiana State University, Baton Rouge,* [2]*School of Animal Sciences, LSU AgCenter, Baton Rouge,* [3]*LSU AgCenter, Hill Farm Research Station, Homer,* [4]*LSU AgCenter, Baton Rouge.*

Two hundred forty Angus and Angus × Charolais cross calves (BW = 217 ± 20.6 kg) were used to evaluate performance and ruminal pH from feeding bermudagrass (*Cynodon dactylon*) or ryegrass (*Lolium multiflorum*), and rye (*Secale cereale*) baleage in hay rings. Calves were stratified by BW, age, gender, and breed, and assigned to 1 of 12 paddocks (0.40 ha each) with 4 treatment diets and fed for a 7-d adaption and 60-d backgrounding period. Diets included: early boot stage bermudagrass harvested for hay, CP = 8.2%, TDN = 59.9%, and DM = 88.8%, (BERH); early boot stage ryegrass and rye harvested for baleage, CP = 12.8%, TDN = 64.5%, and DM = 37.2%, (ERRG); bloom stage ryegrass and rye harvested for baleage, CP = 9.2%, TDN = 62.7%, and DM = 55.7%, (LRRG); and early boot stage bermudagrass harvested for baleage, CP = 9.2%, TDN = 57.4%, and DM = 49.1%, (BERB). Calves on BERH, LRRG, and BERB had free-choice access to a 34% CP (as-fed basis) liquid protein supplement. Two-day BW were collected on d -1, 0, 29, 30, 59, and 60 for comparison of BW, BW gain, and ADG. Ruminal pH was measured from randomly selected calves (n = 5/paddock) on d 0, 30, and 60. There was a treatment by day interaction ($P < 0.01$) for BW and ruminal pH. Initial BW was similar among treatments ($P > 0.05$). Calf BW was heavier ($P < 0.05$) for LRRG compared with BERB and BERH, and heavier ($P = 0.01$) for ERRG compared with BERB on d 60, respectively. Body weight gain and ADG were greater ($P < 0.01$) for calves fed LRRG (34.6 ± 1.2 kg and 0.58 ± 0.02 kg), compared with calves fed ERRG (27.9 ± 1.2 kg and 0.46 ± 0.02 kg), BERH (22.2 ± 1.2 kg and 0.37 ± 0.02 kg), and BERB (19.2 ± 1.2 kg and 0.32 ± 0.02 kg). The BW gain and ADG were greater ($P < 0.01$) for ERRG compared with BERB and BERH, but similar among BERB and BERH, respectively. There was a treatment effect for ruminal pH where ERRG calves had higher ($P < 0.01$) pH compared with LRRG, BERH, and BERB calves. Performance of backgrounded calves fed ryegrass and rye baleage with or without supplementation, based on harvest stage, was improved over feeding bermudagrass hay with supplementation.

Key Words: backgrounding, baleage, beef cattle

0140 Early metabolic imprinting for improvements in finishing feed efficiency and beef carcass characteristics. J. K. Smith[*], M. D. Hanigan, S. P. Greiner, and M. A. McCann, [1]*Virginia Polytechnic Institute and State University, Blacksburg.*

Recent research has indicated the ability of early nutritional intervention to metabolically imprint beef steers for enhanced carcass marbling. As such, metabolic imprinting (IMP) has been suggested as an alternative management strategy to enhance beef quality. The objectives of this experiment were to evaluate the impact of early IMP on finishing average daily residual feed intake (RFI), residual ADG (RADG), and carcass characteristics of backgrounded steers. Angus- and Simmental-sired steer progeny from 4 calving seasons were stratified by sire and age within contemporary group and randomly assigned to metabolically imprinted (MI; weaned at 105 ± 18 d of age; n = 63) or conventionally weaned (CW; weaned at 210 ± 18 d of age; n = 42) treatment groups. Following weaning, MI steers were adapted to and received a concentrate-based ration in a feedlot setting for 105 ± 45 d immediately before commingling with previously unsupplemented CW steers at the time of conventional weaning. Commingled steers were then backgrounded for 150 ± 60 d before being finished on a concentrate-based ration for 110 ± 34 d. Finishing ADFI and metabolic body weight collected at 28-d intervals were used to calculate RFI and RADG. Steers were harvested in groups on reaching an ultrasound-predicted common 12th rib subcutaneous fat thickness (SFT) of ~1 cm. Hot carcass weight was measured immediately before chilling. Chilled (24 h) carcasses were evaluated by a trained panel of analysts to determine ribeye area, SFT, KPH, and marbling score, as well as to calculate yield grade. All statistical analyses were conducted using the Fit Model procedure of JMP Pro. Analysis of a compiled data set for main effects of treatment revealed that IMP resulted in an improvement in RFI ($P < 0.05$; -0.13 vs. 0.19 kg of TDN for MI and CW steers, respectively) without affecting RADG ($P = 0.50$; -0.01 vs. 0.01 kg for MI and CW steers, respectively). Although ribeye area, SFT, KPH, marbling score, and yield grade did not differ ($P > 0.05$) for carcasses of MI steers when compared with those of CW steers, IMP increased HCW ($P < 0.05$; 341 vs. 332 kg). Collectively, interpretation of these results suggests the ability of IMP to increase HCW and decrease the amount of TDN required by finishing steers without negatively impacting ADG.

Key Words: beef, efficiency, imprinting

0141 Linear and nonlinear estimates of the efficiency of metabolizable energy use for maintenance and gain in beef cattle. C. A. Old[*1] and H. A. Rossow[2], *[1]A3 Cattle Company, Le Grand, CA, [2]Veterinary Medicine Teaching and Research Center, University of California, Tulare.*

Efficiencies of ME utilization for maintenance (k_m) and gain (k_g) have historically been determined using ordinary least squares (OLS); these differ from efficiencies determined from known biochemical pathways. We evaluated the relationship between retained energy (RE) and ME intake, using OLS and nonlinear (NL) regressions, using the data set from which the California Net Energy System (CNES) was developed. Parameter estimates from OLS regression were similar to classical estimates. In the nonlinear estimate, ME required for maintenance (ME_m) was a first order function of ME intake; efficiency of ME used for maintenance was calculated as the first derivative of that function. Efficiency of ME use for gain was linear and calculated as (ME intake– ME_m) × k_g. Parameter stability was evaluated using Markov Chain Monte Carlo (MCMC) simulation for both linear and nonlinear estimates. Linear and nonlinear estimates of ME_m, k_m and k_g were different ($P < 0.05$); the nonlinear equation fit the data better ($R^2 = 0.850$) than the linear equation ($R^2 = 0.777$). Linear estimates of ME_m, k_m and k_g were $0.133BW^{0.75}$ (a static estimate), 0.588, and 0.432, respectively. A lack of fit F test indicated that the OLS model was correctly specified. However, parameter estimates for OLS solutions, determined by MCMC simulation, were highly unstable, an indication that the model is incorrectly specified. Nonlinear estimates of ME_m were dynamic and, on average, greater than OLS estimates. Efficiency of ME use for maintenance was 0.382, a value similar to the efficiency of ATP synthesis. Efficiency of ME use for gain was 0.614; theoretical estimates of gain for growing beef cattle are from 0.70 to 0.75. A lack of fit F test indicated that the NL model was correctly specified. Nonlinear parameter estimates were stable, indicating that the model is correctly specified. While it was possible to describe the NL relationship used in this study in the 1960s, the solution of that equation was extremely difficult to perform due to the lack of computing power at that time. This analysis indicates that, while OLS models are adequate to the task for which they were developed, prediction of animal output from feed input, and vice versa, efficiencies calculated for these models are not in concert with animal biology. Efficiencies determined for NL models are similar to those calculated for biochemical pathways and may improve prediction of animal performance.

Key Words: efficiency, metabolizable energy, nonlinear

0142 Relationships among feeding behaviors and performance traits of growing and finishing phase Red Angus cattle. M. McGee[*1], C. M. Welch[1], J. A. Ramirez[2], G. E. Carstens[2], W. Price[1], J. B. Hall[3], and R. A. Hill[1], *[1]University of Idaho, Moscow, [2]Texas A&M University, College Station, [3]University of Idaho, Carmen.*

The progeny ($n = 37$) of Red Angus bulls were performance evaluated during both growing and finishing phase residual feed intake (RFI) tests. Data for RFI evaluation and 7 behavior traits were collected, using a feed intake monitoring system (GrowSafe Systems) over standard 70-d RFI test periods for both phases (BW growing: initial 331 ± 28 kg, final 451 ± 37 kg; finish: initial 499 ± 39 kg; final 587 ± 44 kg). Seven feeding behavior traits: bunk visit frequency (BVFREQ), bunk visit duration (BVDUR), feed bout frequency (FBFREQ), feed bout duration (FBDUR), meal frequency (MFREQ), meal duration (MDUR), and average meal intake (AMINT), and their relationships with RFI, DMI, and ADG were evaluated. Dry matter intake was correlated with BVDUR and FBDUR ($r = 0.44$; $P = 0.01$ for both behaviors) during the growing phase. Residual feed intake and BVDUR or FBDUR showed little to moderate correlations in growing phase ($r = 0.30$, $P = 0.07$; and $r = 0.27$, $P = 0.10$, respectively). There were no significant correlations between ADG and the 7 behavior traits during the growing phase RFI test. However, during the finishing phase RFI test, ADG was correlated with BVFREQ and FBFREQ ($r = 0.43$, $P = 0.01$ for both behaviors). Neither DMI nor RFI were correlated with any of the 7 feeding behavior traits during the finishing phase RFI test. Combining correlated traits into the RFI base model to predict DMI reduced the mean standard error by 13% for growing phase and 17% for finishing phase RFI tests. As these animals were offered different diets during growing and finishing phases (roughage-based vs. concentrate, respectively), the relative contribution of feeding behaviors in predicting DMI may be partially diet-type dependent. Inclusion of correlated feeding behaviors improved feed intake prediction by 13 to 17%, providing evidence that the study of behavior traits has potential to improve our understanding of the biological drivers of feed intake.

Key Words: feeding behavior, Red Angus, RFI

0143 Phenotypic relationships between residual measurements of finishing feed efficiency and visceral organ mass of backgrounded beef steers. J. K. Smith[*1], A. R. Murray[1], D. D. Harmon[2], M. D. Hanigan[2], S. P. Greiner[1], and M. A. McCann[2], *[1]Virginia Tech, Blacksburg, [2]Virginia Polytechnic Institute and State University, Blacksburg.*

Residual measurements of feed efficiency for beef cattle have recently gained popularity among producers, breed associations, and researchers, alike. Efforts devoted toward identify-

ing the underlying physiological mechanisms have been met with limited success. Visceral organs play major roles in nutrient digestion, absorption, and metabolism, and are considered to be substantial contributors to animal energy requirements for maintenance. As such, an experiment was conducted to determine phenotypic relationships between individual visceral organ mass (VOM) and residual measurements of finishing feed efficiency of backgrounded beef steers. Conventionally and early-weaned steer progeny (n = 105) from 4 calving seasons within a single herd were finished on a concentrate-based ration for 110 ± 34 d within contemporary group, immediately following a 150- ± 60-d backgrounding period. Finishing ADFI and BW were collected at 28-d intervals throughout the duration of the finishing period and used to calculate average daily finishing residual feed intake (RFI) and residual ADG (RADG), using a relatively large sample population. A subsample of steers (n = 28) from the sample population used to determine RFI and RADG were harvested on reaching an ultrasound-predicted 12th rib subcutaneous fat thickness of 1 cm and used to measure emptied and cleaned individual VOM. Visceral organs measured included heart, liver, gallbladder, lungs, kidneys, spleen, rumen, reticulum, omasum, abomasum, small intestine, pancreas, cecum, and colon and rectum. All statistical analyses were conducted using JMP Pro. Multivariate analysis of VOM and RFI, as well as VOM and RADG using the multivariate and correlations procedure, revealed inverse relationships ($P < 0.05$) between RFI and mass of lungs, spleen, and rumen (r = -0.57, -0.44, and -0.46, respectively), as well as a correlation ($P < 0.05$) between RADG and lung mass (r = 0.42). No relationships existed ($P > 0.05$) between RFI and mass of the heart, liver, gallbladder, kidneys, reticulum, omasum, abomasum, small intestine, pancreas cecum, and colon and rectum, or between RADG and mass of the heart, liver, gallbladder, kidneys, spleen, rumen, reticulum, omasum, abomasum, small intestine, pancreas, cecum, and colon and rectum. Collective interpretation of these results suggests a direct phenotypic relationship between mass of the lungs and residual measurements of finishing feed efficiency for backgrounded steers. Further research is necessary to evaluate the metabolic implications of the lungs and spleen to nutrient metabolism, cattle growth, and feed efficiency.

Key Words: beef, efficiency, intake

BEEF SPECIES: **FEED ADDITIVES**

0144 Comparison of feed technologies for backgrounding of weaned beef calves. M. J. Hersom*, T. A. Thrift, and J. V. Yelich, *University of Florida, Gainesville.*

The use of feed technologies in supplements is a means to positively affect performance and health status of newly-weaned calves during backgrounding. Our objective was to evaluate the response of weaned calves to different feed technologies in a supplement (CP = 14.6%, TDN = 67%) to improve calf performance and mitigate the stress response observed during weaning and subsequent backgrounding period. At weaning 160 calves (227 + 2.5 kg) were stratified by BW, sex, and breed and were randomly allotted to 1 of 4 treatments (n = 40 calves/treatment): 1) supplemented without feed technologies or control (CON); 2) supplement with added chlortetracycline, 350 mg/d (CTC); 3) supplement with added Rumensin, 175 mg/d (RUM); 4) supplement with added Actigen, 5 g/d (ACT). Calves were held in 1 of 4 drylot treatment pens (n = 40 calves/pen) for 7 d after weaning and offered ad libitum access to hay and 2.27 kg/d of supplement before placement in 1 of 32 0.8-ha pastures (5 calves/pasture) for a total of 8 pastures/treatment and supplemented at 1.0% BW. Calf BW were collected on d 0, 1, 3, 7, 14, 50, 52, 55, 59, and 65. After 44 d on pasture, calves were placed on 2 trucks and transported for 24 h. Upon return, calves were placed in 4 pastures with hay and fed their respective supplements for 14 d. Data were analyzed by the MIXED procedure of SAS. The model included the main effect of treatment, pasture was the experimental unit. During the 7 d after weaning, BW change did not differ (P = 0.65, -0.53 kg/d) among treatments. Over the 50-d post-weaning period there was no difference (P = 0.20, 0.52 kg/d) in BW gain response among treatments. After transportation, 7- and 14-d BW change were least (P < 0.005) for ACT and CTC (0.04 and -0.13 kg/d) compared to CON and RUM (-0.64 and -0.48 kg/d). Feed cost of gain and profitability ($P \geq$ 0.15, mean = \$2.49/kg and \$73.51) were not different among treatments. Use of feed technologies did not improve calf performance over CON during a backgrounding period and ACT was as effective as CTC or RUM during a post-transportation period.

Key Words: beef, backgrounding, supplement

0145 Effects of dose and duration of ractopamine hydrochloride supplementation on growth performance and carcass characteristics of feedlot heifers. B. M. Edenburn*[1], N. A. Pyatt[2], and T. L. Felix[1], [1]*University of Illinois at Urbana-Champaign, Urbana,* [2]*Elanco Animal Health, Greenfield, IN.*

Previous work has shown that ractopamine hydrochloride improves live BW gains, G:F, and HCW; however, data are lacking regarding duration of feeding 300 mg to heifers on growth performance and carcass characteristics. Objectives of this study were to determine the effects of dose, 0 or 300 mg/hd d^{-1}, and duration, 28 or 41 d, of ractopamine hydrochloride (RAC, Optaflexx, Elanco Animal Health, Greenfield, IN) supplementation on growth performance and carcass characteristics of feedlot heifers. Charolais cross heifers (n = 128) were blocked by BW into 2 blocks and allotted to 20 pens. Pens were randomly assigned 1 of 4 treatments in a 2 × 2 factorial arrangement: (1) 0 mg RAC/hd d^{-1} for 28, (2) 0 mg RAC/hd d^{-1} for 41 d, (3) 300 mg RAC/hd d^{-1} for 28, or (4) 300 mg RAC/hd d^{-1} for 41 d. Heifers were fed a basal diet of 50% dry rolled corn, 20% DDGS, 20% corn silage, and 10% supplement. Ractopamine hydrochloride was top dressed immediately following feed delivery. Cracked corn was removed from the diet and 300 mg RAC per 0.454 kg of ground corn carrier was top dressed. Data were analyzed using the mixed procedures in SAS. There were no day × RAC interactions ($P \geq$ 0.31) for heifer growth performance. There was no effect ($P \geq$ 0.22) of RAC on DMI, ADG, or G:F; however, feeding 300 mg RAC to increased (P = 0.03) final BW by 8.4 kg, regardless of duration fed. There were no day × RAC interactions ($P \geq$ 0.27) for heifer carcass characteristics. Furthermore, there were no effects ($P \geq$ 0.11) of duration of RAC feeding on heifer carcass characteristics. However, heifers fed RAC had an average increase (P < 0.01) of 9 kg of HCW, regardless of duration fed. Heifers fed RAC also had greater ($P \leq$ 0.03) LM area and dressing percentage. There was no effect ($P \geq$ 0.14) of RAC on marbling, 12th rib fat, KPH, or YG. Therefore, supplementing RAC at 300 mg/hd d^{-1} to heifers increased HCW, LM area, and dressing percentage and increased final BW without affecting other measures of performance.

Key Words: beef, carcass, heifers, ractopamine

0146 A meta-analysis of zilpaterol and ractopamine effects on feedlot. I. J. Lean[1], J. M. Thompson[2], and F. R. Dunshea*[3], [1]*SBScibus, Camden, Australia,* [2]*The University of New England, Armidale, Australia,* [3]*The University of Melbourne, Parkville, Australia*.

This study is a meta-analysis of the effects of the β-agonists zilpaterol hydrochloride (ZH) and ractopamine hydrochloride (RAC) on feedlot performance, carcass characteristics of cattle and Warner Bratzler shear force (WBSF) of muscles. It was

conducted to provide data that would be useful in considerations on the effect of these agents on meat quality in Meat Standards Australia evaluations. We conducted a comprehensive literature search and study assessment. Data were extracted from more than 50 comparisons for both agents and analyzed using a random effects meta-analysis and meta-regression using Stata (Stata 13.0). Results included forest plots, funnel plots, raw and weighted means, and estimates of effects size for each of ZH or RAC, independently. There was little evidence of publication bias on evaluation of funnel plots. Both agents markedly increased final body weight as indicated by the effect size (ES) 0.45 95% confidence interval (95% CI) 0.28 to 0.62 and weighted mean difference (wmd) 8.15 kg, (95% CI 5.63 to 10.67 kg) for ZH, RAC ES 0.40 (95% CI 0.24 to 0.56) and wmd 7.67 kg (95% CI 5.58 to 9.55 kg), hot carcass weight for ZH ES 1.32 (95% CI 1.03 to 1.61) and wmd 15.18 kg (95% CI 13.62 to 16.74 kg), RAC ES 0.47 (95% CI 0.31 to 0.63) wmd 6.18 kg (95% CI 4.55 to 7.82 kg) and longissimus muscle area (ZH ES 2.30 (95% CI 1.90 to 2.71) wmd 8.01 cm^2 (95% CI 7.05 to 8.96 cm^2), RAC ES 0.39 (95% CI 0.20 to 0.58) wmd 1.84 cm^2 (95% CI 1.17 to 2.52 cm^2) and increased the efficiency of gain:feed ratio (ZH ES 0.88 (95% CI 0.67 to 1.11) wmd 0.15 kg (95% CI 0.11 to 0.19), RAC ES 0.77 (95% CI 0.58 to 0.96) wmd 0.018 kg (95% CI 0.014 to 0.022). These effects were particularly large for ZH; however, ZH decreased fatness (by either ribfat or marbling score) with an ES of about -0.8 SD. For RAC the effects on fatness were much smaller with an ES of 0.0 and -0.1 for ribfat and marbling score, respectively. Zilpaterol also markedly increased WBSF by 1.2 standard deviations and more than 0.8 kg, while RAC increased WBSF by 0.43 standard deviations and 0.2 kg. This work has provided critically needed information on the effects of ZH and RAC on production, efficiency and meat quality.

Key Words: zilpaterol hydrochloride, ractopamine hydrochloride, meta-analysis

---

0147 Evaluation of objective and subjective mobility variables in feedlot cattle supplemented with zilpaterol hydrochloride.

W. C. Burson*[1], A. J. Thompson[1], M. A. Jennings[1], J. A. Carroll[2], N. C. Burdick Sanchez[2], B. J. Ragland[1], J. E. Hergenreder[1], J. O. Baggerman[1], K. S. Sharon[1], T. R. Schmidt[1], E. S. Murray[1], F. R. B. Ribeiro[1], B. J. Johnson[1], and R. J. Rathmann[1], *[1]Texas Tech University, Lubbock, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX.*

The objective of this study was to examine the effects of zilpaterol hydrochloride (ZH) on mobility in feedlot cattle. Black-hided steers and heifers (n = 96) were sourced from a commercial feedlot and transported to the Texas Tech University Beef Center in New Deal, TX. Cattle were weighed and scanned using real-time ultrasound. Resulting data were used to predict empty body fat percentage (pEBF %). Steers (n = 48; BW = 520 ± 30.4 kg; pEBF % = 26.2 ± 1.9) and heifers (n = 48; BW = 466 ± 29.5 kg; pEBF % = 26.7 ± 1.7) were blocked within gender by pEBF % in a completely randomized block design and randomly assigned to pen (2 pens/block; 4 hd/pen) and treatment (6 pens/treatment): 1) control heifers (HC), 2) ZH heifers (HZ), 3) control steers (SC), 4) ZH steers (SZ). Movement differences were objectively assessed on Day 0, 5, 10, 15, and 20 with several measures of mobility: exit velocity from chute (EV), velocity traveling from the pen to chute (VT) and velocity traveling from chute to pen (VF). Chute scores (CS) were assigned to all cattle based on a scale ranging from 1 to 5 (1 = no distress, 5 = high distress). Before shipping, individual locomotion scores (LS) were recorded based on a 1 to 4 scale (1 = no lameness, 4 = severe lameness). No significant gender × treatment interactions were found for any measured variable ($P \geq 0.46$). A significant treatment × day interaction ($P = 0.03$) was detected for EV, indicating that ZH cattle became progressively slower throughout the treatment period. No significant effects were found for VT or VF ($P \geq 0.31$). Fisher's exact test for count data was used to analyze the frequency distributions for both subjective measures. On d 20, a greater proportion ($P = 0.01$) of ZH cattle exhibited elevated chute scores (CS $\geq$ 3) relative to control. There was a tendency ($P = 0.09$) for increased locomotion score (LS $\geq$ 2) in ZH fed cattle. However, the proportion of cattle with locomotion scores indicating sufficiently sound movement (LS = 1&2) versus cattle that were moderate or severely lame (LS = 3&4) was not significantly different between treatment groups ($P = 0.24$). These data suggest that ZH supplementation may slightly limit mobility of cattle; nonetheless, the magnitude of these effects is not sufficient to deduce a detriment to cattle soundness.

Key Words: cattle, zilpaterol hydrochloride, mobility

0148 Comparison of real-time ultrasound measurements for body composition traits to carcass data in feedlot cattle fed zilpaterol hydrochloride.

B. J. Ragland, F. R. B. Ribeiro*, W. C. Burson, B. J. Johnson, and R. J. Rathmann, *Texas Tech University, Lubbock.*

The objective of this study was to compare measurements of real-time ultrasound (RTU) and carcass data to determine body composition in feedlot cattle (n = 96) fed zilpaterol hydrochloride (ZH). Black-hided cattle were weighed and scanned using RTU 32 d before the start of the ZH treatment period. Resulting data were used to predict empty body fat (EBF %). Steers (n = 48; BW = 520 ± 30.4 kg; EBF % = 26.2 ± 1.9) and heifers (n = 48; BW = 466 ± 29.5 kg; EBF % = 26.7 ± 1.7) were blocked within gender by EBF % in a complete randomized block design and randomly assigned to pen (2 pens/block; 4 hd/pen) and treatment (6 pens/treatment). Measurements of RTU were taken by a certified ultrasound technician approximately 24 h before slaughter using an Aloka 500-V instrument with a 17-cm 3.5 MHz transducer. Hair was clipped

to less than 0.64 cm and vegetable oil was applied. The RTU measured traits consisted of 12-13th rib backfat thickness (uBF, mean = 12.4 mm), 12--13th LM area (uREA, mean = 93.9 cm^2), and marbling score (uMARB, mean = 5.1). Intramuscular fat was converted to uMARB by using the equation: uMARB = ((769.7 + (56.69×uIMF))/100)– 5. Overall means for carcass data were 12-13th rib backfat thickness (cBF, 13.6 mm), 12-13th LM area (cREA, 92.0 cm^2; measured using tracing paper), and marbling score (cMARB, 5.2). Marbling scores were converted to a numeric cMARB ($Slight^{00}$ = 4, $Small^{00}$ = 5, and $Modest^{00}$ = 6). Data were analyzed using the PROC REG, MEANS and CORR procedures of SAS. Results show that both methods were highly correlated to each other. Overall correlations were 0.83, 0.61, and 0.69 for BF, REA and MARB, respectively. The accuracy statistics for cattle (heifers and steers pooled together) fed ZH and Control were almost identical. Correlations for ZH and control cattle were 0.83, 0.60, 0.68 and 0.83, 0.59, 0.70 for BF, REA, MARB for ZH, respectively. The low correlation for REA could be a result of the method of collecting carcass REA data. Overall RTU underpredicted BF and MARB and overpredicted REA (bias = -1.32, -0.18 and 1.47, respectively). These results show that RTU can be used to predict carcass traits before slaughter and feeding ZH seems to have no effect in predicting carcass traits using RTU in live animals.

Key Words: ultrasound, carcass traits, zilpaterol hydrochloride

---

0149 The effect of zilpaterol supplementation and RFI on growth performance. L. J. Walter*[1], T. J. McEvers[1], N. D. May[1], J. A. Reed[1], J. P. Hutcheson[2], and T. E. Lawrence[1], [1]*West Texas A&M University, Canyon,* [2] *Merck Animal Health, Summit, NJ.*

Supplementation of zilpaterol hydrochloride (ZH) impacts live cattle performance. Research has not focused on individual intake or the impact on residual feed intake (RFI) when cattle are supplemented ZH. A 308 d serial-harvest trial was conducted in Holstein steers (n = 110) blocked by 11 harvest dates (d 252−534) and assigned to ZH or control treatments (n = 5 per treatment per harvest). Individual DMI was collected using the GrowSafe system and rations were sampled monthly for proximate analysis (CP = 14.5 ± 0.7; NE_m = 2.2 ± 0.1 Mcal/kg; NE_g = 1.5 ± 0.03 Mcal/kg). Every 28 d, DMI, ADG and SBW (BW*0.96) were calculated. Within each 28 d period, before ZH supplementation, RFI was calculated for each steer with a regression equation (coefficients of metabolic BW and shrunk BW gain); steers were assigned to a high or low RFI. Statistical analysis for data generated before ZH supplementation was conducted using a mixed model with fixed effects of RFI and days on feed (DOF) and random effects of harvest group and head count per feeding node; DOF was a repeated measure. Analysis of data during the ZH supplementation period was conducted using a mixed model with the fixed effects of ZH, DOF, and RFI and the random effect of harvest group. Intake before ZH supplementation was associated with RFI ($P < 0.01$); the high group consumed more DM than the low group (10.7 vs. 9.4 kg). A quadratic relationship between DMI and DOF was observed ($P < 0.01$); an inflection point occurred at Day 392. Gain efficiency (G:F) was also influenced ($P < 0.01$) by RFI; steers in the high RFI exhibited a G:F of 0.13 whereas low RFI steers were 0.15. As DOF increased, ADG and G:F exhibited a linear decrease ($P < 0.01$). During the ZH supplementation period, steers of the high RFI consumed more DM ($P < 0.01$; 10.6 vs. 9.5 kg) than those of the low RFI. However, steers supplemented ZH consumed less ($P = 0.03$) DM (9.7 vs. 10.3 kg). No ZH x RFI interaction ($P = 0.42$) was observed for DMI. Daily gain was not different ($P \geq 0.22$) between ZH treatments or RFI group. However, G:F tended ($P = 0.07$) to be greater for steers supplemented ZH; RFI did not affect G:F ($P = 0.39$).

Key Words: DMI, RFI, zilpaterol

0150 Effects of zilpaterol hydrochloride on internal body temperature and respiration rate of black-hided feedlot steers and heifers during moderate heat stress. W. C. Burson*[1], A. J. Thompson[1], M. A. Jennings[1], J. A. Carroll[2], N. C. Burdick Sanchez[2], J. E. Hergenreder[1], J. O. Baggerman[1], B. J. Ragland[1], E. S. Murray[1], T. R. Schmidt[1], K. S. Sharon[1], F. R. B. Ribeiro[1], B. J. Johnson[1], and R. J. Rathmann[1], [1]*Texas Tech University, Lubbock,* [2]*USDA-ARS, Livestock Issues Research Unit, Lubbock, TX.*

The objective of this study was to examine the effects of zilpaterol hydrochloride (ZH) on the internal body temperature and respiration rate of feedlot cattle during moderate heat stress. Black-hided steers and heifers (n = 96) were sourced from a commercial feedlot and transported to the Texas Tech University Beef Center in New Deal, TX. Cattle were weighed and scanned using real-time ultrasound. Resulting data were used to predict empty body fat percentage (pEBF %). Steers (n = 48; BW = 520 ± 30.4 kg; pEBF % = 26.2 ± 1.9) and heifers (n = 48; BW = 466 ± 29.5 kg; pEBF % = 26.7 ± 1.7) were blocked within gender by pEBF % in a completely randomized block design and randomly assigned to pen (2 pens/block; 4 hd/pen) and treatment (6 pens/treatment): 1) control heifers (HC), 2) ZH heifers (HZ), 3) control steers (SC), and 4) ZH steers (SZ). During the ZH treatment period the climatic conditions were: mean maximum temperature, 29.67°C; mean minimum temperature, 15.18°C; mean relative humidity, 60.69%; mean wind velocity, 8.37 km/h. Immediately preceding the ZH treatment period (d -1), cattle were fitted with an indwelling rectal temperature probe. Rectal temperatures (RT) were recorded at 5-min intervals throughout the treatment period. Panting scores (PS) were assigned to cattle every other day from 1500

to 1700 h during the ZH treatment period based on a scale ranging from 1 to 4 (1 = normal respiration, 4 = extremely elevated respiration). Repeated measures analysis of RT revealed a significant treatment × gender interaction ($P < 0.0001$). The HC group recorded higher RT relative to the HZ group ($P \leq 0.0009$; 38.83°C versus 38.76°C, respectively). Alternatively, the SC group recorded lower RT relative to the SZ group ($P \leq 0.0009$; 38.96°C versus 38.98°C, respectively). Although highly significant differences were detected for RT, the marginal effect size may be insufficient to deduce biologically significant implications. Fisher's exact test for count data was used to analyze the frequency distribution of PS. No differences were detected in PS between treatments at any single point of data collection or for the entire treatment period ($P \geq 0.32$). Collectively, the variables measured in the present study do not provide compelling evidence to suggest that ZH treated black-hided cattle of either sex have more difficulty coping with moderate heat stress relative to their control counterparts.

Key Words: cattle, zilpaterol hydrochloride, heat stress

0151 Effects of zilpaterol hydrochloride on blood gas, electrolyte balance and pH in feedlot cattle.

W. C. Burson*[1], A. J. Thompson[1], M. A. Jennings[1], J. A. Carroll[2], N. C. Burdick Sanchez[2], J. E. Hergenreder[1], J. O. Baggerman[1], B. J. Ragland[1], K. S. Sharon[1], T. R. Schmidt[1], E. S. Murray[1], F. R. B. Ribeiro[1], B. J. Johnson[1], and R. J. Rathmann[1], *[1]Texas Tech University, Lubbock, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX.*

The objective of this study was to examine the effects of zilpaterol hydrochloride (ZH) on blood gas, electrolyte balance and pH in feedlot cattle. Black-hided steers and heifers ($n = 96$) were sourced from a commercial feedlot and transported to the Texas Tech University Beef Center in New Deal, TX. Cattle were weighed and scanned using real-time ultrasound. Resulting data were used to predict empty body fat percentage (pEBF %). Steers ($n = 48$; BW = 520 ± 30.4 kg; pEBF % = 26.2 ± 1.9) and heifers ($n = 48$; BW = 466 ± 29.5 kg; pEBF % = 26.7 ± 1.7) were blocked within gender by pEBF % in a completely randomized block design and randomly assigned to pen (2 pens/block; 4 hd/pen) and treatment (6 pens/treatment): 1) control heifers (HC), 2) ZH heifers (HZ), 3) control steers (SC), 4) ZH steers (SZ). Venous blood was collected in lithium heparinized tubes through the use of jugular venipuncture on Day 5, 10, 15, and 20 of the ZH treatment period. Blood samples were placed on ice and transported to an on-site station for prompt analysis. Data were analyzed as repeated measures to assess effects due to treatment. ZH treatment significantly increased potassium (K) concentration ($P < 0.0001$). Calcium (Ca) concentration was reduced in both genders, but, a significant gender × treatment interaction ($P = 0.0376$) revealed that ZH decreased Ca with a greater magnitude in steers relative to heifers. ZH treated cattle expressed a tendency for a lower partial pressure of oxygen (pO_2; $P = 0.082$) relative to control. No significant gender × treatment interactions or main effects were detected ($P \geq 0.14$) for blood pH, partial pressure of carbon dioxide (pCO_2), oxygen saturation (SO_2C), sodium (Na) concentration or percentage of hematocrit (Hct). Collectively, these data suggest that only minor differences exist between ZH and control cattle with respect to blood gases and pH, such that a causative effect cannot be assumed. The alterations in K and Ca indicate that biologically significant differences in the cation-anion difference (CAD) may exist when comparing treatment groups. Furthermore, the significant reduction in blood Ca concentration in ZH treated cattle provides more insight to the well-known reduction in post-mortem tenderness associated with cattle fed a β-adrenergic agonist.

Key Words: cattle, zilpaterol hydrochloride, blood gas

BREEDING AND GENETICS: APPLICATIONS AND METHODS IN ANIMAL BREEDING—DAIRY I

0152 Calculation and delivery of US genomic evaluations for dairy cattle. G. R. Wiggans*[1], T. A. Cooper[1], P. M. VanRaden[1], D. J. Null[1], J. L. Hutchison[1], O. M. Meland[2], M. E. Tooker[`], and H. D. Norman[2], [1]*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD,* [2]*Council on Dairy Cattle Breeding, Columbus, OH.*

In April 2013, the responsibility for calculation and distribution of genomic evaluations for dairy cattle was transferred from the USDA to the US dairy industry's Council on Dairy Cattle Breeding; the responsibility for development of evaluation methodology remained with the USDA. The Council on Dairy Cattle Breeding has implemented a fee schedule to provide operational funds as well as an incentive for continued submission of phenotypic data necessary for estimation of genomic effects. Since April 2013, substantial improvements have been made to the evaluation system. The number of SNP used for all evaluations has been increased to 61,013 from 45,195. The Jersey reference population has been increased by 1186 Danish bull genotypes obtained through an exchange with Viking Genetics International (Skara, Sweden). Genomic evaluations for Ayrshires were released to the industry. Cutoff studies to assess the accuracy of data available 4 yr earlier for predicting current data showed the mean gain in reliability across traits for Holsteins was 0.5% points from adding 15,818 SNP, 1.2% points for adding the Jersey bulls, and 8.2% points over parent average for Ayrshires. The weighting for cow evaluations used to estimate SNP effects has been reduced. Also, the deregression of the traditional PTA is jointly across animals instead of 1 animal at a time. Each animal gets credit for its own records and for records of its non-genotyped progeny. This prevents double counting of traditional information when parents and progeny are both genotyped. For yield traits, genotyped-daughter evaluations are not removed because the cow adjustment made them incompatible. Adjustment of cow weights improved the regression of genomic evaluation on future performance and reduced bias. Multitrait traditional evaluations for heifer and cow conception rates are used to estimate SNP effects for those traits. Imputed values are now provided for gene tests for bovine leucocyte adhesion deficiency, complex vertebral malformation, deficiency of uridine monophosphate synthase, syndactyly, Weaver Syndrome, spinal dismyelination, spinal muscular atrophy, red coat color, and polledness. Four tests for haplotypes that affect fertility or stillbirth rate were added (HH4 and HH5 for Holsteins, BH2 for Brown Swiss, and AH1 for Ayrshires). As of February 2014, over 538,000 genotypes are used in genomic evaluation with a mean of 18,000 added monthly. Genomic evaluations are released for animals from 36 countries, an indication of the global demand for them.

Key Words: dairy cattle, genomic evaluation, holstein

0153 An updated version of lifetime net merit incorporating additional fertility traits and new economic values. J. B. Cole* and P. M. VanRaden, *Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD.*

Lifetime net merit (NM$) is an economic selection index intended for use by commercial dairy producers. The current version of NM$ was most recently updated in 2010 and includes information from 13 traits in Holsteins, 11 in Brown Swiss, and 9 in the other dairy breeds. A new version of the index, 2014 NM$, now includes heifer (HCR) and cow (CCR) conception rates to provide more complete information about fertility. Additional benefits of fertility that are not included in productive life (PL) are earlier age at first calving, decreased units of semen needed per pregnancy, decreased labor and supplies for heat detection, synchronization, inseminations, and pregnancy checks, additional calves produced, and higher yields because more optimal lactation lengths are achieved. The total value of HCR including age at first calving, insemination costs, heat detection, pregnancy checks, and reproductive culling was $2.25; CCR was $2.25; and DPR was $11. Replacement heifers were previously assumed to cost $1940, but current prices are only about $1200 to 1500. Lower replacement prices will reduce the value of PL and daughter pregnancy rate (DPR) because fewer lactations are needed to recover costs. Fertility traits will receive a combined emphasis of 8.6%, less than the 11% on DPR in 2010 NM$. Relative emphasis for PL will decrease to 17% from 22% in 2010. DHI mean SCC has decreased from 230,000 in 2002 to 200,000 in 2012. Therefore, the actual change in SCC from a 1-unit change in SCS and actual SCC differences among bull daughters are now much less than when SCC premiums were introduced. The premium/1,000 cells increased only slightly since 2010 and contributes much of the SCS economic value, but the smaller phenotypic mean and SD for SCC will decrease the relative emphasis to 8% on SCS from 10% in 2010. Only slight revisions are needed to the milk and components prices forecast in 2010 NM$, but yield traits will receive more relative emphasis if PL, SCS, and fertility get less emphasis. These changes will increase the relative emphasis on yield to 42% from 35% in 2010. The 2014 NM$ index is correlated by 0.966 with 2010 NM$ for recent progeny-tested bulls. An increase in genetic progress worth $8 million/year is expected on a national basis, assuming that all of the changes are improvements and that all breeders select on NM$.

Key Words: economic values, lifetime net merit, selection index

0154 Gains in reliability with genomic information in US commercial holstein heifers. F. A. Di Croce*, J. B. Osterstock, D. J. Weigel, and M. J. Lormore, *Zoetis Inc., Kalamazoo, MI.*

Genomic selection allows producers to accurately identify genetically superior animals at a much earlier age than traditional parent averages. The objective of this study is to quantify the gain in reliability from including genomic information in a commercial US Holstein dairy female population. Genomic Predicted Transmitting Abilities (GPTAs) from two Zoetis Low Density Panels consisting of 6836 markers (LD) and 10,932 markers (ZLD) and Parent Averages (PAs) for 73,480 Commercial US Holstein heifers were available for this study. Predicted transmitting abilities (PTAs) from the December 2013 USDA-CDCB evaluation for non-parent animals born in 2012 and 2013 were compared to corresponding GPTA from the December 2013 predictor population. Means were derived and daughter equivalents (DE) were estimated as described by VanRaden and Wiggans (1991). Mean reliabilities for the LD and ZLD panels were 66.85%, 71.15%, 71.15%, 71.15%, 64.48%, 67.45% and 63.10% for Lifetime Net Merit (NM$), Milk, Fat, Protein, Productive Life (PL), Somatic Cell Score (SCS) and Daughter Pregnancy Rate (DPR), respectively (not shown). Average gains in reliability above parent average ranged from 42.69% to 45.44% for LD and from 44.93% to 47.62% for ZLD across the selected yield, health and fertility traits. Mean Daughter Equivalent (DE) above Parent Average across the selected traits ranged from 23.9 to 142.0 and 24.9 to 147.5 for LD and ZLD, respectively (Table 0154). These results suggest that including genomic information in the genetic evaluation of young commercial Holstein females substantially increases reliability over the traditional parent averages.

Key Words: dairy, genomic, reliability

Table 0154. Observed reliabilities in December 2013 for Traditional Parent Averages and their December 2013 Genomic Evaluation by trait and DNA panel (Chip)

Trait[1]	Chip[2]	Parent Average	Genomic Value	Gain[3]	DE[4]
NM$	LD	23.21	66.76	43.55	30.7
	ZLD	21.54	67.21	45.68	32.0
Milk	LD	25.61	71.05	45.44	23.9
	ZLD	23.93	71.56	47.62	24.9
Fat	LD	25.61	71.05	45.44	23.9
	ZLD	23.93	71.56	47.62	24.9
Protein	LD	25.61	71.05	45.44	23.9
	ZLD	23.93	71.56	47.62	24.9
PL	LD	20.44	64.39	43.95	74.4
	ZLD	18.72	64.84	46.12	77.5
SCS	LD	23.13	67.44	44.31	55.5
	ZLD	21.37	67.92	46.55	57.8
DPR	LD	20.34	63.03	42.69	142.1
	ZLD	18.47	63.40	44.93	147.6

[1]NM$ = Lifetime Net Merit Dollars, PL = Productive Life, SCS = Somatic Cell Score, DPR = Daughter Pregnancy Rate.
[2]LD = Low Density Panels consisting of 6836 SNPs, ZLD = Low Density Panels consisting of 10,932 SNPs.
[3]Gain = Genomic REL– Parent Average REL.
[4]DE = Daughter Equivalent.

0155 Genome-wide association analysis in Italian Simmental cows for lactation curve traits using a low density (7K) SNP panel. N. P. P. Macciotta*[1], D. Vicario[2], C. Dimauro[1], G. Gaspa[1], M. Cellesi[1], A. Puledda[3], S. Sorbolini[1], and P. Ajmone-Marsan[4], *[1]Università di Sassari, Sassari, Italy, [2]ANAPRI, Udine, Italy, [3]Dipartimento di Agraria, Università di Sassari, Sassari, Italy, [4]Università Cattolica del Sacro Cuore, Piacenza, Italy.*

In genomic selection (GS) programs of dairy cattle breeds, bulls are currently genotyped using medium or high density SNP platforms. Genome wide association studies (GWAS) are then performed on variables (as polygenic breeding values or deregressed proofs) that are derived from phenotypes recorded on females. It could therefore be of interest to perform GWAS directly on cows that now are being genotyped in GS programs, often by using low density SNP panels. In this study, GWAS was performed on 1211 lactations of 337 Italian Simmental cattle, genotyped with the 7K Illumina bead-chip. Edit on markers was performed on call rate (> .99) and minor allele frequency (> .01). After edits, 6891 markers were retained for the analysis. Phenotypes were scores of the first two principal components obtained by performing principal component analysis on the test day records (seven for each lactation) for milk yield, fat and protein percentages, and somatic cell scores (SCS). The first component describes the average level (LEVEL) of the lactation curve, i.e., the average level of milk yield and percentages along the whole lactation, whereas the second is related to the shape of the lactation curve (SHAPE). Data were analyzed with a mixed linear model that included fixed effects of calving month, calving year, parity, SNP genotype (coded as 0,1,2), and random effects of herd, animal additive, permanent environment. Multiple testing was accounted for by performing the Bonferroni correction (uncorrected P × number of tests). Two markers were associated to LEVEL for milk yield according to the Bonferroni corrected statistical significance ($P < 0.05$). One was located on BTAs 6, close to the casein cluster. Nine significant SNPs were highlighted for LEVEL of fat percentage. Most important ($P < 0.001$) were on BTA23, close to the desmoplakin gene, which is involved in the turnover of epithelial cells, and on BTA7 close to the Ring Finger protein 145. Moreover, two significant SNP were located on BTA14, close to the CYP11B1 gene, previously reported to be associated to dairy traits in Holstein. Six markers were associated to protein percentage. The most significant was on BTA12, close to the HSTRA locus, reported to be associated to type traits in Chinese Holstein. Finally, one marker was found to affect SCS on BTA22, close to the LANCL2 locus. No markers were found to be associated to the SHAPE component for any of the four considered traits

Key Words: GWAS, LD panel, Italian Simmental Cattle

0156 Genetic parameters for pre-calving feed intake.
B. N. Shonka* and D. M. Spurlock, *Iowa State University, Ames.*

The objective of this study was to estimate genetic parameters for dry matter intake (DMI) measured during lactation and the dry period in Holstein cows. Daily individual feed intake data collection started approximately 30 d before the expected calving date and continued through the first half of lactation. Pre-calving DMI traits were defined as average DMI on d -17 through -15 (cows) or d -10 through −8 (heifers) relative to parturition (DRYDMI), average DMI for d -1 through -3 relative to parturition (CALVEDMI), and the slope of the regression line fit through the last 14 (cows) or 7 (heifers) days before parturition (DECLINE). These traits were compared to DMI during lactation, defined as average DMI for 100 through 102 d in milk (LACDMI). The final data set included 242 and 214 primiparous and multiparous cows, respectively. Genetic parameters were estimated by mixed model analyses using a 5-generation pedigree. Fixed effects included lactation, year by season of calving, age at calving, sex of calf (male, female or twin), and status of calf (live or dead). Heritability estimates were 0.37, 0.60, 0.28, and 0.41 for DRYDMI, CALVEDMI, DECLINE, and LACDMI, respectively. Genetic correlations between all traits except DECLINE and LACDMI were significantly greater than zero. The correlation between DRYDMI and DECLINE was 0.37, but all other correlations were greater than 0.70. In particular, the genetic correlation between DRYDMI and LACDMI was 0.93. Results from this study demonstrate that DMI measured during the dry period or lactation is a moderately heritable trait. The high genetic correlation between DRYDMI and LACDMI was unexpected because DMI during lactation is also highly influenced by milk production. However, results of this study suggest the genetic regulation of DMI during the dry period and lactation is very similar. This result has potential implications for the measurement of feed intake for the purpose of calculating feed efficiency because in some situations, measurement of feed intake during the dry period is more feasible than measurement during lactation. However, this study is based on a relatively small number of cows and would benefit from verification in a larger population.

Key Words: Holstein cow, heritability, pre-calving intake

0157 Phenotypic and genetic correlations among milk energy output, body weight, and feed intake, and their effects on feed efficiency in lactating dairy cattle.
M. J. VandeHaar*[1], Y. Lu[1], D. M. Spurlock[2], L. E. Armentano[3], K. A. Weigel[3], R. F. Veerkamp[4], M. Coffey[5], Y. de Haas[4], C. R. Staples[6], E. E. Connor[7], M. D. Hanigan[8], and R. J. Tempelman[1], *[1]Michigan State University, East Lansing [2]Iowa State University, Ames, [3]University of Wisconsin, Madison, [4]Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, Wageningen, Netherlands, [5]Scottish Agriculture College, Edinburgh, United Kingdom, [6]Dep. of Animal Sciences, University of Florida, Gainesville, [7]USDA-ARS, Bovine Functional Genomics Laboratory, Beltsville, MD, [8]Virginia Polytechnic Institute and State University, Blacksburg.*

Continued improvements in feed efficiency are essential for a thriving and sustainable dairy industry. Gross efficiency (GrEff) is defined as the energy captured in milk and body tissues as a percentage of gross energy intake. Our objective was to characterize the relationships among component traits for feed efficiency in lactating Holsteins and to determine their relationships to GrEff. Milk energy output per day (MilkE), calculated from milk, fat, protein, and lactose yields, dry matter intakes (DMI), body weights (BW), and body condition scores (BCS), were collected on 4452 lactating Holstein cows ranging from 50 to 200 d in milk from Scotland, the Netherlands, and the United States. The first 42-d records were analyzed with multivariate animal model in ASREML 3.0. Daily body energy change (dBE) was estimated from body weight change and BCS. Metabolic BW (MBW) was BW to the 0.75 power. GrEff was calculated as (MilkE + dBE)/Gross Energy intake, assuming all diets were 4.5 Mcal/kg. For these cows, MilkE was 26 ± 6 Mcal/d, BW was 600 ± 70 kg, DMI was 22 ± 5 kg/d, and intake as a multiple of maintenance was 3.9 ± 0.6. Genetic correlations for feed efficiency traits were 0.07 ± 0.04 for MilkE and MBW, 0.73 ± 0.03 for MilkE and DMI, and 0.40 ± 0.03 for MBW and DMI. Phenotypic correlations for feed efficiency traits were 0.16 ± 0.02 for MilkE and MBW, 0.60 ± 0.01 for MilkE and DMI, and 0.37 ± 0.01 for MBW and DMI. All correlations were reasonably consistent across countries. Genetic correlations of GrEff with MilkE, MBW, and DMI were 0.61 ± 0.04, -0.14 ± 0.05, and 0.04 ± 0.06, respectively. Phenotypic correlations of GrEff with MilkE, MBW, and DMI were 0.47 ± 0.01, -0.05 ± 0.02, and -0.17 ± 0.01, respectively. We conclude that, for Holsteins at a multiple of maintenance around 4, selection for milk component yield remains the overwhelming determinant of feed efficiency, and that selection for smaller body size may benefit feed efficiency but its impact will be slight compared to selection for more milk. Moreover, selection for greater milk will have a

Table 0158. Conception rate (CR) by month for lactating Holstein (HO) and Jersey (JE) cows

Year Month	2011 Apr	2011 May	2011 Jun	2011 Jul	2011 Aug	2011 Sep	2011 Oct	2011 Nov	2011 Dec
CR-JE	47.2%[a]	45.3%[a]	42.3%[a]	34.5%[b]	34.0%[b]	31.2%[c]	35.6%[b]	41.0%[a]	43.2%[a]
CR-HO	37.3%[a]	37.5%[a]	33.2%[b]	28.2%[c]	27.6%[c]	25.9%[c]	28.7%[c]	35.0%[a]	38.5%[a]

[a,b,c] different letters within rows ($P < 0.05$).

greater impact on profitability than would selection for BW. We suggest that that direct selection for body size (either larger or smaller) is likely not warranted as a means to enhance milk production or feed efficiency.

Key Words: lactating dairy cow, feed efficiency, body weight

0158 Benchmarking reproductive efficiency in commercial dairy herds in California.

A. H. Souza*[1], N. Silva-Del-Rio[2], E. O. S. Batista[3], W. VerBoort[4], P. S. Baruselli[3], and P. J. Ross[2], *[1]University of California Cooperative Extension, Tulare, [2]University of California, Davis, [3]University of Sao Paulo-VRA, Sao Paulo, Brazil, [4]AgriTech Analytics, Visalia, CA.*

Our objective was to benchmark reproductive efficiency for both Holstein (HO) and Jersey (JE) dairy herds in California (CA). Reproductive records from DHIA's database (AgriTech Analytics) for all cows that calved in CA in 2011 were used. The initial dataset included artificial insemination records from 511 dairy operations and 554,523 lactating cows (501,616-HO; 52,907-JE) in a total of 1377,729 breedings (1262,926-HO; 114,803-JE). Only herds reporting at least 200 breedings and having overall conception results within 15% to 75% were included in the analysis. Breeding intervals that were less than 3d or greater than 150 d were discarded from final analysis. In addition, cows that were sold or died before pregnancy confirmation or re-inseminated (and assumed non-pregnant) were disregarded. Conception rate (CR) was defined as number cows pregnant by total number of AIs. Service rate (SR) was calculated based on the average interval between breedings (Woods-index). Statistical analyses were performed with the Proc HPMIXED of SAS (version 9.3), with herd and cow used as random effects in the model. Overall, milk production level 305ME did not affect ($P > 0.10$) CR or SR results for either HO or JE cows. However, CR and SR from JE cows (CR = 38.8%; SR = 66.7%) were better ($P < 0.05$) than in HO-cows (CR = 32.8%; SR = 60.1%), but with great variation in milk production and reproductive performance within each breed. As suspected, CR was drastically affected ($P < 0.05$) by season, with a major decrease for both breeds during the warmer months of the year—as shown in Table 0158. In contrast, SR remained fairly constant throughout seasons and this was independent from cow breed. In summary, these results indicate a major detrimental effect of summer heat stress on fertility of California dairies that seems to disturb both HO and JE cows.

Key Words: dairy cows, heat stress, breed

0159 [Withdrawn]

0160 [Withdrawn]

0161 [Withdrawn]

0162 [Withdrawn]

BREEDING AND GENETICS: GENETIC AND GENOMIC METHODS

0163 Evaluation of predictive ability of Cholesky factorization of genetic relationship matrix for additive and non-additive genetic effect using Bayesian regularized neural network. H. Okut*[1], D. Gianola[2], K. A. Weigel[2], and G. J. M. Rosa[2], [1]*University of Yuzuncu Yil, Van, Turkey,* [2]*University of Wisconsin, Madison.*

This study aimed to explore the effects of additive and non-additive genetic effects on the prediction from using Bayesian regularized artificial neural network (BRANN). The data sets were simulated for two hypothetical pedigrees with five different fractions of total genetic variance accounted by additive (σ^2_a/σ^2_G), additive x additive (σ^2_{aa}/σ^2_G) and additive x additive x additive ($\sigma^2_{aaa}/\sigma^2_G$) genetic effects. A feed forward artificial neural network (ANN) with Bayesian regularization (BR) was used to assess the performance and predictive ability of different nonlinear ANNs and linear models for genetic architectures. Effective number of parameters (γ) and sum of squares error (SSE) in test data sets were used to evaluate the performance of ANNs. Distribution of weights (w_{ij}) and correlation between observed and predicted values in the test data set were used to evaluate the predictive ability. There were clear and significant improvements in terms of the predictive ability of linear (equivalent Bayesian ridge regression) and nonlinear models when the proportion of additive genetic variance in total genetic variance (σ^2_a/σ^2_G) increased. On the other hand, nonlinear models outperformed the linear models at each genetic architecture. The weights for the linear models were larger and more variable than for the nonlinear network, where distributions were leptokurtic, indicating strong shrinkage towards 0. In conclusion, our results showed that: a) inclusion of non-additive effects did not improved the prediction ability compared to purely additive models, b) The predictive ability of BRANN architectures with nonlinear activation function were substantially larger than the linear models for the scenarios.

Key Words: artificial neural networks, Bayesian regularization, additive and non-additive genetic effects

0164 Using recursion to compute the inverse of the genomic relationship matrix. I. Misztal*[1], A. Legarra[2], and I. Aguilar[3], [1]*University of Georgia, Athens,* [2]*INRA, Castanet-Tolosan, France,* [3]*INIA, Las Brujas, Uruguay.*

A traditional algorithm to invert the numerator relationship matrix is based on the observation that the conditional expectation for an additive effect of one animal given the effects of all other animals depends on the effects of its sire and dam only, each with a coefficient of 0.5. With genomic relationships, such an expectation depends on all other genotyped animals, and the coefficients do not have any set value. For each animal, the coefficients plus the conditional variance can be called a genomic recursion. If such recursions are known, the mixed model equations can be solved without explicitly creating the inverse of the genomic relationship matrix. Several algorithms were developed to create genomic recursions. In an algorithm with sequential updates, genomic recursions are created animal by animal. That algorithm can also be used to update a known inverse of a genomic relationship matrix for additional genotypes. In an algorithm with forward updates, a newly computed recursion is immediately applied to update recursions for remaining animals. The computing costs for both algorithms depend on the sparsity pattern of the genomic recursions. An algorithm for proven and young animals assumes that the genomic recursions for young animals contain coefficients only for proven animals. Such an algorithm generates exact genomic EBV in GBLUP and is an approximation in single-step GBLUP. That algorithm has a cubic cost for the number of proven animals and a linear cost for the number of young animals. All algorithms were evaluated with a simulated data set of 1500 genotypes and ssGBLUP. In the algorithm with sequential updates, setting very small elements in recursions to zero resulted in little sparsity. Setting larger elements to zero caused large errors in G^{-1} due to accumulation of errors. However, this algorithm worked very well for inv(A_{22}), especially when the pedigree depth was limited. When complete recursions were computed and small elements were set to 0, the accuracy of GEBVs was almost unaffected but the sparsity level was moderate. The sparsity level increased to > 60% when G was blended with 20% of A_{22}. In all computations involving the algorithm for proven and young animals, the correlations of GEBV with those using the regular algorithm were > 0.99. The genomic recursions can provide new insight into genomic evaluation and possibly reduce costs of genetic predictions with extremely large numbers of genotypes.

Key Words: genomic selection, single-step GBLUP, efficiency

0165 Advantage of supernodal methods in restricted maximum likelihood when dense matrices are involved in a coefficient matrix of mixed model equations. Y. Masuda*[1,2], S. Tsuruta[2], and I. Misztal[2], [1]*Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan,* [2]*University of Georgia, Athens.*

The objective of this study was to determine speed-up of an average-information (AI) REML algorithm with a supernodal sparse-matrix package. Comparisons included twenty-three models with data sets from broiler, swine, beef and dairy cattle. Models included single-trait, multiple-trait, maternal, and random regression models with phenotypic data; selected models

used genomic information as a genomic relationship matrix in single-step GBLUP. The AIREMLF90 program was used to compare two sparse-matrix packages: FSPAK and YAMS; the latter package used supernodal methods for faster computing when sparse matrices contain large dense blocks. The program was compiled with the Intel Fortran Compiler 13.1 using the Intel Math Kernel Library and ran on a computer with 16-core CPUs. Computations with YAMS were on average over 10 times faster than with FSPAK and had greater advantages for large data and more complicated models including multiple traits and random regressions and with genomic effects. The highest speed-up with YAMS over FSPAK was over 20 times faster in AI REML iteration and over 80 times faster in sparse inversion. In a model with 213,297 pedigreed and 15,723 genotyped animals, a single-trait analysis with FSPAK took about 5 h and multiple-trait analyses did not converge in 1 d. With YAMS, a single-trait analysis took about 20 min and a 4-trait analysis took about 5 h. Supernodal methods dramatically improve the computing cost if the AI REML for larger and more complex analyses, especially when genomic information is included in the single-step GBLUP models.

Key Words: AIREML, supernodal methods, sparse-matrix package

0166 Use of genomic recursions and APY algorithm for single-step GBLUP analyses with large number of genotypes. B. D. Fragomeni*[1], I. Misztal[1], D. Lourenco[1], S. Tsuruta[1], and Y. Masuda[1,2], [1]*University of Georgia, Athens,* [2]*Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan.*

The purpose of this study was to examine accuracy of genomic selection in single-step genomic BLUP (ssGBLUP) when the inverse of the genomic relationship matrix (G) is derived by the algorithm for proven and young animals (APY). This algorithm implements the inversion of G by genomic recursions, with recursions for young animals involving only the proven animals. With efficient implementation, the algorithm has a cubic cost for proven animals but only a linear cost for young animals. Simulated data set included 142k phenotypes in 6 generations under selection for EBV, with 170k animals in the relationship matrix. Genomic data consisted of 20k animals genotyped for 45k SNP; the simulated genomic data mimicked the bovine genome. The proven animals were 10k genotyped parents selected from the first 5 generations, and the young 10k genotyped animals were selected from the last generation. For animals treated as young, 5k had a single record and 5k had no records. Comparisons involved GEBVs obtained by ssGBLUP evaluation with either the exact G (G-REG) and the G inverted by APY algorithm (G-APY). The correlations between GEBV with the G-REG and G-APY were 0.97 overall, 0.94 for animals treated as young without records, and 0.98 for animals treated as young with records. The true accuracies for the animals with records with G-REG and G-APY were 0.57 and 0.58, respectively; for the animals without records, the accuracies for REG and APY were both 0.43. When the status of the young and proven animals was switched, the accuracies remained identical. A separate analysis involved a national data set for final score in Holsteins. Out of 74,980 genotypes for bulls, 29,552 for bulls with daughters were treated as proven and 45,428 without daughters were treated as young. The correlations of GEBV obtained with the REG and APY algorithms were > 0.99 for both groups of bulls. When the number of high-accuracy animals with genotypes is limited (< 100k), the APY algorithm may drastically reduce the cost of the ssGBLUP evaluation without affecting the accuracy. The APY algorithm may allow using all the available genotypes in one ssGBLUP analysis to reduce biases due to preselection of young animals.

Key Words: single step method, genomic selection, genetic evaluation

---

0167 Genomic prediction accounting for residual heteroskedasticity. Z. Ou*[1], R. J. Tempelman[2], J. P. Steibel[2], C. W. Ernst[2], R. O. Bates[2], and N. M. Bello[1], [1]*Kansas State University, Manhattan,* [2]*Michigan State University, East Lansing.*

Classical genomic selection (GS) models that use single-nucleotide polymorphism (SNP) marker information to predict genetic merit of animals and plants usually assume homogeneous residual variance. However, this assumption seems questionable as environmental variability can be heterogeneous and it may affect the genetic control of a given quantitative trait. This study extends classical GS models, namely RR-GBLUP, BayesA, BayesB and BayesC, to explicitly account for residual heteroskedasticity using a hierarchical Bayesian mixed-models framework implemented with Markov Chain Monte Carlo methods. Competing GS models assuming homogeneous or heterogeneous residual variances were fitted to training data under simulation scenarios reflecting a gradient of increasing residual heteroskedasticity. Model fit of competing homoskedastic and heteroskedastic GS models was compared using prediction accuracy of genomic breeding values and pseudo-Bayes factors, both computed on a validation data subset one generation removed from the training dataset. Competing models were also fitted to two quantitative traits selected from a Michigan State University swine resource population dataset, namely carcass temperature and loin muscle pH 45 min after slaughter. These traits had been pre-screened for homoskedasticity and heteroskedasticity, respectively. Using a fivefold cross-validation approach, competing GS models were compared based on predictive ability of phenotypes. Overall, under the conditions considered in this study, heteroskedastic GS models showed improved model fit and enhanced prediction accuracy compared to homoskedastic GS models under conditions of extreme residual variance

heterogeneity; however, the magnitude of the improvement was too small (approximately 1% to 2% net gain in prediction accuracy) to confer practical relevance.

Key Words: genomic selection model, heterogeneous residual variance, genomic breeding values.

0168 Are past generations contributing to evaluations on young genotyped animals? D. Lourenco*[1], I. Misztal[1], S. Tsuruta[1], I. Aguilar[2], T. J. Lawlor[3], S. Forni[4], and J. I. Weller[5], *[1]University of Georgia, Athens, [2]INIA, Las Brujas, Uruguay, [3]Holstein Association USA Inc., Brattleboro, VT, [4]Genus Plc, Hendersonville, TN, [5]ARO, The Volcani Center, Bet Dagan, Israel.*

Datasets of US and Israeli Holsteins and pigs from PIC were used to evaluate the impact of different number of generations on ability to predict GEBV of young genotyped animals. The inclusion of only two generations of ancestors (A2) or all ancestors (Af) was also evaluated. A total of 34,506 US and 1305 Israeli Holsteins bulls, and 5236 pigs were genotyped. The evaluations were computed by traditional BLUP and single-step GBLUP, with respective computing performance recorded. For the two Holstein datasets, coefficients of determination and regression of deregressed evaluations from a full dataset with records up to 2011 on EBV or GEBV from the reduced dataset (up to 2006 for Israeli and 2007 for US) and truncations were computed. The thresholds for old data deletion were based on generation intervals of 5 yr. For the PIC dataset, correlations between corrected phenotypes and EBV or GEBV were used to evaluate the predictive ability on young animals born in 2010 and 2011. The reduced dataset contained data up to 2009 and the thresholds were based on generation interval of 3 yr. The number of generations that could be deleted without reduction in accuracy was dependent on data structure and trait. For US Holsteins, removing 3 and 4 generations of data did not reduce accuracy of evaluations for final score in Af and A2 scenarios, respectively. For Israeli Holsteins, the accuracies for milk, fat, and protein yields were the highest when only phenotypes recorded on year $\geq$ 2000 and full pedigrees were included. Of the 135 Israeli validation bulls with genotypes and daughter records only in the complete dataset, 38 and 97 were sons of Israeli and foreign bulls, respectively. While more phenotypic data increased the prediction accuracy for sons of Israeli bulls, the reverse was true for sons of foreign bulls. For PIC dataset, removing data up to five generations did not erode predictive ability for genotyped animals for litter size and number of stillborn. Given the data used in this study, truncating old data does not decrease the accuracy on young genotyped animals, while reducing computation requirements and helping to find problems due to population structure. For populations that include local and imported animals, the truncation may be beneficial for one group of animals and detrimental to another.

Key Words: ssGBLUP, pedigree depth, genomic selection

0169 Use of linear models with normal, Student-t or Slash distributed error for the analysis of quantitative traits. B. Mestav*[1], K. Kizilkaya[2], and S. O. Peters[3], *[1]Canakkale Onsekiz Mart University, Canakkale, Turkey, [2]Adnan Menderes University, Aydin, Turkey, [3]Berry College, Mount Berry, GA.*

Some symmetric and heavy-tailed distributions, such as Student's-*t* and Slash, have been suggested for robust inference in linear mixed models. These robust models are characterized by the degrees of freedom of these distributions and include the normal distribution when the degrees of freedom approach infinity. The objective of this this study was to investigate joint estimation of degrees of freedom for the residual and all other genetic and non-genetic parameters. In a simulation study, five different populations with five replicates were simulated using multivariate linear mixed effects animal models with Normal (NOR), three (ST3) or ten (ST10) degrees of freedom Student-t, and one and half (ST1.5) or three (SL3) degrees of freedom Slash distributions. Multivariate data within each replicate were generated for 18,000 progeny from 10 sires and 20 dams mating, which is selected through three generations. Models with multivariate Student's-*t*, Slash and Normal residuals were fitted to each dataset using a hierarchical Bayesian approach. Predictive log-likelihood (PLL) values strongly favored the multivariate Student's-*t* and Slash models over the Normal models for simulated heavy-tailed datasets. Posterior mean estimates of degrees of freedom parameters seemed to be accurate and unbiased. Estimates of sire and herd variances were similar, if not identical, across fitted models. Posterior mean and 95% posterior probability interval (PPI) estimates of error variances in simulated datasets were found to be (downwardly or upwardly) biased when the fitted model was not the true model. Reliable estimates of degrees of freedom were obtained in all simulated heavy-tailed and normal datasets. The predictive log-likelihood was able to identify the correct model among the models fitted to heavy-tailed datasets. The results obtained indicated that there was no disadvantage of fitting a heavy-tailed model when the true model was normal.

Key Words: multivariate heavy-tailed distributions, robust linear mixed model, MCMC

BREEDING AND GENETICS: APPLICATIONS AND METHODS IN ANIMAL BREEDING—LIVESTOCK II

0170 Genetic gain and economic weights in selection for boar fertility traits in a cross-breeding system. D. Gonzalez-Peña Fundora[*1], R. V. Knox[1], J. Pettigrew[1], M. D. MacNeil[2], and S. L. Rodriguez Zas[1], *[2]University of Illinois, Urbana, [2]Delta G, Miles City, MT.*

Four boar fertility traits: semen volume (VOL, mL), semen concentration (CON, x10^3/mm^3), progressive motion of spermatozoa (MOT, %), and abnormal spermatozoa (ABN, %) provide complementary information about boar fertility. It is now feasible to include these traits in genetic improvement programs. However, there is limited information on the genetic and economic parameters necessary to assess the impact of selection for these traits. Objectives of this study were to estimate economic weights for these traits and to evaluate genetic gain that results from including them in a three-tier, three-way crossbreeding scheme (maternal nucleus lines A and B and paternal nucleus line C). Three cases were simulated in ZPLAN. Case I (baseline case) encompassed genetic selection for number of pigs born alive (NBA), litter birth weight (LBW), adjusted 21-d litter weight (A21), number at 21 d (N21), days to 113.5 kg (D113), backfat (BF), average daily gain (ADG), feed efficiency (FE), and lean carcass % (LEAN). Case II included Case I and a novel fertility indicator called DOSES that combines the four boar fertility traits (VOL * CON/1000) * (MOT/100 * (1 − (ABN/100))/(number of spermatozoa per dose). Case III included Case I and the four boar fertility traits individually. Estimated economic weights represent the net economic gain per unit of genetic improvement in VOL, CON, MOT, ABN, and DOSES ranged from 0.21 to 1.44 $/ml, 0.12 to 0.83 $/x$10^3$/$mm^3$, 0.61 to 12.66 $/%, -0.53 to -10.88 $/%, and 2.01 to 41.43%/dose as number of semen collections per week was reduced from 7 to 1. Average genetic gains remained stable for the maternal traits (NBA, LBW, A21, N21) in Case II and III, relative to Case I. Genetic gains in Cases II and III relative to Case I dropped by 59.2% and 25.8% (BF), 50% and 50% (FE), and 84.4% and 59.4% (LEAN), respectively. The relative economic weights decreased in Case II and III relative to I by 21% and 15% (line A), 18% and 12% (line B) and 32% and 23% (line C), respectively. Selection including the four boar fertility traits separately (Case III) was preferable to using one combined indicator (Case II) by enabling genetic gains in these traits without compromising the genetic gains in the maternal traits.

Key Words: boar fertility traits, economic weights, three-way crossbreeding scheme

0171 A genome-wide association study for egg shell strength in the genome of brown-egg layers. R. A. Ghebrewold[*1,2], M. Heidaritabar[1], A. Vereijken[3], B. J. Ducro[4], and J. W. M. Bastiaansen[4], *[1]Wageningen University, Wageningen, Netherlands, [2]Norwegian University of Life Sciences, Ås, Norway, [3]Hendrix Genetics, Boxmeer, Netherlands, [4]Animal Breeding and Genomics Centre, Wageningen University, Wageningen, Netherlands.*

Egg shell quality is important for commercial egg production. The objective of this study was to identify single nucleotide polymorphisms (SNPs) that are significantly associated with egg shell strength using either own phenotype or deregressed estimated breeding values (DEBV) in brown-egg laying chickens. In this study egg shell strength data were available for 8113 purebred line chickens, of which 2220 had 60k SNP genotype data. Genetic background of shell strength was confirmed by a heritability estimate of 0.29 (SE = 0.03) from this data. The number of chickens with both genotypes and phenotype was 650. Three genome wide association analyses (GWAS) were performed. Single SNP regression (SSR) was used to estimate the SNP effects. The first GWAS analysis was performed on 650 chickens and the model for SSR used own phenotype as the response variable and identified no significant associations (FDR $\leq$ 0.05). To increase the statistical power, DEBV, with their weights, were used as the response variable for two additional association analyses. Chickens with reliabilities of DEBV less than 0.05 were removed from the data set, resulting in 1429 chickens and 36,103 SNPs. In the second GWAS study, we found two significant SNP (FDR $\leq$ 0.05) associated with egg shell strength on GGA1 and GGA2. The third GWAS analysis was performed with a more stringent data filtering, only chickens with reliabilities of DEBV greater than 0.08 were kept (N = 1147). With the more stringent filtering, no significant SNP associations were found (FDR $\leq$ 0.05). Less stringent data filtering can lead to more significant results, probably due to higher power from including more animals, but could also indicate false positive results from including unreliable data points. In addition, GWAS analysis with DEBV as phenotypes may not be a simple solution that works well in any species. The utility of DEBV for GWAS in chickens may be smaller because more information comes from half and full sib families in comparison to for instance cattle.

Key Words: egg shell strength, GWAS, deregression

0172 The identification of a putative mutation for SLICK hair coat in Senepol cattle.

T. S. Sonstegard[*1], D. Bickhart[2], H. J. Huson[3], A. Landaeta[4], L. R. Porto-Neto[5], A. Reverter-Gomez[6], W. Barendse[7], D. J. Null[8], M. P. Morales[9], P. J. Hansen[10], D. Serdal[11], J. F. Garcia[12], R. W. Godfrey[13], and C. P. Van Tassell[1], *[1]USDA, ARS, BFGL, Beltsville, MD, [2]USDA-ARS-AIPL, Beltsville, MD, [3]Cornell University, Ithaca, NY, [4]Universidad del Zulia, Maracaibo, Venezuela, [5]CSIRO Food Futures Flagship, Brisbane, Australia, [6]Food Futures Flagship, CSIRO Animal, Foodand Health Sciences, Brisbane, Australia, [7]CSIRO Animal, Health and Food Science, St. Lucia, Australia, [8]Animal Improvement Programs Laboratory, Agricultural Research Service, United States Department of Agriculture, Beltsville, MD, [9]University of Puerto Rico, Mayaguez, [10]Department of Animal Sciences, University of Florida, Gainesville, [11]University of Florida, Gainesville, [12]Faculdade de Medicina Veterinária de Araçatuba, Univ Estadual Paulista, Araçatuba, Brazil, [13]University of the Virgin Islands, St Croix, US Virgin Islands.*

The slick hair coat (SLICK) is a dominantly inherited trait typically associated with tropically adapted, Criollo-derived cattle breeds. The trait is of interest relative to climate change, due to its association with improved thermo-tolerance and subsequent increased productivity. The goal of this work was to identify the mutation underlying the *SLICK* locus, which was previously mapped to a 4 cM region on chromosome (Chr) 20. To refine this map position, BovineHD genotypes were generated from a sampling (N = 195 animals) of Senepol, Carora, Romosinuano, three additional slick-haired cross-bred lineages and a group of non-slick ancestral breeds. Genome-wide association analysis narrowed the SLICK locus to a 0.8Mb (37.7-38.5 Mbp UMD 3.1) consensus region, which contains *SKP2* and *SPEF2* as possible candidate genes. Three specific haplotype patterns were identified in slick individuals, all with zero frequency in non-slick individuals. In an attempt to identify candidate causative mutations in this region, whole genome re-sequencing was completed for one Romosinuano and five Senepol animals. SNP discovery and annotation analyses revealed a putative causative polymorphism within *prolactin receptor* (*PRLR*), which would truncate an encoded domain involved in JAK/STAT5 signaling. Validation testing of this SNP and 37 others was done across a DNA panel (N = 466) that included representation from five SLICK and seven non-SLICK breeds. The results strongly suggest the frameshift mutation in *PRLR* is the causative mutation underlying SLICK in Senepol and some Romosinuano cattle. However, no associations between this SNP and SLICK animals from Limonero and Carora breeds were found. This information along with accompanying population structure information supports potentially two independent SLICK mutations, one common to Senepol and Romosinuano and another in Limonero and Carora.

Key Words: slick hair coat, cattle, prolactin receptor

0173 Genomic selection of Nili-Ravi buffalo.

M. Moaeen-ud-Din[*1], G. Bilal[1], and M. S. Khan[2], *[1]PMAS-Arid Agriculture University, Rawalpindi, Pakistan, [2]University of Agriculture, Faisalabad, Pakistan.*

Among three well-documented breeds of buffalo dairy breeds in Pakistan, Nili-Ravi is the best milk producer owing to its characteristic of disease and parasitic resistance, and a better convertor of roughages into useful products than cattle. A selection program to enhance the genetic potential for milk production of Nili-Ravi using progeny testing program is going on. Traditional progeny testing program has made a remarkable improvement in the genetic potential of dairy cattle in the developed world. However, this program faces severe implementation issues in buffalo improvement due to limitation of resources and basic infrastructure. Simulated studies have shown the potential of genomic selection in shortening generation interval and increasing the accuracy of selection (especially young bulls) that can bring a relatively rapid genetic improvement. The current study intends to explore the application of genomic selection in a typical buffalo breeding perspective using Nili-Ravi in Pakistan as an example. The assumed size of the training population for genomic selection was 15,860 present with BRI, Pattoki. Our calculations indicated that genomic selection can reduce the generation intervals in the male to male selection pathway from 9.5 yr down to 3.3 yr. It can result in almost 2 times increase in response to selection compared to that in a progeny testing program. Furthermore, it reduced the costs of proving bulls by 88%. The present study suggests the initiation of the program of genomic selection for Nili-Ravi in Pakistan and may serve as an example for other developing countries. The findings of the current study may encourage researchers and policymakers to use genomic selection for improvement in the productivity of dairy cattle of developing countries.

Key Words: developing country, genomic selection, Nili-Ravi buffalo

BREEDING AND GENETICS: APPLICATIONS AND METHODS— MOLECULAR BIOLOGY

0174 Variation in toll-like receptor genes and susceptibility to clinical mastitis in Holstein cows. C. M. Seabury[1], K. N. Galvao[2], K. Lager[3], and P. J. Pinedo[*4], *[1]Department of Veterinary Pathobiology, College of Veterinary Medicine & Biomedical Sciences, Texas A&M University System, College Station, [2]Department of Large Animal Clinical Sciences and D. H. Barron Reproductive and Perinatal Biology Research Program, College of Veterinary Medicine, University of Florida, Gainesville, [3]Iowa State University, Extension and Outreach, Ames, [4]Texas A&M AgriLife Research, Amarillo.*

Toll-like receptor proteins (TLRs) recognize conserved pathogen-associated molecular patterns (PAMPS) and initiate signaling pathways that coordinate the innate immune response. The primary objective of this study was to investigate potential associations between bovine single nucleotide polymorphisms (SNPs) and insertion-deletion (indel) mutations occurring in 7 bovine *TLR* genes (*TLR*s 1, 2, 4, 5, 6, 9, and 10) and clinical mastitis (CM) in dairy cows. Clinical mastitis cases were diagnosed by herd personnel in the milking parlor if milk from one or more quarters was abnormal in color, viscosity, or consistency, with or without accompanying heat, pain, redness, or swelling of the quarter, or with generalized illness, and all treatments were recorded in the on-farm software. Cows were considered as cases if they had at least two CM episodes in the current lactation with the first case occurring within the first 100 d after calving. Cows were included in the control group if they had no CM events during the complete lactation. Each case was matched with 3 control herd-mates in the same parity and with a calving date within 2 mo relative to the case cow. The final study population consisted of 686 Holstein cows (269 primiparae; 417 multiparae) in three farms located in Florida and Texas, including 510 cases and 176 controls. Custom allele-specific genotyping assays derived from multiple bovine *TLR* sequencing studies were utilized. Genotypes for 110 loci (SNPs and indels) that are known to be variable in domestic cattle were determined, resulting in 46 monomorphic loci and 64 loci with two alleles. Collectively, 35 loci did not meet our case-control inclusion criterion for minor allele frequency (MAF $\geq$ 0.10). The association between specific *TLR* genotypes and CM was evaluated by logistic regression with evaluation and correction for potentially confounding variables including: year and season of calving; parity; ME 305 d milk yield; and farm. Overall, five SNPs (*TLR2, TLR9*) produced uncorrected *P*-values $\leq$ 0.05 with respect to CM; four of these SNP associations (3 in *TLR2*, 1 in *TLR9*) endured corrections for multiple testing (*P*-values $\leq$ 0.05). Several confounding variables including year and season of calving, and milk yield remained significant after correction for multiple testing. Our analysis of these data suggests that naturally occurring bovine *TLR2* and *TLR9* variation may potentially elicit tangible effects on udder health in Holstein cows.

Key Words: mastitis, toll-like receptors, candidate gene

0175 Experimental intramammary challenge with *Staphylococcus chromogenes* in dairy heifers with specific *CXCR1* genotypes. J. Verbeke*, K. Piccart, S. Piepers, M. Van Poucke, L. Peelman, and S. De Vliegher, *Ghent University, Ghent, Belgium.*

The *CXCR1* gene encodes one of the two receptors for interleukin 8 (IL-8), named chemokine (C-X-C motif) receptor 1 (CXCR1). Foregoing experiments suggested that single nucleotide polymorphism (SNP) *CXCR1*c.980A > G (rs43323012) influences mammary gland immunity and mastitis resistance. To further investigate these findings, 8 mid-lactating Holstein heifers were challenged intramammarily with coagulase-negative staphylococci (CNS) species. Four heifers had genotype c.980AG and 4 heifers had genotype c.980GG. Each heifer was inoculated with 1.0×10^6 colony-forming units (CFU) of *Staphylococcus chromogenes*, originating from a chronically infected quarter. The quarter bacterial count (qBC) and quarter milk somatic cell count (qSCC) were measured at 4, 6, 9, 12, 18, 24, 28, 32, 36, 48, 54, 60, 72, and 78h post inoculation. Additionally, quarter milk production (qMP) was recorded at 12, 24, 36, 48, 60, and 72h post inoculation. Differences in the three outcome variables between c.980AG and c.980GG heifers were analyzed using linear mixed regression models with heifer as random effect and genotype, sampling time and their interaction as fixed effects. None of the quarters/heifers showed symptoms of clinical mastitis. All heifers cleared the inoculated *S. chromogenes* before the end of the trial. No significant differences in qBC and qMP were observed between c.980AG and c.980GG heifers. However, the change of qSCC over time tended to be associated with the heifer's genotype (interaction sampling time × genotype: $P = 0.06$). The increase in qSCC was more pronounced and persistent in c.980AG heifers compared to c.980GG heifers. In conclusion, increase in qSCC following an intramammary challenge with *S. chromogenes* tended to be associated with SNP *CXCR1*c.980A > G. Heifers expressing genotype c.980AG showed a higher immune response than heifers expressing genotype c.980GG.

Key Words: *CXCR1* genotype, *Staphylococcus chromogenes*, intramammary challenge

0176 Association of *CXCR1* gene polymorphisms with incidence rate of clinical mastitis, somatic cell count, and milk production in dairy cattle.
J. Verbeke*, M. Van Poucke, L. Peelman, S. Piepers, and S. De Vliegher, *Ghent University, Ghent, Belgium*.

The objective of this study was to analyze associations between single nucleotide polymorphisms (SNPs) in the *CXCR1* gene (NCBI Gene ID: 100125580), potential genetic markers for mastitis resistance, and the incidence rate of clinical mastitis (IRCM), test-day somatic cell count (SCC) and test-day milk production (MP). Clinical mastitis was monitored on 50 randomly selected Flemish dairy herds for a period of 1 yr. Each case was sampled and cultured according to NMC (National Mastitis Council) guidelines. Incidence rate of clinical mastitis (cases/days at risk) was calculated independently of the culture results and for *Staphylococcus aureus*, *Streptococcus uberis*, *Streptococcus dysgalactiae*, and *Escherichia coli*, separately. Dairy herd improvement records including SCC and MP were available on 32 herds. A fluorescent multiprobe PCR assay was designed to genotype simultaneously SNP *CXCR1*c.735C > G (rs208795699) and SNP *CXCR1*c.980A > G (rs43323012). In total, 3107 cows were genotyped. Associations between the SNP and (pathogen-specific) IRCM were analyzed using mixed Poisson regression models. Linear mixed regression models were fit to test associations between the SNP and SCC and MP. In total, 681 CM samples were analyzed with *S. uberis* (23% of the culture positive samples), *E. coli* (20%), *S. aureus* (10%), and *S. dysgalactiae* (9%) being the most frequently isolated pathogens. Both SNPs were significantly associated with MP ($P < 0.05$) but not with (pathogen specific) IRCM or SCC. Milk production was higher in c.735GG cows (28.6 kg/day, $n = 571$) compared to c.735CG (28.1 kg/day, $n = 1043$) and c.735CC (28.0 kg/day, $n = 516$) cows. Additionally, MP was higher in c.980GG cows (28.4 kg/day, $n = 1277$) compared to c.980AG cows (27.9 kg/day, $n = 743$). In conclusion, SNP *CXCR1*c.735C > G and *CXCR1*c.980A > G were not associated with the studied udder health traits but were with test-day MP.

Key Words: *CXCR1* genotype, udder health, milk production

0177 *Calpastatin* and μ-*calpain* differ in their control of genotype specific residual variance of beef tenderness in Angus and MARC III steers.
R. G. Tait, Jr.*[1], S. D. Shackelford[2], T. L. Wheeler[2], D. A. King[2], E. Casas[3], T. P. L. Smith[1], and G. L. Bennett[1], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]USDA/ARS, Clay Center, NE, [3]USDA. ARS, National Animal Disease Center, Ames, IA*.

Genotype variant effects of *calpastatin* (*CAST*) and μ-*calpain* (*CAPN1*) on mean beef tenderness have been widely characterized. We have tested whether these genetic variants also control residual (non-genetic) variation, and subsequently total phenotypic variation, of tenderness. Observation of rare genotypes is important for understanding the role of these genetic markers on beef tenderness. Two populations at USMARC (Angus and MARC III) were subjected to marker-assisted selection for multiple years to equalize allele (*CAST*) and haplotype (*CAPN1*; CAPN1_316 with CAPN1_4751) frequencies. Within each population, analyses were conducted for 14-d slice shear force (SSF) in steers (Angus, $n = 199$; MARC III, $n = 254$) to estimate genotypic effect size, mode of inheritance, and polygenic effects utilizing 5-generation pedigrees. Beyond the traditional analyses with a single residual variance (Angus, $\sigma_e = 1.79$ kg; MARC III, $\sigma_e = 3.58$ kg), *CAST* and *CAPN1* genotype specific residual variance models were tested. In both populations, *CAST* genotype specific residual variance models fit significantly better (Angus, $P < 0.001$; MARC III, $P < 0.001$) than single residual variance models and were progressive in their effect. Across populations, *CAST* genotype specific residual variance models identified the homozygous tender genotype as having the smallest residual variance (Angus, $\sigma_{e\text{-}TT} = 1.22$ kg; MARC III, $\sigma_{e\text{-}TT} = 2.54$ kg), the heterozygous genotype had intermediate residual variance (Angus, $\sigma_{e\text{-}CT} = 1.99$ kg; MARC III, $\sigma_{e\text{-}CT} = 3.98$ kg), and the homozygous tough genotype had the largest residual variance (Angus, $\sigma_{e\text{-}CC} = 2.82$ kg; MARC III $\sigma_{e\text{-}CC} = 4.86$ kg). In comparison, *CAPN1* genotype specific residual variance models were not as well supported (Angus, $P = 0.05$; MARC III, $P = 0.03$) and in both populations the effects were not progressive, with a heterozygous *CAPN1* genotype (having an intermediate effect on mean) having the smallest residual variance. Effects of *CAST* and *CAPN1* on mean tenderness were maintained under all genotype specific residual variance analyses. These results indicate that beyond changes in the mean, *CAST* also influences phenotypic variation in beef tenderness, which may be important for management and marketing of beef. USDA is an equal opportunity provider and employer.

Key Words: carcass quality, marker effects, tenderness

0178 Investigation of polymorphisms at the *MUC4*, *MUC13*, *MUC20*, and *TFRC* candidate genes for *F4ab/ac* resistance in South African pig populations.
N. S. Chaora*, *Agricultural Research Council, Pretoria, South Africa*.

Selection for *E. coli* F4*ab/ac* resistance has become common due to the increasing resistance of the bacteria to antibiotics. Four candidate genes were studied in three South African breeds, Exotic (Large White, Landrace and Duroc), indigenous and crossbred (Exotic × indigenous), to identify polymorphisms conferring resistance to *E. coli* F4*ab/ac*. A total of 225 pigs aged 3-12 wk were genotyped to target restriction sites in *MUC4*, *MUC13*, *MUC20* and *TFRC* candidate genes. Four polymorphisms of c.8227G > C for *MUC4,* c.576C > T for

MUC13, g.191C > T for *MUC20* and c.291C > T for *TFRC* were detected. The susceptible allele *C* was close to fixation at over 90% in all three breeds for the *TFRC* and *MUC13* loci and there was a genic and genotypic significant difference ($P < 0.05$) amongst breeds for the *TFRC* loci. The resistant *TT* genotype was found in less than 2% of the entire population for the *TFRC* locus and was not found in any pigs for the *MUC13* locus. Both *TFRC* and *MUC13* were not polymorphic in the studied population. The *MUC4* and *MUC20* genes were polymorphic in the population. The resistant alleles *G* for *MUC4* and *C* for *MUC20* were present in the population with the highest frequency observed in the Exotic pigs. There was a significant difference in genotypic distribution amongst breeds at the *MUC20* and *MUC4* loci ($P < 0.05$). An excess of homozygotes in *TFRC* and *MUC20* was observed, leading to a deviation from HWE in the Exotic pigs at these loci. All three breeds were in HWE at the *MUC4* loci although an excess in heterozygotes was observed. The subpopulations at the *TFRC*, *MUC13* and *MUC20* loci were inbred and those at the *MUC4* locus were outbred. There was no significant linkage disequilibrium observed amongst the loci analyzed. The results showed that *MUC4* and *MUC20* were informative and the presence of the resistant alleles makes it possible to use them as markers for selection against susceptibility to F4 *E. coli*.

Key Words: pigs, polymorphisms, *E. coli* F4

0179 Buffalo and cattle sequence diversity and molecular evolution. M. Moaeen-ud-Din* and G. Bilal, *PMAS-Arid Agriculture University, Rawalpindi, Pakistan.*

Identification of genes of importance regarding production traits in buffalo is impaired by a paucity of genomic resources although buffalo genome is sequenced. An alternative to fill this gap is to exploit the plenty of data available for cow, including SNPchips. The cross-species application of comparative genomics tools, i.e., microarrays and comparative sequencing, to identify single nucleotide polymorphisms are potential gear to investigate the buffalo genome. However, both tools are dependent on nucleotide sequences similarity between the two species. Therefore, the objective of this study was to explicate the sequence diversity between cattle and buffalo for comprehending buffalo genome using available cattle genomic resources. In this study, gene diversity between buffalo and cattle was determined by applying 86 gene orthologues taken from NCBI consisting of over 273 kb of aligned sequences using MEGA program V6.0. Results for relative rate test were assessed with the chi-squared test using all available sites (over 273 kb) using MEGA program V6.0. There was approximately 3% difference in all genes in terms of nucleotide diversity; and 0.267 ± 0.134 in amino acids, indicating the possibility for successfully using cross-species strategies for genomic studies. There were significantly higher non synonymous substitutions both in cattle and buffalo. This higher rate of non-synonymous substitutions at similar level in buffalo and cattle indicates a similar positive selection pressure in both species. Results for relative rate test revealed no significant difference in unique mutations between cattle and buffalo lineages at synonymous sites. However, there was a significant difference in unique mutations for non synonymous sites. This indicated that the mutagenic process that generates substitutional mutation is taking place at approximately the same rate at silent sites in cattle and buffalo. However, there was greater variation in mutation rates at non-synonymous sites in both species. Moreover, despite common ancestry, our results indicate a different divergent time among genes of cattle and buffalo. The present study, for the first time, revealed that variable rates of molecular evolution may be present between cattle and buffalo suggesting usefulness in comparative genomics analysis.

Key Words: buffalo, cattle, gene diversity, molecular evolution

COMPANION ANIMALS:
COMPANION ANIMAL NUTRITION AND PET FOOD PROCESSING

0180 [Withdrawn]

0181 Indirect calorimetry, real-time interstitial glucose monitoring, and blood sampling to determine effects of low, medium, and high glycemic index cat foods. K. D. Berendt*[1], A. K. Shoveller[2], and R. T. Zijlstra[1], [1]*University of Alberta, Edmonton, AB, Canada,* [2]*Procter & Gamble Pet Care, Mason, OH.*

The amount and source of dietary starch affects glucose and insulin responses and contributes to dietary glycemic index (GI) in omnivorous monogastrics. However, limited information exists for GI in carnivorous monogastrics such as cats. Thus, the objective was to study a range in dietary GI in relation to indirect calorimetry and postprandial serum glucose and insulin and interstitial glucose. We used 19 domestic shorthair cats in an incomplete replicated 3 × 3 Latin squares for 19 observations per diet. Initial BW averaged 4.9 kg and ranged from 3.4 to 7.1 kg. Three premium cat diets varying in GI based on ingredient composition (chicken & rice, chicken & chicken by-product meal, and turkey & chicken for high, medium, and low GI respectively) and starch content (36.8, 30.7, and 23.6%, respectively) were fed. Diets contained 38 & 23%, 36 & 22%, and 42 & 16% CP and ether extract, respectively. The respiratory quotient (RQ) decreased ($P < 0.001$) with decreasing GI (0.78, 0.77, and 0.76 for high, medium and low GI, respectively), indicating increased lipid oxidation. Daily resting energy expenditure (REE) did not differ among diets. Postprandial (22 h) fat oxidation was inversely related to GI (0.64, 0.68, and 0.69 g/h for high, medium and low GI, respectively; $P < 0.05$). Postprandial carbohydrate oxidation decreased with reducing GI (0.61, 0.52, and 0.46 g/h for high, medium and low GI, respectively; $P < 0.001$). Postprandial (20 h) interstitial glucose decreased with reducing GI (73.4, 64.4, and 59.7 mg/dL d^{-1} for high, medium and low GI, respectively; $P < 0.05$). Postprandial (10 h) serum glucose did not differ among diets and did not peak postprandially followed by return to baseline as expected based on data from responses of omnivorous monogastrics. Interstitial glucose may be more sensitive than a limited number of sequential blood samples to study starch metabolism in cats. Postprandial serum insulin was greatest ($P < 0.05$) for the high GI diet and lowest for the medium GI diet. In conclusion, responses of cats to changes in dietary starch content are unique, i.e., more prolonged and less pronounced than in humans or dogs.

Key Words: glycemic index, calorimetry, cat

0182 The effect of extrusion and elevated storage temperatures on vitamin retention in pet food. A. K. Mooney*, *Kansas State University, Manhattan.*

Little research has been published in recent years regarding the magnitude of vitamin losses through extrusion manufacturing and storage of pet food. The matrixes of pet diets have changed dramatically within the past twenty years since vitamin degradation was last published. Therefore the objective of our research was to determine the effects of processing conditions and dietary protein content on vitamin retention (vitamin A, vitamin D_3, vitamin E, folic acid and thiamine) during extrusion and drying and the subsequent effect during storage at elevated temperatures. Three diets differing in protein (21.7, 25, and 30% CP; Low, Medium, and High, respectively) were produced. Diets were extruded at 350 and 450 rpm screw speed on a Wenger X-20 single screw extruder (Wenger Mfg, Sabetha, KS) and dried at 104°C for 6 min at each pass or 127°C for 10 min at each pass in a Wenger (Wenger Mfg, Sabetha, KS) triple pass dryer. Samples from each treatment were analyzed immediately following production. Without current established criterion for accelerated shelf life studies of pet food, conditions by industry laboratories were practiced using 50°C and 75% relative humidity for 3, 6, 12, and 18 wk before vitamin analysis. Retention of all vitamins evaluated in this study was not affected ($P > 0.05$) by extruder screw speed or dryer conditions. As time in storage (50°C) increased through 3, 6, 12, and 18 wk vitamin A ($P < 0.05$; 153,708, 95,542, 62,491, 21,713, and 6689 IU/kg, respectively), vitamin D_3 ($P < 0.05$; 6956, 4652, 3572, 1824, and 1421 IU/kg, respectively), vitamin E ($P < 0.05$; 855, 970, 834, 837, and 803 mg/kg, respectively), folic acid ($P < 0.05$; 1.75, 1.81, 2.37, 1.45, and 0.98 mg/kg, respectively), and thiamine ($P < 0.05$; 22.9, 19.7, 16.1, 7.4, and 3.3 mg/kg, respectively) concentrations decreased. These results suggest that the processing parameters in this study had little effect on vitamin losses; but, elevated temperature during storage for 18 wk could reduce vitamin content from initial by 95.65, 79.57, 6.08, 44.00, and 85.86% for vitamin A, vitamin D_3, vitamin E, folic acid and thiamine, respectively. Vitamin fortification of extruded pet diets must take into account these changes to avoid deficiency diseases.

Key Words: vitamin stability, effects of thermal processing, vitamin retention

0183 Effects of processing on water soluble B-vitamins in a canned cat diet. S. DeNoya*, G. Aldrich, and C. K. Jones, *Kansas State University, Manhattan.*

There has been very little research published regarding the degradation of B-vitamins in a canned cat food. The objectives of these experiments were to evaluate the effect of batter temperature and moisture, or retort-cooking time on B-vitamin retention. In Exp. 1, cat food was produced at a batter temperature of 60°C and moistures of 65, 75, and 85%. In

Exp. 2, cat food was produced at a batter moisture of 78% and temperatures of 50, 60, and 70°C. All foods were held in the retort (121°C) for 45, 60, and 90 min. In Exp. 1, (n = 3) thiamine concentration decreased (P = 0.0031; 5.11, 4.30, and 2.96 mg/kg for 45, 60, and 90 min, respectively) as time in the retort increased. As batter moisture decreased, thiamine (P = 0.0072; 3.57,3.67, and 5.12 mg/kg for 65,75, and 85% moisture, respectively), riboflavin (P = 0.0320; 10.41,9.89, and 13.00 mg/kg for 65, 75, and 85% moisture, respectively), pantothenic acid (P = 0.0240; 46.32, 49.52, and 67.31 mg/kg for 65, 75, and 85% moisture, respectively), and vitamin B-12 (P = 0.0004; 0.0220, 0.0180, and 0.0400 mg/kg for 65, 75, 85% moisture, respectively) concentration decreased. In Exp. 2, (n = 3) thiamin (P = 0.0002; 5.11, 3.86, and 2.53 mg/kg for 45, 60, and 90 min, respectively), and niacin (P = 0.0170; 228.51, 200.51 and 202.60 mg/kg for 45, 60, and 90 min respectively) decreased as retort time increased. Pantothenic acid (P = 0.0360) concentration initially increased slightly at 60 min, but returned back to its initial level by 90 min. Folic Acid declined (P = 0.0330; 0.85, 0.83, and 0.03 mg/kg for 50, 60, and 70°C, respectively) as batter temperatures increased. In both experiments, thiamine and folic acid losses exceeded 90%, while vitamin B12 losses exceeded 50%. Fortification of canned cat food diets must take these substantial losses into account to avoid nutrient deficiencies.

Key Words: B-Vitamins, pet food, thermal processing

0184 Feeding frequency and dietary water content affect voluntary physical activity in young lean adult female cats. M. R. C. de Godoy*[1], K. Ochi[2], L. F. de Oliveira Mateus[3], A. C. C. de Justino[3], and K. S. Swanson[1,4,5], *[1]Department of Animal Sciences, University of Illinois, Urbana, [2]Nippon Pet Foods Co. Ltd, Tokyo, Japan, [3]Department of Animal Sciences University of São Paulo State, Jaboticabal, Brazil, [4]Division of Nutritional Sciences, Urbana, IL, [5]Department of Veterinary Clinical Medicine, Urbana, IL.*

Obesity is the most common form of malnutrition in the pet population in western countries. Approximately 58.3% of cats are considered overweight or obese in the U. S. It is imperative that in conjunction with the development of effective strategies to manage obesity, preventive measurements for this disease are also exploited. Therefore, the objective of this study was to investigate whether increased dietary water content and feeding frequency increased voluntary physical activity of young lean adult female cats. A replicated 4 × 4 Latin square design with a 2 × 2 factorial treatment arrangement (feeding frequency and water content) was used. The four treatments consisted of: 1) One meal daily dry (without added water); 2) One meal daily wet (dry diet with added water to reach 70% moisture); 3) Four meals daily dry; and 4) Four meals daily wet. Eight healthy adult, lean, intact, young, female domestic shorthair cats were used in this experiment. Voluntary physical activity was evaluated using Actical activity monitors placed on collars and worn around the cat's neck for the last 7 d of each experimental period of 14 d. Food anticipatory activity (FAA) was calculated based on 2h before feeding periods and expressed as a percentage the total daily voluntary physical activity. The interaction between feeding frequency and water content was not statistically significant (P > 0.05). Increased feeding frequency (four vs. one meal daily) resulted in greater average daily activity (P = 0.0147), activity during the light period (P = 0.0023), and light:dark activity ratio (P = 0.0002). In contrast, physical activity during the dark period was not altered by feeding frequency (P > 0.05). Cats fed four meals daily had increased afternoon FAA (P = 0.0029) compared with cats fed once daily. Dietary water content did not affect any measure of activity. Increased feeding frequency is an effective strategy to increase the voluntary physical activity of cats. Thus, it may assist in the prevention and management of obesity.

Key Words: feline, meal frequency and moisture content, physical activity

---

0185 Effects of graded dietary resistant starch concentrations on apparent total tract macronutrient digestibility, fecal characteristics, and fecal fermentative end-products in healthy adult dogs. A. N. Beloshapka* and K. S. Swanson, *Department of Animal Sciences, University of Illinois, Urbana.*

Resistant starch (RS) is fermentable by gut microbiota and effectively modulates fecal short-chain fatty acid (SCFA) concentrations in pigs, mice, and humans. Resistant starch may have similar beneficial effects on the canine gut; however, the dose of a single source of RS that is effective in manipulating fecal fermentative end-products but does not negatively affect stool quality has yet to be determined. Thus, the objective of this study was to evaluate the effects of 0, 1, 2, 3, and 4% dietary high-amylose maize cornstarch (HI-MAIZE 260; RS) on apparent total tract macronutrient digestibility, fecal characteristics, and fecal fermentative end-product concentrations in healthy adult dogs. An incomplete Latin square design was used, with each treatment period lasting 21 d (d0-17 adaptation; d18-21 fresh and total fecal collection) and each dog serving as its own control. Seven dogs (mean age = 5.3 yr; mean BW = 20 kg) were randomly allotted to one of five treatments, which were formulated to be iso-energetic and consisted of graded amounts of 100% amylopectin cornstarch, RS, and cellulose, and fed as a top dressing on the food each day. All dogs were fed the same amount of a basal diet throughout the study and fresh water was offered ad libitum. Data were evaluated for linear and quadratic effects using SAS. Because the RS used in this study is approximately 40% digestible and 60% indigestible starch, the dogs received the following amounts of indigestible starch daily: 0% = 0 g; 1% = 1.8 g; 2% = 3.6 g; 3% =

5.4 g; and 4% = 7.2 g. Dry matter, organic matter, crude protein, fat, and gross energy digestibilities were linearly decreased ($P < 0.05$) in dogs with increased consumption of RS. Fecal output was linearly increased ($P < 0.05$) in dogs with increased consumption of RS. Fresh fecal pH was linearly decreased ($P < 0.05$) in dogs with increased consumption of RS. Fecal scores and fecal fermentative end-product concentrations, including ammonia, SCFA, branched-chain fatty acids, phenols, and indoles, were not affected by the consumption of RS. The results observed in this study compared to previous studies performed in other animal models and humans seem to indicate that RS is slowly fermentable in dogs and may not greatly impact large bowel health in this species.

Key Words: resistant starch; canine; digestibility

0186 Evaluation of common analysis methods for oxidation in rendered protein meals used to produce pet foods. M. Gray*, G. Aldrich, and C. K. Jones, *Kansas State University, Manhattan.*

A significant amount of rendered protein meal is used in pet food to meet the pets' dietary protein and fat needs. These protein meals contain approximately 15-20% fat, which can oxidize and lead to unusable material. Peroxide value (PV) is a common method used to evaluate oxidation in commercial proteins, but it has been criticized as inconsistent and imprecise. Therefore, our objectives were to evaluate alternative methods to measure fat quality in rendered protein meals and to compare the results among different animal sources and rendering plants. It was hypothesized that PV was an inconsistent and unrepresentative method of analysis for measuring fat stability for rendered protein meals. In this experiment, samples of five chicken byproduct meals (CBPM) from each of three locations, and five beef meat and bone meals (BMBM) from each of two locations were evaluated. Samples were analyzed for proximate constituents, anisidine value (AV), thiobarbituric acid reactive substances (TBARS), PV via titration by two laboratories and PV via rapid method (SafTest; peroxysafe). Fat content differed among plants ($P < 0.0001$; BMBM = 8.44 vs. 11.87% and CBPM = 13.24 vs. 15.11 vs. 16.59%) and when aggregated into protein meal type, the ash concentration was greater for BMBM and protein concentration greater for CBPM ($P < 0.0001$). Again, for compiled least square means between the protein meal types, the peroxide values for the BMBM and CBPM were 10.42 and 58.08 meq/kg, respectively from laboratory 1; 4.65 and 3.01 meq/kg, respectively from laboratory 2; and 11.52 and 42.96 meq/kg, respectively from the rapid method test. There was a direct correlation ($r = 0.98$) between PV titration results from laboratory 1 data and the rapid method, but not with titration results from laboratory 2 ($r = 0.46$). This variation among labs is consistent with the anecdotal field evidence and our hypothesis. As expected, the PV from laboratory 1 did not correlate to the AV ($r = 0.61$); a measure of secondary oxidation products. Oxidation indicated by TBARS differed among both protein meal and plant ($P < 0.0001$). Our data corroborate the inconsistencies noted from commercial quality control laboratories. Combined with the results from the AV and TBARS, there is a clear need for further research to create a more accurate and precise analytical method for fat oxidation in rendered protein meals.

Key Words: oxidation, rendered protein meal, pet food

0187 Broken beans (*Phaseolus vulgaris*) use on extruded diets for cats. B. P. Neto[1], F. C. Sa[2], N. Musco[3], A. P. Maria[2], B. Agy[2], B. A. Kamimura[4], R. S. Vasconcellos[1], and A. C. Carciofi[*5], *[1]Universidade Estadual de Maringa, Maringa, Brazil, [2]Sao Paulo State University, Jaboticabal, Brazil, [3]Universitá degli Studi di Napoli Federico II, Napoli, Italy, [4]Universidade de Campinas, Campinas, Brazil, [5]Sao Paulo State University- UNESP, Jaboticabal, Brazil.*

Broken beans (BB) is the result of bean selection for human consumption, mainly composed of open seeds in good sanitary and nutritional quality, with a potential use as protein and energy source for companion animals. Beans have antinutritional factors, among them protease inhibitors (PI) and hemagglutinin (HA) that reduces the ingredient nutritional value. These factors are thermolabile, and the extrusion process used to produce kibble diets for cats may possibly inactivate them. We evaluated the inclusion of BB on extruded diets for cats, and the effect of the extrusion process on PI and HA inactivation. Thirty adult cats, with 7.6 ± 0.3 yr old and 5.0 ± 0.3 kg of BW were used. Five diets with similar composition (average: 94% DM, 30% CP, 16% fat, 2.8% crude fiber, 7% ash) were formulated for cat maintenance, presenting increasing amounts of BB: 0.0%, 7.5%, 15.0%, 22.5% and 30.0%. The BB sample presented 22.1% of CP, 1.5% of fat, 3.7% of crude fiber, and 2.9% of ash, and was included at the expense of the poultry by-product meal. Diets were extruded under similar conditions in a laboratory scaled complete extrusion system, with a single screw extruder. Samples from the mash diet and the food after the preconditioner, extruder, and dryer were collected and used to measure TI and HA. The experiment followed a complete randomized block design, with 2 blocks of 15 cats, and 3 cats per diet in each block, totaling 6 cats per diet. The blocking factor was time. The coefficients of apparent total tract digestibility and nitrogen balance was determined through total collection of feces and urine. Cats were kept in metabolism cages during 14d, and feces and urine were totally collected on the last 7d. Data were submitted to analysis of variance, and means compared by polynomial contrasts ($P < 0.05$). The extrusion process was very efficient

in inactivating the PI and HA of the BB. After the preconditioner, the activity of these compounds was reduced in 40% to 50%, after the extrusion, they were reduced more than 90%, and after the dryer their values were practically zero. Addition up to 30% BB did not change food intake, nutrient and energy digestibilities (average digestibility: DM, 81%; OM, 84%; CP, 85%; acid-hydrolyzed fat, 89%; gross energy, 86%), fecal traits (dry matter, production, and score), and nitrogen balance, suggesting that bean is a suitable ingredient for extruded diets for cats.

Key Words: co-products, protein, antinutritional factors

COMPANION ANIMALS: **COMPANION ANIMALS AND SUSTAINABILITY: TODAY'S IMPACT ON THE FUTURE**

0188 Nutritional sustainability of pet foods.

R. A. Carter*[1], P. R. Buff[1], K. S. Swanson[2], T. P. Yount[1], and J. H. Kersey[1], [1]*The Nutro Company, Franklin, TN,* [2]*Department of Animal Sciences, University of Illinois, Urbana.*

The ability to provide adequate, safe nutrition is a critical component of a food system's sustainability. Nutritional sustainability is the ability of a food system to provide sufficient energy and the amounts of essential nutrients required to maintain good health of the population without compromising the ability of future generations to meet their nutritional needs. The intention of nutritional sustainability is to advance health and nutrition in parallel to advances in food system sustainability. Nutritional sustainability can be influenced by several factors, including ingredient selection, nutrient composition, digestibility, and consumption rates of diets. The pet food system is unique in regard to sustainability because it is based largely on secondary products and tightly interlinked with livestock production and the human food system. Secondary products of the human food system vary widely in their quality and food safety. The concept of nutritional sustainability calls for the evaluation of these ingredients from a nutritional perspective, and to use ingredients with the appropriate quality and food safety to support pet health. The use of secondary products also introduces challenges to the assessment of the environmental impact of a diet. Consequently, the principles used for human food system sustainability in regard to ingredient selection or dietary nutrient composition may not directly apply to the pet food system. An additional uniqueness of the pet food system is the influence of anthropomorphism on pet owner preferences for specific pet food products. Promoting more sustainable practices from an environmental perspective may not have the greatest overall impact on sustainability because of varying penetration into the marketplace. Therefore, it is critical to balance consumer expectations and pet health considerations in advancing sustainability initiatives. The complexities of pet owner preferences introduce challenges with ingredient selection and dietary nutrient composition, given the increasing preference for ingredients that compete with the human food chain and diets that contain high concentrations of protein and animal-based products. Additionally, as the prevalence of human obesity increases, so does the prevalence of pet obesity, along with the impacts on pet health and food wastage associated with food overconsumption. Companion animals play an important role in our lives, providing a positive impact on the emotional and physical health of people with whom they have contact. Advancing the sustainability of the pet food system through nutritional sustainability is a key enabler to maintaining responsible pet ownership in the future.

Key Words: companion animal, nutrition, pet food, sustainability

0189 How sustainability influences ingredient sourcing, quality, and safety.

D. L. Meeker*, *National Renderers Association, Alexandria, VA*.

The rendering industry collects and safely processes approximately 50 billion pounds of animal byproducts each year in the U.S. Rendering plants process a variety of raw materials from animal agriculture, principally offal from slaughterhouses, but including whole animals that die on farms or in transit and other materials such as bone, feathers, and blood. By recycling these byproducts into various protein, fat and mineral products, including meat and bone meal, hydrolyzed feather meal, blood meal, and various types of animal fats and greases, the sustainability of animal agriculture is greatly enhanced. The rendering industry is conscious of its role in the prevention of disease and microbiological control while providing safe feed ingredients for livestock, poultry, aquaculture, and pets. A HACCP-based Code of Practice is followed to ensure that cooking destroys microbes, and that recontamination does not occur after the rendering process. Recently published FDA animal feed safety regulations follow the same hazard analysis and prevention concepts renderers have used for many years. The processing of otherwise low value organic matter from the livestock production and meat processing industries through rendering drastically reduces the amount of waste. If not rendered, biological materials would be deposited in landfills, burned, buried, or inappropriately dumped with large amounts of carbon dioxide, ammonia, and other compounds polluting air and water. When rendered, these products are dried, stabilized, and recycled for animal feed, energy, fertilizer, and other uses. Even though cooking these high moisture materials is an energy intensive process, for each metric ton of CO_2 produced (scope 1 emissions) by operating rendering plants, 5.68 metric tons of CO_2 are removed from the environment. The majority of rendered protein products are used as animal feed. Rendered products are especially valuable to the livestock and pet food industries because of their high protein content, digestible amino acid levels (especially lysine), mineral availability (especially calcium and phosphorous), and relatively low cost in relation to their nutrient value. Rendering facilities produce many species specific meals as well as mixed species meals, and often meet special specifications required by pet food manufacturers by devoting individual plants or processing lines to certain products. The use of these reclaimed and recycled materials in pet food is a much more sustainable model than using human grade food for pets.

Key Words: rendering, sustainability, ingredients, byproducts

0190 Sustainability of non-traditional companion animals. G. Ballam*, *Purina Animal Nutrition, St Louis, MO.*

In the next 10 yr, the changing demographics within the United States will play an important role in the diversity of food selection and agricultural practices. In addition consumer attitudes will continue to demand products that are locally grown, fresh, safe and sustainable. Changes in attitudes and purchasing behaviors over the last 10 yr are reflected in the emergence of retailers and Farmer's Markets providing a greater variety of natural and sustainable foods. The change in purchasing behavior provides an opportunity for small producers to provide sustainable and non-conventional sources of food such as specialty eggs, meats and fish, free-range or pasture-raised chickens, and artisanal cheese from goats and sheep. The entrepreneurial spirit of sustainability is not limited to food production. There is rising interest in using nutrition to increase pond and lake productivity and sustainability to meet the needs of the recreational sport fisherman. Agricultural professionals have the opportunity to provide information on nutrition, health, and management to help these enterprises develop innovative products, meet the challenges of their industry and affect their sustainability.

Key Words: non-traditional, sustainable, companion

0191 Sustainable ecosystems: Free-ranging cats and their effect on wildlife populations. S. E. Kitts-Morgan*, E. I. Parsons, and K. A. Hilburn, *Berry College, Mount Berry, GA*

Feral and domestic cats are estimated to kill billions of small mammals and birds each year. In certain areas of the world, it is not uncommon for either feral or domestic cats to have high population densities, creating concern regarding their level of hunting. Interest centers on free-ranging cats, as they roam freely and receive care and food from humans. Arguments abound regarding the presence of cats in the habitats of native small mammals and birds, and whether or not local ecosystems can sustain this predator-prey relationship. Studies have attempted to determine the effects of cats on local wildlife populations using various methods. Some research has focused on determining the home range of free-ranging cats using either radio telemetry techniques or the Global Positioning System (GPS). Because home-range size differs for each cat, we can estimate the size of an area where potential damage on local wildlife might occur. Another technique used to determine the effects of cats on wildlife includes evaluating feline scat for prey items. This is a valuable tool, as prey teeth can usually be used to identify the genus and sometimes species of the prey. Unfortunately, it is impossible to accomplish complete collections of all scat from each cat, as they usually eliminate in multiple latrine areas within their home range. Incomplete scat collections increase the difficulty of estimating the true kill rate of prey by free-ranging cats. However, scat analysis has allowed us to determine that cats receiving cat food from humans continue to hunt and at least partially consume prey. Furthermore, the prey species identified in the scat often represent native species killed and consumed by the cats. Lastly, live animal trapping is another technique that may be used to estimate the population of small mammals in an area where cats are known to reside and hunt. Along with determination of home-range size and feline scat analyses, trapping provides another tool to help estimate the effect of free-ranging cats on native wildlife populations. Free-ranging cats certainly have the potential to roam and hunt in very large areas inhabited by native small mammals and birds. It remains questionable as to whether or not local ecosystems can sustain hunting by free-ranging cats.

Key Words: cats, wildlife, hunting

0192 Future aspects and perceptions of companion animal nutrition and sustainability. K. S. Swanson*, *Department of Animal Sciences, University of Illinois, Urbana.*

With an increasing world human population and resources becoming scarce, sustainable practices are of utmost importance. The world pet population also continues to grow. Because pet foods are based largely on secondary products from the human food system and often compete with the human food and livestock feed industries for ingredients, sustainability is also an important issue for the pet food industry. Land, water, air, and waste management, species biodiversity, and energy use are key issues to consider. Although the environmental impact of an ingredient or food usually receives the most attention, one cannot ignore the social and economic factors involved, especially when it comes to pet foods. The anthropomorphism of pet dogs and cats greatly impacts the expectations and purchases of consumers and marketing strategies and products sold by pet food companies. Pet owner preferences introduce challenges in regard to ingredient selection and dietary nutrient composition, with increasing preference for ingredients that compete with the human food chain, including many high-protein, animal-based products. Research focused on pet food sustainability is seriously needed in the future. The carbon- or water-footprint comparisons of animal- vs. plant-based ingredients for human foods have received a lot of attention. However, not only are the published footprint values hotly contested, but they are only applicable to human-grade ingredients. To date, nobody has provided insight as to the footprint of secondary products, an issue that needs to be addressed to provide accurate calculations for pet foods. Further research is also needed to compare farm-raised vs. wild-caught fish, livestock raised under conventional vs. free-range systems, and ingredient processing, packaging, storage, and handling

practices, and to search for acceptable alternative protein sources. Finally, even if an ingredient source is available for use, its nutritional quality, safety, price, and marketability must also be considered. Although many challenges exist, a coordinated effort across the industry, including ingredient buyers, formulators, and nutritionists may result in a more sustainable pet food system.

Key Words: pet food, canine, feline

COMPANION ANIMALS: GEORGE C. FAHEY COMPANION ANIMAL NUTRITION SYMPOSIUM: PREPARING FUTURE COMPANION ANIMAL BIOLOGISTS

0193 Challenges in training companion animal biologists: Missing the research component, how to overcome it? J. P. McNamara*, *Washington State University, Pullman.*

The basic missions of Departments of Animal Sciences are to train leaders in endeavors related to domesticated animals and to conduct and disseminate research related to domesticated animals. For agricultural animals we have been successful and society has benefitted greatly. Yet, as a result of this success and many other factors, the number of people involved in agriculture has declined over half in the last 50 yr. We have seen a major change in demographics of our undergraduate and graduate students, who are now overwhelmingly suburban and urban and interested in companion animals. Yet we still have a mission and a need to train and do research with agricultural animals. Many departments have responded to the changing demographics with expanded course offerings related to companion animals, by including examples from companion animals in our core disciplinary classes and in some cases by opening and expanding research into the biology of companion animals. The future, as always, does hold some great promise and great challenges for furthering these efforts. The research and teaching endeavors will not be similar across states. A few states will maintain significant activity in agricultural animals and have some effort in companions. But many more states will (if they have not already done so) shift significant effort to study and training with companion animals. Recent research and applications with animal behavior, welfare and training; use of service and therapy animals; the social and economic relevance and challenges with companion animals (the horse slaughter issue and increases in drop-offs to animal shelters as examples); the equine, canine and feline genome projects; and the revival of 'dual purpose' animal research at the federal level provide many opportunities for classroom learning and undergraduate research. Many of our undergraduates have experience at animal shelters, with service and therapy animals and in animal training. We should tap that expertise, provide education, and work with the communities (service learning courses; community outreach by faculty and students) to improve and expand the use of such animals and reduce the unwanted animal population. The "Masters in Agriculture" programs that train individuals to improve production provide a successful model that can be adapted to companion animals. Dogs, cats and horses make up the vast majority of 4H projects and this is an opportunity to expand the role of Animal Sciences.

Key Words: companion animals, curriculum, undergraduate

0194 Extension outreach: Use of technology in companion animal biology and nutrition. L. Karr-Lilienthal*, *University of Nebraska, Lincoln.*

Today's technology has changed the way teaching and extension programs are provided and will continue to do so. With changes in technology, we must evaluate the best practices for providing companion animal biology information to youth and students globally. Distance education has become increasingly popular with universities and students. Using technology effectively in the classroom should foster relationships between student and instructor to continue to provide a personal connection. It should be easily accessed from a variety of platforms and locations. There are many options available to educators looking to use technology. Using a combination of tools is probably most effective in student learning. Repetition, practice, and variety of delivery methods will help to reinforce concepts students may struggle with. Student performance in the Companion Animal Nutrition course offered at the University of Nebraska-Lincoln does not differ between online and in class sections. However, different approaches must be taken to ensure student connections and participation. Students tend to ask questions for clarification less frequently in the online section. Providing clear methods to obtain feedback helps to open lines of communication. Often university teaching and outreach programs have limited personnel resources. Technology is a key way to improve collaboration between experts at other universities and within the industry. Online meeting rooms can increase your pool of guest speakers and decrease costs related to speaker fees for programs. Using programs such as Adobe Connect that allow for streaming video and an audio connection will improve the learner experience. The Companion Animal Community of Practice at eXtension.org is one way to improve collaborations among extension and outreach professionals. The use of eXtension provides educators with a simple system for delivering online material to the general public through webinars, articles, and short courses. Published content on eXtension is peer reviewed and is based in science. Effective use of technology should provide ease of use, accessibility, and allow for increased target audience. For learners to feel comfortable with technology, a sense of community should be established both for online teaching as well as online extension efforts. Community can be developed through social media tools, discussion posts, regular communication, and videos. Requesting feedback from the learners improves use of technology in classroom.

Key Words: companion animal, technology, teaching, outreach

0195 A circuitous route: Preparing for a career in the companion animal industry. A. K. Shoveller*, *The University of Guelph, Guelph, ON, Canada.*

Today's companion animal industry refers to food and products for the pet owner and predominantly includes products for dogs and cats. US Pet Industry expenditures in 2012 were ~53.3 billion and have been steadily increasing over the past 20 yr, suggesting a large growth opportunity. There is also growing interest from undergraduate and graduate students to pursue companion animal biology. Professionals are needed to do research in animal biology (health, metabolism, behavior); communicate complex findings to academics, industry professionals and pet owners; develop and market food and products; and maintain the regulatory requirements that tend to be different between countries. "Pet passion" is a necessary attribute for a career in the pet care industry. Individuals need to be effective in multi-functional teams, have strong communication skills and thought processes. These processes also require collaboration outside of internal teams with academic, government and business partners and effective professionals need to be able to utilize a diverse knowledge set. These individuals need to be strategically and operationally agile, enabling them to see the big picture yet know when to be detail oriented. Successfully acquiring knowledge and experience in animal biology will put you in a solid position to compete in the companion animal industry. Despite this requirement, there are still few companion animal programs in North America outside of veterinary school, and because of that, the majority of professionals in the companion animal industry are trained in production animal or human biology. While an individual can build and continue to acquire new knowledge and skills outside of a formal academic program, academia has historically been, and continues to be, responsible for teaching the base of knowledge in undergraduate programs and deeper knowledge and problem-solving skills in graduate school. Programs and funding that encourage collaboration between government, industry and academia, with a solid commitment to generate the next generation of highly-trained technologists and future leaders for the pet care industry, are needed. Furthermore, long-term strategic programs with greater levels of collaboration among academic institutions may help to provide continuity in basic training. Educated and experienced individuals working together across government, academia and industry can help set strategies that would further enable advancements in companion animal health and well being and enhance our knowledge of the role of companion animals in improving the lives of their families.

Key Words: pet care, career, opportunities

0196 How to effectively communicate science with pet owners and society: Understanding pet owner purchasing decisions and sensory characteristics of pet foods. K. Koppel*, *Kansas State University, Manhattan*.

Science communication to targeted communities is a topic that has received a great deal of attention and published research. For the sake of human health there has been an emphasis on food-related communication and comprehension in publications such as human nutrition guidelines, labeling, and risk management of different types of foods. Only recently have pet food related issues been covered extensively in the media. There is a growing awareness of pet owners regarding pet food ingredients and health concerns surrounding pet obesity issues. While traditional animal science has focused on efficiency and yield, companion animal science redirects the target to perceptions about quality, animal wellness, and the pet-owner relationship. This changes the opportunities in research and communication through to the classroom. Recent trends in companion animal and pet food research include understanding drivers behind purchase decisions, relating pet owner behavior characteristics to issues with pets' weight management, and understanding pet food characteristics in association with food composition and animal preference. At Kansas State University our lab is focusing research activity on sensory properties and volatile compounds of pet food, ingredient effects on sensory and palatability aspects, and pet owner behavior studies. This research is being transferred to the classroom and shared with the scientific community and the pet food industry. This presentation describes how pet food science is being studied, taught, and communicated at Kansas State University in the Sensory Analysis Center and Department of Grain Science to educate and train the next generation of companion animal specialists.

Key Words: companion animals, pet food, ingredients

COMPARATIVE GUT PHYSIOLOGY SYMPOSIUM: COMPARATIVE PHYSIOLOGY OF LOWER GUT

0198 Integrated responses to feeding, comparative aspects. J. Furness*, *University of Melbourne, Parkville, Australia.*

The optimal utilization of nutrients requires an integrated response of the gastrointestinal tract to ingested food. Broad mechanisms are similar in all mammals and involve sensing food components through olfaction, taste and specialized receptors within the stomach and intestines. The sensing of food components leads to release of gut hormones and activation of nerves, which in turn modify digestive functions. Bacteria, viruses, fungi and potentially injurious substances in foods activate tissue defense mechanisms. While the responses to nutrients lead to broadly similar changes in appetite, satiety and food-seeking behavior, gastrointestinal motility, release of digestive enzymes and induction of nutrient transporters, the requirements in different animals differ. To simplify discussion, we can divide species into ruminant foregut fermenters (such as cattle and sheep), non-ruminant foregut fermenters (e.g., kangaroo, colobus monkey), hind-gut fermenters (such as horse), and auto-enzyme dependent digesters (pig, human) that also gain nutrition from hind-gut fermentation. Ruminants are efficient digesters because the rumenal movements are able to stratify food into gas, fluid and particle components, retaining food to be digested in the forestomach and passing more fully digested material into the abomasum and duodenum, and also being able to return food from the forestomach to the mouth for mastication and limited enzyme exposure. Poultry have multiple stomachs that allow for storage, digestion and tituration, but not fermentation. Ruminants lose efficiency in that most carbohydrate is utilized by gastric bacteria and very little glucose reaches the small intestine. Thus glucose must be synthesized from short chain fatty acids produced by bacteria, whereas species such as pig and human convert carbohydrate to glucose enzymatically. Thus ruminants are more prone than other groups to enter into negative glucose balance, for example during post-partum lactation. Obligatory by-products of fermentation are carbon dioxide and methane. Foregut fermenters are also advantaged by being able to readily utilize vitamins produced by fermentation. It is thought that coprophagy by hind-gut fermenters, such as rabbits, provides access to such vitamins. Foregut fermentation also contributes to detoxification, for which hindgut fermenters and autoenzymic digesters rely primarily on the liver. With these differences in mind, it is necessary to closely consider what information can be readily extrapolated between species. Conversely, we can point to similarities in neural and hormonal signaling systems and products of digestion, achieved in different ways that are available for energy utilization and incorporation into tissues.

Key Words: digestive physiology, fermentation, glucose, comparative

0199 Expression of nutrient transporter mRNA in the jejunum of high and low efficiency steers. H. C. Cunningham[1], Z. T. L. Gray[1], S. I. Paisley[1], K. J. Austin[1], K. M. Cammack[1] and A. M. Meyer*[2], *[1]Department of Animal Science, University of Wyoming, Laramie, [2]Division of Animal Sciences, University of Missouri, Columbia.*

We hypothesized that small intestinal expression of nutrient transport-related genes contributes to differences in metabolic efficiency in beef cattle. The objective was to investigate jejunal expression of glucose transporter 2 (GLUT2), glucose transporter 5 (GLUT5), sodium-dependent glucose transporter 1 (SGLT1), and peptide transporter 1 (PepT1) in finishing steers classified as high and low efficiency based on residual feed intake (RFI). Hereford-Angus crossbred steers (yr 1, $n = 59$, 461 ± 4.5 kg initial BW; yr 2, $n = 75$, 412 ± 3.8 kg initial BW) from a single contemporary group in each year (birth through slaughter) were used. Steers were fed a finishing diet (yr 1, 11.4% CP, 2.0 Mcal NE_m/kg, 1.35 Mcal NE_g/kg; yr 2, 13.2% CP, 1.8 Mcal NE_m/kg, 1.19 Mcal NE_g/kg; DM basis) for 57 (yr 1) or 80 d (yr 2) using the GrowSafe system. Residual feed intake was calculated as the difference between actual and expected feed intake of each individual, where expected intake was determined by regressing ADG and metabolic midweight on actual intake. Following the intake test in each year, the 20% most efficient (low RFI, $n = 8$/yr) and 20% least efficient (high RFI, $n = 8$/yr) steers with 12th rib fat thickness $\geq$ 1.02 cm were slaughtered between 5 and 8 d after the feed intake test conclusion. At slaughter, jejunal mucosa was flash-frozen for real-time RT-PCR determination of GLUT2, GLUT5, SGLT1, and PepT1. Data were analyzed with PROC MIXED in SAS 9.2 using RFI class (high vs. low efficiency), year, and their interaction as fixed effects. Expression of SGLT1 was affected ($P = 0.02$) by the RFI class × year interaction, although there were no differences ($P \geq 0.12$) within each year. Jejunal expression of GLUT2, GLUT5, and PepT1 were not affected ($P \geq 0.18$) by RFI class; however, expression of each was greater ($P \leq 0.03$) in yr 2 than yr 1. It was previously reported in this study that jejunal expression of y^+LAT2, a basolateral membrane cationic AA transporter, was greater for low efficiency than high efficiency steers in yr 2. Additionally, low efficiency steers had greater jejunal expression of vascular endothelial growth factor (VEGF, a major regulator of angiogenesis) than high efficiency in both years. These data suggest that nutrient absorption and transport in the small intestine may play a role in whole animal feed efficiency of beef cattle.

Key Words: feed efficiency, nutrient transport, small intestine

0200 Comparative physiology of glucagon-like peptide 2—Implications and applications for production and health of ruminants. E. E. Connor*, M. P. Walker, C. M. Evock-Clover, T. H. Elsasser, and S. Kahl, [1]*USDA-ARS, Bovine Functional Genomics Laboratory, Beltsville, MD*.

Glucagon-like peptide 2 (GLP-2) is a 33-amino acid peptide derived from proteolytic cleavage of proglucagon by prohormone convertase 1/3 in enteroendocrine L-cells. Studies conducted in humans, rodent models, and in vitro indicate that GLP-2 is secreted in response to the presence of molecules in the intestinal lumen including fatty acids, carbohydrates, amino acids, and bile acids, which are detected by luminal chemosensors. The physiological actions of GLP-2 are mediated by its G protein coupled receptor expressed primarily in the intestinal tract on enteric neurons, enteroendocrine cells, and myofibroblasts. The biological activity of GLP-2 is further regulated by dipeptidyl peptidase IV, which rapidly cleaves the N terminus of GLP-2 that is responsible for GLP-2 receptor activation. Within the gut, GLP-2 increases nutrient absorption, crypt cell proliferation, and mesenteric blood flow, and decreases gut permeability and motility, epithelial cell apoptosis, and inflammation. Outside the gut, GLP-2 reduces bone resorption, can suppress appetite, and is cytoprotective in the lung. Thus, GLP-2 has been studied intensively as a therapeutic to improve intestinal function of humans during parenteral nutrition and following small bowel resection, and more recently, as a treatment for osteoporosis, obesity-related disorders, and to reduce cellular damage associated with inflammation of the gut and lungs. Recent studies demonstrate that GLP-2 has many similar biological actions and properties in ruminants as in monogastrics, including the potential to reduce intestinal nitro-oxidative stress in calves caused by parasitic diseases like coccidiosis. Due to its beneficial impacts on nutrient absorption, gut healing, and normal gut development, GLP-2 therapy offers significant opportunities to improve calf health and production efficiency. However, GLP-2 therapies require an extended time course to achieve desired physiological responses, as well as daily administration due to the hormone's short half-life. Thus, practical means of administration and alternative strategies to enhance basal GLP-2 secretion (e.g., through specific feed additives), which are more likely to achieve consumer acceptance, are needed. Opportunities to address these challenges are discussed.

Key Words: cattle, glucagon-like peptide-2, gut health

0201 Differential subcellular and cellular storage of GLP-1 and PYY and its implications. J. Furness*[1], H. J. Cho[1], S. Kosari[1], and D. M. Bravo[2], [1]*University of Melbourne, Parkville, Australia,* [2]*PANCOSMA SA, Geneva, Switzerland.*

Intestinal L cells have key roles in the detection of the chemical environment in the gut lumen, to which they react by the release of hormones that influence appetite, proximal gut motility, insulin secretion and mucosal function (Furness et al., Nature Gastroenterology, 10, 729–740, 2013). Important amongst L cell hormones are glucagon-like peptide1 (GLP-1) and peptide tyrosine-tyrosine (PYY), which are products of separate genes. The conventional description of their localization is that GLP-1 and PYY are in the same storage vesicles in the same cells. However, GLP-1 and PYY have different functions, particularly in relation to insulin secretion and mucosal function. We have used super-resolution (3D-SIM) microscopy and double-labelling immunohistochemistry to investigate the subcellular localizations of the hormones, and digital scanning microscopy to investigate cell populations. Super-resolution microscopy revealed that GLP-1 and PYY are in separate storage organelles in enteroendocrine cells from mouse, rat, pig and human. The majority of the organelles were 150-170 nm or less in diameter, and are concluded to be secretory vesicles. Only 10-20% of organelles had immunoreactivity for both hormones. Even this may be an overestimate, as touching or very close vesicles may not be effectively resolved, even with super-resolution microscopy. In investigating co-localisation at the cell level, we included glucagon-like insulinotropic peptide (GIP), an incretin of K cells, in the analysis. The work shows that there is a K/L cell gradient in the mouse intestine. From the duodenum to the distal colon, there are populations of cells with GIP alone, GLP alone, PYY alone and all combinations of the three hormones. Greatest numbers of GIP cells were in the doudenum and jejunum, where 30—40% contained only GIP and the remainder also contained GLP-1. A small proportion also contained PYY. Similar patterns of overlap occurred in the proximal and distal ileum, where GLP-1 was the dominant peptide, which was often alone, or co-localised with PYY. In the large intestine the majority of cells contained both GLP-1 and PYY, but cells with only one of these and cells with all three hormones were found. The findings reveal a structural basis for the separate or preferential control of GLP-1, PYY (and possibly GIP) release. A number of physiological studies imply that there can be differential release of GLP-1 and PYY. This should be investigated further.

Key Words: enteroendocrine cells, incretins, glucagon like peptide, peptideYY

0202 The role of the microbiome in gut immune system development in newborn and mature cattle. P. J. Griebel[*1], N. Malmuthuge[2], G. Liang[2], M. Zhou[2], and L. L. Guan[2], *[1]Vaccine and Infectious Disease Organization, University of Saskatchewan, Saskatoon, SK, Canada, [2]University of Alberta, Edmonton, AB, Canada*.

There is increasing evidence in a variety of mammalian species that the commensal microbiome has diverse effects on mucosal immune system development and function. It is difficult, however, to clearly delineate the effects of the microbiome from other contributing factors, such as diet, environment, and host genetics. The bovine gastrointestinal tract (GIT) is rapidly colonized during birth and these pioneer species are then replaced by a succession of changes, involving both increased microbioal density and diversity. This succession occurs rapidly during the first week of life and then progresses much more slowly. Characterization of the microbiome in the neonatal bovine GIT at both a family and species level revealed marked bacterial variation among individual animals. Furthermore, the composition of the microbiome varied significantly when comparing ingesta- and mucosa-associated communities within individual GIT regions. The first week postpartum is also a very dynamic developmental period in the bovine GIT with significant changes in both mucosal barrier and immune function. These developmental changes were analyzed by profiling miRNAs expressed throughout the small intestine. This analysis confirmed the greatest changes in GIT development occurred during the first week of life with differential expression of miRNAs involved in regulating a broad range of GIT developmental and immunological processes. Relatively few miRNAs were differentially expressed when comparing tissues collected from 6 wk old calves and 3 wk old calves. Correlation analyses between total bacterial numbers and specific families revealed significant associations between the commensal microbiome and the expression of genes involved in regulating both mucosal barrier and innate immune function. It appears the microbiome is an important factor influencing age-dependent changes in the expression of immune function genes. These correlation analyses also suggest that regional differences in the microbiome may be associated with significant regional differences in the expression of innate immune genes. This information provides the baseline to begin analyzing the role of individual bacterial species and interactions among bacterial species in regulating mucosal immune system function in healthy animals and during enteric infections. New experimental models will be required, however, to clearly delineate the role of specific bacterial species in the complex interaction between microbiome and host.

Key Words: microbiome, innate immunity, miRNA

0203 The effects of intentionally-induced leaky gut on metabolism and production in lactating Holstein dairy cows. S. K. Stoakes[*1], M.Abuajamieh[1], D. B. Snider[1], M. V. Sanz Fernandez[1], J. S. Johnson[1], P. J. Gorden[1], N. K. Gabler[1], H. B. Green[2], K. M. Schoenberg[2], and L. H. Baumgard[1], *[1]Iowa State University, Ames, IA, [2]Elanco Animal Health, Indianapolis, IN.*

Presumably, intestinal barrier dysfunction negatively affects productivity, but it has never been studied in a controlled lactation experiment. Objectives were to elucidate consequences of leaky gut in otherwise healthy mid-lactation dairy cows. Twelve Holstein cows (170.0 ± 15.1 DIM, 670 ± 13 kg BW, parity 1 to 5) were enrolled in two experimental periods. Period 1 (P1) lasted 5d and served as baseline for period 2 (P2), which lasted 7d in which cows received one of two treatments I.V. twice daily: 1) sterile saline (control) or 2) γ secretase inhibitor (GSI; 1.5 mg/kg BW). GSI specifically inhibits crypt stem cell differentiation into enterocytes via disrupting Notch signaling. Control animals were pair-fed (PF) to GSI-treated cows (to eliminate the confounding effects of dissimilar feed intake). GSI administration caused a progressive reduction in DMI ($P < 0.01$; 82%) and milk yield ($P < 0.01$; 57%), but there was no treatment effect on milk components. Cows in both treatments lost a similar amount of BW (56 kg) by the end of P2. Histological analysis indicated GSI increased jejunum goblet cell area (3.3 vs. 1.0%; $P = 0.02$), tended to: deepen villous crypts ($P = 0.06$), reduce villous height ($P = 0.07$) and alter villous height to crypt depth ratio ($P = 0.08$). No treatment effects were detected in ileum or colon morphology, but manure score (a measure of fecal consistency) was decreased 36% ($P < 0.01$) in the GSI-treated vs. PF controls. By d5−7 of P2, circulating lipopolysaccharide (LPS) was increased > threefold in PF controls compared to GSI-treated cows. Plasma LPS binding protein (LPB) levels progressively increased in both treatments but were increased (42%, $P < 0.01$) in GSI-treated vs. PF controls by d5−7 of P2. By the end of P2, the LPS:LPB ratio was increased 3.6-fold ($P < 0.05$) in PF controls compared to GSI-treated cows. Haptoglobin and serum amyloid-A concentrations progressively increased (> 400 and > fivefold, respectively) similarly in both treatments. Circulating IFNγ, TNFα and IL-6 were unaffected by treatment or time. GSI-treated cows tended to have increased plasma insulin ($P = 0.07$) and decreased circulating NEFA ($P = 0.06$) vs. PF cows. For both treatments, plasma glucose decreased with time ($P = 0.05$), while BHBA progressively increased (87%; $P = 0.08$). There were no treatment differences in spleen weight, liver weight, liver moisture, or liver lipid content. In summary, based on all the data, GSI-treatment compromised intestinal integrity and markedly reduced feed intake and milk yield. Further, we have demonstrated progressive feed reduction also negatively influenced intestinal integrity.

Key Words: lipopolysaccharide, insulin

0204 Manipulating goblet cell function to protect against enteric infection. M. Wlodarska*, *University of British Columbia, Vancouver, BC, Canada.*

Mucus production by goblet cells serves as one of the crucial mucosal defenses at the interface between the eukaryotic and prokaryotic cells and yet the immunoregulatory pathways involved remain uncharacterized. The inner mucus layer of the intestine functions as a barrier, which serves to minimize microbial translocation, prevents excessive immune activation, and decrease infection. Here we have described methodology to alter the thickness of the inner mucus layer through treatment with antibiotic or a phytochemical. We showed that the antibiotic metronidazole caused a significant thinning of the inner mucus layer accompanied by a dramatic change in the microbial community structure. In contrast, treatment with the phytochemical eugenol resulted in a significant thickening of the inner mucus layer that was accompanied by a change in the microbial community. These changes in community structure were complimentary; sequencing showed that groups depleted by metronidazole treatment were more abundant with eugenol treatment. To investigate how changes in the integrity of the inner mucus layer affect intestinal defense, Citrobacter rodentium (Cr) was used to examine susceptibility to enteric-induced colitis. Metronidazole-induced reduction in mucus thickness correlated with exacerbated severity of Cr-induced colitis. Thickening of the inner mucus layer with eugenol treatment resulted in protection from Cr-induced colitis. Further, we identified a novel innate immune pathway involved in regulation of goblet cell function and mucus layer production. The NLRP6 inflammasome was shown to regulate mucus secretion and deficiency in any component of the NLRP6 inflammasome resulted in impaired goblet cell function preventing mucin granule exocytosis and mucus layer formation. Abrogated mucus secretion led to increased invasiveness and pathology of Cr infection. Mechanistically, NLRP6 deficiency led to stalled autophagy in goblet cells, providing a link between inflammasome activity, autophagy, mucus exocytosis, and antimicrobial barrier function.

Key Words: mucus, goblet cell, *Citrobacter rodentium,* phytochemical, eugenol

0205 Nutritional immunology in swine. Y. Liu*[1], D. M. Bravo[2], and J. Pettigrew[1], [1]*University of Illinois at Urbana-Champaign, Urbana,* [2]*PANCOSMA SA, Geneva, Switzerland.*

The immune system of pigs is vital as its proper functioning protects the pig from disease and health. It also causes inflammation, which contributes to the animal's ability to fight off infection but also inhibits growth performance by reducing feed intake and diverting amino acids and nutrients away from growth to the immune response. It is now clear that reducing inflammation would benefit pig health. We have shown that several plant extracts can do just that, as shown here. Our in vitro study reported that several plant extracts (anethol, capsicum oleoresin, carvacrol, cinnamaldehyde, eugenol, garlicon, and turmeric oleoresin) suppressed ($P < 0.05$) pro-inflammatory cytokines' secretion from lipopolysaccharide-stimulated porcine alveolar macrophages, which indicates the in vitro anti-inflammatory effects of these plant extracts. Results from an in vivo *Escherichia coli* (*E. coli*) challenge study showed that feeding capsicum oleoresin, garlicon, or turmeric oleoresin reduced ($P < 0.05$) diarrhea of *E. coli*-challenged pigs. Feeding these 3 plant extracts also decreased inflammatory responses of *E. coli*-challenged pigs, as indicated by reduced ($P < 0.05$) white blood cell numbers, serum pro-inflammatory cytokines, and acute phase proteins when pigs were fed plant extracts compared with pigs fed control diet. A potential mechanism of action is that plant extracts may enhance gut mucosa health and attenuate the overstimulation of the immune system. The microarray data from the same in vivo study indicated that these plant extracts counteracted ($P < 0.05$) the effects of *E. coli* by reducing the expression of genes involved in antigen presentation or other biological processes of immune responses. Another in vivo study was conducted with porcine reproductive and respiratory syndrome virus (PRRSV) challenge. The results of this study indicated that feeding these 3 plant extracts to nursery pigs enhanced the pigs' immune responses to a PRRSV challenge and may help alleviate negative impacts of infection, as indicated by reducing ($P < 0.05$) viral load and serum concentrations of inflammatory mediators, and shortening ($P < 0.05$) the time of fever in PRRSV-infected pigs. In conclusion, feed additives, such as certain plant extracts, may potentially improve pig health and disease resistance by modulating inflammation.

Key Words: immunology, pigs, plant extracts

0206 Mucosal IgA responses to members of the gut microbiota in healthy vs. malnourished Malawian children. A. Kau*, *Center for Genome Sciences & Systems Biology, St. Louis, MO*.

Childhood malnutrition is a major contributor to childhood morbidity and mortality worldwide. While inflammatory conditions, such as recurrent infection and environmental enteropathy, have been implicated in pathogenesis, the role of the interaction between the host immune system and the gut microbiota in shaping the outcomes remains poorly understood. To identify microbes that were targeted by the host gut mucosal immune response, we developed a flow cytometry-based method to recover and characterize viable gut microbes based on their binding to immunoglobulin A (IgA). Fecal microbiota from Malawian twins discordant for a form of severe acute malnutrition (Kwashiorkor) were transplanted into different groups of adult germ-free C57BL/6J mice that were fed a representative Malawian diet deficient in macro- and micronutrients. IgA-targeted microbes in the fecal micro-

biota of these 'kwashiorkor-Malawian diet–fed' (KM) mice were purified by FACS and transferred to a second group of germ-free mice, also fed the Malawian diet. KM-IgA+ consortia produced (i) dramatic weight loss; (ii) pronounced gut barrier dysfunction manifest by sepsis, and histopathologic changes that were most severe in the colon but also manifest in the small intestine where disruption of the intracellular pattern of epithelial cell adhesion molecule (EpCAM) staining and evidence of extrusion of cells along the length of villi rather than just at the apical region was evident, and (iii) high mortality phenotype in recipient animals. This phenotype was both diet-dependent and microbiota dependent: we did not observe it in mice fed a macro- and micronutrient replete diet or those receiving IgA targeted taxa from mice harboring the healthy co-twin's microbiota. The barrier dysfunction and mortality phenotypes transmitted by the IgA+ consortium could be mitigated through the administration of IgA-targeted microbes from a mouse colonized with a healthy microbiota, including *Akkermansia muciniphila* and *Clostridium scindens*. Applying this FACS-based approach directly to the fecal microbiota of two cohorts of Malawian children, we found that members of Enterobacteriaceae are prominent targets of IgA responses in individuals with severe acute malnutrition. Targeting to other bacterial taxa, including members of Veillonellaceae and Lactobacillaceae, were correlated with the degree of stunting. These findings indicate that this approach for identifying and quantifying mucosal immune responses to members of the fecal microbiota has potential diagnostic and therapeutic applications to childhood malnutrition, and perhaps other diseases affecting the gut mucosal immune system.

Key Words: gut microbiota, gut immunity, nutritional immunology

---

0207 Gut immune system: A new frontier for nutritional modulation of gut health.

H. Lillehoj*, *ARS USDA, Beltsville, MD.*

The gut represents a continuously evolving ecosystem consisting of trillions of commensal bacteria living in symbiosis with the host. This host-microbe interplay plays a crucial role in host physiological development and health. There is increasing evidence that shows a dynamic interaction between the gut microbiota and the development and function of the host immune system. Particularly, the intestinal microflora influences diverse aspects of host metabolic and immunological functions and this "crosstalk" with the various immune component of mucosal immunity, comprising cellular and soluble elements, is critical in maintaining gut homeostasis and gut health. Various chronic inflammatory conditions and metabolic diseases are closely associated with altered symbiotic relationship. Furthermore, probiotics, when used for the treatment of diseases caused by the dysregulation of the immune system, can exert a beneficial immune response. In this regard, as shown in our recent studies, the dietary immunomodulation of gut immunity in broiler chickens using natural dietary supplements, such as TLR ligands, DFMs and plant-derived phytochemicals that interact with innate sensing molecules to stimulate innate immunity, is a promising alternative strategy that can be applied to many infectious diseases where traditional prevention methods show limitations. Furthermore, application of high-throughput functional genomics tools in delineating detailed immune mechanisms associated with alternative disease control strategies will lead to enhanced understanding of how different alternative strategies function. As we move into the 21st Century and the demands for animal food products increase to meet the nutritional needs of a growing world population, developing drug-free alternative strategies to prevent and control animal diseases and to maintain gut homeostasis is a global issue and a critical component of our long-term efforts to alleviate poverty and world hunger.

Key Words: gut health, innate immunity, antibiotic alternatives

---

0208 Effect of dietary supplementation of *Capsicum* extract on immune responses, blood cell counts, blood chemistry, and oxidative stress markers in lactating dairy cows.

J. Oh*[1], S. Walusimbi[1], F. Giallongo[1], H. L. Weeks[1], T. W. Frederick[1], A. N. Hristov[1], J. L. Pate[1], R. J. Elias[2], L. Tao[2], and E. H. Wall[3], *[1]Department of Animal Science, The Pennsylvania State University, University Park, [2]Department of Food Science, The Pennsylvania State University, University Park, [3]Pancosma, Geneva, Switzerland*

The objective of this experiment was to investigate the effects of dietary *Capsicum* extract (CE) on T cell phenotypes, phagocytotic and oxidative burst activity of neutrophils, blood cell counts, blood chemistry, and oxidative stress markers in lactating dairy cows. Eight multiparous Holstein cows (DIM, 50 ± 9.6 d; BW, 591 ± 32.6 kg), including 3 ruminally-cannulated, were used in a replicated 4 × 4 Latin square design with 25-d periods. Treatments were 0 (CON), 250, 500, and 1000 mg CE/cow/d, in which the principal active compounds were capsaicin and dihydrocapsaicin. The CE was mixed with a small portion of the TMR and topdressed. Compared with CON, CE did not affect concentration of cluster of differentiation antigen (CD) 4 positive, $CD8^+$, $CD25^+$, and $\gamma\delta^+$ cells. The phagocytosis of neutrophils tended to quadratically increase ($P = 0.07$) with CE. Relative to CON, total white blood cells, neutrophils, and eosinophils were linearly increased ($P = 0.04$, 0.01, and 0.03, respectively) with CE supplementation. Treatments had no effect on lymphocytes, monocytes, and basophils. Red blood cells quadratically increased ($P = 0.04$) with CE. Hemoglobin was higher ($P < 0.01$) for CE than CON and responded quadratically to CE level of supplementation. Platelets were lower for CE than CON and linearly decreased ($P = 0.04$) with CE supplementation. Glucose, creatinine, al-

bumin, and total protein in blood plasma were not affected by CE. Blood urea N was increased ($P = 0.02$) by CE relative to CON and blood plasma P concentration tended to be lower ($P = 0.09$) for CE than CON. Although there was no effect of CE on oxygen radical absorbance capacity (ORAC) and thiobarbituric acid reactive substances (TBARS), CE tended to decrease ($P = 0.09$) 8-isoprostane relative to CON (14.7 vs. 16.5 pg/mL, respectively). In conclusion, dietary supplementation of CE did not affect T cell phenotypes and neutrophil activities in this study. However, CE increased total white blood cells, neutrophils, and eosinophils, and tended to decrease 8-isoprostane. It is suggested that CE may facilitate cells with function in innate immunity and reduce blood oxidative stress markers in lactating dairy cows.

Key Words: capsicum extract, immune response, oxidative stress

---

0209 Host-microbiome interactions during gut development across species: the role of milk.

T. B. McFadden*, *University of Missouri, Columbia.*

In humans, the benefits to babies of consuming whole colostrum and breast milk are now universally recognized. As a result, colostrum and breast milk are in high demand and are even donated and banked for use by mothers who are unable to lactate but still want to feed their babies breast milk instead of formula. Despite numerous studies on the functions and properties of human colostrum and breast milk, we have only scratched the surface in describing the specific bioactive factors and the mechanisms by which they protect the baby and promote GIT development, as well as programming future health and function. The same is true of all mammals as all mammalian offspring rely on mammary secretions (colostrum and milk) to provide nutrients and bioactive factors necessary for survival and subsequent growth and development. Although young of various species can be reared successfully on milk from other species, it is generally accepted that homologous milk provides the optimal match of components to requirements of the young. From this perspective, there is much potential to gain understanding from comparative studies of the unique relationships between milk composition and requirements of the suckling young across various species. In addition, recent recognition of the role of the gut microbiome as a key determinant of immunological and digestive system development opens new avenues by which milk components can have long term effects on future health and vitality of offspring. This paper will review current knowledge of milk composition and bioactive components and the effects they have on the young of various species. In addition, the effects of these components and temporal changes in the gut microbiome will be considered.

Key Words: gut microbiome, milk

CSAS GRADUATE STUDENT ORAL COMPETITION

0212 Effects of butyrate during subacute ruminal acidosis on VFA transport capacity in the rumen epithelium of holstein dairy cows. A. H. Laarman[*1], L. Dionissopoulos[1], O. AlZahal[2], S. L. Greenwood[3], M. A. Steele[4], and B. W. McBride[2], *[1]University of Guelph, Guelph, ON, Canada, [2]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [3]University of Vermont, Burlington, VT, [4]Nutreco Canada, Guelph, ON, Canada.*

This study examined the effects of exogenous butyrate during subacute ruminal acidosis (SARA) on the membrane VFA-transport proteins in the rumen epithelium. Sixteen mid-lactation Holstein cows fed a TMR including a pelleted concentrate supplement consisting of 60% barley grain, 20% corn grain, and 20% wheat grain on a dry matter basis. For 2 pre-trial days, all cows were adapted to the full amount of concentrate supplement to increase the dietary NFC to 44.0%. Cows were blocked by DIM and assigned either a butyrate treatment or control treatment for 7 d. Cows assigned the butyrate treatment were ruminally dosed twice daily with a calcium butyrate salt at 2.5% of their pre-trial DMI. Cows assigned the control treatment were ruminally dosed with a carrier. On Days 1 and 7, blood, rumen fluid, and rumen biopsies were sampled for serum BHBA concentrations, VFA profiles, and transport protein abundance, respectively. Rumen pH was continuously measured on Days 6 and 7 using an in-dwelling pH-measuring device. There was no difference in SARA between control and butyrate treatments (rumen pH < 5.6 for 598 ± 97 min/d vs. 536 ± 89 min/d, $P = 0.65$). Ruminal butyrate concentration were higher in the butyrate treatment compared to control treatment on both Days 1 (9.88 vs. 22.60 ± 0.94 mM, $P < 0.05$) and 7 (8.60 vs. 21.60 ± 0.94; $P < 0.05$). Serum BHBA was also elevated in the butyrate treatment animals on Day 1 (910 vs. 4201 ± 265 μM, $P < 0.05$) and Day 7 (800 vs. 3262 ± 265 μM, $P < 0.05$) compared to control animals. Immunofluorescence showed an increase in the abundance of monocarboxylate co-transporter isoform 1 (MCT1), sodium/proton exchanger isoform 3 (NHE3) and sodium/bicarbonate co-transporter isoform 1 (NBC1) in all cows between Days 1 and 7. By Day 7, butyrate dosing increased the abundance of MCT1 (11,275 ± 953 vs. 14,747 ± 953 A.U., $P < 0.05$) and decreased the abundance of NBC1 (15,065 ± 992 vs. 11,122 ± 992 A.U., $P < 0.05$) compared to control cows. These results suggest SARA increases the capacity for proton expulsion from the cytosol as well as VFA export into the bloodstream. Butyrate increases the capacity for VFA uptake by increasing the abundance of MCT1 on the basolateral membrane and decreasing NBC1 to maintain intracellular pH.

Key Words: butyrate, epithelium, transport

0213 Nutrient composition and degradation characteristics of anthocyanidin containing alfalfa transformed with Lc, C1, and Lc × C1 regulatory genes. R. G. Heendeniya Vidanaral[*1], M. Y. Gruber[2], Y. Wang[3], D. A. Christensen[1], J. J. McKinnon[1], B. Coulman[1], and P. Yu[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Agriculture and Agri-Food Canada, Saskatoon, SK, Canada, [3]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Alfalfa (*Medicago sativa* L.) is rich in nutrients. However, utilization of its nutrients in ruminants is restricted due to rapid rumen degradation of protein. This may be prevented if adequate protein binding proanthocyanidins are present in the aerial part of the plant. Proanthocyanidins are synthesized by the flavonoid pathway. The Lc gene and C1 genes synthesize bHLH and MYB transcription factors associated with the flavonoid pathway regulation. The objective of this study was to investigate the influence of single gene (Lc and C1) and double gene (Lc × C1) transformation on chemical composition and degradation characteristics of protein and carbohydrate compared to non-transgenic (NT) parental plants. Samples were collected from plant populations of C1 genotype, two Lc genotypes (Lc1 and Lc3), two Lc × C1 genotypes (Lc1C1 and Lc3C1), NT and AC-Grazeland (ACGL) and maintained in a growth chamber. Plants were harvested at late-bud stage, freeze-dried and ground (1 mm). Chemical composition was determined by AOAC methods. Protein and carbohydrate sub-fractions were estimated according to Cornell Net Carbohydrate and Protein System (CNCPS ver. 6.1). Anthocyanidin was extracted with aqueous acetone and hydrolyzed with butanol-HCl to measure spectrometric absorbance. The extractable anthocyanidin contents in Lc alfalfa and Lc × C1 averaged 149 ± 85 and 185 ± 74 μg/g DM, respectively. The single gene had a higher total carbohydrate (CHO; 70% vs. 68%; $P = 0.03$) and non-fiber carbohydrate (NFC; 44% vs. 40%; $P < 0.001$) than double gene transformed alfalfa. There was no difference ($P > 0.05$) in structural carbohydrate (ADF and NDF) content. The single gene alfalfa had a lower CP (19% vs. 21%; $P = 0.02$) than double gene transformed alfalfa. The profiles of protein (PA, PB1, PB2, and PB3), and carbohydrate (CA, CB1, CB2, and CB3) varied among different genotypes, resulting in different degradation profiles. Double gene genotypes had a higher ($P < 0.01$) rumen degradable crude protein (RDCP) but lower ($P < 0.01$) RD-CHO than single gene genotypes. This caused an increase ($P < 0.01$) in total degradable N to CHO ratio in double gene transformation by 10 g N/kg CHO. In conclusion, the gene transformation influenced anthocyanidin accumulation in aerial parts as well as accumulation of nitrogenous compounds and non-structural carbohydrates, thereby changing chemical composition and degradation characteristics. The single gene transformed alfalfa had a lower N to CHO balance than double gene alfalfa.

The C1 gene influences nutrient composition of alfalfa differently, when co-expressed with two Lc lines (Lc1 and Lc3).

Key Words: alfalfa, Lc and C1 genes, gene transformation

0214 Comparative analyses of the bovine rumen microbiota using RNA and targeted DNA-based sequencing approaches. F. Li*[1], X. Sun[2], G. Henderson[3], F. Cox[3], P. H. Janssen[3], and L. L. Guan[2], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]University of Alberta, Edmonton, AB, Canada, [3]AgResearch Limited, Grasslands Research Centre, Palmerston North, New Zealand.*

The bovine rumen microbiota comprises diverse populations, including bacteria, archaea, protozoa, and fungi. Defining rumen microbiota structures and their activities can enhance our understanding of the role of microbes in regulating rumen fermentation. We hypothesized that sequencing total RNA without rRNA removal (RNA-Seq) can be used to study the active microbiota, avoiding potential biases introduced by PCR-amplification of bacterial and archaeal 16S rRNA genes before sequencing. Total DNA and total RNA were isolated from the rumen contents of five steers maintained on a feedlot diet. Partial amplicons of bacterial and archaeal 16S rRNA genes were sequenced (Amplicon-Seq). RNA-Seq was performed in parallel. The data were processed using a QIIME-based pipeline in combination with Greengenes and SILVA-derived taxonomic frameworks. In total, five major bacterial phyla, with a relative abundance greater than 0.1% in any one sample, were identified in both Amplicon-Seq and RNA-Seq datasets; namely *Proteobacteria*, *Bacteroidetes*, *Firmicutes*, *Spirochaetes*, and *Synergistetes*. *Bacteroidetes* was more abundant in Amplicon-Seq than RNA-Seq datasets (52.6 ± 8.8% versus 23.7 ± 7.7%, mean ± SEM), whereas *Proteobacteria* was predominant in RNA-Seq datasets (45.7 ± 14.1% versus 13.0 ± 7.7%). *Euryarchaeota* was the most abundant archaeal phylum in both Amplicon-Seq (100.0 ± 0.0%) and RNA-Seq (94.2 ± 2.5%) datasets. Despite some differences in individual animals, microbial community compositions obtained using Amplicon-Seq and RNA-Seq techniques were broadly comparable. Of particular interest is that *Proteobacteria* appear to be more abundant in RNA-Seq datasets. Whether they are indeed more active relative to their abundance (Amplicon-Seq) than other bacteria warrants further investigation. Our results suggest that total RNA sequencing without rRNA removal can be used to study the active rumen microbiota.

Key Words: Amplicon-Seq, RNA-Seq, rumen microbiota

0215 Effect of pelleting at different conditions on ruminal degradation kinetics and intestinal digestion of canola meal in dairy cattle. X. Huang* and P. Yu, *Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

Pelleting has been adopted and widely used in the animal feed industry with its positive improvements in feed quality. Canola meal, an important protein source for ruminants in Canada, is usually prepared in mash or in pellets in feed mills. The objective of this study was to investigate the effects of pelleting at different conditions on in situ ruminal degradation kinetics and in vitro intestinal digestion of canola meal. Two batches of canola meal were pelleted after conditioning at different temperatures (70, 80, and 90°C) for different time (30s and 60s). Five rumen-cannulated lactating Holstein cows were used in an in situ trial to determine ruminal degradation kinetics. Intestinal digestibility was detected using a three-step in vitro method. Samples conditioned at 80°C had highest degradation rates (K_d) for crude protein (CP) and dry matter (DM) among pellets due to the quadratic effect of conditioning time ($P < 0.05$). The soluble fraction (S) of protein in pellets was greater than that in the unprocessed mash (9.84 vs. 5.68% CP, $P < 0.01$). The unprocessed mash had a greater content of bypass CP (BCP) but a lower content of effectively degraded CP (EDCP) than pellets (BCP: 44.20 vs. 39.30% CP; EDCP: 55.81 vs. 60.70% CP), indicating pelleting reduced ($P < 0.01$) BCP but increased ($P < 0.01$) EDCP contents of canola meal. However, bypass carbohydrates (BCHO) and effectively degraded CHO (EDCHO) were not affected by pelleting. The unprocessed mash had a lower ratio of effective degradability of N to carbohydrates (ED_N/ED_CHO) than pellets (126.17 vs. 142.85; $P < 0.01$). Conditioning temperature had a significant impact on ED_N/ED_CHO among pellets ($P < 0.05$). In the in vitro trial, intestinal digestible protein (IDP) content was greater in the unprocessed mash than in pellets (113.28 vs. 94.85 g/kg DM, $P < 0.05$), indicating that pelleting decreased IDP content of canola meal. There was no difference detected among samples on intestinal digestion characteristics for carbohydrates. In conclusion, pelleting increased ruminal degradation of protein while intestinal digestion of protein decreased in the current study. However, ruminal degradation and intestinal digestion characteristics of carbohydrates were not affected.

Key Words: pelleting, canola meal, rumen degradation, intestinal digestion kinetics

0216 Evaluation of corn and barley varieties in backgrounding grazing programs for beef calves.
S. A. McMillan*[1], B. Lardner[2], J. J. McKinnon[1], K. Larson[2], and G. B. Penner[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Western Beef Development Centre, Humboldt, SK, Canada.*

A study evaluated the effects of grazing either swathed barley (*Hordeum vulgare;* cv. Ranger*)* or standing corn (*Zea mays;* cv. Pioneer P7443R) as compared to drylot calves fed barley hay on forage quality, dry matter intake (DMI), calf backgrounding and feedlot performance, and backgrounding production costs. Each year, 120 spring born Angus calves (278.2 ± 5 kg) were fall weaned, stratified by body weight and randomly allocated to 1 of 3 replicated (n = 2) backgrounding systems: 1) field grazing standing whole plant corn (CORN); 2) field grazing swathed whole plant barley (BAR); or 3) dry lot (DL) bunk fed processed barley hay. CORN and BAR calves were limit grazed in 4-ha paddocks for 3 d grazing periods using electric fencing for 68 d, with all groups receiving a pelleted supplement (78% TDN, 16% CP) daily at 0.8% BW. Forage samples were collected every 21 d to determine CP, TDN, ADF, and NDF. DMI was estimated using the herbage weight disappearance method. After backgrounding, replicates of calves were divided into 2 and placed in a feedlot. Calves were fed a barley silage based diet with either barley or corn grain for 203 d to a target weight of 615 kg, at which point they were slaughtered and carcass data was collected. Data were analyzed as a one-way ANOVA using the Proc Mixed Model procedure of SAS. Protein content was greatest (P < 0.05) for DL and BAR (12.6% and 12.3%, respectively) compared to CORN (8.0%). Forage TDN, ADF, NDF, and forage DMI did not differ *(*P > 0.02) among backgrounding systems. Final BW and ADG were greatest (P < 0.05) for DL calves compared to CORN and BAR (331.7 vs. 311.9 and 311.2 kg, respectively) and (0.9 vs. 0.6 and 0.6 kg/d, respectively). There was no difference in costs of gain among systems but the total cost of production was greatest (P < 0.05) for DL calves ($2.20/calf/day). Feedlot performance and carcass characteristics did not differ among systems, suggesting that backgrounding calves by field grazing either standing whole plant corn or swathed barley can result in lower backgrounding production costs compared to feeding in drylot.

Key Words: backgrounding, barley, corn

0217 Transcriptomic analysis of rectal-anal junction tissue from super-shedders vs. cattle negative for *E. coli* O157:H7.
O. Wang*[1], G. Liang[1], X. Sun[1], B. Selinger[2], K. Stanford[3], G. S. Plastow[1], T. A. McAllister[4], and L. L. Guan[1], *[1]University of Alberta, Edmonton, AB, Canada, [2]University of Lethbridge, Lethbridge, AB, Canada, [3]Alberta Agriculture and Rural Development, Lethbridge, AB, Canada, [4]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

E. coli O157:H7 is a foodborne pathogen that causes hemorrhagic colitis and hemolytic uremic syndrome in humans. Cattle are the main reservoir for *E. coli* O157:H7 and individuals shedding > 10^4 CFU/g of feces are defined as super-shedders. To date, the molecular mechanisms responsible for the high level of carriage and shedding in super-shedders is unknown, but presumably is mediated by a host-microbial interaction. We hypothesized that changes in gene expression related to immune responses in tissues from the rectal-anal junction (RAJ) may be associated with the super-shedder phenomenon. In this study, we performed transcriptomic analysis of tissues from the RAJ, the reported main colonization site of *E. coli* O157:H7. Total RNA was extracted from RAJ tissues collected from five super-shedder steers and four non-shedder pen mates. RNA sequencing was done using Illumina sequencer Hiseq 2000 with average of 29.7 M ± 4.2 M paired-end reads generated from each sample. After mapping the reads to the bovine genome using Tophat, a total of 15,614 expressed genes (FPKM > 0.3) were detected at least once in at least one of the steers, with expression of 13,047 of genes (FPKM > 0.3) detected in non-shedders and 11, 846 (FPKM > 0.3) in super-shedders. The top functions of these genes enriched by GO terms include metabolic process, cellular process, and biological regulation which were not different between the two groups. In total, 20 genes were downregulated in super-shedders as compared to non-shedders (FDR < 0.1, using EdgeR). Of those genes downregulated in super-shedders, 11: CXCL13, CCL21, CCR7, IL2RA, LTB, S100A12, CD19, BANK1, CD19, MS4A1, KLHL6 were predicted to be associated with traits related to immune function; including movement of T cells, recruitment of leukocytes as well as the levels of B-cells and IgG. This is the first study to report transcriptomic analysis of the RAJ as it relates to the shedding status of the host. Our results suggest that immune homeostasis in super-shedders may play a role in the high levels of shedding observed in these individuals.

Key Words: *E. coli* O157, super-shedder, transcriptomic analysis

0218 Influence of steeping DDGS on growth performance and digestive function in liquid fed weanling pigs. M. Wiseman*, J. Zhu, D. Wey, and C. F. de Lange, *University of Guelph, Guelph, ON, Canada.*

Liquid feeding of high-fiber co-products with supplementary fiber-degrading enzymes may increase feeding value and influence gut development. This study assessed the effect of extended steeping of DDGS on performance and digestive function in newly-weaned pigs (weaned at 20 d) fed corn-soybean meal based liquid diets (28% DM). Enzymes (67.2 IU/g DDGS β-glucanase; 15.36 IU/g DDGS Xylanase; AB Vista) were used in both treatments: steeped (sDDGS; DDGS with enzymes fed between Day 5 and 14 of steeping in 39°C water at 16% DM) and unsteeped (usDDGS; DDGS and supplement mixed with water at time of feeding). Diet DDGS inclusion levels were 7.5% in phase 1 (d 0−7) and 25% in phase 2 (d 7-20) and 3 (d 21-35). The study was a randomized block design (n = 6 pens, 14 pigs/pen). Results are lsmean ± SEM (sDDGS vs. usDDGS, respectively), except fermentation characteristics (mean ± SD). On d 7, 14, and 35, 3 pigs per pen were euthanized for determination of liver, stomach, and small intestine (SI) weights, SI length, and digesta pH. VFA concentration was determined in d14 and d35 jejunal, ileal, and cecal digesta pooled among pigs in a pen. sDDGS batch (n = 5) characteristics (d5 and d14, respectively) revealed average pH 3.54 ± 0.16 and 3.04 ± 0.08, lactic acid 127.1 ± 22.3 and 72.5 ± 26.6 mM, and n-Butyric acid 38.7 ± 14.5 and 41.6 ± 27.1 mM. Unsteeped diets had pH 5.97 (n = 1), lactic acid 11.9 ± 11.8 mM (n = 3),and n-Butyric acid 7.1 ± 6.5 mM (n = 3). Steeping did not affect (P > 0.10) growth performance (Day 0-35 ADG 289 ± 15.8 and DMI 416.9 ± 10.3 g/d (n = 6) vs. ADG 290 ± 17.5 and DMI 415.7 ± 11.4 g/d (n = 5)), d7 physiological parameters (P > 0.10), or any gastrointestinal section weights (P > 0.05). Liver weight relative to BW was higher (P < 0.05) in sDDGS pigs on d14 while absolute liver weight was higher (P < 0.05) on d35 (30 vs. 27 ± 1 g:kg BW and 638 vs. 542 ± 21 g). sDDGS increased (P < 0.05) d14 jejunal formic and n-butyric acid (84.6 vs. 9.0 ± 16.8 and 61.8 vs. 42.1 ± 6.0 mM) without altering pH (P > 0.10). On d35 sDDGS increased (P < 0.05) cecal formic acid and decreased pH (P < 0.05) (71.7 vs. 153.7 ± 18.8 mM and 5.49 vs. 5.74 ± 0.07). No other VFA concentrations were affected (P > 0.05). sDDGS decreased (P < 0.05) d35 colon pH (5.64 vs. 5.85 ± 0.07) without altering pH elsewhere (P > 0.10). Results indicate steeping DDGS with enzymes results in altered enteric fermentation without affecting growth performance.

Key Words: digestive function, enzymes, liquid feeding pigs

0219 Selection of hybrid bromegrass for increased NDF digestibility. C. L. Rosser*[1], B. Coulman[1], and G. B. Penner[2], [1]*University of Saskatchewan, Saskatoon, SK, Canada,* [2]*Department of Animal and Poultry Science, University of Saskatchewan, Saskatoon, SK, Canada.*

The objective of this study was to determine whether selecting hybrid bromegrass for improved NDF digestibility would improve NDF digestibility and the performance of growing lambs. In 2010, 128-hybrid bromegrass (*Bromus riparius Rehm. × Bromus inermis Leyss.;* cv. AC Knowles) plants were clipped (5-cm stubble height) and used to determine 24-h in situ NDF digestibility (NDFd). Individual plants with the greatest (HNDFd; n = 20) and least (LNDFd; n = 20) digestibility values were selected (34.5 and 23.5%, respectively; P < 0.001) and polycrossed in isolation to produce seed. Seedlings were established in a field nursery June 8, 2011 and harvested July 23, 2012 and July 11, 2013 for in situ NDF digestibility determination. The DM yield tended to be greater for the LNDFd population (350 vs. 380 g/plant; P = 0.072) than HNDFd, while the degradable DM (37.2 vs. 33.6%; P = 0.098) and OM (39.8 vs. 35.7%; P = 0.092) fractions tended to be greater for HNDFd than LNDFd. Degradation rates for DM, OM, CP, NDF and ADF were not affected by treatment ($P \geq 0.398$). Additional plots of the HNDFd and LNDFd hybrid bromegrass populations were swathed on July 11, 2013, dried, and baled for an in vivo digestibility experiment. Twelve Suffolk × Canadian Arcott wether lambs were randomly assigned to the HNDFd or LNDFd treatments. The bromegrass hay was fed ad libitum and all lambs were supplemented with a pellet fed at 0.88% of initial BW. Total DMI and forage intake were not affected by treatment (P = 0.219). Nutrient intake (OM, CP, NDF, ADF, and ether extract; $P \geq 0.143$) was also not different between lambs fed LNDFd or HNDFd. However, NFC intake tended to be greater for HNDFd than LNDFD (0.34 vs. 0.29 kg/d; P = 0.070). Feeding the HNDFd or LNDFd bromegrass for 21 d did not affect final body weight or ADG ($P \geq 0.189$), but cumulative weight gain was greater for lambs fed HNDFd (P = 0.013). Total tract digestibility of DM, OM, NDF, ADF and NFC were not affected by treatment ($P \geq 0.328$), but CP and ether extract digestibility values tended to be greater for LNDFd than HNDFd ($P \leq 0.068$). These data suggest that although there were improvements in the degradable fractions of DM and OM and cumulative weight gain of the lambs fed HNDFd, the hybrid bromegrasses did not differ in NDF digestibility.

Key Words: digestibility, forage intake, hybrid bromegrass

0220 Effect of feeding different sources of nitrogen on performance of growing pigs fed diets deficient in non-essential amino acid nitrogen.

W. D. Mansilla[*1], J. K. Htoo[2], and C. F. de Lange[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Evonik Industries AG, Hanau-Wolfgang, Germany.*

When formulating diets with low nitrogen (N) content, the supply of dietary non-essential amino acids (NEAA) is reduced and essential amino acid (EAA) may be catabolized to supply N for endogenous synthesis of NEAA, which can lead to compromised pig performance. The objective of this study was to evaluate the effect of supplementing different sources of N in diets deficient in NEAA-N on performance of growing pigs. In total 36 barrows (BW 15.5 ± 1.0 kg) were randomly assigned to 9 different diets: a basal cornstarch and casein-based diet, not deficient in EAA but low in CP (N × 6.25; 8.01%); and the basal diet supplemented with 4 different sources of N (urea, ammonium citrate, glutamic acid and a mix of NEAA) at 2 levels each, supplying 1.37 and 2.75% additional CP, respectively. The mix of NEAA was based on body composition of NEAA of 20 kg pigs, and aimed to minimize endogenous synthesis of NEAA. Pigs were housed individually and fed at 3.0 × maintenance requirement for ME during 3 consecutive weeks. BW gain was monitored weekly. BW gain and gain:feed of pigs fed urea were lower than any other sources of N ($P < 0.05$), but they were similar across the other treatments ($P > 0.10$). As the level of N increased, BW gain and gain:feed increased ($P < 0.05$). Feeding ammonium to pigs is as efficient as supplementing glutamate or NEAA mix to support growth performance when diets are deficient in NEAA-N, while utilization of urea-N is lower.

Key Words: growth, nitrogen, pig

Table 0220. BW gain, feed intake and gain:feed in growing pigs fed a diet deficient in NEAA-N supplemented with different sources of N at different levels of N supplementation

		BW gain, g/d	Feed intake, g/BW$^{0.6}$/d	Gain:feed
Source	Urea	367[a]	169	0.381[a]
	Ammonia	399[b]	169	0.415[b]
	Glutamate	404[b]	169	0.421[b]
	NEAA mix	402[b]	169	0.418[b]
	SEM	7.5	0.1	0.008
Level	0.0	363[a]	169	0.378[a]
	1.37	387[b]	169	0.403[b]
	2.75	429[c]	169	0.445[c]
	SEM	6.4	0.01	0.007
P-value	Source	0.006	0.219	0.004
	Level	< 0.001	0.286	< 0.001
	Interaction	0.070	0.247	0.069

[a,b,c] Values in the same column followed by different superscripts differ ($P < 0.05$).

0221 Comparison of winter feeding systems for the evaluation of beef cow performance, reproductive efficiency and system costs.

D. Jose[*1], G. B. Penner[1], J. J. McKinnon[1], K. Larson[2] and, B. Lardner[1,2], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Western Beef Development Centre, Humboldt, SK, Canada.*

Extensive winter grazing has been proven as a successful strategy to reduce production and labor costs in a cow-calf operation without much adverse effects on animal health and performance. Two experiments were conducted during the winter of 2012-2013, to evaluate 3 winter feeding systems: (i) field grazing standing whole plant corn (SC; TDN = 59.5%, CP = 7.8%), (ii) field grazing swathed barley hay (SB; TDN = 66.2%, CP = 8.5%) and, (iii) barley hay bales fed in drylot pens (DL; TDN = 60.1%, CP = 12.7%). The specific objectives were to compare beef cow performance, reproductive efficiency and system costs in experiment 1 (EXP 1), and ruminal pH parameters in experiment 2 (EXP 2). In EXP 1, dry pregnant Angus cows ($n = 60$, body weight (BW) = 651.2 ± 7 kg), stratified by body weight and days pregnant were randomly allocated to 1 of 3 replicated ($n = 2$) winter grazing treatments for 77 d. Cow BW, body condition score (BCS), and rib and rump fats were measured at the start and end of the trial. Increases in rump fat were greater ($P = 0.002$) for SC cows compared to DL cows (1.90 mm vs. 0.55 mm, respectively). Calves born to cows on SC were heavier ($P < 0.001$) at birth compared to calves from SB cows (42 vs. 40 kg respectively). In EXP 2, 9 cannulated beef heifers were cycled through the 3 winter systems concurrently within EXP 1, in a replicated 3 × 3 Latin square design, for 63d to evaluate effect of forage type on rumen pH. Results from EXP 2 indicated that SB heifers had the lowest ($P < 0.003$) mean, minimum and maximum rumen pH and greatest duration and area under pH < 5.8 ($P < 0.001$) compared to heifers on SC and DL winter systems. Economic analysis revealed that total costs were greatest for the DL ($2.29/head/d) compared to SC ($1.78/head/d) and SB ($1.65/head/d) systems. Results suggest that both SC and SB systems are cost effective alternatives to DL system, and do not negatively affect cow body weight or reproductive performance in winter.

Key Words: winter grazing, corn grazing, swath grazing, reproductive performance

0222 Dietary supplementation with excess leucine transiently improved whole body nitrogen retention in young pigs challenged with bacterial lipopolysaccharide.

M. Rudar* and C. F. de Lange, *University of Guelph, Guelph, ON, Canada.*

The increase in circulating pro-inflammatory cytokines following a bacterial lipopolysaccharide (LPS) challenge causes a disruption in normal nitrogen (N) and amino acid (AA) me-

tabolism. The reduction in whole body N retention during inflammation can be attributed to an increase in hepatic protein synthesis at the expense of muscle protein synthesis, which may be modulated by leucine (Leu) intake. The objective of this study was to explore the effect of excess dietary Leu on the dynamics of N retention in young pigs following an LPS challenge. A total of 24 starter pigs (13.93 ± 2.05 kg) were used in a 2 × 2 factorial design (n = 6). Pigs were fed isoenergetic and isonitrogenous diets formulated to contain all essential AA 10% above requirements for protein deposition (Con; 1.36% SID Leu) or Leu supplemented at twice that amount (+Leu; 2.72% SID Leu). Pigs were housed in metabolic crates and fed six times daily according to their body weight. Pigs were challenged with either saline (−LPS) or repeated and increasing doses of LPS (+LPS; 30 μg·kg^{-1} injected intramuscularly on Days 1, 3, 5, and 7 of a 7-d N-balance period). Blood was collected on Days 1 and 7 1 h after feeding to determine plasma AA concentrations. Whole body N retention was determined daily. Pigs fed +Leu had higher plasma Leu than pigs fed Con (319 vs. 159 μmol·L^{-1}, SE 10.3, $P < 0.01$). There was no effect of diet on N retention across the 7-d N balance period ($P > 0.10$). However, LPS reduced N retention during the first 3 d of the N balance period ($P < 0.05$). For +LPS pigs, the effect of diet on N retention changed over time ($P < 0.05$); on Day 2, N retention was lower in +LPS pigs fed Con than +LPS pigs fed +Leu (10.5 vs. 12.3 g/d, SE 0.66, $P < 0.05$). Moreover, N retention was higher in −LPS pigs than in +LPS pigs fed Con (13.0 vs. 10.5 g/d, SE 0.66, $P < 0.01$) whereas N retention was not different between–LPS pigs and +LPS pigs fed +Leu (12.3 vs. 12.3 g/d, SE 0.66, $P > 0.10$) on Day 2 post-challenge. In this study, excess dietary Leu partly attenuated the reduction in body protein gain after an LPS challenge.

Key Words: endotoxin, leucine, nitrogen retention

0223 The relationship between trailer motion and carcass bruising in market cows during transport.

C. E. Kehler[*1,2], K. H. Ominski[1], L. L. Connor[1], T. G. Crowe[3], and K. S. Schwartzkopf-Genswein[4], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]Agriculture and Agri-food Canada, Lethbridge, AB, Canada, [3]University of Saskatchewan, Saskatoon, SK, Canada, [4]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Increased trailer motion, coupled with large accelerations and decelerations, have been associated with decreased carcass quality and increased stress indicators in cattle, sheep and hogs. However, motion of livestock trailers has not been measured in North-American cattle semi-trailers over long distances (> 1000 km). The objective of this study was to describe the acceleration within each of the 5 compartments of a cattle semi-trailer and to determine the relationship between trailer acceleration and bruising severity. The root mean square (rms) of acceleration was measured at a sampling rate of 200 Hz in 3 orthogonal axes; x (vertical, positive upward), y (front-to-rear, positive forward) and z (lateral, positive leftward as viewed from rear) by rigidly clamping an accelerometer to the cross beam below each of the five compartments of 8 trailers transporting 331 animals from assembly yard to a processing facility. Journeys ranged in duration from 780 min to 942 min. A bruise severity score was obtained before trimming for n = 291 carcasses using the number of bruises weighted by the size of bruise on a 3-point scale (1 $\leq$ 6.5 cm; 2 = 6.5 to 12 cm and 3 $\geq$ 12 cm). Due to limitations in the battery capacity of the sensors, the acceleration was only measured for the first half of the journey for all but 2 journeys. The percent difference in rms between the entire journey and the first half of those 2 journeys ranged from 7.22% to 14.54%. The mean rms of acceleration for all trailers (34 accelerometers) was 1.43 ± 0.42 m/s^2, 1.32 ± 0.53 m/s^2 and 1.67 ± 0.50 m/s^2 for x, y and z axes, respectively. Mean bruise number and severity per carcass were 4.52 ± 2.43 and 5.31 ± 2.84, respectively. When measured by trailer a quadratic relationship was observed between acc (rms) and bruise severity in the z-axis (r = 0.69, P = 0.09) however, no relationship was observed between either the x or y axes and bruise severity. Acceleration varied slightly between trailer compartments in the z (P = 0.10) and y-axes (P = 0.10) but not in the x axis. Bruising also varied slightly by trailer compartment (P = 0.11). Results indicate that reductions in side to side trailer movements could decrease bruising, thereby improving carcass quality and animal welfare. Extension and replication of this research is required to further understand the relationships between trailer motion, carcass bruising and overall animal welfare.

Key Words: cattle, transport, acceleration

0224 Impact of reducing dietary crude protein concentration on serum lysine concentration and lysine utilization efficiency in lactating sows.

L. A. Huber[*1], C. F. de Lange[1], U. K. Larsen[2], D. Chamberlin[3], and N. L. Trottier[3], *[1]University of Guelph, Guelph, ON, Canada, [2]Aarhus University, Foulum, Denmark, [3]Michigan State University, East Lansing*.

It was hypothesized that reducing dietary crude protein (CP) concentration while maintaining available Lys intake will improve Lys utilization efficiency for milk production in sows. Forty lactating multiparous Yorkshire sows were used to determine the effect of reducing dietary CP concentration and supplementing with crystalline amino acids on dietary Lys utilization efficiency during early (d3−7) and peak (d14-18) lactation. Sows were assigned to 1 of 4 diets: [1] 16.0% CP (as-fed; analyzed contents; HCP); [2] 15.7% CP (0.1% crystalline Lys; MHCP); [3] 14.3% CP (0.2% crystalline Lys; MLCP); [4] 13.2% CP (0.3% crystalline Lys; LCP); diet HCP was formulated using soybean meal and corn as the only Lys sources. Across diets, standardized ileal digestible (SID) content of Lys was 0.77%, based on analyzed

content and estimated SID. Other essential amino acids were included to exceed requirements. Litters were standardized to 10 piglets within 24h of birth. Milk yield was estimated based on litter size and growth rate. Blood was collected from fasted sows on d3, 7, 14, and 18 for free amino acid analysis. The efficiency of using SID Lys intake for Lys output in milk (Klys) was calculated according to NRC (2012), accounting for maternal maintenance requirements and the contribution of maternal body protein mobilization based on sow BW change. Sow feed intake and litter growth rate during the 21d lactation period did not differ between dietary treatments (overall means: 5670 ± 138 and 2263 ± 94 g/d, respectively). Serum Lys concentration was influenced by day in lactation ($P < .0001$); there tended ($P = 0.08$) to be a quadratic effect of dietary CP concentration (142.8, 105.6, 127.5, and 167.7 ± 22.7, and 84.8, 63.2, 61.7, and 79.6 ± 11.9 µmol/L; HCP, MHCP, MLCP, and LCP on d7 and d18, respectively). In early lactation, reduced dietary CP concentration did not affect Klys (67.5, 70.9, 64.2, and 66.7 ± 6.63%; HCP, MHCP, MLCP and LCP, respectively; $P > 0.10$). In peak lactation Klys was higher for MHCP than HCP ($P < 0.05$), but a further reduction in diet CP concentration did not affect Klys ($P > 0.10$; 59.8, 68.3, 65.1, and 67.6 ± 2.92%; HCP, MHCP, MLCP and LCP, respectively). There appears to be an association between plasma Lys levels and Klys, which needs to be explored further. In peak lactation the use of up to 0.1% crystalline Lys to replace protein bound Lys in the diet improved Klys.

Key Words: amino acids, lactating sows, lysine utilization

0225 Diurnal variations in enteric methane emissions from non-lactating dairy cows offered diets differing in forage to grain ratio. A. J. Kotz*[1], S. C. Li[2], E. J. McGeough[1], E. Khafipour[3], and J. C. Plaizier[2], *[1]University of Manitoba, Winnipeg, MB, Canada, [2]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [3]Department of Medical Microbiology and Infectious Diseases, University of Manitoba, Winnipeg, MB, Canada*.

This experiment determined how level of dietary grain inclusion affected daily enteric methane emissions and their diurnal variation in dairy cows. Six mature non-lactating Holstein dairy cows were offered one of three diets with forage to grain ratios of 100:0 (F), 75:25 (M), and 50:50 (H). The forage portion of the diet consisted of 80% grass hay and 20% alfalfa hay (DM basis). The concentrate was a barley-corn based ration (DM = 893 g/kg, CP = 198 g/kg DM). Feed was offered three times daily at 0900, 1300, and 1700. The experiment was a replicated 3 × 3 Latin Square Design, with each animal receiving each of the three diets over the course of the three 5-wk periods. Experimental diets were switched gradually during the first week of every period. This was followed by 3 wk dietary adaptation. Sample collection and enteric methane output measurement were conducted on two separate days during the fifth week of every period. Rumen fluid was collected using a stomach tube and a fecal grab sample was taken to determine pH at 0830 and 1500 on the day preceding enteric methane output. An open-circuit hood calorimetric system was used to determine methane output over a 24 h period. Increasing the grain content of the diet decreased rumen pH (F = 7.02, M = 6.82, H = 6.77, $P < 0.01$) and fecal pH (F = 7.09, M = 6.85, H = 6.66, $P < 0.01$) and increased DMI (F = 12.2, M = 14.3, H = 16.6 kg/d, $P < 0.01$). Increasing the dietary grain content increased daily enteric methane emissions (F = 361.6, M = 423.0, H = 445.0 L/Day, $P < 0.01$). However, when methane production was expressed per kilogram of DMI, increasing the dietary grain inclusion reduced daily emissions (F = 29.8 L/kg DMI, M = 29.7 L/kg DMI, H = 27.2 L/kg DMI, $P < 0.01$). Methane emissions clearly exhibited a diurnal pattern that coincided with feeding events, irrespective of diet offered. The highest rate of methane production observed was concurrent with afternoon feeding at 1300 (0.38 L/min); while the lowest rate of methane production was observed 2 h before morning feeding (0.20 L/min). The diurnal pattern differed among diets ($P < 0.01$). In conclusion, dietary grain inclusion increased daily methane production and altered the diurnal pattern of methane emission rate.

Key Words: cattle, enteric methane emission, grain to forage ratio

---

0226 Long-term supplementation of diets with 3-nitrooxypropanol resulted in a sustained reduction in methane production in beef cattle. A. Romero-Perez*[1,2], E. K. Okine[1], S. M. McGinn[2], L. L. Guan[1], M. Oba[1], S. M. Duval[3], and K. A. Beauchemin[2], *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada, [3]DSM Nutritional Products France, Research Centre for Animal Nutrition and Health, Saint Louis Cedex, France.*

The objective was to evaluate whether long-term supplementation of diets with 3-nitrooxypropanol (NOP), a synthetic compound proven to reduce enteric CH_4 emissions in short-term studies, results in a sustained reduction in enteric CH_4 emissions in beef cattle. Eight ruminally cannulated heifers (637 ± 16.2 kg of BW) were used in a completely randomized design with 2 treatments: Control (0 g/d of NOP) and NOP (2 g/d of NOP). Treatments were mixed by hand into the TMR (60% forage, DM basis) at feeding time. Feed offered was restricted to 65% of ad libitum DM intake (DMI; maintenance energy intake) to avoid excessive growth. Duration of the experiment was 146 d, including an initial covariate period without NOP supplementation (18 d), 4 periods with NOP supplementation (28 d each), and a final recovery period without NOP supplementation (16 d). Methane was measured at the

end of each period for 3 d using metabolic chambers. Volatile fatty acid (VFA) concentration and microbial populations were measured using rumen samples collected 0, 3, and 6 h after feeding. Data were analyzed using the PROC MIXED procedure of SAS. Average DMI for the experiment was 7.0 ± 0.2 kg. Methane intensity was reduced by 60% when NOP was supplemented (22.6 vs. 8.9 g/kg DMI; $P < 0.01$) with no signs of adaptation (period × treatment, $P = 0.2$). Total VFA concentrations were not affected ($P = 0.12$); however, acetate concentration was reduced and propionate concentration increased when NOP was supplemented ($P < 0.01$), which led to a reduction in the acetate to propionate ratio (3.9 vs. 2.9; $P < 0.01$). NOP had no effect on the copy number of the 16S rRNA gene of total bacteria ($P = 0.5$) but the copy numbers of the 16S rRNA gene of methanogens ($P < 0.01$) were reduced and copy numbers of the 18S rRNA gene of protozoa ($P = 0.03$) were increased. All effects of NOP observed during the measurement periods were absent during the recovery period when supplementation was discontinued. These results showed that reduction of CH_4 production in ruminants is sustained with long-term dietary supplementation of NOP.

Key Words: 3-nitrooxypropanol, beef cattle, methane

0227 Measuring animal productivity and rumen efficiency from extensively overwintered beef cows on the Canadian prairies.

G. R. Donohoe*, K. M. Wittenberg, D. N. Flaten, B. D. Amiro, and K. H. Ominski, University of Manitoba, Winnipeg, MB, Canada.

Many producers in the Prairie region have adopted the use of low-cost, extensive overwintering strategies. Although the economic benefits of these practices are well-documented, rumen efficiency and animal productivity have not been fully characterized. Evaluation of such strategies is challenging because of our limited capacity to measure individual animal intake in extensive overwintering systems. In an attempt to address these knowledge gaps, sixty mature, non-lactating, pregnant beef cows were fed low-quality forage (8.8% crude protein and 4.3 Mcal kg^{-1} gross energy (GE), DM basis) ad libitum and monitored over two, 28-d periods. Cows were divided into three treatment groups: intensively overwintered (drylot; DL), extensively overwintered (bale grazed; BG) and extensively overwintered supplemented with dried distillers' grains with solubles (DDGS) at a rate of 8.31 kg DM every third day (BG+DDGS). Measurements included temperature, body weight, DM intake, enteric methane emission, and serum urea nitrogen (SUN). Average daily air temperature over the trial was -17.1 ± 6.5°C (± SD). Localized temperatures, measured with iButtons near the animal body surface, showed that cows in the extensive treatments were exposed to colder temperatures, at -14.7 ± 0.6°C, compared to cows overwintered intensively, at -11.9 ± 1.4°C (± SD). Average daily gain over the trial was greater ($P < 0.01$) for DL cows when compared to BG cows, but not different ($P > 0.20$) when comparing DL to BG+DDGS. Intake was greater ($P = 0.04$) in period one for DL cows compared to BG cows, measured using GrowSafe and alkane bolus techniques, at 13.4 ± 0.38 and 12.1 ± 0.44 kg DM d^{-1}, respectively (± SE). This resulted in greater ($P < 0.01$) enteric methane emission from the BG cows in period one, at 5.62 ± 0.49 and 8.46 ± 0.49%GEI, for the DL and BG treatments, respectively (± SE). The addition of DDGS every third day in the extensive treatment reduced enteric methane in both periods. Average SUN concentrations over the trial were below the acceptable range of 2.1 mmol L^{-1} at 1.00 ± 0.40 and 1.40 ± 0.60 mmol L^{-1} for cows in the DL and BG treatments, respectively (± SD). When measured at 24 and 72 h after feeding DDGS, SUN concentrations for cows in the BG+DGSS treatment were 5.14 ± 1.67 and 2.65 ± 0.57 mmol L^{-1}, respectively (± SD), indicating that supplemental DDGS was an effective strategy to increase SUN when feeding low-quality forage. This data demonstrates that animal nutrient requirements may differ in intensive and extensive overwintering environments, and therefore require further characterization to improve metabolic and production efficiency of cattle.

Key Words: enteric methane, beef cows, overwintering

0228 Adding sera enriched in PUFA with different n-6/n-3 ratio advanced bovine in vitro embryo development from both high- and inferior-quality oocytes.

R. Salehi*[1], A. Ruiz-Sanchez[1], M. G. Colazo[2], M. Oba[1], M. Dyck[1], and D. J. Ambrose[3], *[1]University of Alberta, Edmonton, AB, Canada, [2]Alberta Agriculture and Rural Development, Edmonton, AB, Canada, [3]Alberta Agriculture and Rural Development, Livestock Research Branch, Edmonton, AB, Canada.*

Diets containing sunflower (SUN; high linoleic acid, LA) or flaxseed (FLX; high α-linolenic acid, ALA) positively affect early embryonic development (EED) in dairy cows. Also, a FLX-based diet decreased the proportion of non-viable embryos in vivo. Oleic acid (OLA), abundant in canola (CAN), improves oocyte competence in vitro but its influence on EED is not known. Our objectives were to: (1) compare the effects of adding serum collected from cows fed CAN, SUN or FLX on in vitro development of bovine embryos derived from high-quality oocytes (Exp-1), and (2) determine the effect of FLX-fed-cow-serum on development of embryos derived from inferior-quality oocytes (Exp-2). Estrus-cow-serum was harvested from Holsteins fed hay (8.8 DM kg/d) and concentrates (3.8 DM kg/d) supplemented with 1 of 3 rolled oilseeds (8% of total DM) for ≥ 21 d: CAN ($n = 4$); SUN ($n = 4$); or FLX ($n = 4$). Cumulus-oocyte-complexes (COC) aspirated from abattoir ovaries were categorized into Grade 1+2 (high-quality) and Grade 3 (inferior-quality) for Exp1 and 2, respectively. The COC were matured and fertilized (Day-0) in vitro; presumptive zygotes ($n = 977$ from Grade 1+2, Exp-1; $n = 359$ from Grade 3 COC, Exp-2 in 5 replicates each) were cultured with corresponding sera (5%) until Day-8. Se-

rum fatty acid profile (% total fatty acid) were OLA 12.1, total polyunsaturated fatty acids (PUFA) 49.4, n-6/n-3ratio 4.7 (CAN); LA 52.5, PUFA 57.5, n-6/n-3ratio 10.5 (SUN); ALA 17.9, PUFA 54.3, n-6/n-3ratio 2.0 (FLX). In Exp-1, SUN (78.0) and FLX (78.8) increased ($P < 0.05$) % cleaved compared with CAN (65.0) but not with fetal calf serum (FCS; 72.1). Blastocyst (BL) developmental rate (%) was higher ($P < 0.05$) on Day-7 in FLX (15.5) and SUN (15.5) than in CAN (9.1) and FCS (9.2) treatments, but not on Day-8 (overall, 23.3). More ($P < 0.05$) advanced stage embryos (expanded- and hatched-BL, %) were present on Day-8 in SUN (85.0) compared to FLX (69.8), CAN (61.5) and FCS (64.0). In Exp-2, although % cleaved did not differ (41.8), FLX tended ($P = 0.12$) to increase BL developmental rate on Day-7 (6.73) compared to FCS (3.01). More advanced stage embryos (BL and expanded-BL) were present in FLX vs. FCS (84.6 vs. 0.0%). In Exp-2, BL developmental rate (11%) and advanced stage embryos (95%) did not differ on Day-8. In summary, adding serum from cows fed FLX or SUN enhanced BL developmental rate on Day-7 and the proportion of advanced stage embryos on Day-7, even from inferior quality oocytes.

Key Words: oilseed, embryo, serum

CSAS SYMPOSIUM: **UNDERSTANDING FEEDING BEHAVIOR TO IMPROVE ANIMAL WELL-BEING AND PRODUCTIVITY**

0229 The psychology and sociology of feeding behavior. J. J. Villalba*, *Agricultural Experiment Station, Utah State University, Logan.*

Food intake (how much to eat) and preference (what to eat) dictate nutrient balance and ultimately an individual's fitness and productivity. Emerging evidence suggests that the mechanisms underlying hunger and satiety are not only governed by physiological signals associated with the homeostatic control of food intake but also by their interaction with pathways involved in the control of food reward and hedonics. The hedonic value of a food—or how pleasurable to the animal such food results—is in part motivated by the individual's previous experiences with its orosensorial and biochemical properties. Taste (as well as smell and sight) allows animals to discriminate among foods and is a source of hedonic sensations. Postingestive feedback calibrates such sensations with its homeostatic utility, influencing food preference and chemical composition of the diet. This mechanism identifies foods adequate in nutrients (or in chemicals that enhance health) and foods with nutrient deficiencies/imbalances (or in chemicals that are toxic), thereby increasing or decreasing preference, respectively. The cultural inflection is manifest through mother and peers, representing a model from which naïve observers learn new behaviors and are exposed to novel environmental experiences. These experiences begin in utero and continue after birth, priming individuals to learn from their individual orosensorial and postingestive experiences. In turn, the new knowledge created within a social group is maintained and transmitted by mothers across generations. It is proposed that a strategic management of an animal's experiences with food, i.e., a certain target food presented early in life with mother/peers, or in close temporal association with other nutritious/medicinal foods, has the potential to enhance animal health, productivity and well-being.

Key Words: food choice, behavior, preference

0230 Physiological mechanisms controlling feeding behavior. M. S. Allen* and P. Piantoni, *Michigan State University, East Lansing*.

Mechanisms controlling feed intake are dependent on the interaction between diet and physiological state of animals. Physiological state is affected by age, pregnancy, lactation, and adiposity and is characterized by differences in insulin sensitivity of tissues and plasma concentrations of insulin, growth hormone, and leptin. The interaction between diet and physiological state affects feeding behavior (e.g., meal size and frequency) depending on the type and temporal supply of absorbed fuels. These fuels (e.g., glucose, fatty acids, amino acids) derive from the diet directly or indirectly as a result of gastrointestinal fermentation and are metabolized or stored by different tissues at different rates. Other fuels (e.g., long chain fatty acids, glycerol, amino acids) originate from body reserves. Effects of fuels on endocrine response and gene expression affect energy partitioning, which in turn affects feeding behavior by altering clearance of fuels from the blood. Various signals are integrated in brain feeding centers and dominant mechanisms controlling feed intake change with physiological state. Signals that affect feeding behavior include those from gut distension, which likely dominates control of feed intake under conditions of high-energy requirements with low-energy diets, as well as those from the release of gut peptides stimulated by certain nutrients. There is a growing consensus of the importance of fuel-based sensing among tissues. Signals to brain feeding centers via hepatic vagal afferents are also affected by oxidation of fuels. While oxidation of fuels has been linked to feeding behavior, evidence suggests that the mechanism is specifically related to hepatic energy charge (degree of phosphorylation of adenine nucleotides). Synergistic effects of metabolic inhibitors have been demonstrated in rodents, which suggests an integrated mechanism with a common signal related to hepatic energy status from oxidation of a variety of fuels. Utilization of high-energy phosphate bonds vary with liver function and their production is determined by the flux of carbon through acetyl CoA and activity of the tricarboxylic acid cycle. Hepatic concentration of acetyl CoA varies diurnally and is highly variable across cows, depending on lipolytic state (e.g., early postpartum period, shipping stress). Therefore, acetyl CoA is likely a key metabolite involved in both circadian control of feeding behavior and control of feed intake across physiological states. This presentation will discuss control of feed intake in animals varying in physiological state considering the effects of diet on energy partitioning and hepatic oxidation of fuels.

Key Words: feeding behavior, hepatic oxidation, metabolic fuels

0231 Feeding behavior, productivity and welfare of dairy cows. M. A. G. von Keyserlingk* and D. M. Weary, *University of British Columbia, Vancouver, BC, Canada.*

Over the last decade there has been a growing scientific interest in feeding behavior of dairy cattle, in part because dairy nutritionists are now becoming interested in how changes in feed intake are mediated by changes in behavior and, in part, because changes in feeding behavior are increasingly recognized as a useful indicator of cow health. Feeding behavior can be described using several measures, including the number and duration of meals, as well as intake and feeding rate. However, it is now clear that changes in feeding behavior are mediated in part by changes in other primary behaviors such

as social and lying behavior. It is also well established that the delivery of fresh feed is a primary factor stimulating feeding behavior by intensively housed dairy cows. Moreover, management factors such as competition at the feed bunk and regrouping can profoundly affect feeding behavior, with subordinate animals often showing the most pronounced effects. Many types of diseases are common after calving; these include illnesses caused by infectious agents and disturbances in metabolism. Much of our work has focused on identifying links between feeding behavior and a common infectious disease of the uterus, metritis. For example, over a series of studies, we now provide solid evidence that feeding behavior is altered in cows during the period of illness, but even more interesting is that this behavior is altered in the weeks leading up to parturition, long before clinical signs are evident, compared to healthy cows. We also review the relationship between lying, social, and feeding behavior as work now indicates that each of these behaviors impacts the other and collectively they play a role in expression of sickness behavior by cattle.

Key Words: social behavior, lying behavior, disease

0232 Good eating habits lead to good growth and welfare of dairy calves. T. J. DeVries*, *University of Guelph, Kemptville, ON, Canada.*

The dairy calf needs access to milk in sufficient quantities to maintain health and high-levels of growth. In addition, solid feed consumption must also occur early in life to establish fermentation in the rumen, and initiate the process of physical and metabolic development of the rumen. There is good empirical evidence that the feeding behavior patterns of adult dairy cattle, in meal patterning and dietary selection, can impact health, productivity, and welfare. It has also been demonstrated in more recent research that the feeding behavior patterns of dairy calves may also be just as important. In particular, feeding behavior can have immediate impact by influencing nutrient consumption and growth. Further, as behavior patterns are learned early in the life of a ruminant, these may have long-term implications if and when they persist over time. Thus, there is potential for various nutritional, housing, and management factors early in the life of a dairy calf to impact both short- and long-term feeding behavior patterns. This review will provide several examples of early-life factors influencing the eating habits of dairy calves and, in turn, influencing calf growth and welfare. For example, providing continuous, ad libitum access to milk may result not only in greater growth, but also in more natural feeding patterns, both of milk and solid feed. As another example, there is new data to reinforce the idea that providing forage to calves is important for rumen development, and consequent growth and efficiency. However, the physical form and presentation of that forage may also have a significant impact on the feeding patterns of calves, in particular feed sorting, impacting both their immediate nutrient intakes as well as the development and persistence of that behavior. Housing management also has the potential to impact calf feeding behavior and growth. Housing calves in pairs (vs. individually) can promote intake and growth, particularly at weaning. However, competition for feed access for grouped calves can impact the expression and learning of less desirable feeding patterns. Continued research in this area is needed to assess how long some of these learned behaviors persist and what factors may influence their persistence or diminishment.

Key Words: calves, behavior, sorting

DAIRY FOODS SYMPOSIUM: ADVANCES IN DELIVERY OF DAIRY INGREDIENTS FOR HEALTH AND FUNCTIONAL BENEFITS

0233 Market opportunities for dairy proteins. A. Bienvenue*, *U.S. Dairy Export Council, Arlington, VA.*

The protein trend, popular among athletes for decades, has now reached several mainstream segments. Consumers – especially in the United States and Western Europe – have become increasingly aware of the benefits of protein in the diet for satiety, weight management and muscle-related benefits such as exercise recovery and healthy aging. Food manufacturers now offer beverages, bars, cereals, meals and yogurts formulated to deliver increased levels of protein, while maintaining a good taste profile. In Asia and the Middle East, the protein trend is at the cusp of what we are seeing in the United States and Europe. Growth in demand for protein-rich foods is expected as consumers in these regions achieve greater financial prosperity, become aware of health trends in other countries, and move toward a more Western diet. The demand for protein-rich foods presents a huge opportunity for dairy's many products and ingredients. Dairy protein can deliver good taste, functionality, fast and/or slowly digested proteins and superior nutrition in a product formulation. In order to capitalize on formulators' desire to increase protein levels in foods and beverages, dairy suppliers must offer ingredients that will meet buyers' specifications, consistently perform and deliver a high-quality finished product. Dairy ingredient performance depends on the protein type, structure, pH, ionic strength, interactions with other ingredients in the formula and processing conditions of the finished product. Therefore, it is crucial for suppliers to understand formulators' parameters to help in selecting the best dairy ingredient functionality for a food system. In a highly competitive marketplace, formulators have choices of ingredients to increase protein levels in food formulation. The Digestible Indispensable Amino Acid Score (DIAAS), the new FAO-recommended method, demonstrates the higher bioavailability of dairy proteins when compared to plant-based protein sources. Dairy proteins can therefore distinguish themselves by the excellence of the nutrition they deliver. To allow for more dairy protein to be used in a wide variety of food applications, the dairy industry must accelerate innovation to expand the offering of cost-effective ingredients that will perform consistently under diverse processing conditions and challenges. Examples of the attributes requested include: for beverages, improved heat stability across a wide pH range, greater clarity and a very clean flavor profile; in bar applications, a dairy protein that can resist hardening over time. Dairy protein ingredients that maintain flavor, color, solubility and flowability throughout their shelf life, even in hot and humid environments, are highly desired for export markets..

Key Words: dairy protein, functionality, export.

0234 Using charged membranes to improve dairy protein ingredients. M. Etzel*, *University of Wisconsin, Madison*.

This research examines two hypotheses: (1) negatively charged ultrafiltration (UF) membranes can be used to manufacture whey protein and milk protein ingredients at enhanced flux, and (2) positively charged UF membranes can be used to make dairy protein fractions without the use of chromatography. Charged UF membranes are fabricated from normal uncharged UF membranes. The membrane charge combines with the membrane molecular weight cutoff to control whether or not proteins permeate or are retained by the membrane. At the neutral pH of milk and whey, the major proteins are charged negative and are rejected by a negatively charged UF membrane, allowing the use of wide pore size membranes that operate at high flux. Compared to current uncharged 10 kDa membranes, 100 to 300 kDa charged UF membranes have a 2−5× higher flux at the same or increased protein retention. We scaled up this technology 1400× from 50-1000 cm^2 flat sheet systems to 70,000 cm2 spiral wound systems. In the fractionation of proteins from milk or whey, chromatographic purity can be obtained without the use of chromatography. For example, by attaching a positive charge to a 300 kDa UF membrane, selectivity increased by a factor of 3 for fractionating bovine α-lactalbumin from β-lactoglobulin in milk-serum, compared to an unmodified membrane. Thus, like-sized proteins that differed only somewhat in isoelectric point and size and that were about 15-20 times smaller than the membrane molecular weight cutoff were fractionated using charged UF membranes.

Key Words: proteins, membranes, processing

0235 Emerging uses of new dairy ingredients in cheese, yogurt, beverages, and other products. L. Metzger*, *Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

The application of membrane based filtration processes to isolate and concentrate a variety of protein fractions present in milk has led to the development of a new generation of dairy protein based ingredients. These new protein based ingredients can be broadly classified into three groups: protein isolates containing milk proteins in the same ratio as found in milk, protein isolates fractionated into casein or whey protein; and isolates of individual milk proteins. Protein isolates containing milk proteins in the same ratio as milk have been further modified with enzyme treatments as well as modifications in the mineral content. These modifications have led to improved functionality in process cheese applications, protein bars and UHT processed beverages. Protein isolates that primarily con-

tain casein or whey protein created a new class of ingredients that take advantage of the unique properties of these two categories of protein. For example clear acidic beverages can be produced with whey protein isolates whereas heat stable high calcium meal replacement beverages can be made with casein isolates. Individual protein fractions such as β-casein or α-lactalbumin can also be isolated from milk using a combination of several filtration processes. These individual protein fractions have unique functional or nutritional properties and can be used in produce specialty products such as whipped toppings and beverages that target for stress reduction. The availability of filtration based processes to isolate a wide variety of protein based ingredients containing different fractions of milk proteins in conjunction with enzyme and mineral modification has provided product developers with a tool kit of new ingredients that can be utilized to modify the functionality of existing products as well as create new products.

Key Words: proteins, processing, filtration

0236 An update on carrier and delivery systems using casein micelles from bovine milk. F. Harte*, *University of Tennessee, Knoxville.*

Although the structure-function relationships of casein micelles remain under discussion, there is strong evidence suggesting that casein micelles in bovine milk are natural delivery systems not only for calcium but also for other biomacromolecules. Recent research and development in the structure-function properties of casein micelles has put emphasis on processing operations to improve the binding of low molecular weight hydrophobic molecules. Improved binding properties of casein micelles has been achieved by using enzymatic processes (e.g., transglutaminase) or through environmental modifications including pH, ionic strength, solvent properties, pressure, and shear. Researchers are starting to understand the mechanisms that trigger delivery (e.g., pH, enzymatic digestion) and the role that individual casein proteins play in binding and delivery of bioactives compounds important in the food (e.g., flavor and color delivery), and pharmaceutical (drug delivery) fields. This symposium is designed to update the academic and industry communities on current and future developments on the use of a natural nano-delivery system such as the casein micelles from bovine milk.

Key Words: casein, encapsulation, delivery

0237 Protein modification for health benefits. J. A. Lucey*, *Department of Food Science, University of Wisconsin, Madison.*

Proteins can be modified by the covalent attachment of polysaccharides utilizing the Maillard reaction. Recently, a novel method was developed at University of Wisconsin where conjugation was achieved in (liquid) batch processed mixtures. Protein denaturation/aggregation was inhibited by conducting the process in the presence of a crowding agent (such as dextran). A food-grade chromatography method was developed to purify these conjugates. Conjugated proteins produced by this method had excellent solubility and heat stability and did not exhibit browning or off-flavors. Using an in vitro infant digestion model (i.e., physiological amounts of enzymes that matched in vivo infant digestion rate of β-lactoglobulin), we also demonstrated that conjugated proteins were digested more slowly than unmodified proteins, which could help avoid the high titers of immunoreactive proteins for sensitive infants. We obtained blood sera from patients that had cow's milk protein allergy. The IgE binding capacity of conjugates was tested using the ImmunoCap method. Conjugation of allergenic protein significantly reduced IgE binding but we observed large individual (patient) differences for the level of reduction in IgE binding. Conjugation may be helpful in reducing the allergenicity of food proteins.

Key Words: Maillard, digestion, allergenicity

DAIRY FOODS: **TECHNICAL ORAL SESSION: CHEESE/YOGURT/ICE CREAM**

0238 Microbial production of conjugated linoleic acid: Development of functional dairy products-an overview. S. Abd El Ghani* and W. K. Bahgaat, *National Research Centre, Giza, Cairo, Egypt.*

Conjugated linoleic acid (CLA) is a generic name for a group of positional and geometric isomers of linoleic acid (LA), *cis*-9, *cis*-12, octadecadienoic acid) in which the double bonds are conjugated instead of the methylene interrupted configuration of LA. Of these isomers, *cis*-9, *trans*-11 and *trans*-10, *cis*-12 octadecadienoic acid (C 18: 2) has been reported as the most biologically active fatty acids that confer beneficial health effects on human. CLA isomers are found mostly in milk, dairy products and meat of ruminant animals. Interest in the beneficial health effects of CLA was reported over the years since the 1990s. Such benefits are: increased metabolic rate, decreased abdominal fat, enhanced muscle growth, lower cholesterol and triglycerides, lower insulin resistance, reduced risk of vascular diseases and anticarcinogenic effect. Microbiological production of CLA has recently attracted considerable research studies. The capability of several bacterial genera to convert linoleic acid in the forage of ruminants into CLA has been highlighted in many studies. The major CLA producing bacteria are lactic acid bacteria (LAB), bifidobacteria, and propionibacteria. Lactic acid bacteria (LAB) comprised 13 genera namely,*Carnobacterium*,*Enterococcus*, *Lactobacillus*, *Lactococcus*, *Lactosphaera*, *Leuconostoc*, *Melissococcus*, *Oenococcus*, *Pediococcus*, *Streptococcus*, *Tetragenococcus*, *Vagococcus* and *Weissella*among phylum Firmicutes. LAB were isolated from milk, fermented milk, cheese and other plant sources. They inhabit human and animal intestinal tracts and positively affect the health of the host. LAB are regarded as a unique group of bacteria having probiotic effect due to their capability to produce bioactive compounds such as peptides including antimicrobials, fatty acids, vitamins, and antioxidants. Probiotics refer to a live microbial feed or food supplement that beneficially affects the host by improving its intestinal microbial balance. LAB metabolites play a significant role in metabolism and detoxification of foreign substances and free radical entering the body of the host. Recently, manufacture of functional dairy products such as cheese and yogurt rich in CLA, using unique adjunct probiotics as vehicles to provide adequate dietary CLA for human consumption, has received considerable interest by dairy processors. The aim of the present overview was to highlight some aspects in the production of functional dairy products to satisfy modern consumer interest looking for their life betterment through increased tendency toward functional food consumption.

Key Words: microbial CLA, probiotic bacteria, functional foods, LAB

0239 Chemical and organoleptic characteristics of cheese from dairy cows supplemented with soya and partially hydrogenated vegetable oils. E. Vargas-Bello-Pérez*[1], G. Iñiguez-González[1], K. Fehrmann-Cartes[1], and P. C. Garnsworthy[2], *[1]Pontificia Universidad Católica de Chile, Santiago, Chile, [2]The University of Nottingham, Loughborough, United Kingdom.*

Lipid supplements have been used to improve the fatty acid profile of dairy products; however, little information is available concerning the effect of dietary vegetable oils on the sensorial properties of cow's milk cheese. The objective of the present study was to examine the effects of soya (SO) and partially hydrogenated vegetable (PHVO) oils supplementation in dairy cow diets on the chemical composition of milk and cheese and organoleptic characteristics of cheese. Nine multiparous Holstein cows averaging 169 ± 24 DIM (average ± SD) at the beginning of the study were used in a replicated (n = 3) 3 × 3 Latin square design that included three periods of 21 d. All cows received a basal diet formulated with a 56:44 forage:concentrate ratio. Dietary treatments consisted of the basal diet (C; no fat supplement), and fat-supplemented diets containing SO (unrefined oil; 500 g/d/cow) and PHVO (manufactured from palm oil; 500 g/d/cow). Individual milk samples were taken at 0700 h on Day 20 of each period. Milk collected on Day 21 from the same treatment and period across Latin squares was pooled and made into cheese. Three cheeses per treatment per period were allowed to mature for 14 d and analyzed for moisture, ash, fat and total protein contents. Sensory evaluation of cheeses was performed in relation to 16 attributes: appearance (color homogeneity and holes), odor (overall odor, ripe cheese odor and cow milk odor), flavor (salty, acid, bitter, overall flavor and ripe cheese flavor), and texture (sharpness, toughness, graininess, screeching, moisture and greasiness). Except for ash, milk composition was not affected by treatments. Cheese chemical composition was not affected by dietary treatments. Sensory attributes were not affected by treatments, however four principal components explained around 0.64 of the overall variance in the data. The outcome of this study showed that supplementing dairy cow diets with SO or PHVO do not have detrimental effect on the chemical composition of milk and cheese and the organoleptic characteristics of cheese. *This study was sponsored by a research grant from FONDECYT 11121142 (Fondo Nacional de Desarrollo Científico y Tecnológico, Chile).*

Key Words: cheese, milk, organoleptic characteristics

0240 Comparison of the effect of Holstein-Friesian and Jersey milk on Cheddar cheese production. J. H. Bland*, C. C. Fagan, and A. S. Grandison, *University of Reading, Reading, United Kingdom.*

The objective of this study was to compare the effect of using Holstein-Friesian or Jersey milk on the Cheddar cheese mak-

ing process, cheese composition and sensory quality. Cheddar cheese was produced using Jersey and Holstein Friesian milk and various blends ($n = 11$) in the University pilot plant (100L vat) each month over a year to take into account seasonal variation. A significant difference in actual yield and moisture adjusted yield (37% moisture) was found between the two breeds with Jersey milk yielding 34.6% and 40.9% more respectively ($P < 0.001$). The yield of whey for Jersey milk was significantly lower (−3.7%, $P < 0.001$), as was the yield of protein in whey (−13.5%, $P = 0.014$). However, concentrations of lactose and solids in whey for Jersey milk were higher (+3.6% and +3.8% respectively, $P < 0.001$) and no difference was detected in the yield of fat in whey. The recovery of both fat and protein in cheese was higher for Jersey by 22.9% ($P < 0.001$) and 11.9% ($P = 0.026$), respectively, compared to Holstein-Friesian. Cheese making time for Jersey milk was significantly higher (+13.1%, $P = 0.008$) even though coagulation time was significantly shorter (−44.5%, $P = 0.002$). The longer cheese making time was due to the increase in time required for acidity development, which has not been observed previously. In terms of cheese composition, Jersey milk produced cheese with higher levels of fat (+15.5%) and lower moisture content (−7.54%, $P < 0.001$). No differences in protein, pH and salt were observed. Jersey milk showed a higher suitability for cheese making with higher recovery of component and higher yield. The influence of seasonality on yield was studied and neither the actual yield nor moisture adjusted yield were significantly affected by season. Fat in whey was lowest in summer (−23.8%), while protein in whey was lowest in winter (−18.1%, $P < 0.05$). These changes in recoveries had, however, no significant effect on cheese composition. Results to date suggest that using Jersey milk to produce Cheddar cheese may be more efficient than using Holstein-Friesian. Differences in the fat and moisture content of the cheese could impact on the sensory quality of the cheese. Sensory analyses are still in progress and will include texture, color and standardized grading tests.

Key Words: Cheddar cheese, cheese yield, breed

0241 Adding citrate to ice cream mix for enhanced protein functionality.

A. Gilbert, J. Prost, and H. D. Goff*, *University of Guelph, Guelph, ON, Canada.*

High-pressure processing has been shown to greatly improve the structure and texture of ice cream by modifying casein micelles, the net effect of which is to enhance protein functionality through increased air adsorption and enhanced protein-protein interactions in the aqueous phase. The addition of citrate to milk also modifies casein micelles, enhancing soluble casein levels through the chelation of calcium from within the micelle. This has been shown to enhance foamability in skim milk. It has been documented that citrate will decrease fat partial coalescence in ice cream mix, through enhanced soluble protein adsorption to the fat globule. Given these established relationships, the effect of citrate addition to ice cream mix was re-examined to determine if advantage could be gained from enhanced soluble proteins at air interfaces or within the serum phase, to either provide enhanced structure and air bubble stability and/or enhanced mouthfeel and texture. In this study, citrate triphosphate/citric acid was added to a typical ice cream mix at 0.1M/kg milk solids-not-fat (SNF) or 0.2M/kg SNF, balanced to keep the pH at 6.8, in the presence of either 0.15% saturated or unsaturated monoglyceride. Ice cream mix was batch pasteurized and batch frozen. Analyses included fat droplet size, soluble protein and protein adsorption to fat droplets in the mix; and structural collapse during melting, fat destabilization and structural analyses by transmission electron microscopy in the ice cream. Results indicated that serum proteins were enhanced in the mix due to citrate addition. However structural collapse during melting was enhanced by citrate in the presence of either surfactant, due to reduced fat partial coalescence. Adsorbed protein levels to the fat droplet were reduced by the addition of citrate, but TEM analyses indicated that the proteins were more homogeneously distributed around the fat droplets in the mix and emulsifiers were less able to displace these proteins than they were native casein micelles. Thus the soluble caseins over-stabilized the emulsion by creating a more continuous thin layer around the fat globules, which prevented the formation of a partially coalesced fat globule network necessary for air stabilization in ice cream. Consequently, while the citrate did successfully modify the casein micelles by increasing soluble casein, it did not result in enhanced foamability or protein structure in the aqueous phase.

Key Words: casein, citrate

0242 The nutritional value of kishk: dried wheat fermented milk Egyptian native dairy food.

S. Abd El Ghani*[1] and W. K. Bahgaat[2], *[1]National Research Centre, Dairy Department, Giza, Cairo, Egypt, [2]National Research Centre, Giza, Cairo, Egypt.*

Kishk is dried wheat fermented milk mixture originated during Pharonic period since 3200 B.C. in Upper Egypt and continued until nowadays. It is considered a good source of carbohydrates, proteins, vitamins and minerals. Egyptian farmers prepared kishk as a home made product mainly for their consumption. However, considerable amounts of the product may be marketed to gain additional profit. The aim of this proposal was to evaluate the nutrition value of kishk. Therefore, gross composition and minerals content were determined. Quality and quantity of fatty acids as parameters of functionality were also analyzed. Forty kishk samples were procured from four provinces encoded as A, B, F, and G located in Upper Egypt (10 samples from each). Gross composition and minerals were examined according to (APHA, 2004). Moreover, quality and quantity of FAs methyl ester were pursued using

Agilent Technologies 6890 N GC/MS equipped with a flame ionization detector (FID) and a HP-5% Phenyl Methyl Silixane capillary column. Helium was used as a carrier gas. The oven temperature was 70°C with a 2 min. hold. Injector and detector temperatures were 250° and 280°C, respectively. FAMEs were identified by comparing its retention times with those of standard FAMEs mixture (Sigma, USA). Mean gross compositions were: moisture, 6.82, 7.24, 7.02 & 7.23; total solids, 93.18, 92.69, 92.98 & 92.77; and total carbohydrates, 65.43, 69.83, 73.09 & 69.43 g/100-g sample for A, B, F, and G kishk, respectively. Mean protein and fat contents were 18.84, 11.60, 11.87, 11.43; and 4.85, 3.21, 3.51 & 3.43 g/100 g dry matter in the same order, respectively. Po, K, Ca, Mg, Na, Fe, Mn, Zn and Cu were determined in varying concentrations. FA profile includes saturated, monounsaturated and polyunsaturated fatty acids from C10 to C21. Octadecadieonic and octadecatrienoic acids were detected in all kishk samples examined. However, Kishk A contained conjugated linoleic acid 10*t*,12*c*CLA. Perhaps this was the first report to document presence of beneficial CLA isomer in kishk. In conclusion, kishk is a very nutritive functional food containing carbohydrates, protein, fat and minerals. Moreover, occurrence of essential PUFA and CLA ensure its functionality for human health.

Key Words: kishk, CLA, functional food

0243 Bacterial community shifts in geriatric subjects in response to probiotic intervention revealed by high throughput DNA sequencing. G. H. Meletharayil[1], S. Senan[*2], P. Jashbhai[2], and C. G. Joshi[3], *[1]South Dakota State University, Brookings, [2]SMC College of Dairy Science, Anand Agricultural University, Anand, India, [3]Faculty of Veterinary Science, Anand Agricultural University, Anand, India*

Evidences on the association between bacterial shifts in human gut microbiota and disorders such as inflammatory bowel disease, diabetes and obesity are mounting. A comprehensive catalogue of gut microbiota is thus essential for personalized microbiome focused treatments. The microbiota of older people displays greater inter-individual variation than that of younger adults. Gastrointestinal disorders are a major cause of morbidity in the geriatric population. Probiotic interventions are known to have been shown to inñuence the composition of the intestinal microbiota in the geriatric. As most of the bacteria present in the gut are non culturable, we attempted to study the bacterial community structure of the geriatric gut using Ion torrent 16s rRNA sequencing. There remains considerable variability in response to probiotic intervention among subjects, hence we hypothesized that a signature gut metagenome could be the deciding biomarker for a successfully probiotic therapy. Among the 72 geriatric subjects who participated in the trial, we could identify 10 respondents who showed positive results in the primary outcome of cholesterol reduction and 10 who showed an increase in cholesterol with a decreasing lactobacilli population indicating non response to probiotic therapy. DNA from the fecal samples of these 20 respondents during baseline and end of feeding was analyzed. Amplicons from the hypervarialbe region of the 16S rRNA gene were generated and sequenced each on a 316 chip. Sequencing reads were clustered into operational taxonomic units described by community metrics and taxonomically classified. Reads per sample were clustered and studied for diversity and richness using MG-RAST. All the community members in our samples were from the domain bacteria. The most prevalent phyla in all samples were: *Firmicutes*, *Proeobacteria*, *Actinobacteria* and *Bacteroidetes,* with *Firmicutes* dominating in all samples. All the samples taken before treatment showed an abundance in *Blautia, Bifidobacterium, clostridium, Escherichia, Eubacterium, Fecalibacterium, Lactobacillus, Prevotella, Roseburia, Ruminococcus* and *Shigella*. It was strikingly evident that the non respondents harbored more *Shigella, Escherichia* and less *Runinococcus and Clostridium* (compared to positive respondents). *Lactobacilli and Prevotella* showed an increase in abundance values after probiotic treatment with a decrease in *Shigella, Ruminococcus, Bacillus* and *Bifidobacterium*. Such metagenomic analysis gives new insights into differences in response towards the same probiotic intervention due to host community profiles. Modulation of the community structure using probiotics can prove beneficial for geriatric intestinal well-being and cholesterol reduction.

Key Words: metagenome, probiotic, gut, geriatric

0244 Microbial population dynamics during aging of Cheddar cheese. B. Ganesan*, C. Brothersen, and D. J. McMahon, *Western Dairy Center, Utah State University, Logan.*

The dynamics of bacterial microflora changes in Cheddar cheese during ageing are largely unknown. Normally, the unwanted bacteria may die out and not survive through 60 d of storage of hard and semi-hard cheeses. However, the beneficial flavor producers such as starter and adjunct LAB may survive longer, as may some unwanted bacteria that have a competitive advantage due to shorter growth times and fewer nutritional requirements. Traditional estimates of bacterial populations depended on the ability to grow bacteria from cheese on specific media. While this is possible for the dominant bacterial species, it still does not define the breadth of the bacterial diversity adequately. A slightly broader picture of bacterial classes can be obtained by culture-independent techniques such as quantitative PCR analysis (qPCR) or phylogenetic microarrays, which are based on the levels of a gene of a particular organism estimated from DNA extracted from cheese. Challenges for DNA extraction such as interference from dairy components such as milk fat and protein in not allowing DNA separation and inability to lyse bacteria inside solid matrices have been tackled. We recently demonstrated that probiotic bacteria survive up to 6 mo of aging without

population reduction by measuring their levels using qPCR. However, the high number of simultaneous assays needed to define the diversity of bacteria and the necessity for prior knowledge of bacteria that may exist in cheese are both limitations for qPCR's or microarrays' applicability to cheese. Currently, the bacterial ecology research arena largely depends on sequencing of amplified 16s ribosomal gene segments at a very high throughput to characterize the populations in diverse extreme environments. This approach surmounts some of the drawbacks of array-based technologies where we only target short (11 probes that are each 20-25 bases long), discontinuous portions of the gene sequences, whereas with sequencing, we seek to identify bacteria based on 200 base-long continuous DNA sequences. Our objective was to study the changes in bacterial populations in cheese during manufacture and aging using the 16s pyrosequencing approach. While lactococci and lactobacilli were the dominant microbial species ($P < 0.05$) as expected, the presence of hitherto unknown species was also identified. This demonstrates that 16s DNA sequencing is a nonrestrictive approach towards surveying both known bacterial types and relatively unknown or previously unexpected cheese microflora members.

Key Words: Cheddar cheese, mciroflora, lactococcus, lactobacillus

---

0245 The influence of protein content of milk protein concentrates on the rheological properties of Greek style acid skim milk gels. G. H. Meletharayil[*1], H. A. Patel[2], and T. Huppertz[1], [1]*South Dakota State University, Brookings,* [2]*Dairy Science Department, South Dakota State University, Brookings.*

Greek-style yogurt (GSY) derives its popularity from combining nutritionally desired high protein content with a rich smooth texture. The straining process traditionally applied in GSY manufacture leads to large amounts of acid whey, which is an industrial concern in terms of further processing or disposal. An alternative process, preventing the creation of acid whey, is producing GSY from suitable milk protein ingredients for attaining the desired protein concentration. The aim of this study was to evaluate the rheological properties of Greek-style acid milk gels prepared from milk protein concentrates (MPCs) of varying protein content. MPC powders containing 50% (MPC50) to 85% (MPC85) protein were prepared by ultrafiltration and spray-drying from the same lot of milk. Solution (7.5% protein and 15% total solids) were prepared with these MPCs and lactose and pH was adjusted to pH 6.7 before preheating at 90°C for 10 min. Acid gels were prepared using glucono-δ-lactone to obtain final pH 4.6 after 4h of incubation at 30°C. Small amplitude oscillatory rheology (SAOR) measurements at 1% strain and a frequency of 1 Hz were performed for rheological characterization. pH was also monitored continuously during acidification. The pH of gelation (pH_G) and time of gelation were taken as the point where elastic modulus (G') was > 1 Pa. Statistical significance ($P < 0.05$) of effects observed was tested by ANOVA. The SAOR measurements showed a significant differences ($P < 0.05$) in G' of acid milk gels prepared from MPC60–MPC85 compared to gels prepared with MPC50. This was also reflected in a significant increase ($P < 0.005$) in the gelation pH and decrease in gelation time of acid gels. Such differences in the rheological properties, gelation time and gelation pH could be attributed to increased diafiltration during the preparation of MPC powders with higher protein contents, thereby reducing serum calcium and phosphate, increasing calcium ion activity and increasing the amount of denatured whey proteins associated with the casein micelles after heating. From these studies, it can be concluded that the use of MPC60−MPC85 in the manufacturing of GSY has a positive influence on G', gelation pH and gelation time. There was no significant differences in the rheological properties of gels manufactured with MPCs with > 60% protein. Hence, opportunities exist to produce GSY without acid whey as a by-product using MPC like MPC60 or MPC70, which are not prone to excessive solubility loss during storage.

Key Words: Greek style yogurt, milk protein concentrate. rheology

---

0246 Investigating the refrigerated performance shelf-life of high pressure treated, reduced sodium, low moisture part skim Mozzarella cheese. M. Ozturk[*1], S. Govindasamy-Lucey[2], Y. Lu[2], J. J. Jaeggi[2], M. E. Johnson[2], and J. A. Lucey[1,2], [1]*University of Wisconsin, Madison,* [2]*Wisconsin Center for Dairy Research, Madison.*

Physical, or performance, properties of low moisture part skim (LMPS) Mozzarella cheese are acceptable for only a relatively short time period (e.g., 4−6 wk) when stored under refrigeration conditions (4°C). During longer term storage (such as for exporting), cheese becomes soft and pasty due to physicochemical changes in para-casein matrix and ongoing protein breakdown, which results in poor shredding properties for unmelted cheese. We proposed that the performance and sensory properties of reduced Na LMPS-Mozzarella cheese could be extended by decreasing microbial and enzymatic activity with the application of high hydrostatic pressure (HHP). Camel chymosin was also used as a coagulant to help reduce cheese proteolysis. Average composition of reduced Na (1.0 ± 0.1% NaCl) LMPS-Mozzarella cheeses were 48.6 ± 0.7% moisture, 22.6 ± 0.4% fat, and 24.4 ± 0.7% protein. Cheeses were divided into three groups randomly after manufacture and stored at ~4°C. One group was non-pressurized and kept as control. Two wk after manufacture, the two groups of cheese samples were HHP-treated at 500 or 600 MPa for 3 min. Analysis was performed at 2, 4, 6, 8, 12, 16, and 20 wk after cheese manufacture. Texture profile analysis (TPA) and dynamic low-amplitude oscillatory rheology was used to

monitor cheese functionality during ripening. Quantitative descriptive analysis was conducted with 9 trained panelists to evaluate texture and flavor attributes using a 15 point scale. Pressure treatments at 500 and 600 MPa resulted in ~1 and ~2 log reduction in starter culture numbers at 2 wk of ripening, respectively, compared to control cheese. High pressure treatment of LMPS-Mozzarella cheese resulted in an initial (at 2 wk of ripening) increase ($P < 0.05$) in pH values; however, by 4 wk of ripening we did not observe any statistical difference in pH values between control and HHP-treated samples. At 2 wk of ripening, pressure treatment significantly ($P < 0.05$) decreased cheese hardness; however, by 16 wk the 600 MPa HHP-treated cheeses exhibited significantly ($P < 0.05$) higher TPA hardness values compared to control. Sensory panels also indicated that by 16 wk of age, the 600 MPa HHP-treated sample was significantly ($P < 0.05$) firmer than the control. Pizza panels indicated that 600 MPa HHP-treated cheese was significantly ($P < 0.05$) chewier and exhibited lower blister quantity and higher strand thickness compared to control. Pressures of 600 MPa produced LMPS-Mozzarella cheese with acceptable performance on pizza for a greatly extended refrigerated storage period.

Key Words: high pressure, reduced sodium, camel chymosin

0247 Impact of potassium substitution for sodium on pH, proteolysis, organic acids, and microbial populations during storage of Cheddar cheese.

D. J. McMahon*[1], C. J. Oberg[2,3], M. Drake[4], N. Farkye[5], L. V. Moyes[2], and M. R. Arnold[5], *[1]Western Dairy Center, Utah State University, Loga, [2]Department of Microbiology, Weber State University, Ogden, UT, [3]Western Dairy Center, Utah State University, Ogden, [4]Southeast Dairy Foods Research Center, North Carolina State University, Raleigh, [5]Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo.*

Sodium reduction in cheese can assist in reducing dietary Na intake, yet saltiness is an important aspect of cheese flavor. Our objective was to evaluate impact of substitution of KCl for NaCl on cheese pH, organic acid content, extent of proteolysis as water soluble nitrogen (WSN) and protein profiles using urea-PAGE in Cheddar cheese in relation to changes in starter lactic acid bacteria (LAB) and nonstarter LAB (NSLAB) during 9 mo storage. Cheddar cheeses with molar salt contents equivalent to 1.7% salt and Na replacement of 0% (control), 10%, 25%, 50% and 75% were manufactured as well as a low-salt (0.7% NaCl) negative control cheese. The 1.7%-salt cheeses had mean composition of 352 g/kg moisture, 259 g/kg protein, 17.5 g/kg salt (measured as Cl^-) and 50% fat on a dry basis. After salting there was a faster initial drop in pH in the 0.7%-salt cheese and cheeses with high levels of K substitution, and the pH remained lower throughout storage. No difference in intact casein levels or %WSN levels between the various cheeses was observed with %WSN increasing from 5% at d 1 to 25% after 9 mo. There was a greater decrease in intact α_{s1}-casein than β-casein, and a linear relationship was observed between the ratio of α_{s1}-casein (f121–199) to α_{s1}-casein and storage time suggesting this ratio could be used as an index of cheese ripening. Lactic acid content increased with K substitution and throughout storage. Propionic acid concentration in the cheese increased earlier in the control cheese than in cheeses with $\geq$ 25% K substitution or cheese with only 0.7% salt. This increase corresponded to the time after NSLAB numbers in the cheeses became dominant. There were few other obvious trends in organic acid concentration observed as a function of Na or K content. Typical changes in bacteria microflora occurred during storage with lactococci gradually decreasing and NSLAB increasing. Lowering the Na content, even with K replacement, extended crossover time when NSLAB became the dominant microflora from 4.5 mo to 5.2, 6.0, 6.1 and 6.2 mo for cheeses with 10%, 25%, 50% and 75% K substitution. This was, however, still shorter than the 7.3 mo for the low-salt cheese. By 9 mo, NSLAB levels in all cheeses had increased from initial levels of $\leq 10^2$ to ~10^6 CFU/g. Lactococci remained at 10^6CFU/g in the low-salt cheese even after 9 mo storage.

Key Words: cheese, sodium, potassium

DAIRY FOODS SYMPOSIUM: PROTEIN FUNCTIONALITY IN CHEESE SYSTEMS: NATURAL, PROCESS CHEESE AND ANALOGS

0248 Commercial and functional considerations when formulating foods with dairy proteins. T. McCarthy*, *Schreiber Foods, Green Bay, WI.*

Global milk production is estimated at 1600 bn lbs/yr. and cheese production at 45 bn lbs/yr. The dairy industry is among the most highly regulated when it comes to international trade and only about 5% of production is traded internationally. The greatest surpluses of milk being found in New Zealand, US, Germany, France, Australia and Ireland, whereas the greatest deficits are in China, Italy, the Russian Federation, Mexico, Algeria and Indonesia. This presentation will explore some of the commercial and technical challenges in moving dairy proteins around the globe and formulating them into cheese and related products

Key Words: milk production, cheese production, markets

0249 A model for the formation of the aggregated network in process cheese products that can be used to predict functional properties. L. Metzger*, *Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Process cheese products are produced by mixing and heating natural cheese and other dairy and non-dairy ingredient in the presence of emulsifying salts. It is well established that during manufacture of process cheese, the para-casein network in natural cheese is modified as a result of calcium chelation by emulsifying salts. This modification results in an increase in the emulsion capacity of the casein and gives process cheese its unique functional characteristics. Extensive research on process cheese has been conducted and the critical formulation parameters (composition, intact casein, calcium content, pH, type and amount of emulsifying salt) and critical manufacturing parameters (mixing speed, cooking temperature, cooking time and cooling rate) have been identified. Although we know these parameters are important, a model that links these parameters to the functional properties of process cheese has not been developed. The objective of this work is to propose a theoretical model to predict the impact of formulation and manufacturing parameters on the functionality of process cheese. The proposed model divides process cheese manufacture into four stages: 1) para-casein network de-aggregation; 2) para casein hydration and induction of casein-fat and casein-casein interactions; 3) casein re-aggregation and gelation; and 4) re-orientation of the gelled network. The theoretical impact of critical formulation and manufacturing parameters on each stage of the model and their relation to functional properties are also proposed.

Key Words: cheese, models, casein

0250 Autocatalytic multistage gel formation reaction in dairy based systems in relation to compositional factors. U. Kulozik*, *Technische Universität München, Freising-Weihenstephan, Germany*.

A multistage structure formation reaction is described in this paper that seems to be typical for the gel formation process in protein model system similar to products such as fresh cheese or processed cheese. Therefore, it was the objective of this study to identify and to assess the influencing factors driving the reaction. The effect of the fat and protein content, rework as well as the fat globule size influenced by an upstream treatment were studied in this work to develop a deeper understanding of the complex reactions taking place in such systems, where the underlying reaction mechanisms are insufficiently understood so far. It is shown that a fat level of 15-20% is required for the multistage structure formation course to occur. By means of an upstream homogenization of the fat phase and with an increasing protein content, the structure formation can be accelerated. It can be concluded that two parallel or partially sequential reactions seem to take place, inducing the formation of a finely dispersed emulsion as well as a protein network in the continuous phase, the latter one being sourced from proteins at the emulsion droplet interfaces. Compositional factors including the addition of rework affect the structure formation process, rework probably acting as a starter in an autocatalytic reaction.

Key Words: gel, protein, fat

0251 Protein functionality in processed cheese—Fundamental principles and practical observations. D. C. Reid*, *Fonterra Research and Development Centre, Palmerston North, New Zealand.*

Functionality of the protein in the raw materials determines the outcome of processed cheese manufacture. However, making processed cheese is fundamentally an exercise in cost optimization. The biggest cost is the young cheese. This provides unproteolysed casein, sometimes known as intact casein or functional protein, that will form the structural backbone of the processed cheese. Innovation around functional protein is often hindered by cost, regulation or IP. One concept that is often overlooked by manufacturers is optimization of functional protein. Optimizing and standardizing the functional protein not only minimizes the cost of the formulation but increases product quality, increases throughput and reduces rework generation. The challenge is that natural cheese is inherently variable due to proteolysis. Standardization requires measurement of

the functional protein in cheese. There are several approaches to measuring functional protein. Graders can gauge the body of cheese using finger and thumb. Others map the composition of the cheese against its history and predict the maturity. Wet methods are available such as relative casein content or water soluble nitrogen. Gold Peg markets Caseus Pro—a package that combines an NIR-based measurement system with optimization software. Fonterra has been working on a new method that uses viscosity to predict functional protein. To simplify standardization, manufacturers have developed ingredients that are slower to ripen or are more consistent sources of functional protein. One approach is to slow maturation of cheese while another is to use dry proteins. Using powders brings some challenges—not the least of which is hydration in a competitive and moisture-constrained environment. The problem is exacerbated by short processing times in cookers. MPCs have been developed with improved hydration characteristics that help alleviate this problem. Manufacturers have also looked at ways to increase the functional protein value for an ingredient beyond its casein content, for example functionalizing the whey protein component. Fonterra developed an MPC that delivers the same body to processed cheese as rennet casein, despite 20% of the protein being whey. An alternative approach is to functionalize the whey protein during manufacture of the processed cheese. In the future, optimum levels of functional protein could be totally redefined if work with casein fractions comes to fruition. Ingredients enriched in a_s–casein could deliver significantly more body to processed cheese without compromising other properties.

Key Words: intact casein, functional protein, processed cheese

0252 Impact of emulsifying salts on milk proteins and process cheese properties. J. A. Lucey*, *University of Wisconsin, Madison.*

Emulsifying salts, like citrate and phosphates, are widely used to modify the properties of caseins via a range of chemical and physical reactions. During the manufacture of process cheese, emulsifying salts have the ability to influence several critical events, such as Ca^{2+} binding (including complex formation), pH adjustment, casein dispersion (or crosslinking), fat emulsification, and structure formation. The impact of single emulsifying salts on casein properties and process cheese functionality has been studied. However, in many cases confounding effects like pH changes due to variation in the amount/type of emulsifying salt were not addressed in the experimental approach. Trisodium citrate and disodium phosphate are widely used to make many process cheese products whereas pyrophosphates are used for restricted melt applications. Pyrophosphates are very efficient at causing an initial casein dispersion of cheese, but during the heating phase they can cross-link these dispersed caseins to greatly increase viscosity (creaming). Mixtures of emulsifying salts alter casein properties and process cheese functionality in a complex fashion depending on the proportion, concentration and type of emulsifying salts present in these mixtures.

Key Words: processed cheese, pyropshosphates, salts

DAIRY FOODS SYMPOSIUM: MILK PROTEIN-HYDROCOLLOID INTERACTIONS: RECENT IMPACTS

0253 Exopolysaccharides from lactic acid bacteria—A world of opportunities. A. Hassan*, *South Dakota State University, Brookings*.

Exopolysaccharides (EPS) are polysaccharides secreted outside the cell wall of microorganisms. Exopolysaccharide-producing lactic acid bacteria are used to modify the textural and functional properties of fermented milk. The selection criteria of EPS-producing cultures depend on the desired physical properties of the fermented product. Exopolysaccharides provide functions that also benefit reduced-fat cheeses. They bind water and increase the moisture in the nonfat portion, reduce rigidity, and increase viscosity of the serum phase. Whey, the cheese byproduct, is concentrated or fractionated by membrane separation, and dried to produce a variety of products. The residual EPS in cheese whey have been demonstrated to enhance the functional properties of whey protein concentrate. On the other hand, application of EPS-producing cultures in cheese making may impact biofouling of whey filtration membranes. Exopolysaccharide can either enhance or prevent biofilm formation, depending on their characteristics and interaction with the membrane surface. Fermented milks made with some EPS-producing strains have also shown chemopreventive effects against azoxymethane-induced tumors in rats. In conclusion, EPS from lactic acid bacteria can improve body and texture of dairy products and modify functionality of whey protein concentrates. As functional foods are gaining popularity, EPS as natural chemopreventive agents become an attractive choice.

Key Words: lactic acid bacteria, exopolysaccharides, functionality, dairy

0254 A tale of in-body magnetic resonance imaging of foods and gut feelings. L. Marciani*, *University of Nottingham, Nottingham, United Kingdom.*

Assessment of the behavior and transit of food materials in the human gastrointestinal (GI) tract adds value when manipulating food design and improves the understanding of satiety mechanisms. Previous methods to assess the macroscopic, physiological impact of foods in the GI tract were invasive, used ionizing radiation and had a number of other limitations. Magnetic resonance imaging (MRI) is a non-invasive, high resolution, dynamic imaging technique that is developing rapidly in this field. MRI can provide in-body imaging of food materials and assess gastric emptying, intestinal fluid volumes and the colonic response in combination with other physiological and behavioral techniques. This paper presents an overview of the technique with specific examples from human healthy volunteers' studies using fat emulsions, hydrocolloids, milk-based products, poorly digested carbohydrates and dietary fiber supplements.

Key Words: MRI, in vivo, human

0255 Functionality and structure of hydrocolloids in dairy foods. H. D. Goff*, *University of Guelph, Guelph, ON, Canada.*

Stabilizing gums, e.g., guar or cellulose gum or modified starches, have been used in dairy products such as yogurts and ice cream mix for many years, for thickening and enhanced eating pleasure and for enhanced stability and shelf-life. Some unique gums rely on specific milk protein interactions, e.g., carrageenan in chocolate milk or pectin in acidified milk beverages. Many of the polysaccharide stabilizers are incompatible with milk proteins, particularly casein micelles, and carrageenan plays a unique role in inhibiting phase separation. While this body of knowledge regarding "traditional" usage of hydrocolloids is well established, there has been much research to expand the understanding and scope of hydrocolloid utilization in dairy products. Novel dairy products have been introduced into the markets, an example could be squeezable-tube products, and these products create unique demands for physical functionality, which leads to creative product development in the application of hydrocolloids. Novel hydrocolloids, particularly from agricultural by-products such as flaxseed gum or soy soluble polysaccharide, are continually being examined for potential applications. Hydrocolloids have been shown to form complexes with both casein and whey proteins under certain conditions of processing, and these complexes offer potential for new structures in dairy products. Hydrocolloid addition is also being viewed for health benefits, as most are soluble dietary fibers. Hydrocolloids in dairy products offering enhanced glycemic index reduction is an area of exciting research and product development potential, particularly in the light of rapidly rising Type II diabetes rates in the population. Hydrocolloids such as sodium alginate can also help to confer post-prandial satiety, which may present another opportunity for dairy product positioning in the context of rising rates of obesity in the population. Given this growing demand for more functional and nutritional foods, it is critical that opportunities from within the hydrocolloids sector continue to be exploited in dairy products.

Key Words: stabilizers, functionality, dietary fiber

0256 Impact of starch on milk protein functionality in food applications. M. E. Yildiz*, *Ingredion, Bridgewater, NJ*.

Dairy foods are increasingly formulated with several functional ingredients such as milk proteins, starch and hydrocolloids. Functional ingredients provide several key properties to dairy

foods, including process robustness, texture, eating quality and shelf stability. Starch has been a very important component of dairy foods including yogurt, cheese and dairy beverages. To formulate consumer winning dairy products, it is very important to understand the mechanisms and interactions as well as true synergies between functional ingredients. However, both starch and milk proteins are very complex and shedding light to the precise nature of the starch-milk protein interactions requires fundamental studies focusing on physic-chemical properties of starch and milk proteins, starch base and granular nature (intact vs. fragmented/solubilized), starch surface properties (protein content/location, etc.) to list the few key points. Additionally, it is very important to understand the processing parameters such as temperature and pressure on starch-protein interactions. In this presentation we will review the current understanding of starch-protein interactions. We will discuss the impact of starch base (waxy corn, tapioca and dent corn) on bulk properties of fermented dairy products, and relate the starch gelatinization temperature, granular integrity, process temperature and pressure on starch protein interactions and bulk properties of fermented dairy products. We will also discuss the instrumental and sensory measurements of observed behavior and propose mechanisms of starch impact on protein functionality.

Key Words: starch, dairy, yogurt, processing, protein, interactions

DAIRY FOODS: **TECHNICAL ORAL SESSION: ANALYTICAL/PROCESSING**

0257 Modification of the functionality of micellar casein concentrates by changing the structure of casein micelles using high pressure processing. C. I. Moraru[*1], M. Walkling-Ribeiro[1], I. Aprodu[2], and M. V. Karwe[3], *[1]Cornell University, Ithaca, NY, [2]Dunarea de Jos University, Galati, Romania, [3]Rutgers University, New Brunswick, NJ.*

Growing interest in food products with high protein content has led to an increased demand for protein ingredients. Micellar casein concentrate (MCC) is an emerging dairy ingredient obtained by membrane filtration. MCC is characterized by a bland, clean taste and has potential for use in applications ranging from beverage fortification to manufacturing of soft gel products. High pressure processing (HPP) is a physical process that can be used to induce controlled changes in the structure of casein micelles and thus modify the properties and functionality of MCC. In this study, MCC suspensions with 2.5, 5, 7.5, and 10% protein content were processed at 150, 250, 350, and 450 MPa for 15 min, at cold (4-24°C) and warm (53−60°C) temperatures. Particle size, turbidity, and viscosity were assessed directly after HPP and during refrigerated storage. The study was replicated and data analyzed statistically. Under cold HPP conditions, casein micelle size decreased significantly with increasing pressure ($P < 0.05$) due to disruption of the casein micelle structure. The average micelle diameters ranged from 192 to 81 nm for 2.5% MCC and from 216 to 173 nm for 10% MCC after treatment at 150 and 450 MPa, respectively. These effects were concentration dependent, indicated by increased micelle size and turbidity in samples with higher casein concentration ($P < 0.05$). By contrast, HPP under warm conditions led to an increase in particle size, indicating a re-association of caseins. The increase in particle size was concentration dependent: for 2.5% MCC treated under warm conditions, particle sizes ranged between 175 and 216 nm, while for 10% MCC they ranged between 192 and 778 nm when treating the samples at 150 and 350 MPa, respectively. Particle size and turbidity did not change significantly during storage at 4°C of cold HPP treated samples, whereas samples treated under warm HPP conditions were less stable. Interestingly, cold HPP treated 10% MCC formed a weak gel above 250 MPa. The present study suggests that HPP is effective for modifying MCC functionality by inducing structural changes of the casein micelles. Most notably, cold HPP can induce shelf-stable size reduction of casein micelles and improved transparency at low casein concentrations, and gel-like structure at high casein concentrations. This data can be used as a basis for developing new food applications involving HPP treatment of MCC.

Key Words: micellar casein concentrate (MCC), high pressure processing (HPP), nonthermal processing

0258 Microfiltration of milk protein concentrate using ceramic membranes: Determination of limiting flux and serum protein removal at 8, 9, or 10% protein in the recirculation loop. E. E. Hurt[*1,2], M. C. Adams[1,2], and D. M. Barbano[1,2], *[1]Cornell University, Ithaca, NY, [2]Northeast Dairy Foods Research Center, Ithaca, NY.*

In designing a MF process to separate SP. from casein, both the amount of SP. removed and flux are likely to be a function of the protein concentration in the recirculation loop (RL). Our objective was to determine the limiting flux and SP. removal at 8, 9 or 10% protein in the RL using 0.1µm ceramic graded permeability membranes with 4 mm channel diameters. The MF feed was an 85% milk protein concentrate diluted to an average protein of 5.5 ± 0.1%. The concentration factor was chosen to achieve 8, 9 or 10% protein in the RL. The MF was operated with a longitudinal pressure drop of 220 kPa at 50°C. The MF was started at an average flux of 55 ± 2kg/m^2 per h and flushed until the protein concentration in the RL was near the target. Once the target protein was reached, the MF was run at 55 kg/m^2 per h for 1h, the flux was then increased in steps and run for 1h at each new flux. The flux was increased until the new flux could not be maintained. The limiting flux was the last flux the MF could run at for 1h. Transmembrane pressure averaged 66 kPa at 55kg/m^2 per h and 190 kPa at the limiting flux and transmembrane pressure did not vary with protein concentration in the RL ($P > 0.05$). Retentates and permeates at each flux were analyzed for true protein (TP) using Kjeldahl methods. SP. removal as a percentage of theoretical removal (SPR) was calculated as TP in the permeate divided by SP. in the permeate portion of the feed. TP concentrations in the RL averaged: 8.2 ± 0.1, 9.2 ± 0.1 and 10.1 ± 0.2%. Cross-flow velocities depended on the protein concentration in the RL ($P < 0.05$) and were: 7.09, 7.01 and 6.90m/s at 8, 9, and 10% protein, respectively. Limiting fluxes decreased with increasing protein in the RL ($P < 0.05$) and were: 154 ± 1, 133 ± 1 and 117 ± 6kg/m^2 per h. SPR was not a function of the protein concentration in the RL ($P > 0.05$), but SPR decreased ($P < 0.05$) from 80% at 55 kg/m^2 per h to 75% at the limiting flux, indicating fouling may have impacted passage of SP. through the membrane. The protein concentration in the RL that the MF operated at had an impact on the limiting flux, but not passage of SP. However, as flux increased to the limiting flux, there was reduced SP. passage through the membrane, likely caused by membrane fouling.

Key Words: limiting flux, microfiltration, milk protein concentrate

0259 Impact of membrane channel diameter on limiting flux and serum protein removal during milk protein concentrate microfiltration. M. C. Adams*, E. E. Hurt, and D. M. Barbano, *Cornell University, Ithaca, NY.*

The design of a ceramic microfiltration membrane will impact its ability to remove serum proteins (SP) from milk. Our objectives were to determine the limiting fluxes and SP. removal as a percentage of theoretical (SPR) of 0.1 μm ceramic graded permeability membranes with either 3 mm or 4 mm diameter flow channels. A microfiltration process was fed with an 85% milk protein concentrate that had been standardized to 5.62 ± 0.06% protein with reverse osmosis water. Retentate and permeate were continuously recycled to the feed tank. Limiting fluxes were determined by incrementally increasing flux once per h from 55 kg/m^2 per h until flux became independent of transmembrane pressure. Experiments were replicated 3 times and the Proc GLM procedure of SAS was used for statistical analysis. Temperature, longitudinal pressure drop (ΔP), and protein concentration in the retentate recirculation loop were maintained at 50°C, 220 kPa, and 9.16 ± 0.08%, respectively. Because the graded permeability membranes are designed to operate at ΔP between 200 and 220 kPa, ΔP was controlled. Consequently, 3mm cross-flow velocity was lower ($P < 0.001$) than 4 mm cross-flow velocity (5.48 vs. 7.00 m/s). In both membranes, cross-flow velocity decreased ($P < 0.05$) between the initial and limiting fluxes. The 3 mm membrane limiting flux was lower ($P < 0.001$) than the 4 mm membrane limiting flux (105 vs. 133 kg/m^2 per h). SPR was calculated by dividing true protein in the permeate by SP. in the permeate portion of the feed to describe the ease of SP. passage through the membrane. In the 4 mm membrane, SPR decreased ($P = 0.03$) between the initial and limiting fluxes due to fouling. No decrease in SPR was detected ($P > 0.10$) in the 3 mm membrane between the initial and limiting fluxes. Experimental variation and the fact that 3mm SPR was lower ($P = 0.07$) than 4 mm SPR at the initial flux contributed to this finding. Despite a lower limiting flux and a higher rejection of SP, the modular SP. removal rate (kg SP. removed/module per h) of 3mm membranes would be higher than that of 4mm membranes because 46% more membrane surface area can be housed in a 3mm membrane module. This relationship could change if the retentate protein concentration were different. A processor should consider both the increased performance of the 4 mm membrane and the reduced cost per module of the 3 mm membrane before proceeding with a purchasing decision.

Key Words: microfiltration, serum protein removal, limiting flux

0260 Using membrane filtration techniques to fractionate acid whey into value added ingredients. B. Chen*, K. E. Smith, J. A. Lucey, R. Kalscheuer, and M. Molitor, *University of Wisconsin, Madison.*

There has been a huge expansion in acid whey production due to the rapid growth in Greek yogurt manufacture; therefore it is critical to find an environmentally friendly and economically feasible way to process acid whey. Membrane filtration techniques have been used for many decades in the dairy industry to fractionate components into different streams. The objective of this study was to determine the suitability of nanofiltration (NF) membranes for fractionating acid whey into value added streams that could potentially be used in food products. Because of the relatively low protein content of Greek yogurt acid whey, our research focused on possible value added components in the UF permeate of acid whey. Potential end products include lactose, lactic acid, dairy minerals, peptides and oligosaccharides. Our initial focus was on reducing the calcium and lactic acid content of this UF permeate. Approximately 1000 L of acid whey was obtained from a Greek yogurt manufacturer for each trial. A 10,000 daltons UF membrane was used to fractionate the protein. The UF permeate was then processed by one of two different NF membranes. An experimental NF membrane was evaluated for divalent ion permeation and compared to a control NF membrane. Permeates were concentrated to 1× and 2×, and sampled at 1380, 2760, and 4140 kPa processing pressures, and at temperatures 4, 21, 43, and 54°C. Flux also was recorded. Total solids, lactose, galactose, lactic acid and calcium were determined. Higher temperatures and higher pressures yielded higher rates of component permeation for each membrane. The experimental NF membrane had higher permeation on all analyzed components compared to control NF membrane. Lactose and calcium were permeated on the experimental NF membrane, in contrast to the control NF membrane. By utilizing various membranes with very different permeation properties, fractionated products could potentially be achieved. We are exploring other membranes to evaluate the potential creation of purified value added fractions from acid whey.

Key Words: acid whey, membrane processing, nanofiltration

0261 Polymerization of lactose to polylactose by twin-screw extrusion. T. C. Schoenfuss*, C. E. Tyl, and E. M. Reid, *University of Minnesota, St. Paul.*

Our objective is to create a value-added product from lactose. We successfully polymerized lactose into polylactose, a mixture of oligosaccharides, via extrusion. Previously, we evaluated one extruder feed rate and two citric acid catalyst concentrations. We hypothesized that a lower residence time in the extruder would achieve similar fiber contents while reducing caramelization side-reactions. The objectives of this project

were to further evaluate acid catalyst concentrations and extruder conditions on fiber yield. We hypothesized that concentrations above 2% citric acid would yield more fiber. We tested the hypotheses by extruding lactose with 2, 4, and 6% citric acid and 20% glucose. Extruder feed rate was at 15 and 30kg/hour for all formulas. Product was extruded on a Buhler twin-screw 44 mm extruder and the screw configuration, rpms and temperature profile were kept constant between runs. Process (temperature, motor torque and specific mechanical energy (SME)) and product responses (color, dietary fiber, degree of polymerization (DP), and residual lactose) were measured in response to the formula and process changes. Color and brown pigments were determined by HunterLab (10° observer and D65 illuminant) and spectrophotometry (420 nm) of an aqueous extrudate solution. Liquid chromatography (LC)-evaporative light scattering detector analysis was used to quantify dietary fiber by the AOAC integrated dietary fiber method (2009.01). DP was determined by LC-Mass Spectrometry with positive electrospray ionization. Residual lactose was quantified enzymatically using a commercial test kit. The higher feed rate resulted in lower SME and higher motor torque, indicating the material had higher viscosity. The higher feed rate resulted in less brown pigmentation, lower b-values, higher *L*-values and more residual lactose and glucose. These results indicate that at the lower feed rate more lactose and glucose were converted to caramelization products. Citric acid concentration effects were more pronounced at the lower feed rate with higher concentrations leading to more browning and higher *b*-values. Residual lactose decreased with higher citric acid concentrations. Dietary fiber profiles were similar between formulas with DPs of generated oligosaccharides ranging from 3–5. In contrast to the higher feed rate, the HPLC profiles at the lower feed rate of 6% citric acid formulas had lower oligomer peak areas when compared to 2% citric acid. This was not the case for the high feed rate. Overall, the higher feed rate resulted in more favorable processing parameters, less caramelization, and maintained dietary fiber concentrations.

Key Words: extrusion, lactose, oligosaccharides, dietary fiber

---

0262 A proficiency test system to improve laboratory and method performance and produce reference values for component calibration samples for infrared milk analysis.

D. M. Barbano*[1,2], K. L. Wojciechowski[1,2], and C. Melilli[1,2], [1]*Cornell University, Ithaca, NY,* [2]*Northeast Dairy Foods Research Center, Ithaca, NY.*

Our objectives were: 1) utilize data from 10 to 12 laboratories running duplicate chemical analyses of 14 milk samples with an orthogonal matrix of fat, protein, and lactose concentration to calculate all-lab mean reference values for fat, protein, lactose, and total solids for each sample, 2) monitor the analytical performance of the reference chemical analysis methods, and 3) evaluate and improve the analytical performance of individual laboratories conducting chemical reference methods. The chemical reference methods used were Mojonnier ether extraction for fat, Kjeldahl for true protein, spectrophotometric enzymatic assay for anhydrous lactose, and forced air oven drying for total solids. Statistical outliers were removed and all-lab mean reference values and within and between laboratory variation (i.e., Sr and SR) were calculated for each sample for each component. The set of 14 milk samples with all lab mean reference values was used to run diagnostic performance evaluation and calibrate infrared milk analyzers. The proficiency of each lab was evaluated utilizing Z-scores, Pareto diagrams, and Euclidian distance (ED) plots. Performance of the ether extraction, Kjeldahl true protein, and oven drying total solids methods were improved ($P < 0.05$) due to the improved ability to identify and trouble shoot between laboratory differences in results when using the modified milks with the orthogonal design of variation in composition. Residual plots of an individual lab's results minus the all-lab mean for each sample provides an evaluation of individual lab bias and proportional deviations from the all-lab mean over a wide range of concentration of each component. Residual and ED plots allow an experienced evaluator to identify the sources of poor performance by an individual lab and recommend corrective measures. Over a period of years, the feedback and method performance trouble shooting based on residual and ED plots has improved within (Sr) and between (SR) laboratory and method performance.

Key Words: proficiency testing, infrared milk analysis, method performance

---

0263 A relatively rapid method for the estimation of the amount of exopolysaccharide produced by lactic acid bacteria during milk fermentation.

S. N. Khanal*[1] and J. A. Lucey[2,3], [1]*Department of Food Science, University of Wisconsin, Madison,* [2]*University of Wisconsin, Madison,* [3]*Wisconsin Center for Dairy Research, Madison*.

The available methods for estimation of exopolysaccharide (EPS) produced in fermented milks are very lengthy (several days). A relatively shorter ($\leq$ 1 d) method has been investigated for the estimation of EPS produced during fermentation of non-fat milk at 40°C by two strains of *Streptococcus thermophilus* (St–143 and St–10255y). Milk samples were analyzed for EPS concentration every 30 min over a fermentation period of 300 min (final pH 4.6). Samples with pH > 5 were adjusted to pH ~5 before protein was removed by heat and acid precipitation. Excess ethanol was added to the neutralized supernatant and precipitated at -20°C for 3 h. The pellet was dissolved in water at 55°C and centrifuged before residual lactose in the supernatant was removed by repeated precipitation by ethanol. The EPS concentration in the final pellet was estimated by the phenol sulfuric acid method. In milk fermented by *S. thermophilus* St–143, the EPS content significantly increased

($P < 0.05$) from 24 to 68 mg/L during the fermentation period from 150 to 300 min. EPS concentration in samples fermented with *S. thermophilus* St–10255y also significantly varied ($P < 0.05$) from 16 to 52 mg/L during a similar fermentation period. Interestingly, both of the strains appeared to start producing significant amounts of EPS after 150 min of fermentation time, which corresponded to pH ~5.2 and was close to when milk gelation occurred. Thereafter, the EPS concentration continued to increase up to pH ~4.6 (end of fermentation). The total amounts of EPS obtained were comparable to the previously reported results in milks fermented by similar bacterial strains. To explore the recovery of EPS by this method, we added different concentrations of dextran (mol wt: 2×10^6 Da) to milk and found that up to ~70% of the added dextran could be recovered, suggesting that this method was reasonably effective in extracting most of the EPS produced in fermented milk.

Key Words: exopolysaccharides, yogurt, fermented milk

0264 Raw milk quality in the dairy industry: Compositional changes correlated with somatic cell counts. C. R. T. Júnior[1], G. C. Ribeiro[2], R. M. Longo[2], M. C. P. P. Oliveira[2], L. M. Fonseca[*3], M. O. Leite[2], and M. P. Cerqueira[2], *[1]Ministry of Agriculture, Poços de Caldas, Brazil, [2]Universidade Federal de Minas Gerais (School of Veterinary Medicine), Belo Horizonte, Brazil, [3]University of Wisconsin, Madison*.

The aim of this study was to evaluate the seasonal correlation of somatic cell count (SCC) and composition of raw milk. A total of 287,000 samples of raw milk were analyzed during twelve consecutive months by the UFMG Milk Quality Laboratory (UFMG/Veterinary School; LabUFMG) for composition and SCC. The data were analyzed using descriptive statistics, according to the months of production and SCC ranges: Range 1: SCC $\leq$ 200,000 cells/mL; 2: SCC from 201,000 to 400,000 cells/ml; 3: SCC from 401,000 to 750,000 cells/ml, and 4: SCC > 750,000 cells/mL. The least significant difference between treatments was evaluated using Tukey's test, with significance level of 5% in a randomized complete block design. SCC indexes (SCC Log/mL) were higher from January to April and from October to December, with peaks of SCC in February and March (rainy season). The lowest results for SCC ($p < 0.05$) were observed from May to September (dry season), with lower average results during the month of May. The highest fat, protein and total solids contents, and the lowest SCC were found during the dry season ($p < 0.05$), while the lowest concentrations were observed during the rainy season (spring and summer). The increase in SCC was correlated with reduction in lactose, solids, nonfat and protein concentrations ($p < 0.05$), except for SCC range higher than 750,000 cells/mL. In this range, protein content was higher if compared to the levels found in SCC range of 401,000 to 750,000 cells/mL ($p < 0.05$), but similar to the levels found in milk with SCC range from 201,000 to 400,000 ($p > 0.05$). This fact may be related to a reduction in milk secretion, and passage of serum proteins into the milk due to a more pronounced inflammatory process. Fat contents were higher ($p < 0.05$) for elevated SCC, which may be linked to lower milk secretion because of mastitis.

Key Words: milk quality, composition, somatic cells

0265 The effect of immunoglobulins and somatic cells on the gravity separation of fat, bacteria, and spores in pasteurized whole milk. D. M. Barbano[*1,2] and S. R. Geer[1,2], *[1]Northeast Dairy Foods Research Center, Ithaca, NY, [2]Cornell University, Ithaca, NY.*

Our objective was to determine the role that Ig and somatic cells (SC) play in the gravity separation of milk. There were 9 treatments: (1) low temperature pasteurized (LTP) (72°C for 17.31s) whole milk, (2) LTP (72°C for 17.31s) whole milk with added bacteria and spores, (3) recombined LTP (72°C for 17.31s) whole milk with added bacteria and spores, (4) high temperature pasteurized (HTP) (76°C for 7 min) whole milk with added bacteria and spores, (5) HTP (76°C for 7 min) whole milk with added bacteria and spores and added colostrum, (6) HTP (76°C for 7 min) centrifugal-separated gravity-separated (CS GS) skim milk with HTP (76°C for 7 min) low SC cream with added bacteria and spores, (7) HTP (76°C for 7 min) CS GS skim milk with HTP (76°C for 7 min) high SC cream with added bacteria and spores, (8) HTP (76°C for 7 min) CS GS skim milk with HTP (76°C for 7 min) low SC cream with added bacteria and spores and added colostrum, and (9) HTP (76°C for 7 min) CS GS skim milk with HTP (76°C for 7 min) high SC cream with added bacteria and spores and added colostrum. The milks in 9 treatments were gravity separated at 4°C for 23 h. Five fractions were collected by weight from each of the columns treatments starting from the bottom of the column: 0 to 5%, 5 to 90%, 90 to 96%, 96 to 98%, 98 to 100%. The SC, fat, bacteria, and spores were measured in each of the fractions. The experiment was replicated in 3 different weeks using a different batch of milk and colostrum. Portions of the same batch of the frozen bacteria and spore solutions were used for all 3 replicates. The presence of both SC and Ig were necessary for normal gravity separation (i.e., rising to the top) of fat, bacteria, and spores in whole milk. The presence of Ig without somatic cells was not sufficient to cause bacteria, fat and spores to rise to the top without SC. The interaction between SC and Ig was necessary to cause aggregates of fat, SC, bacteria, and spores to rise during gravity separation. The SC may provide the buoyancy required for the aggregates to rise to the top due to gas within the SC. More research is needed to understand the mechanism of the gravity separation process.

Key Words: immunoglobulin, somatic cells, gravity separation

DAIRY FOODS: **TECHNICAL ORAL SESSION: PROTEIN/ POLYSACCHARIDE INTERACTIONS**

0266 Production and purification of whey protein glycate conjugated with low molecular mass dextrans. L. Xu[*1], Y. Gong[1], and J. A. Lucey[2,3], *[1]Department of Food Science, University of Wisconsin, Madison, [2]Wisconsin Center for Dairy Research, Madison, WI, [3]University of Wisconsin, Madison.*

An increasing number of people are suffering from food protein allergies, which have become a growing concern around the world. One possible helpful approach could be to glycate food proteins via Maillard reaction, which may block the IgE binding epitopes of the allergen that are responsible for eliciting an immune response. The goal of this research was to optimize processing conditions for creating and purifying whey protein isolate (WPI) glycate with dextran (DX) of 3 different molecular masses. Purification involved a combination of isoelectric precipitation and ion exchange chromatography. Glycates were characterized using size-exclusion chromatography coupled with multi-angle laser-light scattering (SEC–MALLS), glycoprotein analysis using SDS–PAGE and periodic acid Schiff's glycoprotein staining test with fluorescence laser densitometry. The optimal conjugation condition chosen from these experiments were 10% WPI–30% Dextran (DX), pH 6.5, 62°C for 24h for DX of molecular mass = 10 and 3.5 kDa, and 50°C for 12h for 1 kDa DX. The optimal purification process was performed by ion-exchange chromatography: for G10 (glyate with 10 kDa DX) we used pH 2 running buffer, followed by 0.55M NaCl elution buffer; for G3.5 and G1 (glycate with 3.5 and 1 kDa DX, respectively) we used pH 3 running buffer, followed by 0.52 and 0.5M NaCl running buffer for G3.5 and for G1, respectively. The resulting protein–DX molar ratios were estimated as 1:1.6 and 1:1.8 for G10 and G3.5 with a purity of 91% and 88%, respectively. Future work will focus on examining the allergenicity of the different molecular masses of WPI–DX glycates, using blood sera from cow's milk protein allergic patients.

Key Words: dextran, whey protein isolate, Maillard reaction

0267 Impact of Maillard modification on the in vitro carbohydrate digestibility of WP-dextran glycates. Y. Gong[*1], L. Xu[1], and J. A. Lucey[1,2], *[1]Department of Food Science, University of Wisconsin, Madison, [2]Center for Dairy Research, University of Wisconsin, Madison.*

Whey protein (WP) conjugation with dextran (DX) by the Maillard reaction might provide an alternative approach to decrease the immunogenicity of milk proteins. Protein digestibility of whey protein-dextran (WP-DX) glycates has recently been investigated by our group using an in vitro infant digestion model. The digestibility of carbohydrate part of the glycates is unknown. According to human colonic fermentation models, DX can be entirely degraded by the colonic microflora. In this study, we investigated the in vitro carbohydrate digestibility to find out the impact of conjugation on the glucose release of dextran from WP-DX glycates compared with maltodextrin and a mixture with dextran and whey protein isolates (WPI). WP-DX glycates were made with dextran (molecular weight 10 kDa) and WPI via our patented aqueous Maillard reaction method. The glycates were separated and purified by chromatography. The glycates were digested at 37°C by in vitro model using an enzyme mixture including pepsin, pancreatin and amyloglucosidase, which represent enzymes in the digestion system of animals and humans. The free glucose was measured at 0, 10, 20, 60, 120, 180 min and 24 h by HPLC with ion-exchange chromatography and RI detector. The percentage glucose release of dextran and maltodextrin were 6.3 and 64.5% (g glucose/100 g carbohydrates) respectively, during the first 10 min. The glucose release from WP-DX glycates was 9.5, 13.2 and 16.1% at 60, 120, and 180 min, respectively. The glucose release of glycates were lower ($p < 0.05$) than that of dextran alone at 60, 120, and 180 min of digestion. However, no difference was observed in glucose release rate between WP-DX glycates and dextran alone at 0, 10, and 20 min of digestion. The results indicated that both dextran and WP-DX glycates can be digested into glucose by this mixture of digestion enzymes. The rate of glucose release and extent of release were lower for DX compared to maltodextrin. The conjugation of dextran and WP slowed down the glucose release of dextran. Slower digestion of dextran in conjugates might help maintain a possible protective impact of the polysaccharide for reducing WP allergenicity during digestion.

Key Words: in vitro, digestion, WP-DX glycates

0268 Effects of mineral salts and calcium chelating agents on the functionalities of milk protein concentrate prepared by ultrafiltration. X. Luo*, L. Ramchandran, and T. Vasiljevic, *Victoria University, Melbourne, Australia.*

Functionality of milk protein concentrates can be tailored by modifying state of casein micelles through manipulation of processing conditions including temperature, pH and/or addition of calcium chelators. The objective of this study was to investigate the effect of calcium and calcium chelating agents (EDTA and citrate) on the performance of membrane ultrafiltration (UF) process and the functionalities of resulting milk protein concentrates (MPC). Skim milk adjusted to pH 5.9 was pre-treated with EDTA or citric acid (10, 20 or 30 mmol) and ultrafiltered using a polyethersulfone (PES) membrane at 15°C to five times concentration factor. The membrane performance was measured by the permeate flux during UF process. Used membranes were examined using scanning electron microscopy (SEM). The MPC samples were freeze dried and powders were assessed for physical functionalities including solubility, heat stability and emulsification.Addition of chilators led to a shift in a protein-mineral equilibrium and calcium dissociation from the casein micelle. The total calcium in the final MPC was reduced ($p < 0.05$) from 191 (control) to 131 mM or 135 mM for skim milk pre-treated with 30 mmol of EDTA or citrate, respectively. The casein micelle particle size was subsequently reduced ($p < 0.05$) from 200 nm (control) to 28 nm or 24 nm for the milk pre-treated with EDTA or citrate at concentrations equal to or greater than 20 mmol. Consequently, solubility of the MPC increased ($p < 0.05$) from 92% (control) to 98% (ETDA, $\geq$ 20 mmol) or 98.9% (citrate, 30 mmol); heat stability was also enhanced ($p < 0.05$) from 78% (control) to 83% (EDTA, 20 mmol) or 87% (citrate, $\geq$ 20 mmol). The emulsion capacity has increased from 1170 (control) to 1392 or 1459 (g oil/g protein) ($p < 0.05$) when 30 mmol of EDTA or citrate were added, respectively. Addition of EDTA or citrate hindered the membrane performance as observed by reduced permeate flux from 10.5 kg/h.m^2 (control) to 7.9 kg/h.m^2 (EDTA, $\geq$ 20 mmol) and 8.6 kg/h.m^2(citrate, $\geq$ 20 mmol) at the start of UF. Consequently UF processing time increased from 5 h (control) to 7 h (EDTA) or 6 h (citrate). This work has provided new insights into the relationship between calcium, calcium chelators and their influence on the casein micelle size and the physicochemical properties of MPC produced using UF, and also demonstrated the potential of using EDTA and citrate acid to manipulate MPC product functionality using UF.

Key Words: milk protein concentrate (MPC), functionality, ultrafiltration (UF), membrane, calcium chelator, casein micelle

0269 Storage stability of sodium caseinate stabilized oil-in-water emulsions as affected by severe heat treatment and storage temperatures. Y. Liang*[1], G. Gillies[2], H. G. Patel[3], L. Matia-Merino[1], A. Ye[4], and M. Golding[1,4], *[1]Massey University, Palmerston North, New Zealand, [2]Fotnerra Research and Development Centre, Palmerston North, New Zealand, [3]South Dakota State University, Brookings, [4]Riddet Institute, Palmerston North, New Zealand.*

Oil-in-water emulsions are an important basis of many food products such as soup, sauces, salad dressing, processed cheese and whipped cream. In many cases, liquid emulsions are processed at high temperature (e.g., retort or UHT processing) and may be stored at different temperatures. There is little information on how high heat treatment and storage temperatures influence the creaming stability of caseinate-stabilized emulsions. In this study, we investigated the effects of heating and storage conditions on the structural, mechanical and rheological properties of caseinate-stabilized emulsions. The stock emulsion was prepared by mixing a reconstituted sodium caseinate solution (2% w/w) with 60% w/w oil and subjecting it to a high pressure homogenization. Caseinate solutions of different concentration were heated separately at 120°C as a function of time up to 60 min. These heated caseinate solutions were then mixed with the stock emulsion in different ratios to form the model emulsions with 1−8% protein. The creaming stability of unheated emulsions was determined between 20 and 60°C. All experiments were performed at least in duplicate. The creaming kinetics determined by Turbiscan showed that the phase separation of model emulsions was markedly dependent on the duration of the heat treatment. The differences between unheated and heated emulsions were attributed to the heat-induced physicochemical changes in sodium caseinate nanoparticles. At low and moderate caseinate concentrations (2% and 4% respectively), the droplet-droplet interactions were weakened while the droplet-droplet interactions increased at high Na-CN concentration (6%) by the addition of heated sodium caseinate. It seems that the former structural change is predominantly due to reduced depletion attraction, whereas both reduced depletion attraction and decreased continuous phase viscosity influenced the later structural change. Unheated emulsions stored at higher temperature (60°C) resulted in an accelerated phase separation compared to those stored at lower storage temperatures. The main cause was attributed to the weakened depletion energy and decreased viscosity at accelerated temperatures. Both changes lead to a rapid droplet network formation and rearrangement.

Key Words: emulsion, heat-induced degradation, depletion flocculation

0270 Understanding mechanisms of the plasmin-induced dissociation of the casein micelle. H. Bhatt*[1], A. Cucheval[1], C. Coker[1], H. G. Patel[2], A. Carr[3], and R. Bennett[3], [1]*Fonterra Research & Development Centre, Palmerston North, New Zealand,* [2]*South Dakota State University, Brookings, SD,* [3]*Massey University, Palmerston North, New Zealand.*

Bovine plasmin is a highly heat-resistant enzyme that is naturally present in milk. Plasmin can survive severe heat treatments such as UHT and may act on casein during the storage of milk products and lead to proteolysis, gelation, and bitterness. We explored the plasmin-induced dissociation of the casein micelle to achieve a better understanding of gelation and sedimentation mechanisms in different milk products. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) and reverse phase high performance liquid chromatography (RP-HPLC) were used to monitor the extent of hydrolysis of casein. The particle size, turbidity, mineral level in the serum phase, and sedimentation were also analyzed and were correlated with different extents of hydrolysis. The particle size and turbidity decreased during the initial hydrolysis, but increased dramatically towards the end of hydrolysis. This indicated that casein micelle dissociation occurred during early stages and that aggregation of hydrolyzed peptides occurred towards the final stages of hydrolysis. The total calcium and phosphorus level in the serum phase increased linearly with an increase in the extent of hydrolysis, suggesting the release of peptides containing colloidal calcium phosphate from the casein micelle. The SDS-PAGE and RP-HPLC results indicated that hydrophilic peptides, e.g., proteose peptones, were the first to dissociate from the casein micelle on plasmin-induced hydrolysis; hydrophobic peptides, e.g., γ-caseins, dissociated slowly and with dissociation patterns that were identical to those of κ-casein, suggesting that, even after breakage of the anchor points, the release of κ-casein from the micelle was too slow to cause gelation. These results provide new insights into the dissociation pattern of the casein micelle and how this relates to plasmin-induced sedimentation or gelation of UHT milk systems.

Key Words: plasmin, UHT milk, gelation

0271 Heat-induced changes in milk proteins in high-carbohydrate media. T. Huppertz*[1,2] and H. G. Patel[2], [1]*NIZO food research, Ede, Netherlands,* [2]*South Dakota State University, Brookings.*

Casein micelles in milk are unique association colloids, sterically stabilized by a polyelectrolyte brush consisting of κ-casein, and are crucial structure elements in the creation of desirable texture and stability in dairy products such as cheese and yogurt. Casein micelles show remarkable colloidal stability, but when treatment conditions extreme or solvent quality is reduced, the micelles lose their colloidal stability and aggregate. This study investigated the colloidal stability of casein micelles and whey protein at high temperature and in the presence of a high level of carbohydrate, conditions commonly encountered in caramels, sweetened condensed milk and Dulche de Leche. Adding 10−50% carbohydrate to milk reduced their colloidal stability of casein micelles. These effects are more extensive for carbohydrates of lower molar mass. Heating milk at > 110°C increased casein micelle size and turbidity as a result of the aggregation of casein micelles, with contributions from heat-induced denaturation and aggregation of whey proteins. Heat-induced increases in particle size and turbidity were more extensive at higher heating intensity, with increasing carbohydrate concentration and decreasing molar mass of the carbohydrate. The presence of a free aldehyde group in reducing sugars also strongly influence the heat stability of milk through Maillard reaction products. The positive effect of Maillard reaction products on the heat stability of milk was derived from the formation of reductones, which can facilitate the covalent cross-linking of milk proteins and hence increase the heat stability. Whey protein denaturation was impaired by the presence of carbohydrates. Denaturation temperature increased with increasing carbohydrate content, effects being larger for low-molecular-mass carbohydrates. The size of heat-induced whey protein aggregates could be tailored by a combination of carbohydrate type and concentration. The results presented facilitate the extension of our understanding of the behavior of milk proteins in environments strongly deviating from natural physiological conditions. Such insights can be applied to understand and tailor the behavior of milk proteins in environments of high carbohydrate content, e.g., caramels, sweetened condensed milk and Dulche de Leche, and facilitate the design of rules for attaining maximum milk protein functionality in these systems.

Key Words: casein, whey protein, heat, carbohydrate, heat stability, denaturation

0272 Effects of pH on the morphology and mechanical property of heat-induced whey protein aggregates. C. W. Y. Lam* and S. Ikeda, [1]*University of Wisconsin, Madison.*

Whey proteins denature and aggregate when they are heated in aqueous environments. It is known that the morphology of resulting aggregates varies depending on pH. However, the structure-property relationship of heat-induced whey protein aggregates has not been fully understood. The objectives of this study were to study the effect of pH on the morphology of heat-induced whey protein aggregates and to seek correlations between their morphologies and mechanical properties. Whey protein was dissolved in deionized water adjusted to pH 3−7 and heated at 80 ± 0.2°C. Subsamples were taken at pre-specified time intervals and quenched in a 0°C water bath. The sample solutions were diluted to a protein concentration of 10-100 ppm, deposited on to freshly cleaved mica

surfaces, air-dried, and imaged using atomic force microscopy (AFM) operated in peak-force tapping mode in air. Further mechanical tests were done with AFM force spectroscopy, where the whey protein aggregates were indented directly to obtain interaction forces. These force curves were analyzed where the Young's modulus (E) of the samples can be fitted and calculated using the Hertzian model. The data were used to verify the mechanical and surface properties of the samples with different pH obtained with AFM imaging. At pH 3, a relatively small fraction of protein aggregates revealed fibrillar morphologies, while the majority of aggregates appeared to be particulate. At other pHs, only particulate aggregates were observed. All of these particulate aggregates were composed of smaller elementary particles, suggesting that the heat-induced aggregation was a two-step process regardless of pH, consisting of the formation of primary aggregates, followed by the secondary aggregation between primary aggregates. The Feret's diameter, representing the diameter of the smallest circle that entirely covers an individual whey protein aggregate, became more dependent of the aggregate size with increasing pH, indicating that whey protein aggregates became more extended, coarse, or anisotropic with increasing pH. Furthermore, the surface roughness evaluated based on the cross-sectional height data decreased by a factor of 2 with increasing pH from 5.5 to 7. This suggested that the protein aggregates collapsed, meaning that the primary aggregates were denser and more tightly packed within the aggregate. From the force spectroscopy analysis, the samples prepared at pH 7 showed larger E values than the samples prepared at pH 5.5. This suggested that the samples at pH 7 were stiffer, which conformed with the previous morphological results.

Key Words: whey protein, heat-induced aggregation, AFM

0273 Strengthening interfacial whey protein films by conjugation with gellan. B. Cai* and S. Ikeda, *The University of Wisconsin, Madison.*

Whey protein can be used as an emulsifier that forms nanometer-thick rigid layers at hydrophobic-hydrophilic interfaces in dispersed systems and provides stability against coalescence of the dispersed phase. If another surfactant is added, however, whey protein will be displaced competitively from the interface, leading to a loss of stability of the dispersed system. Gellan is a network-forming polysaccharide widely used in the food industry. Whey protein-gellan conjugates are expected to show enhanced resistance against surfactant-induced competitive displacement because gellan is considered to form additional networks at the interface. The objectives of this study were to conjugate whey protein either covalently or electrostatically with gellan and to investigate the effect of the different conjugation methods on interfacial structure and resistance to the surfactant-induced competitive displacement from the interface. Whey protein was conjugated either covalently or electrostatically with gellan. The conjugate was dissolved in water and spread on the air-water interface formed on a Langmuir trough. Food-grade nonionic surfactant Tween 20 was then injected into the aqueous phase to induce competitive displacement. Langmuir-Blodgett interfacial films were sampled at pre-specified surface pressures by dipping a freshly cleaved mica sheet in and out through the interface. The interfacial films thus transferred on the mica surface were imaged using atomic force microscopy. Both covalent and electrostatic conjugates formed close-packed interfacial films at the air-water interface. String-like structures of gellan attached to globular protein molecules were also evident. The thickness and surface pressure of the interfacial films were approximately 0.2-0.4 nm and 8-12 mN/m, respectively. Upon the addition of Tween 20, the surface pressure increased further due to the adsorption of the surfactant to the interface. Nanometer-sized surfactant domains first appeared at a surface pressure around 20 mN/m, and expanded their areas with increasing surface pressure. The thickness of protein domains increased with increasing surface pressure, consistent with the previously proposed orogenic displacement mechanism. At a certain surface pressure (e.g., 23 mN/m), the covalent conjugate occupied a larger interfacial area (83%) than both electrostatic conjugate (74%) and the WPI control (61%), The interfacial area occupied by the covalent conjugate displaced from interface less rapidly than electrostatic conjugate demonstrating a more resistant interfacial structure. These results suggest that covalent conjugation of whey protein with gellan is a more effective approach than electrostatic conjugation in strengthening interfacial protein layers and enhancing their resistance against surfactant-induced competitive displacement from the interface.

Key Words: whey protein, gellan, interface

0274 Enhancement of radical quenching ability of sweet whey and casein hydrolyzate: mutual supplementation with thermally generated maillard reaction products. Z. Z. Haque* and D. Mukherjee, *Food Science, Nutrition & Health Promotion, Mississippi State University, Mississippi State.*

Copiously available sweet whey is a source of nutritious proteins, peptides, free amino acids, and lactose. Abundant N-terminal, ε-amino-groups and the reducing sugar, allows thermal generation of Maillard reaction products (MRPs) on heating. With an aim to develop powerful natural antioxidative foods, this research investigates the enhancement of short (Antioxidative Activity; AA) and long term (Antioxidative Persistence; AP) ROS quenching ability of two types of sweet whey, Cheddar (ChWPC) and Edam (EWPC) whey and enzymatic hydrolyzate of casein (CH) through mutual supplementation with freshly heat-generated MRPs. Whey and CH dispersions (3 and 2%, respectively, w/v) were heated for 0 to 4 h at 90°C in McIlvaine's iso-ionic buffer (pH 7.0), with and without

added lactose (1%, w/v), to generate MRPs. AA and AP were determined from luminol-induced chemiluminescence (CL) caused by unquenched hydroxyl radicals generated by pyrolysis of 2,2'-azobis(2-methylpropionamidine) dihydrochloride (ABAP). Decrease in CL, measured as relative light units (RLU), compared to control (without the test materials) at maximal radical generation within one and 2 h, were respectively measures of AA and AP. Thermal generation of MRPs tended to enhance AA and AP in both sweet wheys though this effect was more dramatic for ChWPC. This was conceivably due to its greater peptide content. CWPC and EWPC heated for 1 h exhibited radical induced CL maxima of 99 and 141 RLU, respectively. Whereas values for ChWPC + lactose and EWPC + lactose were 90 and 140 RLU, respectively. Furthermore, a direct correlation was observed between added lactose induced MRP formation and AA of ChWPC, though this was not so clear for EWPC. AA of CH after heating for 4 h showed a CL of 79 RLU. However, this decreased when lactose, ChWPC and EWPC were added to CH as seen from increasing CL of 164, 107, and 121, respectively. The AP values for the same treatments were 53, 87, 57, and 62 RLU, respectively. The study not only indicated the variable effect of MRPs on antioxidative properties of the sweet wheys and CH, but also depicted the dramatic time-dependent thermal enhancement of AA and AP of ChWPC on MRP formation with added lactose. These data can potentially lead to the development of powerful new antioxidants to alleviate the detrimental effects of cellular oxidative stress.

Key Words: antioxidants, free radicals, reactive oxygen species.

0275 Impact of heat treatments on the functionalities of milk protein concentrate 80. R. M. Horak*, J. A. Lucey, and M. Molitor, *University of Wisconsin, Madison.*

Processing conditions impact the properties and functionality of milk protein concentrate 80 (MPC80). Nonfat dry milk is categorized according to the processing temperatures (low, medium, high) as these treatments greatly influence its functionality and end use. It is unknown how MPC80 properties will be affected by increased pasteurization temperatures of skim milk (before concentration). Increased pasteurization temperatures will denature more whey protein, which could impact solubility, foam stability, and viscosity of the reconstituted powder. Raw skim milk received heat treatments of 72°C for 16 s or 77, 82, or 87°C for 1 min, immediately before ultra- and diafiltration. The retentate (23% TS) was spray dried and outlet temperature was adjusted to maintain consistent moisture content between powders (~4.4%). The powders had similar composition including fat contents (< 2%). Functionality testing included solubility, foaming, tapped bulk density, and reconstituted viscosity. Tests were conducted within 1 wk of production. Powders were also stored at 30°C for 6 mo with functionality tested every 30 d. SDS-PAGE results show higher heat treatments produced more di-sulfide linked aggregates. For all powders, solubility slightly decreased during storage, but higher heating temperatures did not have a significant impact on solubility. Initial foaming experiments indicated that heat treatments of 82°C or 87°C for 1 min produced foams that were stiffer and more stable than samples treated at temperatures of 77°C for 1 min. Bulk density decreased over storage but was not significantly affected by heat treatment. Experiments investigating the viscosity of reconstituted powders are ongoing; however, initial results indicate that viscosity slightly increased with an increase in heating temperature. Based on preliminary results, it was concluded that increased heat treatments had the greatest impact on the foaming properties of MPC80 but has less impact on other functional properties.

Key Words: milk protein concentrate, processing, functionality

DAIRY FOODS SYMPOSIUM: DAIRY FOODS CONSUMPTION, GUT MICROBIOTA, AND HUMAN HEALTH

0276 Probiotics and health benefits with reference to synthesis of γ-aminobutyric acid by selected probiotic bacteria. N. Shah* and Q. Wu, *The University of Hong Kong, Hong Kong.*

Traditionally, probiotics have been added to yogurt and other fermented foods for health benefits. Currently 56 species of *Lactobacillus,* including *L. acidophilus* and *L. casei* and 32 species of *Bifidobacterium,* exist. These probiotic cultures are able to restore the normal balance of microbial populations in the intestine and offer several therapeutic benefits. There has been an increasing demand for health-promoting food ingredients. Different milks fermented with bacteria, yeasts, molds or enzymes offer a broad range of possibilities to cover different health aspects with new bioactive components such as lactoferrin, micronutrients, CLA, sphingolipids and bioactive peptides or synthesize exo-polysaccharides. In particular, milk-proteins and associated bioactive peptides released during microbial or enzymatic fermentation of milk offer a broad spectrum of new functional properties including anti-hypertensive, anti-microbial, anti-oxidative, and immuno-modulatory properties. Gamma-aminobutyric acid (GABA), a non -protein amino acid, is mainly found in the brain and regulates vertebrate physiological and psychological behaviors such as anxiety and depression blood pressure and hormone secretion. The synthesis of GABA in the brain decreases with age, especially in elders. Hence, there has been increasing interest in use of probiotics for GABA production. In this study, several GABA-producing LAB isolates have been isolated from naturally fermented foods such as Korean kimchi. Previous screening methods are time-consuming and inefficient. In the present study, we have developed a novel screening and identification method for GABA-producing LAB from Korean kimchi. Acid treatment was applied to screening procedure to obtain acid-tolerant LAB isolates, and then a simple identification of GABA-producing LAB based on release of gas by these bacteria has been developed. The amount of GABA produced by LAB isolates at various monosodium glutamate (MSG) concentrations and incubation times in MRS medium was quantified by HPLC. Genetic identification of high GABA-producing LAB was performed by both 16S rRNA gene and glutamate decarboxylase gene. Nine potential GABA-producing LAB isolates were selected by observing gas release during fermentation. The conversion ability of MSG into GABA for all nine LAB isolates was 100% (supplementation level 10 g/L MSG, incubation time 24 h), over 80% (supplementation level 30 g/L MSG, incubation 48 h), over 60% (supplementation level 50 g/L MSG, incubation time 72 h) and over 50% (supplementation level 70 g/L MSG, incubation time 72 h). These nine LAB isolates were genetically identified as *Lactobacillus brevis* by 16S rRNA gene and confirmed by glutamate decarboxylase gene.

Key Words: probiotics, γ-aminobutyric acid, health benefits

0277 Gut micrcobiota, probiotics, bioactives (such as CLA, USFA), trans-fatty acids and their relationship to health. H. Gill*, *RMIT University, Melbourne, Australia.*

The human gastrointestinal tract harbors ten times more microorganisms than somatic cells in the human body. These organisms are part of a diverse and complex ecosystem comprising over 3.3 million genes that encode a vast repertoire of enzymes and metabolites with the ability to significantly influence human health and wellbeing. While a majority of these microbes exert health-promoting effects on the host, some possess the potential to cause disease. In a healthy state, the gut microbiota is known to confer a range of health benefits relating to immune function, nutrition, host metabolism and protection against pathogens. Alterations in the normal composition of the gut microbiota are associated with an enhanced predisposition to immunoinflammatory, autoimmune, metabolic and degenerative disorders. Consequently, there has been an increasing interest in developing nutrition/diet-based strategies for correcting gut microbiota dysbiosis. The use of probiotics is one such strategy that has been found to be effective in restoring perturbed gut microbiota composition and function and promoting/restoring optimal health. Amongst the many health benefits associated with probiotics, a large proportion of research attention over the last two decades has focused on their immunomodulatory and anti-infection properties. There is evidence that specific probiotics strains are effective in preventing and/or managing a range of enteric infections and modulating the functioning of the immune system. In healthy subjects and subjects with suboptimal immunity, specific strains are able to boost immune function, whilst in subjects with dysregulated immune system, such as allergy and inflammatory bowel disease, probiotics are effective in restoring immune homeostasis and reducing the severity of immunoinflammatory disorders. A variety of mechanisms by which probiotics mediate their health-enhancing or disease-preventing effects have been suggested. These include direct interaction with the host immune system and through the production of diverse array of bioactive molecules/metabolites. Dairy-based products are common vehicle for delivering probiotics. Being a rich source of essential nutrients and a variety of biologically active substances with synergistic physiological effects, these products offer a significant advantage over other non-dairy products. Milk also contains trans-fatty acid, vaccenic acid, which humans convert into rumenic acid, the biologically active form of CLA. Other fatty acids in milk are also known to exert beneficial health effects. This

presentation will provide an overview of recent advances in health-promoting effects of gut microflora, probiotics and bovine milk fatty acids, especially related to immunoregulation, and novel health-enhancing food products.

Key Words: micrcobiota, probiotics, bioactives

0278 Overview of whey protein based bioactivities (including colostrum) in gut and health promotion.
A. M. Pihlanto* and R. M. Tahvonen, *MTT Agrifood Research Finland, Jokioinen, Finland.*

The high nutritive value and diverse functional properties of milk proteins are well known. In recent years, intense scientific research has focused on the identification of factors within bovine milk that may be relevant to improving human health. The best characterized whey-based bioactive proteins include α-lactalbumin, β-lactoglobulin, immunoglobulins, lactoferrin, lactoperoxidase and growth factors. These proteins exhibit a wide range of biological activities that may influence the digestive function, metabolic responses to absorbed nutrients, growth and development of organs and disease resistance, as well as gut microbiota and microbiome. Some whey proteins may reduce the risks of chronic human diseases. Whey protein constituents have been reported to have functional roles in various biological processes and organ systems in geriatrics, and thus help in the management of geriatric health problems through proper nutrition. Whey components have beneficial effects on intestinal health in four areas: prebiotic effects, antimicrobial and antiviral properties, anticancer properties and gut associated lymphoid tissue. Whey proteins are a good source of various bioactive peptides that are encrypted within the proteins and can be released during gastric digestion or food processing by enzymes or microbes. Whey protein-derived peptides have been shown to exert a wide range of bioactivities affecting the cardiovascular, immune and nervous systems. The efficacy of a few peptides has already been established in animal and human studies. A number of commercial whey-protein based products with potential health effects are on the market and their number is envisaged to increase on global markets.

Key Words: whey protein, bioactivity, health

0279 Milk fat globule membrane components and gut health effects.
R. Ward* and K. Hintze, *Utah State University, Logan, UT.*

Milk fat globule membrane (MFGM) is a complex biopolymer that is primarily composed of polar and neutral lipids and membrane glycoproteins. MFGM is present in all dairy products to some degree, but may be isolated as a co-product from the manufacture of butter and cheese. Based on its composition, it has been suggested that MFGM may have value as a nutraceutical ingredient, yet relatively few studies have been conducted to test this assumption. Individual components of MFGM, such as sphingomyelin and gangliosides, have been shown to reduce the development of preneoplastic lesions in rodent models of colon cancer, and a recent study from our lab extended this finding to MFGM itself. In addition, MFGM itself, and isolated components have been shown to protect the barrier properties of the gut against stress-induced permeability development. Several groups have shown MFGM has antiviral and antibacterial properties, and recent data from our lab indicates MFGM may affect the microbiome composition and metabolism. Lastly, we have recently conducted an acute and a chronic human trial investigating the effects of MFGM on gut health and resilience.

Key Words: milk fat globule, nutraceuticals, gut health

0280 Human gut microbiota, diet and health.
M. Lefevre*, N. Hergert, and G. Rompato, *Utah State University, Logan.*

It is well established that gut microbiota composition and metabolic capabilities can have far reaching effects on host physiology. Further, diet composition can play a major role in modifying gut microbiota. However, the extent to which beneficial effects of dietary modification are mediated through changes in gut microbiota is largely unknown. The Gut Check study was a cross-sectional investigation of the relationship between gut microbiota, habitual diet, intestinal inflammation and selected health biomarkers. Fifty males and eighty-two females between the ages of 18 and 79 provided photograph assisted 3-d food intake records along with stool and blood samples collected immediately following the food records. Diet records were analyzed for selected foods and macro and micronutrient content. Fecal samples were processed for microbiota composition and additionally analyzed for calprotectin levels (a marker of intestinal inflammation). Blood samples were processed for biomarkers of inflammation, insulin sensitivity and endotoxin levels. Despite the recognized limitations associated with assessing dietary intake (even with photo assisted food intake records), strong associations were identified between selected dietary factors and microbiota composition. As an example, we identified a strong positive linear trend ($P < 0.0001$) between tertiles of total milk intake and the relative abundance of the Ruminococcaceae family. A weaker negative association was found between tertiles of milk intake and the Alcaligenaceae family. The relative abundances of the gut microbiota were also associated with parameters of health. Thus the Ruminococcaceae family (members of which have been shown to be higher in controls versus individuals with type 2 diabetes) was negatively associated with diastolic and systolic blood pressure (DBP, SBP) and circulating endotoxin levels. Thus, one would expect that increasing total milk intake would increase Ruminococcaceae and lower blood pressure. Conversely, the relative abundance of the Alcaligenaceae family was negatively associated with BMI, triglycerides, fasting glucose and waist circumference suggesting that increasing milk consumption would adversely affect parameters of metabolic

syndrome. Effects associated with calcium intake were minor, suggesting a primary effect of dairy intake as opposed to generalized effect of calcium intake. In total, these data emphasize the complicated interactions between diet, gut microbiota composition and health parameters and a need to conduct carefully controlled diet intervention studies.

Key Words: microbiota, metabolism, intake

EAAP EQUINE SYMPOSIUM: KNOW-HOW AND FUTURE CHALLENGES FOR DEVELOPING THE HORSE SECTOR IN EUROPE: THE ACTIVITY OF THE EAAP HORSE COMMISSION

0281 Recent aspects in stallion sperm preservation for artificial insemination. M. Magistrini*, *INRA, Nouzilly, France*.

Equine industry needs more and more to improve long-term sperm storage (chilled or frozen) to optimize artificial insemination (AI) and fertility rates and consequently genetic exchanges. In most domestic animal species, sperm extenders are composed of animal products such as milk and/or egg yolk (EY). However, these products are potential sources of bacterial contaminations and have a variable composition. In equine species, milk and egg yolk have been used for years in the composition of extenders. In our laboratory, we have decided to focus our research on the composition of extenders and our objective was to adapt extenders free of milk and or egg yolk for both chilled and frozen sperm. For chilled transported sperm, milk or milk based extenders have been used to dilute and store stallion sperm for AI. However, all milk components are not optimal for sperm protection. So milk fractions were tested and finally we developed an extender named INRA96, containing the purified fraction of native milk caseins, for long-term sperm storage at 4°C or 15°C. INRA96 is a ready to use extender and it can maintain fertility potential for up to 24–72 h. INRA96 has proved itself and many of breeders use it nowadays in many countries. Since the first insemination with frozen semen, the low or fluctuating fertility results have limited the use of this technology. Our objective was to develop a new freezing extender, easy to use and able to improve the success of artificial insemination with equine frozen semen. We first demonstrated that INRA96 extender, used previously for chilled transported sperm, supplemented with EY and glycerol significantly improved significantly the fertility rates of equine frozen sperm. More sterilized EY-plasma afforded the same protection as EY. These results lead to the commercialization of an extender available ready to use and called INRA Freeze. Our next objective was to identify the cryoprotective molecule(s) in egg yolk plasma. EY and more precisely LDL, composed mainly of phospholipids, have long been considered as cryoprotective agents. In our analytical approach to develop a new freezing extender, we have tested the effect of EY-phospholipids instead of EY or EY-plasma. Our results demonstrate that EY-phospholipids as cryoprotective agents are a promising approach that we have to finalize.

Key Words: Equine, INRA 96, sperm storage

0282 The growth of social sciences in equine research: Essential to create new understandings of the horse industry's growth and evolution. C. Vial[1] and R. Evans*[2], [1]*INRA Montpellier, Montpellier, France,* [2]*Norwegian University College of Agriculture and Rural Development, Jaeren, Norway.*

The equine sector is currently growing and evolving worldwide. In Europe, it is estimated that there could be at least 6 million horses in the 27 member countries, grazing 6 million hectares of permanent grassland. 400,000 full time jobs equivalent would be provided by the sector and the numbers of horses and riders are growing in the approximate range of 7% a year. Today, little is known about the horse industry but there is a growing consensus that it has changed from a primarily agricultural and industrial sector activity to one firmly rooted in sports, leisure and consumption. It is impossible to understand these transformations without understanding the society within which they are embedded. Horse welfare, population size, behaviors and potentials depend on those of the societies in which their owners and riders live. Further, contemporary society is changing as it never has before. There is no single 'society.' Different peoples and different places all constitute unique economies, unique social values and mores, and unique formations of the horse industry. To understand the future of the horse sector we must understand these varied social and economic formations. In this context, and given the importance of and the challenges faced by the horse industry, the number of socio–economic studies devoted to this sector has recently multiplied all over the world. The social sciences undertake research, analysis and the development of new understandings of changes in the economy, in cultural values, and in social organization of contemporary society. Working together with traditional equine sciences, we are creating new interdisciplinary knowledge that helps us understand how we got to where we are now and where the equine sector might go in the future. That's why a working group in socio-economy has been created within the EAAP Horse Commission. Today, it includes 67 members from 20 countries. The goal of this group is to share ideas, research and experiences, but also to think about new topics of interest for research and development and to build common projects. This presentation addresses the social and economic issues faced by equine and social scientists who are exploring the contemporary shape of the equine sector, and whose research and analysis can help begin a discussion that enables us to understand what it might become in the future.

Key Words: equine, future of horse sector

0283 Equids contribution to sustainable development in Europe: Modern aspects and transfer of knowledge. N. Miraglia*, *Molise University, Campobasso, Italy.*

Sustainability as a concept comprises the combination of economic, environmental and social elements, never more importantly than when looking at the achievement of local sustainability. The achievement of sustainable development is not only dependent on the sustainability of the environment and its natural resources, but also on the level of economic and social conditions reached by the people using the environment and its natural resources. Europe's rural areas face significant challenges and, between them, the capacity to create sustainable development. In recent years there have been considerable worldwide changes in rural environment, agricultural and feeding systems that affected horse breeding considerably. Farming and forestry remain crucial as the use and the management of natural resources in the EU's rural areas. Rural development is the key tool for the restructuring of the agriculture sector and to encourage diversification and innovation. Equids match an important role in this context because they can make good, productive use of less-favored lands; they are able to develop considerable adaptation mechanisms to resist to very difficult climatic conditions and to low food availability. Diet selection needs to be analyzed to understand livestock performance and their impact on the vegetation in the different sites. So far, the studies concerning the integration between horses and territory are of considerable importance in the recovery of marginal lands and in maintaining their biodiversity. In this context grazing represents a major tool for conservation management because of its effects on habitat structure and biodiversity. Moreover, such activities are more and more linked to the maintenance of population in rural areas, to new relationships between citizen and cultural rural life and consequent preservation of traditional socio-cultural life. This paper will emphasize the role of equids in the rural development from past to future, identifying the farming systems in a general context of environment and landscape safeguard and of biodiversity preservation. It will emphasize the diversity of the "equine culture" and the equine-related activities such as leisure and tourism activities, the preservation of rural socio-cultural life and the most relevant socio–economic issues.

Key Words: equine, sustainability, rural development

0284 Genomic research in horses in Europe — EAAP Interstallion Working Group. K. F. Stock[1]*, L. Jönsson[2], S. Mikko[3], S. Brard[4], B. Ducro[5], S. Janssens[6], and J. Philippson[3], *[1]Vereingte Informationssysteme Tierhaultung, Verden, Germany, [2]University of Copenhagen, Department of Veterinary Clinical and Animal Sciences, Copenhagen, Denmark, [3]Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics, Uppsala, Sweden, [4]Institut National de la Recherche Agronomique (INRA), Génétique, Physiologie et Systèmes d'Elevage, Castanet-Tolosan, and Génétique Animale et Biologie Intégrative, Jouy-en-Josas, France, [5]Wageningen University, Animal Breeding and Genomics Centre, Wageningen, The Netherlands, [6]KU Leuven, Livestock Genetics, Department Biosystems, Heverlee, Belgium.*

With completion of the horse genome sequence in 2007, the potential of close international collaboration of researchers was impressively demonstrated, and an important step for genomic research in horses was taken. Since then, several European scientists have significantly contributed to the development of tools and strategies for using genomic information in the study of hereditary conditions and for improvement of breeding programs. An overview will be given of projects and initiatives in Europe in the field of equine genomics including prospected routine applications. Equine genetic and genomic research in Europe is carried by several strong and experienced research groups with high expertise and access to the latest methods and technologies, such as high-density SNP genotyping and next generation sequencing. The long standing European horse breeding organizations are in transition and have realized the potential of genomics for future practical horse breeding. Some progressive studbooks have accordingly shown considerable engagement and support in recent genomic projects. Because of their importance for the usability and overall quality of horses, health and performance have been and are still in the focus of genomic research in horses in Europe. Skeletal conditions are highly relevant for sport horses, so results of radiological screenings of young horses have been used for identifying ways to improve locomotory health by breeding. Quantitative trait loci have been identified and their routine use for selection purposes has been envisaged in, for example, Dutch, French and German horse populations for osteochondrosis, the most extensively studied single disease condition. Promising results for gaits and jumping have indicated the potential of using genomic approaches for improving complex performance traits in sport horses. However, limited accessibility of high-quality phenotype data has retarded the development of routine genomic applications in horse breeding, which is expected to significantly benefit from the recent initiatives addressing refinement and extension of the phenotypic information basis and R&D collaborations. The exchange of genetic material

between European Warmblood populations, the similarities of breeding goals and the relatively well developed infrastructure in the European horse sector make a good starting point for collaborative work across countries in the field of genomics. Synergistic effects of linking national projects and resources are obvious and have allowed prospecting a joint European genomics project aiming at improved selection for health and performance traits in Warmblood horses.

EXTENSION EDUCATION

0286 Developing, marketing and branding mobile apps for the horse industry. K. L. Martinson[*1], R. J. Coleman[2], and M. E. McCue[1], [1]*University of Minnesota, Saint Paul,* [2]*University of Kentucky, Lexington.*

An app is software that runs on the internet, a computer or phone. There are millions of apps available with about one billion downloads annually. However, relatively few apps have been developed for use in the horse industry. The objective of this abstract is to outline developing, marketing and branding of two mobile apps for use in the horse industry. In 2012, researchers developed a more accurate method for estimating horse body weight, a new equation for estimating ideal horse body weight, and a percentile that resulted in a body weight score to help assess over- and under-weight horses. Since the equations were complex, researchers decided to develop an app, named "Healthy Horse," to encourage use and adoption of the equations. During the same time period, hay prices around the U.S. were at all-time highs. Horse owners normally purchase hay by the bale, which can result in further exaggeration of prices. To help horse owners convert price per bale to price per ton, representing a more economical hay purchasing strategy, the "Hay Price Calculator" app was also developed. In January 2013, a computer science graduate student was hired to develop both apps in collaboration with the research team. App development took about 4 mo and cost approximately $8,000. Because grant funds were used to pay for the development of the apps, the University of Minnesota Office of Technology and Commercialization was consulted and decided to brand and market the apps under the University of Minnesota Board of Regents. In May 2013, both apps were released for use with Apple operating systems at a cost of $1.99 and $0.99 for the Healthy Horse and Hay Price Calculator apps, respectively. In November 2013 and March 2014, the Android version of Hay Price Calculator and Healthy Horse, respectively, were released. During the summer of 2013, the research team was approached by a nutrition company to co-brand the Healthy Horse app. After consulting with University Relations and the Office of the General Council, a contract was finalized to co-brand the app with the company logo and website address in exchange for a monetary contribution and marketing efforts. Since May 2013, over 1100 apps have been sold. Funds from the sale of the apps will help support future equine research at the University of Minnesota.

Key Words: mobile app, horse, body weight

0287 Calving management education program for dairy and beef workers and producers. L. G. D. Mendonça[*1], L. Hollis[1], J. M. Zeller[2], and J. P. Harner[2], [1]*Department of Animal Sciences and Industry, Kansas State University, Manhattan,* [2]*Department of Biological and Agricultural Engineering, Kansas State University, Manhattan.*

Stillborn is defined as a calf born dead or death within 24 h after calving. A stillbirth event is costly to a cattle producer because of the calf loss and the effects on the dam. Calving management education programs in English and Spanish were organized and delivered across Kansas with the objective to educate cattle producers and their workers. Furthermore, the program addressed other important areas; participants learned about management of cows during the pre- and postpartum period, and newborn calf care. A tool was designed and built to assist with the hands-on demonstration part of the educational program. Faculty from the Department of Animal Sciences and Industry collaborated with faculty and staff from the Department of Biological and Agricultural Engineering, Kansas State University, to build a tool to simulate a cow giving birth. A pelvic bone was placed inside a stainless steel box with a plexiglass side panel to allow participants to visualize a number of obstetrical procedures. A dead calf was used for the demonstrations and it was discarded at the end of each session. To date, there were 167 attendees in the educational program; it impacted approximately 15,000 dairy and 5000 beef cows in the state. In 2 training sessions, attendees' perception of the educational program was assessed using a survey, and pre- and post-test questions were used to evaluate participants' knowledge. Audience response system clickers (Turning Point Technologies) were used to collect answers of the pre- and post-test questions. Among the participants that responded, 72% answered they never participated in any "calving school training" before. The survey found that knowledge of understanding calving management increased from 2.8 to 4.0 (scale 1−5) in the first session and 2.0 to 2.6 (scale 1-3) in the second training session. Eighty-six percent of the attendees answered that the information presented about calf presentation and in the hands-on assistance demonstration was new and useful information. In the training sessions, 16% of respondents reported they were very likely, 70% likely and 14% not likely to make management changes. The mean scores for the pre- and post-tests were 51% and 81%, respectively. The mean difference of 30% indicates that using an interactive slide lecture and hands-on demonstration was effective in teaching producers and workers about calving management.

Key Words: calving management, producers and workers, education

0288 Premium beef semen on dairy calculator. G. Lopes*[1] and V. Cabrera[2], [1]*Accelerated Genetics, Baraboo, WI,* [2]*University of Wisconsin Madison, Madison.*

Producers are searching for alternatives to increase net income of their operations. Genetic companies are partnering with livestock sales companies and offering premium alternatives for crossbred calves when using beef semen. Our objective was to develop a decision support tool to analyze the net income of switching inseminations from conventional or sexed sorted dairy semen to beef semen. This partial budgeting calculation is performed considering the genetic value of animals to be inseminated and the expected premium to be received for crossbred offspring. The tool was conceived as an aid to help producers in their decision-making regarding the use of beef semen. Inputs from the herd such as herd size and herd structure, culling rate, pregnancy rate, number of virgin heifers inseminated with female sex-sorted semen, percentage stillborn, and calf mortality are used to calculate the number of replacements needed to maintain herd size and to determine the number of eligible animals for the beef program. Different prices of semen (conventional dairy, sex-sorted dairy, and conventional beef), and different prices paid for the offspring (dairy and beef crossbred) are taken into consideration. Animals are grouped according to parity (nulliparous, first, second, and greater than two lactations), and then further sub-divided according to the number of inseminations to receive (one, two, three, and greater than three). The selection of animals could be made in two different ways: (1) by genetic merit or (2) by reproductive performance. After selection, the tool calculates and shows the number of replacements that will remain in the herd to maintain herd size. Further, the tool estimates the profitability of selling crossbred calves at a premium price, presenting the dollar net return for the crossbred animals, and the net return for the herd as a whole. Herds using beef semen strategies enhance their genetic gain by generating future replacements from genetically superior heifers and cows. The tool will soon be freely available from the UW-Dairy Management Website (DairyMGT.info).

Key Words: premium, beef, dairy

0289 A decision support tool to estimate the economic potential of SCC hot sheet data. D. T. Nolan* and J. M. Bewley, *University of Kentucky, Lexington*.

A DHIA hot sheet ranks cows from the highest to lowest percent of bulk tank somatic cell count (BTSCC) based on their SCC and milk yield. The objective of the Southeast Quality Milk Initiative (SQMI) Hot Sheet Dashboard was to develop a farm specific tool that producers could use to make economic decisions from DHIA hot sheet data. Producers enter production information for the top SCC cows from the DHIA hot sheet including: milk production (kg/d), and percentage of the BTSCC, and herd based inputs including: amount of milk shipped/d, BTSCC, current milk price, and bonus opportunities for milk quality. Producers also determine whether they want to discard or ship milk from a cow with a high percentage of the BTSCC. Results are displayed to show how the current BTSCC and the economic opportunity would change depending on which cows' milk was discarded. An example scenario is presented in Table 0289. The net opportunity for this herd is $24.05/d. This value represents the difference in economic opportunity when milk from the top 2 cows is being shipped compared to being discarded. The price was higher when the cows' milk was discarded because the producer received the bonus opportunity for having a lower BTSCC. The SQMI Hot Sheet Dashboard can be beneficial to producers by allowing producers to make economic decisions from their DHIA hot sheet data. The Southeast Quality Milk Initiative project is supported by Agriculture and Food Research Initiative Competitive Grant no. 2013–68004–20424 from the USDA National Institute of Food and Agriculture.

Key Words: decision support tool, SQMI, hot sheet

Table 0289. Example herd inputs and results generated from the SQMI Hot Sheet Dashboard for a 100-cow herd, shipping 3402 kg of milk per day, with a BTSCC of 492,000 cells/mL and a current milk price of $0.41/kg, with a bonus opportunity of $0.01/kg*

	Cow Information				
	Milk Yield (kg)	% BTSCC	Decision	BTSCC after decision (cells/mL)	Bonus Opportunity ($/L)
Cow #1	19.1	25.6	Discard	284,376	.005
Cow #2	13.7	15.9	Discard	171,708	.01
Cow #3	37.0	10.1	Milk	171,708	.01
Cow #4	28.4	6.8	Milk	171,708	.01
Cow #5	36.9	5.9	Milk	171,708	.01
Economic Opportunity $24.05/d**					

*Bonus opportunity will increase with a decrease in BTSCC depending on producer inputs.
**Net opportunity does not assume discard milk is used as milk replacer substitute.

0290 The Kentucky Master Stocker Program. J. W. Lehmkuhler*[1], W. R. Burris[2], S. R. Smith, Jr[1], G. Halich[1], K. Burdine[1], M. Arnold[1], S. F. Higgins[1], A. Gumbert[1], and K. Laurent[1], [1]*University of Kentucky, Lexington* [2]*University of Kentucky, Princeton*.

The upper Mid-South is home to a large number of farms that utilize available forage and feed resources to add weight to lightweight feeder calves. With the change in the market conditions, it was evident that an outreach program was needed to provide this segment of the industry information related to management of feeder calves. An interdisciplinary team was assembled to develop curriculum related to all aspects of the feeder cattle industry. A total of eight sessions comprised the curriculum including: enterprise budgeting, economic risk management, health, nutrition, handling and welfare, forages, marketing and environmental management. The program was

offered twice during 2011 and 2012. Approximately 380 participants from 30 of the 120 counties attended. A random subsample of 150 were mailed a 50 question survey in 2013 to assess post-program impact. A total of 47 questionnaires were returned (31% return rate). The majority (93%) of respondents indicated the program Exceeded or Far Exceeded expectations. Awareness was increased (95%) related to management and marketing and 66% of respondents indicated they implemented changes. The majority (62%) Agreed or Strongly Agreed that their perception of the impact livestock have on water quality and the environment changed with an outcome of agriculture water quality management plans being completed by 79% and 61% indicating they developed streamside buffers or alternative watering sources for cattle. Increases in knowledge for livestock health were noted where 89% Agreed or Strongly Agreed they had a better understanding of how to use various antibiotic products available, 87% had a better understanding of selecting vaccines, 83% an improved understanding of health risk classification and 71% indicated they were better able to diagnose and properly treat feeder calves. Of those surveyed, 53% made changes to their health protocols and 60% indicated they have seen improvements in the health or response from administered products after having attended the session. Cattle handling was altered with only 19% indicating their handling techniques were unchanged and 57% indicated the use of an electric prod was Slightly or Much Lower. The majority (58%) Agreed or Strongly Agreed to have made changes to their feeding program. Economic risk management tools were utilized by 40% of respondents with 88% indicating the strategy limited their risk. The delivery of an educational program for the stocker and backgrounding industry in Kentucky was well received and increased producers' awareness and adoption of management changes.

Key Words: education, feeder cattle, stocker

0291 The North Dakota Beef Industry Survey; Enterprise management, risk factors, and risk management strategies of beef cattle operations.

D. N. Black*[1], J. C. Hadrich[2], G. P. Lardy[1], and C. R. Dahlen[1], *[1]North Dakota State University, Fargo, [2]Colorado State University, Fort Collins.*

In the spring of 2012 a survey was distributed to 2500 randomly selected North Dakota beef producers to evaluate their attitudes concerning risk factors and risk management on their operations. Five hundred twenty-seven surveys were returned (21.1% response rate), of which, 436 (82.7%) respondents indicated that they were active beef producers. Commercial cow-calf production (94.5%), and backgrounding (37.8%), were the most common enterprises on respondents' operations. Thirteen percent of respondents grazed cattle on federal grasslands, 54.4% grazed crop residue, and 17.7% grazed cover crops. When asked about expansion plans, the majority of respondents indicated they would focus on commercial cow-calf (82.8%) followed by backgrounding (36.6%), feedlot (21.9%), stocker (19.4%), and purebred (15.4%) enterprises, respectively. For recordkeeping, most operations use a paper record book (60.4%), followed by computer spreadsheets (36%), and management software (9.6%), whereas 2.9% do not have a formal recordkeeping method. To determine per-cow cost of production, 23.9% of respondents balanced checkbooks, 22.7% use management software, 22.1% use tax returns, 15.5% do not calculate, 5.1% use a consultant, and 29.3% use other methods not categorized in the survey. On a scale of 1−5 (1 = small negative impact, 5 = large negative impact) respondents identified animal health issues (4.1) and severe weather (4.1) as having a large negative impact on profitability, and labor availability (3.0) was viewed as being a neutral factor. Variability in cattle price (4.3) and input cost (4.3) were factors identified as having the greatest potential negative impact on profitability, whereas variability in soybean price (2.8) had neither a small nor large negative impact on profitability. When asked about the effectiveness of management strategies in reducing risk (scale of 1−5, 1 = not effective, 3 = neutral, 5 = very effective), respondents identified maintaining good animal health (4.6), financial reserves (4.0), and having off farm income (3.7) as being effective strategies, whereas herd management programs (2.8) and hiring ranch management consultants (2.8) were viewed as neither effective nor ineffective strategies to reduce risk. Survey results identify the degree of risk that producers associate with different factors and highlight strategies used to mitigate losses from identified risks.

Key Words: beef industry, profitability, risk management

EXTENSION EDUCATION: **DECISION SUPPORT TOOLS IN EXTENSION**

0292 History and development of the Bovine Estrus Synchronization Planner. S. K. Johnson[*1], G. Dahlke[2], and D. R. Strohbehn[2], [1]*Kansas State University, Colby,* [2]*Iowa State University, Ames.*

The Bovine Estrus Synchronization Planner is an Excel-based tool that aids in the selection and delivery of synchronization protocols. The development was a response to vocal concerns expressed by technicians, veterinarians and producers to Iowa State University extension beef specialists on the difficulty in managing the product delivery and timing elements of estrus synchronization protocols. Errors in protocol follow through were common and the resulting poor conception rates unfairly discredited the technology. As a multi-state extension group (now the Beef Reproduction Task Force) was coming together to deal with similar issues related to clear communication on research-based synchronization protocols, an Iowa State specialist approached the group about working together to update the existing planner with the new task force recommendations. This has been a successful partnership as the group has worked together to improve and update the planner for 10 yr. The original program contained six protocols, but now almost 40 recognized protocols are included. However, the short list of protocols recommended by the task force is highlighted. At one point there was a charge for the software, but over time the group has achieved enough industry sponsorship to provide the program as a free download at http://www.iowabeefcenter.org/estrus_synch.html. Today, the planner has more independent users than any of the other Iowa State University Animal Science software. The most recent development is a shortened version for use on handheld devices (www.estrussynch.com). Through the following steps: identification of research proven protocols, designation of most appropriate use of protocols, direction on proper implementation and stressing the importance of timing through the use of a calendar printout, the Estrus Synch software has clarified the necessary details to the end user. An online survey of AI users in 2013 (42 states represented) indicated 36% had downloaded the planner; of which 41% used it frequently, 15% used it 3−5 times, 31% used it less than twice and 13% had not used it. Users strongly agreed or agreed that the planner was easy to use (79%), made scheduling easier (77%), reduced errors (68%), improved communication (71%), helped achieve timely planning and preparation (73%), and directed them to a more appropriate protocol (57%). Suggestions made by users were included in the 2014 version. The Estrus Synchronization Planner has been a useful tool in the proper implementation of synchronization protocols. Efforts to inform potential users of its availability must continue.

Key Words: estrous synchronization, decision tools, evaluation

0293 Impact of decision support tools available for dairy farm management. V. Cabrera*, *University of Wisconsin, Madison.*

A number of decision support tools are available for dairy farm management and are being used for practical decision-making. The objective of this analysis was to document the level of adoption of decision-support-tools available at the University of Wisconsin-Madison Dairy Management Website (http://DairyMGT.info; > 35 tools) including the *Repro Money*, a Wisconsin extension program to improve reproductive performance. Since its inception in 2008, the DairyMGT.info, conceived as a mechanism to deliver science-based, user-friendly, and practical-application decision-support-tools, has accumulated a number of tools in nutrition, heifer rearing, reproduction, production, replacement, financial, and environment. The domain DairyMGT.info was registered with *Google Analytics* in December 2009 (http://www.google.com/analytics) to record the number of visitors and pageviews. Later, a system to track tool-specific usage by registering user emails was implemented in March 2011. Data indicate that the DairyMGT.info domain has consistently received > 1000 visits and > 3000 pageviews per month with a total of > 55,500 visits and > 179,000 pageviews in the period December 2009 to January 2014. Around 55% of visitors were from the US and the rest from more than other 150 countries, counting as the most important: Australia, Mexico, Brazil, Canada, Argentina, UK, and Italy. To January 2014, a list of 4500 users were registered with the DairyMGT.info domain and there were > 35,000 tool effective uses (a rate of > 1000 accessions a month or > 30 a day). As the number of visitors, tools usage is consistently increasing. The top 5 most popular tools are: FeedVal 2012-feed price valuation, grouping strategies for feeding lactating dairy cattle, value of sexed semen programs, economic reproductive analysis, and the economic value of dairy cow. A special tool for improving dairy herd reproductive management, *Repro Money* consists on facilitating 4+ farm-team meetings with the goal of diagnosing, prioritizing needs, and taking effective actions to improve reproductive performance. *Repro Money* was launched in late 2010 and since then 45 farmers have enrolled. Data from farms that finished the program by January 2014 (n = 30) indicate that reproductive performance (before vs. after) improved significantly at key reproductive indicators such as conception rate (+3%, $P < 0.01$), service rate (+5%, $P < 0.01$), interbreeding interval (−5 d, $P < 0.01$), and overall 21-d pregnancy rate (+3%, $P < 0.01$). This improved reproductive performance was estimated to increase economic gains in an average amount of $55/cow per yr (range $0 to $278) with an estimated overall impact of > $358,000/yr on 11,340 cows.

Key Words: online tools, decision-making, reproductive economic performance

0294 Assessing the need, project development and impact of the National Swine Reproduction Troubleshooting and Management Guide.

D. Levis*[1], M. Estienne[2], W. Flowers[3], R. Baker[4], R. Knox[5], K. Stalder[4], T. Safranski[6], M. Knauer[3], W. Singleton[7], D. Meisinger[8], C. Branderhorst[8] and W. Winkelman[9], *[1]Levis Worldwide Swine Consultancy, Lincoln, NE, [2]Virginia Tech, Suffolk, VA, [3]North Carolina State University, Raleigh, [4]Iowa State University, Ames, IA, [5]University of Illinois, Urbana, [6]University of Missouri, Columbia, [7]Purdue University, Lafayette, [8]US Pork Center of Excellence, Clive, IA, [9]National Pork Board, Clive, IA.*

An assessment of university Cooperative Extension swine programs in the United States revealed lack of a tool for troubleshooting reproductive problems at the farm level. Moreover, there are an extremely small number of extension specialists academically trained in reproductive physiology of pigs who are able to conduct troubleshooting and ongoing educational programs at the farm level. Thus, pork producers rely on themselves, veterinarians, or other consultants to improve reproductive performance of the breeding herd. A major role of university Cooperative Extension/Outreach is to provide scientific based information to help pork producers and consultants solve swine reproductive problems. The United States Pork Center of Excellence organized a group of nine university Extension swine specialists to develop a National Swine Reproduction Troubleshooting and Management Guide (NSR-TMG) for use by all pork producers and pork industry consultants. The NSR-TMG uses a question and answer format. The NSR-TMG has three main areas: (1) Problems with replacement gilts, (2) Problems with sows, and (3) Problems with semen quality. The replacement gilt segment focuses on problems associated with attainment of puberty and expression of estrus, problems resulting from a gilt pool that is too small, and problems that lead to poor litter size or reduced farrowing rate of gilts. The sow segment focuses on problems associated with reduced longevity due to high culling rate, low farrowing rate, low litter size, prolonged weaning-to-service interval and high pre-weaning mortality of pigs. The semen quality segment focuses on record keeping, semen delivery and storage, semen evaluation, and on-farm semen collection and processing. The program has answers for over 1000 questions. The answers are supported by a list of 648 references. Some references are available by linkage. The NSR-TMG is a web-based application, user-friendly, applicable for use by any size of sow farm, and easily accessed through personal computer, smart phones and tablets. Because the NSR-TMG is web-based, it will be easily updated. The project was partially funded by numerous pork industry partners. There is a yearly license fee to obtain access to the NSR-TMG. University and college instructors have free access to train students. The NSR-TMG is being used to improve reproductive performance of the sow herd by independent pork producers, large corporate swine operations, swine genetic companies, veterinarians, swine nutrition consultants, and university instructors. The actual financial impact of the NSR-TMG is difficult to measure at the farm-level.

Key Words: swine reproduction troubleshooting

FOOD SAFETY: **GLOBAL CHALLENGES TO A SAFE FOOD SUPPLY**

0295 Introduction—Global challenges to a safe food supply. R. J. Harmon*, *University of Kentucky, Lexington*.

As we move forward in meeting the global food demands of 2050, food safety will continue to be a high priority. Consumers have an increased interest in how their food is produced, where it is produced and is it safe and healthy for their families. In contrast, we have movements that seem to be counter to providing a safe and wholesome product to consumers, such as the raw milk movement. This symposium proposes to address several issues related to a safe global food supply, including new regulatory approaches to safe animal feeds (and thus food), raw milk issues and safety, and the retail perspective on food safety in international markets. All of these areas, and more, play important roles in assuring a safe global food supply for the future.

Key Words: food safety, raw milk, animal feed

0296 Raw milk—Is it safe? B. Jayarao* and E. Hovingh, *Penn State University, University Park.*

Over the last 20 yr, several surveys in the United States have detected food borne pathogens in raw bulk tank milk and many of the milkborne disease outbreaks have been traced to consumption of raw milk. In contrast, for the same period, fewer milkborne disease outbreaks were associated with consumption of pasteurized milk. These milkborne disease outbreaks following consumption of raw milk and milk products have raised serious public health concerns nationwide. The sale of raw milk has become more relevant than ever before due to the emergence of antimicrobial resistance in food borne pathogens such as *Salmonella* and *Escherichia coli*. Consumption of raw milk is widely prevalent among dairy farm families and their employees. In recent years, the "post baby boom" generation, comprised of a small but growing subset of urban/suburban population that consumes raw milk and raw milk products may account for the rise in the sale of raw milk. There are few reports that suggest urban/suburban consumers of raw milk believe that raw milk has more health benefits than pasteurized milk and these benefits outweigh the risks associated with foodborne pathogens in raw milk. In 1987, the FDA banned the interstate sale of raw milk; however, the sale of raw milk within state boundaries falls under the jurisdiction of each state's government. Nonetheless, in states where sale of raw milk is legal, the farms with permits to sell raw milk have to meet set bacteria count standards, periodic testing of raw milk for the presence of pathogens, and labeling of raw milk offered for sale. The Penn State Veterinary Extension and Field Investigation Team recently undertook a study involving 40 permitted raw milk producers in Pennsylvania. The study collected milk samples on a monthly basis to determine the presence or absence of pathogens, as well as various milk quality parameters. In addition to assessing farm management and milk hygiene practices, a survey of the farms' customers was also conducted. The findings of the study are as follows; 1) raw milk sale is largely driven by consumer demand, 2) farm hygiene level and presence of pathogen are not correlated, 3) most producers are cognizant of pathogens in raw and strive to address the issue of product safety, and, 4) critical points in the raw milk production continuum are yet to be clearly identified.

Key Words: raw milk, food safety

FOOD SAFETY: **ADVANCES IN FOOD SAFETY**

0299 Effectiveness of a mycotoxin binder to minimize transfer of aflatoxin from feed to milk in Nili-Ravi buffaloes. N. Aslam[1], I. Rodrigues[2], A. ul Haq[3], A. Cowling[1], H. M. Warriach[4], D. M. McGill[1], and P. C. Wynn[*1], *[1]Graham Centre for Agricultural Innovation, Charles Sturt University, Wagga Wagga, Australia, [2]BIOMIN-Singapore Pte. Ltd., Singapore,[3]Buffalo Research Institute, Bhunniky, Pakistan, [4]University of Veterinary and Animal Science, Lahore, Pakistan.*

Mycotoxins resulting from fungal contamination of feeds provide a major limitation for dairy production in Pakistan. The objectives of this study were to observe the extent of transfer of aflatoxinB1 in feed to the aflatoxinM1 metabolite in milk in Nili-Ravi buffaloes and to evaluate the efficacy of a mycotoxin binder incorporated into feed to minimize this transfer. Multiparous animals ($n = 28$) were randomly distributed to four groups corresponding to 2 treatments each with 2 levels in a factorial design. Animals were offered mycotoxin contaminated concentrate ration (2.5 or 5 kg/day) and corn (200 or 400 g/day) providing a total of 1475 µg (groups A and B) or 2950 ug (groups C and D) of aflatoxinB1 together with either 80 kg (groups A and B) or 70kg (groups C and D) of aflatoxin free fresh cut berseem clover (17.8% DM). AflatoxinB1 concentrations in feed for the low and high groups were therefore 88.7 and 171.2 ug/kg DM. Groups B and D were given 50 g of mycotoxin binder daily mixed with feed while groups A and C were kept as controls. Feed samples were analyzed by HPLC in Romer Labs Pte. Ltd., Singapore for aflatoxinB1 and milk samples were evaluated by ELISA for the liver metabolite aflatoxinM1. There was a highly significant difference ($P < 0.001$) in total daily aflatoxinM1 concentration in milk between animals fed the two concentrations of aflatoxinB1. The mean for those fed 2950 µg/day was 112.62 µg/kg of milk, almost double the concentration of 62.19 µg/kg in buffalo fed 1475 µg/day (SED = 5.99). The mean daily concentration of aflatoxinM1 in milk of animals from both treatment groups fed with 50 g of mycotoxin binder was 76.51 µg/kg, nearly 22 µg lower than those without mycotoxin binder 98.31 ± 5 µg/kg (SED = 5.99: $p < 0.01$). The interaction between the 2 treatments was not statistically significant. The total carryover of aflatoxinB1 from feed to aflatoxinM1 in milk was 5.06 and 4.14% for group A and C (without mycotoxin binder) and 3.37 and 3.50%, for groups B and D respectively fed the mycotoxin binder. Thus buffaloes are highly efficient at transferring mycotoxins in feed to the aflatoxinM1 metabolite in milk, while mycotoxin binder is capable of alleviating without preventing this contamination risk. In spite of this, the concentrations in milk still exceeded the European Union minimum standard of 0.05 µg/kg by over 150 fold. Strategies to minimize fungal contamination of concentrate feeds remains of importance for food security in Pakistan.

Key Words: aflatoxinM1, aflatoxinB1, transfer, milk, mycotoxin binder, Nili-Ravi buffaloes

0300 Use of silage bacteria as enterosorbents to reduce aflatoxin contamination. Z. Ma*, J. J. Romero, S. K. Williams, and A. T. Adesogan, *Dep. of Animal Sciences, University of Florida, Gainesville*.

The aim was to determine the effects of bacteria strain, viability and pH on the aflatoxin B_1 (AFB_1)-binding capacity of silage bacteria. In Experiment 1, each of 10 silage bacteria strains (Table 0300) was screened for their AFB_1–binding capacity by growing them on de Man-Rogosa-Sharpe broth to a population of 10^9 cfu/ml in quadruplicate. The suspension was centrifuged at 2500 × *g* for 10 min and the pellet was suspended in a 1.5-mL solution (5 µg/ml) of AFB_1 in phosphate buffered saline (PBS) for 24 h at 20°C. Bacterial (bacteria suspended in PBS) and AFB_1 Controls were also incubated. Supernatant samples after centrifuging were used to quantify the presence of unbound aflatoxin by High-Pressure Liquid Chromatography. Data were analyzed as a completely randomized design. Each bacterium bound more than 18% of AFB_1, and the greatest responses occurred with *L. plantarum* R2014 (32.95%), *L. buchneri* R1102 (30.30%) and *P. acidilactici* EQ01 (25.38%). In Experiment 2, the latter 3 strains were tested to determine how pH and bacterial viability influence their ability to bind AFB_1. Bacterial cells (10^9 cfu/ml) were incubated in either 4 mL of PBS (viable cells) or 2M HCL (dead cells) and centrifuged as described above. Pellets were incubated in quadruplicate in AFB_1 solution as above at pH 6, 2.5 and 8 to simulate the pH in the rumen, abomasum and intestine of dairy cows, and AFB_1 binding was quantified. Data were analyzed as a completely randomized design with a 3 × 2 × 3 factorial treatment arrangement. Dead cells of *L. plantarum* R2014 (32.62% vs. 24.78%) and *L. buchneri* R1102 (45.05% vs. 17.77%) bound more AFB_1 than viable cells, whereas a contrasting response was detected for *P. acidilactici* EQ01 (2.44% vs. 21.92%, respectively). The pH of 2.5 increased AFB_1 binding compared with pH 6 and 8 ($P < 0.05$). All bacterial strains showed AFB_1–binding ability but the efficacy was dependent on the bacteria strain, viability and pH. More work is required to test the ability of the bacteria to bind AFB_1 in animal feeds.

Key Words: aflatoxin, silage bacteria, enterosorbents

Table 0300. Bacterial strains tested for AFB_1 binding capacity

Bacteria	Strain
Lactobacillus plantarum	R2014
	EQ12
	PT5B
Lactobacillus buchneri	R1102
Pediococcus acidilactici	R2142
	EQ01
Pediococcus pentosaceus	EQ44
	IA38
Propionibacterium jensenii	SE253
Propionibacterium acidipropionici	EQ42

0301 Effect of starter culture as a source of microbial contamination on the quality and safety of yogurt products in Egypt. M. M. Motawee[*1], W. E. D. I. Saber[2], and S. A. Ibrahim[3], [1]*National Organization for Drug Control and Research, Giza, Egypt,* [2]*Department of Microbiology, Giza, Egypt,* [3]*Food Microbiology and Biotechnology Laboratory, North Carolina A&T State University, Greensboro*.

Yogurt is one of the most common dairy foods in Egypt, yet the stability and shelf-life of yogurt remain a challenge to local producers. Thus, the objective of this study was to examine the effect of starter culture as a source of contamination on the quality and safety of yogurt product. In this study, we examined three groups of yogurt products. In group one, we collected 100 commercial yogurt products available in the marketplace. In group two, we made 10 yogurt batches ourselves using different yogurt starter cultures obtained from the local dairy industry. In group three, we made yogurt using yogurt culture from food microbiology stock culture. We then evaluated the types of microbial groups in relation to spoilage before and after storage of yogurt under chill condition and examined the microbial quality during storage at 7C for 14 d. Our results showed that during storage, there was an undesirable change in the commercial products as well as in yogurt products made with commercial starter cultures. All samples in groups one and two tested positive for *Aspergillus* spp. aflatoxin M1 and *Salmonella* spp. By contrast, the use of the control starter cultures prevented the presence of these contaminants in group three. Our results thus demonstrated that the use of a safe starter culture would be a promising approach to ensure the safety and quality of yogurt when it reaches the consumer.

Key Words: starter culture, yogurt, safety

0302 Effectiveness of pulsed light treatment on the inactivation of pathogenic and spoilage bacteria on cheese surface. J. Proulx[*1], L. Hsu[1], B. Miller[1], G. Sullivan[1], K. Paradis[2], and C. I. Moraru[1], [1]*Cornell University, Ithaca, NY,* [2]*McGill University, Montreal, QC, Canada.*

Cheese products are susceptible to post-processing cross-contamination that can lead to both food safety issues and significant losses due to spoilage. Pulsed Light (PL) treatment, consisting of short, high-energy light pulses, could represent a solution to address this issue since it is a nondestructive technology that can effectively inactivate microorganisms on surfaces. This study examined the effectiveness of PL on the inactivation of the spoilage microorganism *P. fluorescens* and the pathogen surrogates *E. coli* ATCC 25922 and *L. innocua.* The effect of inoculum level, cheese surface topography, and the presence of clear polyethylene packaging were evaluated in a full factorial experimental design. The challenge microorganisms were grown to stationary phase: *P. fluorescens* 1150 was grown at 30°C in tryptic soy broth (TSB) while *E. coli* ATCC 25922 and *L. innocua* FSL C2–008 were grown at 37°C in TSB and brain heart infusion (BHI), respectively. White cheddar and processed cheese, chosen for their different surface topography, were cut into 2.5 cm × 5 cm slices. The samples were then spot inoculated using ten droplets of 10 µL per slice, resulting in an initial concentration of either 5 or 7 log CFU/slice. Inoculated samples were dried overnight at 4°C. For treatments through packaging, sterile UV-transparent low-density polyethylene packaging was placed on top of the inoculated cheese samples immediately before the PL treatment. Cheese samples were then exposed to PL doses of 1.1 to 13.2 J/cm^2. PL-treated samples were stomached for 2 min in Butterfield Phosphate Buffer, the extract then plated on selective media and survivors enumerated by standard plate counting (SPC). When survivor counts fell below the SPC detection limit, the most probable number was used. Experiments were performed in triplicate and data were analyzed using a general linear model. PL was most effective against *E. coli*, achieving a maximum log reduction of 5.4 ± 0.3, at a dose of 13.2 J/cm^2. For *P. fluorescens*, a maximum log reduction of 3.7 ± 0.9 and for *L. innocua* a maximum log reduction of 2.9 ± 0.8 at 13.2 J/cm^2 were obtained. The process parameter effects tested showed varying statistical significance when used in different combinations, but PL treatments through packaging and without packaging consistently resulted in similar inactivation levels. This study suggests that PL has strong potential for decontamination of cheese surface.

Key Words: pulsed light, cheese, pathogenic and spoilage bacteria

0303 Evaluation of heavy metals, phenol, and polycyclic aromatic hydrocarbons on singed skin-on red Sokoto buck goats. O. A. Babatunde*[1], O. O. Olusola[2], O. J. Aremo[2], and W. Y. Akwetey[1], *[1]kwame Nkrumah University of Science and Technology, Kumasi, Ghana, [2]University of Ibadan, Ibadan, Nigeria.*

The safety of skin-on meat obtained from singed carcasses needs to be assessed. This study was therefore performed to investigate the concentration of heavy metals (Pb, Cd, Zn, Mn and Cu), phenol and polycyclic aromatic hydrocarbons (PAH) in red Sokoto buck goat carcasses singed using fire wood, kerosene, scrap tyre and liquefied gas (LG). A total of twenty four good grade red Sokoto buck goats weighing between 18-20 kg were randomly distributed into each of the four treatments in a completely randomized design. Each treatment was replicated six times. PAH levels were highest in scrap tyre singed carcasses (0.040 mg/kg) and least in LG singed carcasses (0.001 mg/kg). Pb and Mn were below detectable limit in carcasses singed with LG while the concentrations were similar ($P >$ 0.01) in the other treatments. Cd was not detected in any of the treatments. Zn concentration was highest in carcasses singed with kerosene (0.005 mg/kg). The level of phenol ranged from 0.02 Gae/kg in LG singed carcasses to 0.38 Gae/kg when scrap tyre was used. Material used in singeing was found to have profound effect on heavy metal, phenol and PAH depositions on skin-on meat from red Sokoto buck goats.

Key Words: skin-on, singed, heavy metal, phenol, polycyclic aromatic hydrocarbon, red Sokoto

FORAGES AND PASTURES I: SILAGES

0304 Effect of corn silage hybrids differing in starch and NDF digestibility on lactation performance and total tract nutrient digestibility by dairy cows. L. F. Ferraretto[*1], A. C. Fonseca[1], C. J. Sniffen[2], A. Formigoni[3], and R. D. Shaver[1], *[1]University of Wisconsin, Madison, WI, [2]Fencrest, LLC, Holderness, NH, [3]Università di Bologna, Bologna, Italy.*

The objective of this study was to determine the effect of feeding a TMR containing a floury-leafy corn silage hybrid (LFY) compared to a brown midrib corn silage hybrid (BMR) for intake, lactation performance and total tract nutrient digestibility in dairy cows. Ninety-six multiparous Holstein cows, 105 ± 31 DIM and 735 ± 18 kg of body weight at trial initiation, were stratified by DIM and randomly assigned to 12 pens of 8 cows each. Pens were randomly assigned to 1 of 2 treatments, BMR or LFY, in a completely-randomized design; a 2-wk covariate period with cows fed a common non-experimental diet followed by a 14-wk treatment period with cows fed their assigned treatment diet. Data were analyzed using Proc Mixed in SAS with covariate, treatment, period, and treatment × period interaction as Fixed effects and pen within treatment as a Random effect. Starch digestibilities, in situ, in vitro and in vivo, were 10%, 6% and 5% units greater ($P < 0.05$), respectively, for LFY compared to BMR; however, the opposite was observed ($P < 0.05$) for NDF digestibility at wk 13 of treatment. Cows fed BMR consumed 1.7 kg/d more dry matter than LFY ($P < 0.01$); feed sorting was minimal and did not differ by treatment ($P > 0.10$). Although milk yield was greater ($P < 0.01$; 49.0 vs. 46.8 kg/d) and energy- and solids-corrected milk yields tended ($P < 0.10$) to be 1.5 kg/d greater for BMR than LFY, feed conversions (kg milk or component-corrected milk per kg DMI) did not differ ($P > 0.10$). Fat-corrected milk (50.3 kg/d on average) and milk fat yield (1.84 kg/d on average) were similar ($P > 0.10$), as milk fat content was greater ($P < 0.01$) for cows fed LFY (4.05%) than BMR (3.83%). Cows fed BMR had lower ($P < 0.001$) MUN concentration and greater ($P < 0.05$) milk protein and lactose yields compared to LFY. Body weight change and condition score were unaffected ($P > 0.10$) by treatment. Total tract starch digestibility was greater for cows fed the LFY corn silage, however, dry matter intake and milk and protein yields were greater for cows fed the BMR corn silage.

Key Words: corn silage, fiber, starch

0305 The interaction of drought stress and heat stress as determinant of dry matter yield and nutritional composition of corn whole-plant for silage. G. Ferreira[*1], H. D. Behl[2], E. Hokanson[2], W. E. Thomason[2], and C. D. Teutsch[3], *[1]Department of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, [2]Department of Crop and Soil Environmental Sciences, Virginia Polytechnic Institute and State University, Blacksburg, [3]Department of Crop and Soil Environmental Sciences, Virginia Polytechnic Institute and State University, Blackstone*.

The objective of this study was to better understand how abiotic stresses affected DM yield and nutritional composition of corn whole-plant destined for silage. We analyzed data from corn hybrids performance trials completed at two sites over the 2011 and 2012 growing seasons within the state of Virginia. The first site is referred to as the Southern Piedmont region (Blackstone, VA). The second site is referred as Shenandoah Valley region (Lynnwood, VA). Data from eight corn hybrids (110 to 117 d to maturity) were tested in both sites and years. Dry matter yield and nutritional composition was analyzed through mixed model analysis, using hybrid as a fixed effect and site-year as a random effect (i.e., blocking factor). Climate data were obtained from weather stations located in Blackstone and Elkton, VA. Whole-plant DM yields did not differ between hybrids, but varied significantly across site-years. The extremely low DM yield observed for the Southern Piedmont region in 2012 (4556 kg/ha) is partially attributed to severe drought conditions (227 mm). However, substantially higher DM yields (12,678 kg/ha) were observed in the Shenandoah Valley region with only slightly more precipitations (262 mm) during the same year. Neutral detergent fiber concentrations did not differ among hybrids, but were significantly different between site-years. That NDF concentration in 2012 was much lower for the Shenandoah Valley region (43.0% NDF) than for the Southern Piedmont region (56.6% NDF) indicates that corn crops were affected differently despite summer drought. For year 2012, the Southern Piedmont region had maximum daily temperatures above 35°C for an extended period right after corn silking, whereas maximum daily temperatures were 7.1 ± 2.3°C milder in the Shenandoah Valley region for the same corn crop stage. We concluded that heat stress had a major adverse effect on kernel development in the Southern Piedmont region, but not in the Shenandoah Valley region and that, therefore, heat stress exacerbated the effects of drought, reducing substantially DM yields and increasing whole plant fiber concentration. As an overall conclusion, low DM yields and poor quality of corn whole-plant for silage are beyond drought stress. Daily maximum temperatures should be considered when planning strategies to ensure good quality forage supply and reduce risk in dairy farming systems.

Key Words: corn, drought, heat, silking

0306 Effects of different levels of corn silage and alfalfa hay on rumen pH, VFA, and milk production in dairy cows. A. Akbari-Afjani[1], A. Zali[2], M. Ganjkhanlou[2], M. Dehghan-Banadaky[*2], and A. Emami[3], *[1]University of Zanjan, Zanjan, Iran, [2]University of Tehran, Tehran, Iran, [3]University of Birjand, Birjand, Iran.*

The present study investigated the effects of different levels of corn silage and alfalfa hay on rumen pH, VFA and milk production of Holstein cows. In this study 15 Holstein cows (39 ± 9 kg milk yield/day; 37 ± 10 d in milk) were used in a completely randomized design experiment. Animals were kept in individual tie-stalls for 9 wk. Treatments included three levels of hay and corn silage: 1) 10% alfalfa hay, 30% silage corn (CS); 2) 20% alfalfa hay, 20% silage corn (AH-CS); and 3) 30% alfalfa hay, 10% silage corn (AH), and the ratio of forage:concentrate was 60:40. Cows were fed the total mixed rations (TMR) twice daily. Individual DMI was measured daily. On 4 and 9 wk of experiment, rumen fluid from the ventral sac was sampled using the rumenocentesis technique. Rumen fluid samples were taken 4 h after morning feed. Ruminal pH measured immediately after sampling using a pH meter. The rumen fluid was stabilized with sulfuric acid (1 cc per 50 mL) and frozen at -20°C until VFA analysis by gas chromatography. Normality of distribution and homogeneity of variance for residuals were tested using PROC UNIVARIATE and adjust Tukey-Kramer (SAS Institute, 2003). Dry matter intake was higher ($p < 0.05$) when cows were fed diets AH-CS (23.20 kg per day) and diet CS (22.95 kg per day) than diet AH (18.64 kg per day). Diet affected milk production with CS and AH-CS being higher ($P < 0.01$) than AH (34.88, 35.21 and 30.78 kg/day for diets CS, AH-CS and AH, respectively. Data from ruminal pH clearly showed replacing AH with CS had a quadratic effect on the rumen acidity ($P < 0.05$). In contrast to ruminal pH, ruminal VFA concentration was not meaningfully affected by the treatments ($P > 0.05$). It is concluded that feeding alfalfa hay more than corn silage reduced dry matter intake, therefore reduced milk production.

Key Words: alfalfa hay, corn silage, dry matter intake

0307 [Withdrawn]

0308 Effects of dairy slurry on the nutritive value and fermentation characteristics of alfalfa silages. W. K. Coblentz[*1], R. E. Muck[2], M. A. Borchardt[1], W. E. Jokela[1], M. G. Bertram[3], and K. P. Coffey[4], *[1]U.S. Dairy Forage Research Center, Marshfield, WI, [2]U. S. Dairy Forage Research Center, USDA-ARS, Madison, WI, [3]University of Wisconsin, Arlington, [4]University of Arkansas, Fayetteville.*

Dairy producers frequently ask questions about the risks associated with applying dairy slurry onto growing alfalfa. Our objectives were to determine the effects of dairy-slurry application on the subsequent nutritive value and fermentation characteristics of alfalfa silages. Dairy slurry was applied to 0.17-ha plots of alfalfa; applications were made to the second and third cuttings during 2012 at mean rates of 42,437 ± 5505.6 L/ha and 41,729 ± 2503.5 L/ha, respectively. Four application strategies were evaluated. These included: i) no slurry; ii) slurry applied directly to stubble immediately after the preceding harvest; iii) slurry applied after 1 wk of regrowth; or iv) slurry applied after 2 wk of regrowth. All harvested forage was packaged in (0.9 × 0.9 × 1.8 m) large-rectangular bales that were ensiled as wrapped balage. Each bale was sampled on both a pre-ensiled (June or August 2012) and post-ensiled basis (May 2013). Yields of DM harvested from the second (2477 ± 175.8 kg/ha) and third (781 ± 73.9 kg/ha) cuttings were not affected ($P \geq 0.19$) by slurry application treatment. By May 2013, all silages appeared to be well-fermented, with no indication of undesirable odor. Only minor differences across manure application treatments were observed for post-storage nutritive value, as well as final pH, unfermented water-soluble carbohydrates, and starch. *Clostridium tyrobutyricum*, which is known to negatively affect cheese production, was not detected in any forage on either a pre- or post-ensiled basis. On a pre-ensiled basis, counts ($\log_{10}$ genomic copies/g) for *Clostridium* Cluster 1 were greater for slurry-applied plots than for those not receiving slurry, and this response was consistent across the second (4.44 vs. 3.29; $P < 0.01$) and third cuttings (4.99 vs. 3.88; $P < 0.01$). Similar ($P < 0.01$) responses were observed on a post-ensiled basis; however, post-ensiled counts also were greater for delayed applications onto growing alfalfa compared with applications onto stubble for both the second (5.51 vs. 5.17; $P = 0.02$) and third (5.84 vs. 5.28; $P < 0.01$) cuttings. For the third cutting, counts also were greater following a 2-wk application delay compared to a 1-wk application delay (6.23 vs. 5.45; $P < 0.01$). These results suggest that the risk of secondary clostridial fermentations in alfalfa silages is greater following manure applications to alfalfa, and that applications to stubble are preferred (and less risky) compared to delayed applications onto growing alfalfa.

Key Words: alfalfa silage, clostridial fermentations, dairy slurry

0309 The effects of combination of lactic acid-producing bacteria and hydrolytic enzyme inoculants on ensiling characteristics of alfalfa and corn.

J. M. Chilson*, P. Rezamand, and M. E. Drewnoski, *University of Idaho, Moscow.*

Before ensiling, inoculants containing lactic acid-producing bacteria (LAB) may be used to promote greater, more rapid lactic acid production causing a faster pH decline, possibly resulting in less DM and nutrient loss. The inclusion of hydrolytic enzymes may increase simple carbohydrate availability, further increasing fermentation rate and pH decline. To test the effects of an inoculant containing four species of LAB and four hydrolytic enzymes, green chopped whole plant corn and alfalfa were treated with water (control) or with water containing the inoculant (treatment), resulting in forage that had 33% DM or 42% DM for corn and alfalfa, respectively. Each forage was packed into mini-silos (1206 cm^3 volume; $n = 3$/treatment per date) to monitor rate of fermentation. The pH was measured on d 1, 2, 3, 7, 13, 17, 21, 28, 45 for alfalfa and on d 1, 2, 3, 7, 10, 17, 28, 45 for corn. Data were analyzed using PROC NLIN and PROC MIXED of SAS significance declared when $\alpha = 0.05$. The rate of decline to terminal pH was faster ($P < 0.01$) in the treatment than control in alfalfa, but demonstrated no difference for corn ($P = 0.91$). Additionally, buckets ($n = 5$ per treatment; 21,504 cm^3 volume) of each forage were ensiled to measure effect on nutrient composition (DM, CP, ammonia, starch in the corn, and sugar in the alfalfa) and pH after 59 d of fermentation. The pH of the treatment tended to be lower than control in alfalfa buckets ($P = 0.07$) on d 59 but did not differ between treatments in corn ($P = 0.92$). The percent DM and DM loss did not differ ($P > 0.5$) between treatments for either alfalfa or corn. The percent sugar and starch did not differ ($P > 0.58$) between treatments for alfalfa and corn, respectively. Crude protein content of alfalfa was lower ($P < 0.01$) in the treatment than control (13.3 vs. 13.0 ± 0.06%) but did not differ ($P = 0.11$) between treatments in corn. Ammonia content did not differ ($P > 0.13$) between treatments for both alfalfa and corn. The inoculant appeared to affect the rate of decline to terminal pH in the alfalfa, but not corn, while having little to no effect on nutrient composition of either ensiled forage.

Key Words: silage, pH, inoculants

0310 In vitro digestibility and gas production kinetic characteristics of corn stover treated by calcium oxide and stored under anaerobic condition.

H. T. Shi*, Z. J. Cao, S. L. Li, W. N. Shi, and Z. H. Wu, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

As a large agricultural country, China is rich in corn stover resource. The nutritional value of corn stover can be improved by calcium oxide (CaO) treatment. Anaerobic storage is an effective method to prevent the treated stover from molding. A 1 plus 3 × 3 design was used to investigate the effect of CaO level and moisture content on the in vitro organic matter disappearance (IVOMD) and gas production in 72h (GP_{72h}). Ground stover was treated with different levels of CaO (3%, 5%, and 7%) and moisture content (40%, 50%, and 60%). Untreated stover was used as control. Treated stover was kept under anaerobic condition for 15 d. Four Holstein cows with ruminal cannulas were used as animal donors of rumen fluid. An automated gas production system was used. Half gram of samples was added to each bottle (4 replicates/sample). Data were analyzed using single degree of freedom contrast to compare all the treatments with the control, and data excluding the control were further analyzed as a 3 × 3 factorial arrangement of treatments. There were no treatment interactions ($P > 0.01$), but differences ($P < 0.01$) were found for main effects of moisture and CaO on IVOMD. The CaO level affected ($P < 0.01$) GP_{72h}, but the moisture content and its interaction with CaO level had no effect ($P > 0.01$) on GP_{72h}. The rate, halftime, and AGPR (gas production rate when gas production is 1/2 of the maxium) of gas production were not affected ($P > 0.01$) by the moisture or CaO level. As CaO level increased from 3% to 7%, IVOMD increased from 45.36% to 52.66%.The combination of CaO level and moisture content that resulted in the highest IVOMD was 7% CaO at 50% moisture content. There were no significant differences ($P > 0.01$) in IVOMD between stover treated with 5% CaO at 50% or 60% moisture content and that treated with 7% CaO at 50% moisture content. Under 50% and 60% moisture content, the level of CaO above 5% was not able to further improve the IVOMD. When treated with 5% CaO at 60% moisture content, the IVOMD and GP_{72h} of corn stover can be improved by 25.94% and 13.91%. Based on this study, the level of 5% CaO at 50% or 60% moisture content seems to be the best treatment combination.

Key Words: corn stover; calcium oxide treatment; in vitro digestibility

0311 Effects of calcium oxide level and moisture content on the in situ degradability of the alkali treated and anaerobically stored corn stover.

H. T. Shi*, S. L. Li, Z. J. Cao, Y. He, and Q. Zhou, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

Corn stover is one of the most abundant agricultural residues in the world. Calcium oxide (CaO) treatment could improve the nutritional value of corn stover. Anaerobic storage is an effective way to keep the treated stover free from molding. The aim of this study was to investigate the in situ degradability of the corn stover treated with different combinations of CaO level and moisture content. Ground stover was treated with different levels of CaO (3%, 5% and 7%) and moisture

content (40%, 50% and 60%), then stored under anaerobic condition for 15 d. Four Holstein cows with ruminal cannulas were used to evaluate the in situ ruminal degradability of DM, OM, and NDF (ISDMD, ISOMD, and ISNDFD) of the corn stover. Stover samples were incubated in the rumen for 0, 4, 8, 12, 24, 36, 48, and 72h. Compared with untreated corn stover, CaO-treated corn stover had greater ($P < 0.01$) ISDMD, ISOMD, and ISNDFD. The moisture content and CaO level affected ($P < 0.01$) ISDMD, ISOMD, and ISNDFD, but no interaction of main effects existed. The greatest improvements in ISDMD, ISOMD, and ISNDFD occurred when stover was treated with 7% CaO and 60% moisture content; however, no differences ($P > 0.01$) in these in situ degradability parameters were observed between the stover treated with 5% CaO at 60% moisture content and that treated with 7% CaO at 60% moisture content. When treated with 5% CaO at 60% moisture content, the ISDMD, ISOMD, and ISNDFD of the stover were increased by 31.72%, 34.03%, and 36.50%, respectively. Based on this study, the level of 5% CaO and 60% moisture content was a proper treatment for corn stover.

Key Words: corn stover, calcium oxide, |in situ degradability

0312 Effects of different silage forages on cecal fermentation in rabbits: In vitro gas production.

M. Gonzalez Ronquillo*, A. Zetina Sanchez, O. Castelan Ortega, and J. Romero Bernal, *Universidad Autonoma del Estado de México, Toluca, Mexico*.

The aim of this study was to evaluate the cecal fermentation of beans (*Phaseolus vulgaris*), faba beans (*Vicia faba*), common vetch (*Vicia sativa*), ryegrass (*Lolium perenne*), and barley (*Hordeum vulgare*) as silages in rabbits. In vitro gas production was performed using cecal contents from three rabbits (New Zealand, LW 2.5 k). Rabbits were fed forage silage and water ad libitum before cecal content collection. The rabbit's caeca was emptied and pooled cecal contents were mixed before being used for in vitro cultures. Chemical composition of forage species was determined and samples were weighed (0.800 g of DM) in 125 mL flasks and incubated with 90 mL of solution and 10 mL of cecal content, which previously diluted (50:50 with buffer solution). Gas production (GP) was measured at 1, 2, 3, 4, 8, 10, 12, 24, 36, and 48 h in three runs of inoculations. GP was calculated (ml/g DM) to evaluate the differences between forage species. Data were analyzed as a completely randomized design with contrasts used to compare means, significance was declared at $P < 0.05$. Crude protein was greater ($P < 0.05$) in common vetch followed by faba beans and beans, than the other species. NDF and ADF contents were lower ($P < 0.05$) in beans and common vetch, ME and SCFA were greater ($P < 0.05$) in faba beans and ryegrass, and less in barley silage. In vitro GP (fraction B) was greater ($P < 0.05$) in rye grass and faba beans than the rest of the silages. Lag time has greater in common vetch ($P < 0.05$) than the rest of the silages. Results suggested that ensiling ryegrass or faba beans are suitable for rabbits feeding compared with barley forage.

Key Words: rabbits, cecal fermentation, in vitro gas production

Table 0312. Chemical composition (g/kg DM) and in vitro gas production (IVGP, ml gas/g DM) of forage silages species in rabbits

Item	Barley	Ryegrass	Beans	Common vech	Faba beans	SEM	P-value
OM	969^{ab}	973^{a}	955^{b}	961^{ab}	965^{ab}	3.0	0.005
CP	46^{d}	139^{c}	146^{bc}	179^{a}	157^{b}	3.5	0.001
NDF	613^{a}	651^{a}	516^{b}	476^{b}	658^{a}	14.3	0.001
ADF	598^{a}	586^{a}	489^{b}	450^{b}	621^{a}	14.6	0.001
ADL	100^{f}	127^{e}	156^{c}	164^{b}	174^{a}	3.5	0.001
ME	10.3^{c}	20.0^{a}	16.6^{b}	17.3^{b}	20.3^{a}	0.5	0.001
SCFA	1.73^{d}	3.13^{a}	2.09^{cd}	1.99^{cd}	2.93^{ab}	0.12	0.001
IVGP							
B	87^{b}	121^{a}	88^{b}	90^{b}	119^{a}	5.3	0.001
C	0.0036^{c}	0.0236^{a}	0.008^{bc}	0.0113^{bc}	0.014^{abc}	0.002	0.001
Lag time	2.10^{b}	0.50^{b}	2.00^{b}	4.63^{a}	2.43^{b}	0.44	0.001

FORAGES AND PASTURES SYMPOSIUM: USE OF MARGINAL LANDS AND FIBROUS BYPRODUCTS IN EFFICIENT BEEF AND DAIRY PRODUCTION SYSTEMS

0313 Improving efficiency of production in pasture/range based beef and dairy systems.
J. T. Mulliniks*[1], A. G. Rius[2], M. A. Edwards[3], K. B. Brantley[3], S. R. Edwards[3], and R. L. Nave[1], *[1]University of Tennessee, Crossville, [2]Present address: University of Tennessee, Knoxville,, [3]University of Tennessee, Knoxville*.

Despite overall advances in technology and livestock production systems in the last century, it is still critical for research to be focused on efficient nutrient and forage utilization to improve efficiency of grazing beef and dairy production systems. Beef and dairy cattle have the advantage to capitalize on the ruminant's ability to utilize these feed resources that are not usable for other production industries. However, poor forage and subsequent energy utilization are often the primary limiting factors associated with decreased efficiency in range- and pasture-based beef and dairy systems. Although forage remains the least expensive nutrient source to maintain productivity of the cow herd, energy utilization of converting forage to a marketable output can be relatively inefficient. Thus, improving energy efficiency of pasture- and range-based grazing systems is essential to maintain long-term profitability and sustainability of livestock industry. Increasing profitability by optimizing grazing management and reproduction requires a rapid adoption of grazing management practices and genetic selection criteria for animals that fit diverse environment. The task of developing efficient production systems is biologically and economically complex and not easily achieved. Forage production and utilization on pasture- and range-based grazing systems varies tremendously across regions in the United States. This variation in forage production and utilization is due to differences in environmental conditions (e.g., temperature, precipitation, humidity, topography) and genetic makeup of the cow, which creates challenges in recommendations for specific genotype and grazing management schemes. However, matching cow type or genetic potential to the production environment and grazing management scheme may provide opportunities to increase energy utilization efficiency. In addition, pasture nutritive value and production varies within forage species across regions (e.g., cool-season vs. warm-season grass), and recommendations for grazing strategies leading to greater pasture utilization should factor differences in pasture composition. Therefore, increasing ruminants' efficiency of forage utilization through selection of energy efficient animals and/or grazing management decisions (i.e., supplementation, grazing management) would result in an increased profitability and sustainability.

Key Words: pasture, range, energy efficiency

0314 Forage breeding programs aimed at increasing productivity of marginal lands.
M. Casler*, *USDA-ARS, Madison, WI.*

The definition of "marginal lands" is highly contentious, subject to a wide range of opinions and contexts. For the purposes of this paper, I define marginal land simply as land with one or more problems that reduce crop productivity or economic sustainability. Numerous production and sustainability problems may be caused by land, soil, or atmospheric issues, including drought, nutrient imbalance, toxicity, pH imbalance, air pollutants, and temperature extremes. Forage crops, particularly perennials, are often relegated to these lands, particularly when crop productivity or sustainability falls below an economic viability threshold. As such, forage breeders have been faced with numerous challenges to breed both grasses and legumes that will tolerate these stresses, providing the basis for profitable and sustainable livestock production on lands that are "marginal" for crop production. The foundation of plant breeding is genetic variation, which has been observed for nearly all of the major stresses that have presented themselves as challenges for forage breeders. Genetic variation often must be coaxed out of a species by designing the proper challenge and screening method for the plants, such as an acid soil that is sufficiently acidic to cause measurable or observable stress, but not so much as to kill all the plants. For many stresses, it is quite common to find very low frequencies of tolerant or resistant plants, sometimes as low as < 1 in 10,000. For this reason, forage breeding is often a "numbers game" in which genetic improvements are directly proportional to the population sizes and efforts expended. Numerous cultivars have been developed and released to the public, often expanding the geographic range and broadening the environmental circumstances under which a forage species can be used for livestock production.

Key Words: forage breeding, genetic variation, stress tolerance, adaptation

0315 Improving soil health and productivity on marginal lands using managed grazing livestock.
R. R. James* and J. Bisinger, *Iowa State University, Ames*.

Beyond grazing, managed grasslands can provide ecological services with indirect and direct economic benefits that offer an incentive for multi-functional uses that provide the opportunity to increase available grazing lands. Increasing biodiversity of the plant community may maximize primary production by optimizing utilization of available light, water, and nutrient resources, enhance forage nutritive value for grazing livestock, improve nutrient retention while reducing nutrient leaching or loading in surface run off, enhance stability of

production in response to disturbance, increase soil organic matter, reduce invasion of exotic species, and provide wildlife feed and habitat. Strategically managed grazing may increase biodiversity of cool season pastures by creating disturbance in the established plant community through diet selection and treading as well as increased nutrient cycling and dispersal of plant seeds. Soil organic matter will increase carbon and nutrient sequestration and water-holding capacity of soils and is greater in grazed pastures than land utilized for row crop or hay production. Studies evaluating the effects of grazing management on soil organic matter in the eastern and central United States are limited. However, greater soil organic matter has been observed in cool season pastures grazed by management intensive than continuous grazing or grazed by mob or strip grazing than ungrazed grasslands. In addition to organic residues, pasture forages provide roots that produce macropores mitigating compactive forces on soils. The reduced soil compaction and increased surface structure provided by plant shoots and residues increase water infiltration. Therefore, water infiltration in cool season pastures managed to maintain 10 cm residual height did not differ from ungrazed pastures, which limits nonpoint-source pollution of surface water resources and provides resilience to floods and droughts. Through increased diversity of the plant community, productivity of selected species, and nutritive quality of the forage with alterations of habitat structure, grazing systems can be developed that enhance habitat for wildlife and insect pollinators. Although grazing management may enhance the ecological services provided by grasslands, environmental responses are controlled by variations in climate, soil, landscape position, and plant community, resulting in considerable temporal and spatial variation in the responses. Furthermore, a single grazing management system may not maximize both forage quality for grazing livestock and each of the potential ecological services provided by grasslands. Therefore, production and ecological goals must be integrated to identify the optimal grazing management for an individual site.

Key Words: grazing, biodiversity, ecological services

0316 Optimizing the use of fibrous residues in beef and dairy diets. J. C. MacDonald*, G. E. Erickson, P. J. Kononoff, and T. J. Klopfenstein, *University of Nebraska, Lincoln.*

Increased corn prices over the past decade have altered land use away from traditional forage in favor of corn. Accordingly, beef and dairy producers have had to adopt non-traditional forage resources into their production systems, many of which have become available as a result of increased corn production. Byproducts of the wet and dry milling industries have been used to replace both corn and forage in beef and dairy diets. Byproducts containing corn bran have large amounts of readily digestible hemicellulose. The use of byproducts may increase milk production, ADG, and G:F in dairy, beef growing, and beef finishing diets, respectively. In beef finishing diets, byproducts allow for use of low quality forages or partial replacement of traditional forages with minimal losses in ADG or G:F by formulating for equal NDF concentrations. Corn residues have become more available due to increases in corn acres and yield. The individual plant components (i.e., husk, leaf, stem) vary in fiber digestibility (NDF digestibility estimates = 40.5%, 31.4%, and 0.6% ± 0.8 for husk, leaf, and stalk, respectively). Selectivity for husks and leaves by grazing cattle likely improves their performance. New technologies that allow for selective harvesting of husk and leaf may result in a higher value feed product. Alkaline treatment is another technology that may improve the feeding value of residues. Concentrations of up to 20% harvested corn residue treated with calcium oxide may be included in finishing diets with an average of 2.3% reduction in G:F when diets contain 40% wet or modified distillers grains. Conversely, when untreated corn residues are included in similar finishing diets, G:F may be reduced by 20%. Calcium oxide treated residues included in beef growing diets increases DMI and ADG without significant improvements in G:F. Calcium oxide treatment of corn residues has been evaluated in dairy diets by replacing corn or corn silage with variable results. Harvesting corn silage rather than separate harvest of corn grain and residue may allow for greater total net energy per acre to be captured. The use of wet and modified corn milling byproducts enhances the use of corn silage in finishing diets. While G:F may be reduced, feeding greater concentrations of corn silage may be economical. Efficient use of non-traditional fiber sources, like corn milling by products and corn residue, are critical to the future viability of ruminant animal production.

Key Words: alternative fiber sources, corn milling byproducts, corn residue

FORAGES AND PASTURES II: **FORAGES FOR LIVESTOCK SYSTEMS**

0317 Interseeding bermudagrass pastures with alfalfa or clovers for growing calves. P. Beck*[1], D. S. Hubbell, III[2], T. Hess[2], and J. Jennings[3], *[1]University of Arkansas SWREC, Hope, [2]University of Arkansas Livestock and Forestry Research Station, Batesville, [3]Department of Animal Science, University of Arkansas, Little Rock.*

Bermudagrass [*Cynodon dactylon* (L.) Pers.] pastures (n = 8; 0.8 ha) were interseeded with 13 kg red clover/ha (Trifolium pretense, cv. Morningstar, Cal/West Seeds, Woodland, CA) and 3.3 kg ladino white clover/ha (*Trifolium repens*, cv. Regal Graze, Cal/West Seeds) or with 28 kg alfalfa/ha (*Medicago sativa*, cv. PGI 459, Producers Choice, Woodland, CA in yr 1 and cv. Rebel, Producers Choice, Woodland, Cain yr 2). Twelve additional bermudagrass pastures received 0, 56, or 112 kg N/ha as ammonium nitrate. Beef steers (n = 283, BW = 243 ± 30.5 kg) were used for BW gain analysis and grazed treatment pastures through the summer over 4 yr in this put and take experiment. In the fifth year of the experiment, clovers and alfalfa were killed before grazing and steers (n = 80, BW = 223 ± 13.3 kg) grazed pastures to determine the carryover N benefit to the bermudagrass following these legumes. Data were analyzed as a completely randomized design with the mixed procedure of SAS. Single df contrasts were used to determine the linear N fertilization rate effect and the effects of alfalfa and clover. Over the 4-yr experiment, ADG, BW, gain per hectare and grazing days per hectare increased (P < 0.01) linearly with increasing N rate. Yet ADG and BW of alfalfa and clover additions did not differ ($P \geq 0.14$) from the 112 kg N rate or each other. During the 4-yr experiment, grazing-d/ha was greater (P < 0.01) for alfalfa than clover, which was greater than all N fertilization rates ($P \leq 0.05$). Gain/ha of alfalfa and clover did not differ ($P \geq 0.31$) but were greater (P < 0.01) than all fertilization rates. In the final year of the experiment, ADG, grazing-d/ha, and gain/ha were not affected ($P \geq 0.19$) by N fertilization rate or carryover N from previous legume stands, indicating that benefit of carryover N from legumes to subsequent grass crops is minimal. Both clovers and alfalfa produced equivalent BW to the 112 kg N/ha fertilization rate and produced more grazing-d/ha and BW gain/ha than N fertilization, indicating improvements in diet quality with greater levels of fertilization or legume additions. Increases in grazing-d/ha and gain/ha with alfalfa or clovers were primarily through extension of the grazing season due to an earlier start of grazing.

Key Words: alfalfa, bermudagrass, clover, growing steers

0318 Grazing novel endophyte-infected fescue following grazing endophyte-infected fescue to alleviate fescue toxicosis in beef calves. T. B. Wilson*, M. R. Milnamow, M. A. West, D. B. Faulkner, F. A. Ireland, and D. W. Shike, *University of Illinois, Urbana*.

The objective was to investigate the efficacy of grazing novel endophyte-infected fescue following grazing endophyte-infected fescue as a means to alleviate fescue toxicosis; exhibited as poor ADG, BCS, hair coat score (HCS; 1−5), increased respiration rate, and decreased serum prolactin (PRL). Fall-born, Simmental × Angus calves (yr 1: n = 36 steers, average BW = 182 ± 28 kg; yr 2: n = 36 heifers, average BW = 240 ± 16 kg) were stratified by BW and randomly allotted into 6 groups within each yr. In yr 1, grazing (139 d) initiated May 2, 2012; in yr 2, grazing (121 d) initiated May 5, 2013. Groups were randomly assigned to 3 treatments: 1) endophyte-infected fescue (KY-31; whole grazing season), 2) novel endophyte-infected fescue (MaxQ; whole grazing season), and 3) KY-31 (early half of season, period 1) followed by MaxQ (late half of season, period 2; KY-31/MaxQ). Groups were rotated every 5 d through 3.24 ha pastures that were subdivided into six 0.54 ha paddocks. Put-and-take cattle were used to ensure forage availability was not different (P = 0.73) between treatments. Period 1 ADG, BCS, HCS and respiration rate were analyzed using a contrast of MaxQ vs. KY-31 and KY-31/MaxQ as both treatments grazed KY-31 pastures during this time. Period 1 respiration rate was not different (P = 0.26); yet, ADG was greater (P < 0.01) for cattle grazed on MaxQ than KY-31. Period 2 respiration rate was greater (P = 0.01) for KY-31 than MaxQ, with KY-31/MaxQ being intermediate. Period 2 ADG and final BCS were greater ($P \leq 0.04$) for MaxQ and KY-31/MaxQ than KY-31. There was a year × treatment interaction (P = 0.02) for final HCS. In yr 1, MaxQ and KY-31/MaxQ had improved ($P \leq 0.01$) final HCS than KY-31. In yr 2, MaxQ had improved ($P \leq 0.04$) final HCS, with no difference (P = 0.10) between KY-31 and KY-31/MaxQ. There was a treatment × time interaction (P < 0.01) for PRL. Mid- and end of period 1 PRL for MaxQ were greater ($P \leq 0.01$) than KY-31 and KY-31/MaxQ; however, mid- and end of period 2 PRL for MaxQ and KY-31/MaxQ were greater ($P \leq 0.01$) than KY-31. Overall ADG was greater (P < 0.01) for MaxQ and KY-31/MaxQ than KY-31. Grazing MaxQ following grazing KY-31 alleviated fescue toxicosis symptoms; thus, cattle experienced compensatory gain resulting in similar overall performance to cattle that grazed MaxQ continuously.

Key Words: beef cattle, endophyte, fescue grazing

0319 Metagenomic analysis of the rumen microbiome in wheat-induced frothy bloat among steers.
D. W. Pitta*[1], W. E. Pinchak[2], B. Veiccharelli[1], R. Sinha[3], and D. Fulford[2], *[1]University of Pennsylvania, Kennett Square, [2]Texas A&M AgriLife Research, Vernon, [3]University of Pennsylvania, Philadelphia.*

Frothy bloat is a serious metabolic disorder that causes reduced performance or mortality in stocker cattle grazing hard red winter wheat forage in the Southern Great Plains. We hypothesized a dysbiosis to develop in the rumen microbiome of stocker cattle when grazed on high quality winter wheat pasture that predisposes them to frothy bloat risk. In this study, rumen contents were harvested from six cannulated steers (mean BW 450 lb; three with bloat score '2' and three with bloat score '0'), extracted for genomic DNA and subjected for shotgun sequencing on 454/Roche platform. Approximately 1.5 million reads were sequenced, assembled and assigned for phylogenetic and functional annotations. Differences in microbial communities between bloated and non-bloated steers were analyzed using Mixed procedure of SAS. Bacteria predominated up to 84% of the sequences while archaea contributed to nearly 5% of the sequences. The abundance of archaea tended to be higher in bloated animals ($P < 0.12$) dominated by *Methanobrevibacter*. Predominant bacterial phyla were *Firmicutes* (65%), *Actinobacteria* (13%), *Bacteroidetes* (10%) and *Proteobacteria* (6%). *Firmicutes* were largely represented by *Eubacteriaceae*, *Ruminococcaceae*, *Lachnospiraceae* and *Eubacteriaceae*. However, only a few genera from Firmicutes such as *Butyrivibrio* and *Lactobacillus* showed differences ($P < 0.05$) between both groups. *Bacteroidetes* showed distinct differences between both groups with lineages from *Prevotellaceae* to be higher ($P < 0.05$) in bloated animals while non-bloated animals had higher ($P < 0.05$) abundance of *Porphyromonadaceae*, and *Bacteroidaceae* members. *Actinobacteria* was dominated by *Coriobacteriaceae* lineages, which tended to be higher ($P < 0.12$) in non-bloated steers. Functional annotations of assembled reads to KEGG database revealed the abundance of several metabolic pathways, with carbohydrate and protein metabolism well represented. Among the carbohydrate metabolism, utilization of monosaccharides was higher ($P < 0.05$) in bloated animals while disaccharide degradation tended to be higher ($P < 0.12$) in non-bloated animals. Assignment of contigs to CaZy database revealed the distribution of Glycosyl Hydrolases across all samples showing the presence of a core microbiome associated with fiber digestion. Principle component analysis based on phylogenetic and functional assignments both revealed the tendency to cluster microbial communities by the incidence of bloat, however validation will require greater sample numbers. It can be concluded that the rumen microbial community structure and metabolic potential are substantially altered under moderate frothy bloat conditions.

Key Words: rumen microbiome, frothy bloat, metagenomics, wheat forage

0320 Stocking density effects in short duration grazing systems on botanical composition and soil characteristics of grasslands.
J. J. Bisinger*, *Iowa State University, Ames.*

To evaluate stocking density effects in short duration grazing systems on grassland forage and soil properties, three replicated pastures containing cool season grass and legume species without (BL1) and with (BL2) warm season grasses were divided into 5 paddocks. In each pasture, one paddock was not grazed (NG) and 4 were strip (moved once daily with a back fence) or mob (moved 4 times daily with a back fence) grazed beginning in May 2011 (BL1) and 2012 (BL2) by 10 cows at a live forage DM allowance of 2% BW/d. Within each pasture, one mob (MR) and strip (SR) paddock were rotationally stocked to remove 50% of the live forage with 35 d rest periods beginning 60 d after mob or strip grazing in yr 1 of each block and in the two (BL1) and one (BL2) subsequent grazing seasons. Water infiltration, soil penetration resistance, soil bulk density, and soil carbon were measured in May and October and botanical composition was determined in May, July, and October of each year. Compared to NG paddocks, water infiltration was lower ($P < 0.05$) in rotationally stocked paddocks in October 2011 and 2012 in BL1 and greater ($P < 0.05$) in all grazed paddocks in October 2012 in BL2. Penetration resistance at 5 cm was greater ($P < 0.05$) in rotationally stocked than NG paddocks from May 2012 to October 2013 in BL1 and in October 2013 in BL2. Bulk density to 7.5 cm was less ($P < 0.05$) in NG than grazed paddocks in BL1 in October 2012 and rotationally stocked paddocks in October 2013 in BL2. Soil carbon content to 7.5 cm was greater ($P < 0.05$) in BL1 SR and BL2 MR paddocks than NG paddocks in May and October 2013, respectively. The proportions of cool season grasses in BL1 were lower ($P < 0.05$) in grazed than NG paddocks in July 2011 and in rotationally stocked paddocks after July 2012. Conversely, in grazed paddocks there were greater proportions of annual grasses ($P < 0.05$) in July 2011 and legumes ($P < 0.10$) in May and October 2012 than NG paddocks. In BL2, proportions of warm season grasses were less ($P < 0.05$) in rotationally stocked than NG paddocks in July 2013. Strategic spring mob or strip grazing will reduce competition from cool season grasses to allow establishment of legumes in perennial grasslands.

Key Words: beef cattle, mob stocking, botanical composition

0321 Seasonal changes in DM, CP, NDF, and NDF digestibility of pasture forage in grazing production systems. J. Paulson[*1], B. J. Heins[2], and D. G. Johnson[2], *[1]University of Minnesota, Hutchinson, [2]University of Minnesota West Central Research and Outreach Center, Morris.*

Nine grazing dairy farms were utilized in a study to measure monthly changes in forage quality of pastures over a 2-yr period. Farms were from a wide geographical area across Minnesota representing a range in soil type and annual rainfall amounts as well as herd size, pasture size and pasture management. Pasture forage was sampled every 2 wk during the growing season and analyzed for DM, CP, NDF, and NDF digestibility concentrations. Data were analyzed using PROC MIXED of SAS. Independent variables for analyses were the fixed effects of farm (n = 9), season (spring, summer or fall), year (1 or 2) and their interactions. Across the 9 farms, spring pasture DM (23.96%) was higher ($P < 0.05$) than summer (23.52%) and fall (19.76%) pasture DM. Average DM for each year was 22.71% and 22.12% for 2004 and 2005, respectively and they were not different. There were ($P < 0.05$) differences in CP concentrations between farms and across seasons on all farms and averaged 21.52% in year 1 and 21.85% in year 2. Seasonal average CP concentrations were 21.01%, 20.11% and 23.93% for spring, summer, and fall, respectively. NDF concentration in the pasture forage was different ($P < 0.05$) across the 9 farms, as well as different ($P < 0.05$) for spring, summer, and fall grazing. However, there were no differences within farm and season or across year for NDF; averaging 46.91% in year 1 and 47.53% in year 2. Seasonal NDF concentrations were 46.63%, 49.25%, and 45.97% for spring, summer, and fall, respectively. There was a difference ($P < 0.05$) across farms for NDF digestibility-30 h and within farm and year. Average NDF digestibility-30 h values for year 1 were 46.33% and for year 2 were 46.55%, and 46.64%, 44.71% and 47.98% for spring, summer, and fall, respectively. In summary, fall pasture growth was higher in CP and NDF digestibility when compared to spring and summer growth across all farms. However, NDF concentrations were highest in summer but CP and NDF digestibility were lowest in summer. There are significant seasonal effects on forage quality.

Key Words: dairy, grazing, forage quality

0322 Relationship between pasture nutritive measurements and plasma urea nitrogen in lambs grazing silvopasture or open pasture. J. P. S. Neel[*1] and D. P. Belesky[2], *[1]USDA-ARS, El Reno, OK, [2]West Virginia University, Morgantown.*

Relationship of herbage energy content relative to crude protein (CP) is an important aspect in nitrogen use efficiency of grazing livestock. Plasma urea nitrogen (PUN) is an indicator of animal nitrogen status, increasing with excessive dietary nitrogen, resulting in greater urinary N excretion. Analytical procedures utilized to estimate herbage energy content can be laborious and expensive. Our objective was to evaluate the relationship between herbage CP and herbage energy content indicators of differing assessment cost (total non-structural carbohydrate [TNC]; total digestible nutrients [TDN]), with animal PUN. We utilized winter born lambs (n = 187; initial weight 28.7 ± 2.1 kg; final weight 41.4 ± 2.9 kg), grazing either open or silvopasture over 4 consecutive grazing seasons. Grazing began in mid-April each year on cool-season mixed pastures and concluded mid-September. Forage nutritive value was determined from clipped samples taken the day before grazing events. Herbage TNC was determined directly, while TDN was estimated from ME (NRC, 1996) via ADF (MAFF/ADAS, 1987). Lambs grazed fresh paddocks (minimum 35 d regrowth after initial grazing) for 2 h and held an additional 1 h in drylot before blood draw. We correlated (Pearson) the relationship of pasture nutritive measurements and PUN. After tallying across treatments and years the number of correlation coefficients within the following categories: $r > 0.5$, > 0.6, > 0.7 or > 0.8, we evaluated the relationships. All nutritive components except TDN performed similarly using the $r > 0.5$ criteria. Within this grouping, the ratio of TDN:CP (a negative relationship, −) had the greatest total number of r values > 0.5 (16 of 22, or 73%), while TDN alone (−) had just 3 of 22 (14%). Using > 0.6 criteria, sampling date (+) and TNC:CP (−) were best, with 11 of 22 (50%) being greater. They were followed closely by TDN:CP (−) and TNC (−), 10 of 22 (45%), and 9 of 22 (41%), respectively. Within the grouping $r > 0.7$, sampling date and TNC:CP remained highest at 9 of 22 (41%), while TDN:CP and TNC were 5 of 22 (23%) and 8 of 22 (36%), respectively. For $r > 0.8$, sampling date and TNC:CP still had approximately 25% of the correlation coefficients falling within this category. The use of TNC:CP appears to be a quick, economical, and useful tool to evaluate pasture energy status relative to crude protein.

Key Words: silvopasture, plasma urea nitrogen, nutritive value, total non-structural carbohydrate

0323 Effect of organic grain supplementation on production, body weight, body condition score, and fatty acid profiles of organic dairy cows. B. J. Heins[*1], M. I. Endres[2], J. Paulson[3], and R. D. Moon[2], *[1]University of Minnesota West Central Research and Outreach Center, Morris, [2]University of Minnesota, Saint Paul, [3]University of Minnesota, Hutchinson.*

Organic cows (n = 153) were used to evaluate the effect of grain supplementation levels during 2 grazing seasons (May to September 2012 and May to September 2013) on production, body weight, body condition score (BCS), and fatty acid profiles of organic dairy cows. Cows were assigned to 1 of 3 replicate supplementation groups: 1) no grain supplementa-

tion (100% pasture, GRS, $n = 51$), 2) low grain (2.72 kg/head/day, LOW, $n = 51$), and 3) high grain (5.44 kg/head/day, HI, $n = 51$), and calved at the University of Minnesota West Central Research and Outreach Center, Morris, Minnesota. Supplement (organic corn and minerals) was fed with a partial mixed ration (PMR) of corn silage and alfalfa haylage, and at least 30% of diet dry matter intake for LOW and HI cows consisted of organic pasture. Milk production, from daily milk weights, was averaged weekly for cows, and body weight and BCS were recorded bi-weekly. Milk for fatty acid analysis was collected monthly and analyzed at R-Tech Analytical Laboratory (Arden Hills, MN). The PROC MIXED of SAS was used for statistical analysis, and independent variables were fixed effects of year (2012 or 2013), season of calving (fall or spring) nested within year, parity (1, 2, 3+) nested within year, supplementation group, breed group; week nested with supplementation group, with replicate nested within year and cow nested within supplementation group and breed group as a random effect with repeated measures. The GRS (14.4 kg/d) cows had lower ($P < 0.05$) energy-corrected milk than LOW (16.2 kg/d) and HI (17.0 kg/d) cows; however, the LOW and HI cows were not different from each other. The GRS, LOW, and HI cows were not different for body weight across the grazing season (491, 498, 498 kg, respectively); however, GRS (3.05) cows had lower ($P < 0.05$) BCS than LOW (3.14) and HI (3.15) cows. Milk urea nitrogen was higher ($P < 0.05$) for GRS (19.5 mg/dl) than LOW (12.0 mg/dl) and HI (9.9 mg/dl) cows. Furthermore, omega-3 fatty acid was higher ($P < 0.05$) for the GRS (0.05%) cows compared to the LOW (0.04%) and HI (0.03%) cows. Organic dairy cows that consume 100% pasture had lower production, but milk from cows that consume 100% pasture compared to pasture and PMR had fatty acid composition of potential benefit to human health.

Key Words: organic, fatty acid profile, pasture

0324 Chemical composition and in vitro gas production of forage cereals associated with common vetch (*Vicia sativa*). M. Gonzalez Ronquillo*, E. Y. Aguilar Lopez, A. Morales, M. G. Gutierrez, and O. Castelan Ortega, *Universidad Autonoma del Estado de México, Toluca, Mexico.*

Cereal grain forages and legume silages are an important part of dairy cattle rations in many parts of the world. The increasing importance of these crops as feedstuffs has highlighted the need to understand the factors that influence their nutritive value. The use of in vitro gas production (GP) techniques to estimate digestibility of feeds was based on empirical relationships between digestibility and in vitro gas production. The objectives were to evaluate forage yield, chemical composition and in vitro gas production of some varieties of spring triticale (T-UAEMex and Siglo XXI), barley (Doña Josefa) and its association with common vetch (CV). The experimental unit consisted in seven rows, each 50 linear meters by 30 cm wide (with two lines of planting and spaced at 80 cm). The planting density was 80,000 plants/ha, harvested at 145 d (milky-dough stage) and ensiled in three repetitions, at 60 d the samples were opened from micro-silos (2 kg FM), and chemical composition was determined, GP profiles were determined using a semi-automated pressure transducer technique. Approximately 800 mg of each substrate was weighed into 125 mL serum bottles and incubated in a water bath at 39°C with 10 mL strained rumen fluid and 90 mL of medium. The volume of gas produced was recorded at 3, 6, 9, 12, 24, 36, 48, 72, and 96 h of incubation. Each sample was incubated in triplicate in three series in different weeks. Data were analyzed by a completely randomized design. There were differences ($P < 0.001$) in DM (dry matter) production, being greater T-Siglo XXI and associated with CV (6.50 and 5.4 ton DM/ha respectively), the greater CP content ($P < 0.001$) was for CV (217 g/kg) and their associations (185 g/kg). No significant differences ($P > 0.05$) were observed among varieties and their associations in NDF contents. Barley had a greater content ($P < 0.05$) of NE_l 1.5, and NE_g 0.9 (Mcal/kg DM). GP was greater for the association Barley−CV ($P < 0.05$) (124 ± 6 mL gas/g DM) compared to the rest (117 ± 3 mL gas/g DM). Considering its nutritional quality and energy content forage cereals associations with CV are an option with higher forage yield and improved nutritional content for feeding livestock.

Key Words: common vetch, silage, in vitro gas production.

GRADUATE STUDENT COMPETITION: ADSA DAIRY FOODS DIVISION ORAL COMPETITION

0325 Improving properties of acid skim milk gels by adjusting non-micellar to micellar protein ratio and controlling protein interactions.

G. H. Meletharayil*[1], H. A. Patel[2], and S. G. Sutariya[1], [1]*South Dakota State University, Brookings,* [2]*Dairy Science Department, South Dakota State University, Brookings.*

In addition to the protein content, the type and status of milk protein in yogurt milk may affect the final rheological properties of yogurts. In the present study, we investigated the effects of altering non-micellar to micellar casein ratio on the rheological properties and microstructure of acid gels. Model acid gel formulations containing 0, 10, 30, and 60% protein substitution from carbon-dioxide-treated milk proteins (T-MPC) as a source of non-micellar casein and non-fat dry milks (NFDM) as a source of micellar casein were developed. All the samples were standardized to 4% w/w protein and 12% w/w total solids. The pH was adjusted to 6.5 before their pre-heating to 90°C/10 min. Acid milk gels were prepared using Glucono-δ-lactone to obtain final pH4.4 ± 0.05 after 4 h incubation at 30°C. The soluble (serum) phases obtained by centrifugation of heated and unheated milk samples at 25000 g/1h were characterized using sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Microstructure and rheological properties of acid gels were characterized using confocal laser scanning microscopy (CLSM) in the fluorescence mode and small amplitude oscillatory rheology (SAOR) (1% strain, 0.1Hz frequency), respectively. Photon correlation spectroscopy was used to study the particle size of the heated milks. ANOVA was used to test the results and statistical significance at $P < 0.05$ was determined, using the statistical software SAS. The SDS-PAGE pattern of model formulations containing T-MPC showed significantly higher ($P < 0.05$) proportion of soluble caseins and disulfide-linked casein-whey protein complexes in the serum phase of unheated and heated milk, respectively. Particle size of formulations containing T-MPC was significantly lower than control samples containing untreated proteins. This can be attributed to the preferential interaction of whey proteins with κ-casein in the soluble phase. SAOR showed a significant increase ($P < 0.05$) in the elastic modulus (G') of acid gels formulated with T-MPC to an optimum level. CLSM images revealed that gels containing treated proteins had smaller, well-connected aggregates with uniform, homogenous pore-sizes, which explained the results of rheological characterization. It can be concluded that the soluble casein-whey protein complexes and optimum non-micellar to micellar casein ratio in the yogurt formulation yielded acid gels with significantly improved rheological properties. Overall, the results suggested that yogurt with varying texture can be made by altering the ratio of non-micellar to micellar casein and by manipulating interactions of milk proteins at soluble and micellar phase. This invention is patent pending.

Key Words: yogurt, carbon dioxide, rheology, microstructure

0326 Controlling the viscosity of milk concentrates through tailored casein-whey protein interactions.

S. G. Sutariya*[1], H. G. Patel[1], T. Huppertz[1,2], and G. H. Meletharayil[1], [1]*South Dakota State University, Brookings,* [2]*NIZO food research, Ede, The Netherlands.*

Heat-induced interactions between caseins and whey proteins form the basis for their functionality in many applications. We have hypothesized that the pH of the milk before preheat-treatment and adjusting preheating temperatures will influence the distribution of casein-whey protein complexes between the micellar and the soluble (serum or continuous) phase of milk and this will affect the viscosity of the continuous phase in concentrated milk. Therefore, the objective of the present study was to investigate the effect of pH and preheating temperatures on the viscosity of skim milk concentrates. Reconstituted milk, 10% w/w total solids (TS), adjusted to pH 6.5, 6.7 (control) and 6.9 was preheated either at 80 or 90°C for 5 min. Following these treatments, the milk was concentrated to final TS of 45 and 50% (w/w) under vacuum at 60°C using a rotary evaporator. Dynamic viscosity of the resulting concentrates was measured at 55°C at a constant shear rate of 100 s^{-1} using a Stresstech Rheometer. Particle size was determined using a Malvern Zeta-sizer-Nano-ZS. The heated and pH adjusted samples were centrifuged at 25,000 g for 1 h to obtain soluble (serum) and micellar phases. The protein interactions in these milk samples were characterized in detail using non-reduced and reduced sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE). The experiments were repeated at least two times and results were tested by ANOVA and statistical significance at $P < 0.05$ was determined, using the statistical software SAS. Significant differences in the viscosity of milk concentrates were observed ($P < 0.05$) when the milk was pre-adjusted to different pH and pre-heated at different temperatures. The results showed that the concentrates obtained from milk preheated at pH 6.5 and 80°C for 5 min had significantly ($P < 0.05$) lower viscosity compared to that preheated at pH 6.7 and 6.9 at both TS levels studied (45 or 50% w/w). The samples pre-heated at pH 6.5 also showed increase in particle size in contrast to the samples preheated at pH 6.7 and 6.9. Such differences can be explained by differences in the interactions of casein and whey proteins and distribution of casein-whey protein complexes distributed at continuous phase and micellar phase as shown by SDS-PAGE. It can be concluded that adjusting the pH and preheating temperature of milks can be used as levers for controlling viscosity of milk

concentrate for powder manufacturing, which ultimately has an influence on the efficiency of drying.

Key Words: milk concentrate, viscosity, casein-whey proteins, pH.

0327 Partial calcium depletion during membrane filtration impacts gelation of reconstituted milk protein concentrates. H. Eshpari*[1,2], P. S. Tong[3], and M. Corredig[4], *[1]University of Guelph, Guelph, ON, Canada, [2]California Polytechnic State University, San Luis Obispo, [3]Dep. of Dairy Science, California Polytechnic State University, San Luis Obispo, [4]Dept Food Science, University of Guelph, Guelph, ON, Canada.*

Solubilization of colloidal calcium phosphate (CCP) from casein micelles during membrane filtration (e.g., through acidification) may affect the structural organization of these protein particles. The aim of this study was to investigate the effects of addition of glucono delta lactone (GDL) to skim milk during membrane filtration on the structural changes of the casein micelles by studying their functionality after reconstitution of the final powders. In particular, the renneting behavior of the casein micelles was examined, as renneting is affected by both the calcium equilibrium and their supramolecular structure. Milk protein concentrate (MPC) powders were manufactured in duplicate, either by ultrafiltration (65% protein, MPC 65) or by ultrafiltration followed by diafiltration (80% protein, MPC80), using pasteurized skim milk, either at the native milk pH (~ pH 6.6), or after addition of GDL to pH 6.0, followed by spray drying. The amount of total calcium for the MPC80 without and with GDL varied with a significant difference ($p < 0.05$) from 18,449.5 ± 265 to 15,954.5 ± 271 (μg/g), respectively. Samples were reconstituted at a 3.2% (w/w) protein to compare their gelation behavior between treatments. Both reconstituted MPC 65 and MPC 80 treated with GDL showed significantly increased amounts of soluble calcium ($p < 0.05$) and non sedimentable caseins compared to their respective controls, as measured by ion chromatography and SDS-PAGE electrophoresis, respectively. The primary phase of rennet gelation was not significantly different ($p < 0.05$) between treatments, as measured by the amount of caseino-macropeptide released, using reverse phase-high performance liquid chromatography (RP-HPLC). Rheological measurements were performed using a controlled stress rheometer on the reconstituted samples immediately after addition of rennet, both before and after dialysis against skim milk, to ensure similar serum composition for all samples. While reconstituted samples before dialysis showed no gelation (defined as tan d = 1), only control MPC 65 and 80 showed gelation after serum re-equilibration. It was concluded that the gelation properties of reconstituted MPC powders were negatively affected by the presence of soluble casein, and positively affected by the amount both soluble and insoluble calcium present after reconstitution. This work, testing the renneting behavior of various reconstituted MPC samples, clearly demonstrated that decrease in pH to 6.0 during membrane filtration affects the structure of casein micelles with important consequences to their processing functionality.

Key Words: milk protein concentrate, calcium depletion, rennet coagulation

---

0328 Utilizing whey protein isolate and polysaccharide complexes to stabilize aerated dairy gels. E. C. O'Chiu* and B. Vardhanabhuti, *University of Missouri, Columbia.*

Previous research has shown that heated soluble complexes of whey protein isolate (WPI) with polysaccharides can improve both foam stability and acid-induced gel strength. We utilized these complexes in aerated dairy gels, which could be formulated into novel-textured high-protein desserts. The objective of this study is to determine the effect of polysaccharide charge density and concentration within a WPI-polysaccharide complex on the properties of aerated gels. Three polysaccharides having different degrees of charge density were chosen: low methoxyl pectin (LM-12), high methoxyl type D pectin (HM-D), and guar gum. WPI-polysaccharide complexes were prepared by heating the mixed solutions (8% protein, 0 to 1% polysaccharide) at pH 7. To form aerated gels, 2% glucono-δ-lactone (GDL) was added to the solutions and foam was generated by whipping with a handheld frother. The foam set into a gel as the GDL acidified to a final pH of 4.2. The aerated gels were evaluated for overrun and rheological properties. Stability was determined by measuring drainage (the volume of liquid separated from the aerated gels). Overrun of aerated gel (179% to 14%) significantly decreased as polysaccharide concentration increased due to increased viscosity, which limited air incorporation. Increased concentration was significantly related to increased stability ($P < 0.001$) which could be due to increased viscosity of the pre-foam solutions limiting the mobility of the air bubbles. A negative logarithmic relationship was found between solution viscosity and drainage. However, charge density played an important role on stability. Plot of drainage against solution viscosity revealed that drainage was lowest in samples with high charge density pectin (LM-12) followed by those with low charge density pectin (HM-D). Aerated gels with guar gum (no charge) did not show improvement to stability as separation still occurred even at highest guar concentration. Rheological results showed no significant difference in gelation time among samples; therefore, stronger interactions between WPI and high charge density polysaccharide were likely responsible for increased stability. Rheological results also revealed that aerated gels with LM-12 pectin had the highest final elastic modulus, followed by guar gum, then HM pectin gels. Stable dairy aerated gels can be created from WPI-polysaccharide complexes. High charge density polysaccharides, at concen-

trations that provide adequate viscosity, are needed to achieve stability while also maintaining solution overrun capabilities. This can inform the formulation of dairy-based gels set by acid or calcium such as whipped yogurts and mousses.

Key Words: acid-induced gelation, aeration, whey protein

0329 pH-triggered intragastric gelation of whey protein/alginate and its effect on sucrose release.

S. Zhang* and B. Vardhanabhuti, *University of Missouri, Columbia, MO.*

Protein digestion is highly influenced by gastric conditions, protein structures, and the presence of other food components in the gastrointestinal tract. Protein and dietary fibers are common food ingredients; however, the effect of dietary fiber on protein digestion is not fully understood. Our previous study showed that whey protein/pectin mixture formed intragastric gel under simulated gastric conditions, which slowed the degradation of protein and could potentially affect the digestion and release of other nutrients. The objective of this study was to investigate the in vitro gastric behavior of mixed whey protein and alginate, and its effect on the digestion pattern of protein and sucrose release. Mixed solutions of 5% whey protein isolate (WPI), alginate (0.01 to 0.05 alginate to WPI wt. ratio) and 10% sucrose were prepared by heating them together at 85°C for 30 min. Simulated gastric fluid (SGF) consisted of 0.034 M NaCl, 3.2 mg/g pepsin, and pH was adjusted to 1.2, 2, 3, and 4. The in vitro digestion was performed using reciprocating cylinder dissolution apparatus, with 10-g sample added to 78 g SGF (pepsin: protein = 1: 2). Rheological properties and electrophoresis were performed to evaluate the gastric behavior of the mixture, and HPLC was used to measure sucrose release during digestion. At low alginate to WPI ratios, alginate did not significantly affect the degradation of whey protein and the bioavailability of sucrose, as shown by SDS-PAGE and HPLC, respectively. Increasing biopolymer ratio to 0.05 led to extensive intragastric gelation immediately when samples were mixed with SGF at pH 1.2. The mechanism behind intragastric gelation is believed to be the cross-linking between oppositely charged protein and alginate molecules when pH was reduced to lower than the pI of protein. Sucrose was entrapped in the gel network since no sucrose was detected in the digestion media once the intragastric gel was formed. During dissolution, physical movement and proteolysis by pepsin led to slow degradation of the gel, which also resulted in the slow release of sucrose from the matrix in 20 min. Intragastric gelation was only observed in SGF at pH 1.2 and 2.0. This study indicated that at certain conditions whey protein and alginate mixtures could form intragastric gel, which delayed protein digestion and sucrose release from the matrix. These results can potentially lead to formulation of whey protein beverage having lowered postprandial glycemic response.

Key Words: intragastric gelation, digestion, sucrose

0330 Evaluation of an adsorbent for the removal of aflatoxin M1 from contaminated milk.

E. D. Womack*, D. L. Sparks, A. Brown, and S. H. Ward, *Mississippi State University, Mississippi State.*

Lactating cows that consume aflatoxin B_1 (AFB_1) contaminated feed containing approximately 20 parts per billion (ppb) may produce aflatoxin M_1 (AFM_1) contaminated milk that exceeds the FDA maximum allowable limit of 0.5 ppb. Current detoxification methods for the reduction of AFM_1 include the use of sequestering agents added to feed. The sequestering agents act as an enterosorbent to ameliorate the toxicity of AFB_1 by reducing intestinal absorption. However, not all AFB_1 is bound and the residual can be metabolized to AFM_1. Once this tolerance level of 0.5 ppb AFM_1 is surpassed, the milk must be discarded because it cannot be used for human consumption resulting in economic losses. The current study examines the proficiency of an adsorbent, powdered activated carbon (PAC) to bind AFM_1 in various milk types as PAC has excellent adsorption properties in an aqueous environment. A total of 24 samples ($r = 3$) contained artificially spiked AFM_1 (0.5 ppb) and 0.1%, 0.25%, and 0.4% PAC in whole, skim, and raw milk. Samples were shaken, extracted using Agilent QuEChERS extraction salts, and analyzed via liquid chromatography with mass spectrometry detection. A concentration of 0.5 ppb AFM_1 was spiked into 10 mL to yield a final concentration in whole (0.54 ± 0.07 ppb), skim (0.46 ± 0.01 ppb), and raw milks (0.56 ± 0.03 ppb). The highest concentration of PAC (0.4%) resulted in a significant decrease in AFM_1 contamination ($p < 0.05$) with a reduction of 65% (0.18 ± 0.08 ppb), 91% (0.05 ± 0.01 ppb), and 52% (0.24 ± 0.03 ppb) of AFM_1 from the whole, skim, and raw milks, respectively. No milk showed any significant difference in percent protein, lactose, or total fat relative to their milk blanks ($p > 0.05$) suggesting that PAC has no effect on milk constituents. Preliminary results show that the use of PAC can reduce the amount of AFM_1 below the FDA safety limit and, as a result, prevent the dumping of milk.

Key Words: AFM_1, activated carbon, milk

0331 Application of FT-IR and flow cytometry to evaluate the effect of sodium chloride on probiotic bacteria.

N. Shah and A. Gandhi*, *The University of Hong Kong, Hong Kong.*

The aim of the study was to investigate the effect of varying sodium chloride concentrations on cell membrane, viability and proteolytic activity of probiotic bacteria. Reconstituted skim milk was inoculated with *Lactobacillus acidophilus* at varying salt concentrations (0-10% NaCl) and pH levels (4.0, 5.0 and 6.0) and ACE-inhibitory activity and proteolytic activity were determined. Additionally, the effects of NaCl reduction and its substitution with KCl on cell membrane of certain probiotic bacteria (*Lb. acidophilus*, *Lb. casei* and *B. longum*) and

a pathogenic bacterium, *Escherichia coli* were investigated using Fourier transform infrared spectroscopy (FT-IR). A critical NaCl concentration that inhibited the growth of *E. coli* without significantly affecting the growth of probiotic bacteria was determined by monitoring cell growth and FT-IR spectra. To evaluate the effect of substitution of NaCl with KCl, substitution was performed at critical total salt concentration at varying concentrations (0%, 25%, 50%, 75% and 100% KCl). Furthermore, the effects of varying NaCl concentrations on viability, membrane integrity and metabolic activity of these probiotic bacteria were studied using conventional technique and flow cytometry. The findings revealed that in *Lb. acidophilus* degree of proteolysis increased with higher salt concentration at pH 5.0 and 6.0 and ACE-inhibitory activity was highest at pH 5.0 at all salt concentrations. Fourier transform infrared spectroscopy results demonstrated significant shifts occurring in amide-I and amide-III regions when *Lb. acidophilus* was subjected to varying salt concentrations. Further, the conventional technique revealed that 2.5% was the critical level of NaCl to inhibit the growth of *E. coli* without significantly affecting the growth of most probiotic bacteria. The FT-IR analysis also highlighted the changes that occurred mainly in amide regions on increasing NaCl concentration from 2.5 to 3% in most bacteria. The findings suggest that 50% substitution of NaCl with KCl at 2.5% total salt could inhibit *E. coli*, without affecting the probiotic bacteria. Lastly, the observations from conventional culture technique were compared with the findings from flow cytometric analysis on metabolic activities of the cells and it was revealed that there was a correlation between culturability and dye extrusion ability of *Lb. casei* and *B. longum*. However, a certain population of *Lb. acidophilus* was viable as per the plate count method but the efflux activity was compromised. The metabolic activity of *Lb. casei* was found to be highest among the three probiotic bacteria.

Key Words: FTIR, flow cytometry, probiotic bacteria

0332 Genomic insights into high exopolysaccharide-producing dairy starter bacterium *Streptococcus thermophilus* ASCC 1275. N. Shah, Q. Wu* and H. M. Tun, *The University of Hong Kong, Hong Kong.*

Streptococcus thermophilus ASCC 1275 (ST 1275) is a typical dairy starter bacterium and produces the highest known amount (~1,000 mg/L) of exopolysaccharide (EPS) in milk within this species. This organism produces both capsular and ropy EPS and possesses textural modifying properties for yogurt and cheese. In this study, de novo shotgun paired-end pyrosequencing was applied to complete the whole genome of ST 1275. The genome size of ST 1275, a plasmid-free bacterium, was ~ 1.85 Mbp with an average GC content of 39.1%. A novel *eps* gene cluster for EPS assembly containing two-pair genes of *eps*C-*eps*D for determining the chain length of EPS was found in ST 1275 genome, which confirms that ST 1275 produces two types of EPSs as found in our previous studies. Compared with other sequenced *S. thermophilus* strains, ST 1275 possessed the lowest numbers of 5 rRNA operons and 55 tRNAs suggesting that this organism may have a more effective protein synthesis machinery. The highest number of four separate CRISPR (clustered regularly interspaced short palindromic repeats)-Cas (CRISPR-associated) loci was found in ST 1275 genome indicating that this organism may have a better adaptive immunity against various bacteriophage infections. Further analysis including carbohydrate utilization, effective proteolytic system, sophisticated stress response systems and defense systems in ST 1275 was performed to provide genomic insights into its adaptation to milk and as a cell factory for EPS production during milk fermentation. The elucidation of ST 1275 genome makes this organism as a model dairy starter bacterium for the research of high EPS yield and capsular/ropy EPS producer from the species of *S. thermophilus*.

Key Words: genome sequencing; EPS biosynthesis; *Streptococcus thermophilus*

0333 Effectiveness of pulsed light treatment on the inactivation of pathogenic and spoilage bacteria on cheese surface. J. Proulx*[1], L. Hsu[1], B. Miller[1], G. Sullivan[1], K. Paradis[2], and C. I. Moraru[1], [1]*Cornell University, Ithaca, NY,* [2]*McGill University, Montreal, QC, Canada.*

Cheese products are susceptible to post-processing cross-contamination that can lead to both food safety issues and significant losses due to spoilage. Pulsed Light (PL) treatment, consisting of short, high-energy light pulses, could represent a solution to address this issue since it is a nondestructive technology that can effectively inactivate microorganisms on surfaces. This study examined the effectiveness of PL on the inactivation of the spoilage microorganism *P. fluorescens* and the pathogen surrogates *E. coli* ATCC 25922 and *L. innocua*. The effect of inoculum level, cheese surface topography, and the presence of clear polyethylene packaging were evaluated in a full factorial experimental design. The challenge microorganisms were grown to stationary phase: *P. fluorescens* 1150 was grown at 30°C in tryptic soy broth (TSB) while *E. coli* ATCC 25922 and *L. innocua* FSL C2–008 were grown at 37°C in TSB and brain heart infusion (BHI), respectively. White cheddar and processed cheese, chosen for their different surface topography, were cut into 2.5 cm × 5 cm slices. The samples were then spot inoculated using ten droplets of 10 μL per slice, resulting in an initial concentration of either 5 or 7 log CFU/slice. Inoculated samples were dried overnight at 4°C. For treatments through packaging, sterile UV-transparent low-density polyethylene packaging was placed on top of the inoculated cheese samples immediately before the PL treatment. Cheese samples were then exposed to PL doses of 1.1 to 13.2 J/cm^2. PL-treated samples were stomached for 2 min in Butterfield Phosphate Buffer, the extract then plated on selective media and survivors enumerated by standard plate

counting (SPC). When survivor counts fell below the SPC detection limit, the most probable number was used. Experiments were performed in triplicate and data were analyzed using a general linear model. PL was most effective against *E. coli*, achieving a maximum log reduction of 5.4 ± 0.3, at a dose of 13.2 J/cm^2. For *P. fluorescens*, a maximum log reduction of 3.7 ± 0.9 and for *L. innocua* a maximum log reduction of 2.9 ± 0.8 at 13.2 J/cm^2 were obtained. The process parameter effects tested showed varying statistical significance when used in different combinations, but PL treatments through packaging and without packaging consistently resulted in similar inactivation levels. This study suggests that PL has strong potential for decontamination of cheese surface.

Key Words: pulsed light, cheese, pathogenic and spoilage bacteria

GRADUATE STUDENT COMPETITION: ADSA PRODUCTION ORAL COMPETITION, MS

0334 Nutrient utilization and metabolism by lactating dairy cows fed high-forage diets with protein supplements. K. Neal[*1], J. S. Eun[1], A. J. Young[1], and K. Mjoun[2], [1]*Utah State University, Logan,* [2]*Alltech, Brookings, SD.*

Due to the increasing cost of soybean meal and concerns of excess N being excreted into the environment, new protein supplements have been developed. Two products that have shown potential in increasing N utilization efficiency are slow release urea (SRU; Optigen, Alltech, Nicholasville, KY) and ruminal escape protein derived from yeast (YMP; DEMP, Alltech). The objective of this study was to assess the effects of feeding these 2 supplements in high-forage (54% of total dietary DM) dairy diets on nutrient utilization, feed efficiency, lactational performance of dairy cows, and their impacts on income-over feed costs (IOFC). Twelve multiparous dairy cows were used in a triple 4 × 4 Latin square design with one square consisting of ruminally cannulated cows. Treatments included: 1) control, 2) SRU-supplemented TMR (SRUT), 3) YMP-supplemented TMR (YMPT), and 4) SRU and YMP-supplemented TMR (SYT). The control consisted only of a mixture of soybean meal and canola meal (SBMCM) in a 50:50 ratio. The SRU and the YMP were supplemented at 0.49% and 1.15% DM, respectively. The experiment consisted of 4 periods lasting 28 d each (21 d of adaptation and 7 d of sampling). Cows fed YMPT and SYT had decreased DMI, and all supplemented treatments had lower CP intake compared to those fed the control. Milk yield tended ($P = 0.08$) to have the greatest increase in YMPT compared with the control (41.1 vs. 39.7 kg/d) as well as a tendency for increased milk fat ($P = 0.10$) and protein yields ($P = 0.07$). Feed efficiencies were improved in all diets with protein supplementation at 10–16% ($P < 0.04$). Cows fed with protein supplements partitioned less energy toward BW gain, but tended ($P = 0.08$) to partition more energy toward milk production. Efficiency of use of feed N to milk N increased by feeding SRUT and YMPT, and milk N to manure N ratio increased in YMPT. Cows fed SRUT or YMPT tended ($P < 0.10$) to improve IOFC. Overall results from this experiment indicate that replacing SBMCM with SRU and YMP in high-forage dairy diets can be a good approach to enhance farm profitability through improved nutrient utilization efficiencies by lactating dairy cows.

Key Words: dairy profitability, high-forage dairy diet, protein supplement

0335 Individual and additive value of conventional and non-conventional technologies in beef steers housed in small research pens. A. R. Harding[1], G. K. Jim[2], C. W. Booker[2], E. J. Behlke[2], S. L. Parr[2], S. J. Hannon[2], T. M. Greer[2], Z. D. Paddock[2], M. L. May[2], L. O. Burciaga-Robles[2], and C. R. Krehbiel[1, 1]*Oklahoma State University, Stillwater, Feedlot Health Management Services, Ltd., Okotoks, AB, Canada.*

This trial was conducted at a research feedlot in Alberta, Canada to evaluate the effects of conventional and non-conventional production technologies identified from previous research in feedlot steers. The study utilized 960 steers stratified by BW and randomly allocated to one of four treatments: rumensin/tylan/growth-promotant free (RT), Oleo/growth-promotant free (O), negative control (NC), or conventional (CON). The RT cattle received Rumensin and Tylan (Elanco Animal Health), and did not receive an implant or β-agonist. The O cattle were fed 1 g/animal/day of Oleobiotec Ruminant (Oleo; Laboratoires Phodé, Terssac, France), and did not receive an implant or β-agonist. The NC cattle received a non-medicated supplement of vitamins and minerals and did not receive an implant or β-agonist. Cattle in the CON group received a hormonal implant (Revalor-200; Merck Animal Health, Intervet Canada Corp., Kirkland, Québec), Rumensin, Tylan and Optaflexx (Elanco Animal Health) at the end of the feeding period. All study animals received a barley-based finishing diet and were housed by treatment in 48 research pens. Data were analyzed using the GLIMMIX procedure (SAS Institute Inc, Cary, North Carolina). Final BW and HCW were lower for the RT, O, and NC ($P < 0.001$) cattle relative to the CON cattle. In addition, RT, O, and NC cattle had decreased ADG and poorer G:F on both a live and carcass adjusted basis ($P < 0.001$) relative to the CON cattle. The RT cattle had improved G:F compared to the O and NC cattle on a live weight basis ($P < 0.001$). The RT cattle also had better G:F compared to the NC cattle on a carcass adjusted basis ($P < 0.001$). Cattle in the O group tended ($P = 0.051$) to have improved G:F compared to NC cattle on a carcass weight basis. No differences in carcass quality or animal health were detected between experimental groups. These results indicate that animal performance can be improved with conventional (implant, β-agonist, ionophore, and antimicrobial) or non-conventional (Oleobiotec) production technologies relative to a negative control.

Key Words: feedlot, cattle, technology

0336 The effects of supplementing two pasteurized milk balancer products to pasteurized whole milk on the health and growth of dairy calves.
K. M. Glosson*[1], B. A. Hopkins[1], S. Washburn[1], S. Davidson[1], G. Smith[1], T. Earleywine[2], and C. Ma[1], [1]*North Carolina State University, Raleigh,* [2]*Land O'Lakes Animal Milk Products, Shoreview, MN.*

Neonatal Holstein heifer calves (n = 72) received one of three dietary treatments: M (no supplement), MB (Land O'Lakes Pasteurized All-Milk Balancer), or MPB (Land O'Lakes Pasteurized Protein-Blend Balancer) from d 1 through weaning at d 56. Two locations were used in this trial, NCSU Lake Wheeler Dairy (Raleigh, NC) and NCDA Piedmont Research Station (Salisbury, NC), with 36 calves on trial at each site. All calves were removed from their dams after birth (d 0) and fed 3.8 L pasteurized colostrum. All calves were fed pasteurized whole milk from d 1 through d 56. Calves were fed 3.8L milk divided into 2 equal feedings from d 1 through d 14 and 5.7L milk divided into 2 equal feedings from d 15 through weaning at d 56. Supplements given to MB and MPB were included at a rate of 0.23kg of their respective balancer per 3.8L of pasteurized whole milk. Calves were weighed and measured for wither height (WH), hip height (HH), and hip width (HW) every 7 d from birth until weaning at d 56. Average daily gain (ADG) and feed efficiency (FE) were calculated from d 0 through d 56. Feed efficiency is the ratio of total gain to total dry matter intake (DMI), which included milk balancer DM and calf starter DM consumed. A contrast statement was used to compare M to the average of MB and MPB, and a second contrast compared the two supplemented treatments, MB versus MPB. Calves fed MB and MPB had greater body weight (BW), ADG, HW and WH when compared to calves fed M. Calves fed MB or MPB performed similarly.

Key Words: calf, milk balancer, pasteurized

Table 0336. BW, HH, HW, WH, ADG and FE as affected by treatment for 72 Holstein heifer calves from birth through weaning at 56 d

	Treatment				M vs. 1/2 (MB+MPB)	MB vs. MPB
	M	MB	MPB	SEM	$P \leq$	$P \leq$
BW, kg	53.8	56.7	58.19	1.0	0.01	0.3
HH, cm	85.0	85.5	86.3	0.7	0.2	0.3
HW, cm	18.8	19.0	19.4	0.2	0.04	0.1
WH, cm	80.4	81.1	82.1	0.7	0.04	0.1
ADG, kg	0.70	0.80	0.77	0.03	0.01	0.3
FE, total gain/ total DMI	0.75	0.69	0.64	0.04	0.09	0.4

0337 Relationship between fertility and postpartum changes in body condition and body weight in lactating dairy cows.
P. D. Carvalho*[1], A. H. Sousa[2,3], M. C. Amundson[2], K. S. Hackbart[2], A. R. Dresch[2], L. M. Vieira[2], J. N. Guenther[2], R. R. Grummer[2,4], R. D. Shaver[1], P. M. Fricke[2], and M. C. Wiltbank[1], [1]*University of Wisconsin, Madison,* [2]*Department of Dairy Science, University of Wisconsin-Madison, Madison,* [3]*University of California Cooperative Extension, Tulare,* [4]*Balchem Corporation, New Hampton, NY.*

The relationship between energy status and fertility in dairy cattle was analyzed retrospectively by: analyzing the effect of early postpartum changes in body condition score (BCS; Expt 1) and post-partum changes in body weight (Expt 2) on fertility. To reduce the effect of cyclicity status, all cows were presynchronized with Ovsynch before to a second Ovsynch and timed AI (TAI after Double-Ovsynch; Expt 1; First GnRH at 53 ± 3 DIM; TAI at 80 ± 3 DIM) or synchronized superovulation (Expt 2). Data were analyzed by logistic regression with GLIMMIX and ANOVA using the MIXED procedure of SAS. In Expt 1, lactating dairy cows on two commercial dairies (n = 1887) were divided by BCS change from calving until third week postpartum. Overall, P/AI at 70 d pregnancy diagnosis differed dramatically ($P < 0.001$) by BCS change and were least for cows that lost BCS, intermediate for cows that maintained BCS, and greatest for cows that gained BCS (22.8% [180/789], 36.0% [243/675], and 78.3% [331/423], respectively). Effects of BCS change on fertility were similar for primiparous and multiparous cows, but differed by farm with BCS change dramatically affecting ($P < 0.001$) P/AI on one farm however there was no effect ($P = 0.35$) on the other farm. In Experiment 2, body weight of lactating dairy cows (n = 71) was measured weekly from first to ninth week postpartum. Cows were divided into quartiles by percentage of body weight change from calving until third week postpartum. (Q1 = +2.39%; Q2 = -0.07%; Q3 = -3.50%; Q4 = −6.84%). Cows were superovulated (TAI = 70 ± 3 DIM) and there was no effect of quartile on number of ovulations (17.9), total embryos/oocytes collected per cow (8.5), or percentage of oocytes that were fertilized (77.5%). In contrast, the percentage of fertilized oocytes that were transferable embryos was greater ($P = 0.04$) for cows in Q1, Q2 and Q3 than Q4 (83.8%, 75.2%, 82.6%, and 53.2%, respectively). In addition, percentage of degenerated embryos was less ($P = 0.02$) for cows in Q1, Q2, and Q3 compared to Q4 (9.6%, 14.5%, 12.6%, and 35.2% respectively). In conclusion, change in BCS during the first 3 wk postpartum had a profound effect on P/AI to first TAI. This effect could be partially explained by the reduction in embryo quality and increase in degenerate embryos 7 d after AI in cows that lost more body weight from first to third week postpartum. Supported by Hatch project WIS01171.

Key Words: BCS loss; body weight loss; embryo quality; fertility

0338 Effect of serum calcium status at calving on survival, health, and performance of postpartum dairy cows and calves. A. Hunter*[1], M. G. Maquivar[2], S. Bas[1], T. A. Brick[1], W. P. Weiss[3], J. S. Velez[4], H. Bothe[4], and G. M. Schuenemann[1], [1]*Department of Veterinary Preventive Medicine, The Ohio State University, Columbus,* [2]*Department of Animal Sciences, Washington State University, Pullman,* [3]*Department of Animal Sciences, The Ohio State University, Wooster,* [4]*Aurora Organic Farms, Platteville, CO.*

Limited evidence is available in the literature about the effect of hypocalcemia (HYPO) of dams at calving on survival and health of calves. The objective was to assess the effect of clinical and subclinical HYPO ($\leq$ 8 mg/dL) at calving on survival, health, and performance of lactating dairy cows and calves. Prepartum dairy cows (primiparous, n = 450; multiparous, n = 334) from one dairy herd were monitored (close-up pen) for imminent signs of birth (appearance of amniotic sac outside the vulva) until birth. Calving ease, time of birth, single or multiple calves, calf sex, and stillbirth (born dead or died within 24 h after birth), BCS immediately after calving, and hygiene score of the perineum were recorded. All female calves were subject to the same newborn care and colostrum management. Total serum Ca (HYPO) of cows was determined within 2 h after calving. The effect of HYPO on survival (died or culled within 30 DIM), metritis, and pregnancy per AI (P/AI) for first services of lactating cows were assessed using GLIMMIX. The effect of HYPO on calf survival, failure of passive transfer (FPT; serum total proteins $\leq$ 5.5 mg/dL), and diarrhea within 10 d of age were assessed using GLIMMIX. Diarrhea was defined as a calf presenting fluid or bloody feces (scores 2-3; 0-3 scale) and > 5% dehydration or fever ($\geq$ 39.5°C). The overall prevalence of HYPO was 15%. Cows experiencing HYPO at calving had greater proportion ($P < 0.05$) of metritis (29.4%) and culling within 30 DIM (23.5%) compared to non-hypocalcemic cows (17.3% and 6.9%, respectively). The proportion of P/AI at first service was not different between HYPO (30%) and non-HYPO cows (37%; $P > 0.05$). The proportion of stillbirth and FPT was not different ($P > 0.05$) between calves born from HYPO or non-HYPO cows. However, calves born from HYPO cows had greater (49%; $P < 0.05$) proportion of diarrhea than those calves born (33.3%) from non-HYPO cows. Dairymen, consultants, and veterinarians often trouble-shoot transition cow diseases and this process requires constant monitoring and comprehensive assessment of several events. Findings from the present study showed that HYPO at calving had significant health implications for both dams and calves.

Key Words: hypocalcemia, cow and calf health, dairy

0339 Sodium salicylate decreases glucose turnover rate in periparturient dairy cows, likely through enhanced liver insulin sensitivity. S. R. Montgomery*, L. Mamedova, A. J. Carpenter and B. Bradford, *Kansas State University, Manhattan*.

Low-grade inflammation has been implicated as a contributor to metabolic disease during the transition to lactation. However, in previous work, administration of sodium salicylate (SS) for 7 d led to hypoglycemia in mature dairy cows in early lactation. The purpose of this study was to identify the mode of action underlying this response to SS. Twenty mature (3+ parity) cows were assigned alternately at time of calving to either control (CON) or SS treatments. CON treatment received a molasses carrier in drinking water while the SS received 2.5 g/L SS with the molasses carrier in drinking water for 7 d after parturition. Blood samples were collected daily. A glucose turnover assay was performed on Day 7, followed by liver, muscle, and adipose tissue biopsies. Results were analyzed in the MIXED procedure of SAS with significance declared at $P < 0.05$. There were no treatment effects on DMI ($P = 0.98$) or water intake ($P = 0.61$). Tumor necrosis factor α (TNFa) mRNA expression was decreased by SS in adipose tissue ($P = 0.09$), but not in muscle ($P = 0.97$) or liver ($P = 0.52$), and plasma haptoglobin was not altered by treatment ($P = 0.34$). Though treatment did not alter plasma glucose or insulin concentrations, RQUICKI, a measure of insulin sensitivity, and plasma glucagon tended to be increased by SS ($P = 0.08$ for both). The insulin:glucagon ratio was increased by SS ($P = 0.01$). Cows on SS had a 25% decrease in glucose turnover rate ($P = 0.05$). There were no differences in mRNA expression of gluconeogenic genes in liver or of GLUT4 transporters in any of the tissues. These results indicate that SS may increase insulin sensitivity in mature fresh cows. This increase in sensitivity of insulin could explain the lower glucose turnover rate because of increased post-transcriptional inhibition of gluconeogenesis by insulin during SS treatment.

Key Words: NSAID, transition cow, insulin resistance

0340 Effects of elevated subcutaneous fat stores on serum nonesterfied and milk fatty acid profile and peripheral blood mononuclear cells gene expression of pro-inflammatory markers and production measures in periparturient dairy cows. C. M. Scholte*, K. C. Ramsey, C. Y. Tsai, A. Hendrickson, Z. M-Amiri, B. Shafii and P. Rezamand, *University of Idaho, Moscow, ID.*

Dairy cows with greater subcutaneous fat stores release greater concentrations of nonesterified fatty acids (NEFA) into the blood during the periparturient period. The objective of this study was to determine the effect of elevated lipid mobilization during the periparturient period on serum NEFA and milk fatty acid (FA) profile, peripheral blood mononuclear cells

(PBMC), gene expression of selected markers of inflammation and production measures. Thirty-four cows were blocked by parity; treatment received a dry cow ration with an additional 10 kg of corn/head per day starting -28 d relative to parturition. The control received the dry cow ration (no additional corn) with 400 mg of monensin/head per day. Immediately postpartum, cows were fasted for 8 h. Serum samples were collected on -28, −7, +1, +6, +15, and +21 d for FA analysis of specific lipid fractions. Milk samples were obtained on +1, +3, +6, +15, and +21 d for composition, yield, and FA analyses. Real-time q-PCR gene analysis for intercellular adhesion molecule 1 (*ICAM-1*), interleukin (*IL*) 1β and 6, and tumor necrosis factor-α (*TNF-α*) was performed on PBMC collected on -28, +3, +12, and +21 d. Data were analyzed as repeated measures analysis of variance using mixed model procedures in SAS (9.3) and significance was declared at $P \leq 0.05$. Within serum NEFA fraction, C16:1, sum of C18:1 *trans*, and C18:3n3 were greater in control than in treatment prepartum, but no significance was detected in postpartum. In contrast, sum of C18:1 *trans* was greater in treatment compared with that of control during postpartum period. Serum concentration of C20:4n6 tended to be greater in treatment compared with that of control (1.12 vs. 0.86 ± 0.11%; $P = 0.06$). In milk fat, C16:1 and C18:2 *cis* were greater for treatment and C15:0, C18:3n3 and C22:2 were lower for treatment compared to with control. Gene expression for *IL-1β* in PBMC was greater for control, whereas *ICAM-1*, *IL-1β*, *IL-6*, and *TNF-α* were greater in primiparous than multiparous cows, without a detectable treatment effect. Prepartum, control cows consumed more feed than treatment. Postpartum intake indicated a marginal treatment × time interaction, with intake wavering until d +11 and treatment consuming relatively more thereafter. In summary, increased subcutaneous fat stores altered FA profile of serum NEFA fraction and milk as well as gene expression of PBMC in periparturient dairy cows.

Key Words: lipid mobilization, fatty acid profile, peripheral blood mononuclear cells

---

0341 Effect of prophylactic and therapeutic antibiotic administration on fecal excretion of antibiotic resistance genes by dairy cows. L. R. Caudle*, H. M. Littier, A. Pruden, X. Feng, and K. F. Knowlton, *Virginia Tech, Blacksburg.*

The objective of this study was to determine the effect of prophylactic and therapeutic antibiotic administration on fecal excretion of antibiotic resistance genes (ARG) in dairy cows. Twelve primiparous lactating Holstein cows were used in a completely randomized design. Four treatments included the administration of cephapirin (intramammary), pirlimycin (intramammary), or ceftiofur (subcutaneous), as well as a control group where no antibiotic was given. Fecal samples were collected from all cows before antibiotic administration on d 0 and then on d 1, 3, 5, 7, 14, 21, and 28 following treatment. Fecal samples were freeze-dried and DNA was extracted using the FastDNA Spin Kit for Soil. Extracted DNA was analyzed using quantitative polymerase chain reaction for genes encoding for resistance to tetracyclines (*tet*O and *tet*W) and β-lactams (*amp*C) as well as a housekeeping gene (16S rRNA) to monitor bacterial abundance. Statistical analysis was performed using Proc Glimmix in SAS with a model including treatment, day, and their interaction with pre-treatment (d 0) abundance as a covariate. Absolute (log10 copies/g feces) and relative (gene copies/16S rRNA) abundance of *tet*O, *tet*W, and *amp*C were not influenced by antibiotic treatment. Absolute abundance of 16S rRNA was lower ($P < 0.04$) in feces of pirlimycin-treated cows than in feces of cephapirin-treated cows and also tended to be lower ($P < 0.06$) than in feces of control cows. This suggests effects of pirlimycin on total fecal bacterial numbers. There was an effect of day on relative abundance of *tet*W ($P < 0.04$) and *amp*C ($P < 0.04$) in all cows, with fecal excretion highest on d 3 post-treatment. Absolute abundance of *tet*W in feces was influenced by day ($P = 0.01$), with excretion highest 28 d post-treatment. In this study, prophylactic and therapeutic antibiotic administration did not increase excretion of the three target ARG by dairy cows. The observed temporal pattern in ARG excretion will help identify the most useful time frame for possible interventions to reduce dissemination of ARG from dairy farms. These results will inform further analysis of the entire complement of known ARG using shotgun metagenomics.

Key Words: antibiotic resistance genes, dairy cow, feces

0342 Effects of oscillating the crude protein content in dairy cow rations. A. N. Brown*[1] and W. P. Weiss[2], *[1]The Ohio State University, Wooster, [2]Department of Animal Sciences, The Ohio State University, Wooster.*

Overfeeding crude protein (CP) is a common practice in the dairy industry to reduce the risk of a loss in milk; however, overfeeding CP increases costs and negatively impacts the environment. We hypothesized that oscillating dietary CP concentrations to equal the average concentration of a diet limited in metabolizable protein (MP) for lactating dairy cows will improve milk protein yield and milk N efficiency because oscillating CP should stimulate nitrogen recycling to the rumen. Twenty-one Holstein dairy cows averaging 123 DIM were randomly assigned to a treatment sequence in seven 3 × 3 Latin Squares with 28-d periods. The control diet contained 16.4% CP (MP allowable milk = 47 kg/d), the low protein diet contained 13.4% CP (MP allowable milk = 31 kg/d), and the oscillating treatment consisted of a diet with 10.3% CP fed for 2 d followed by a diet with 16.4% CP fed for 2 d repeated over the 28 d period to average 13.4% CP. The cows were fed once daily and milked twice daily. Cows on the low protein diet had greater DMI than cows on the oscillating treatment (24. 8 kg/d vs. 24.3 kg/d; $P = 0.04$) but were similar in DMI compared to

cows on the control diet (24.8 kg/d). There was no treatment difference ($P > 0.05$) for milk yield (avg. 34.6 kg/d), feed efficiency, milk fat yield, milk fat content, and milk protein content. Milk protein yield showed a treatment effect; however, treatment contrasts showed no difference between the oscillating treatment and low treatment and between the high and low treatments. Milk urea nitrogen (MUN) increased with protein content of the diet (14.5 mg/dl vs. 9.1 mg/dl; $P < 0.0001$) with no difference in MUN between cows fed the low and oscillating treatments except that MUN followed a cyclic pattern for oscillating cows. Given that cows on the low diet produced more milk than MP allowable milk, cows on the low protein diet used nitrogen more efficiently than expected or the NRC overestimated the requirements. Although milk and milk protein production were not affected by the oscillating treatment, very little research has been done on oscillating CP content of dairy cows rations; therefore, this study is a first step in understanding how oscillating protein affects dairy cows.

Key Words: dairy cow, metabolizable protein, oscillating protein

---

0343 Interaction among energy status and retinoid status in periparturient dairy cows: production, milk retinoid, and metabolic response.

K. C. Ramsey*, J. D. Blickenstaff, C. Y. Tsai, C. M. Scholte, W. Price, M. A. McGuire, and P. Rezamand, *University of Idaho, Moscow.*

An objective of this study was to determine the effect of feeding various amounts of dietary vitamin A (0 or 110 IU/kg BW), crude protein (12.5% or 16%), and an ionophore (monensin at 0 or 400 mg/d per head) on performance measures, retinoid metabolism, immune system, and metabolic response. Multiparous Holstein dairy cows ($n = 80$) were studied from day -35 to +21 relative to expected parturition, in a complete randomized block design with a 2 × 2 × 2 factorial arrangement of treatments. Milk samples were obtained at the first, second, third milking, and every 3 d thereafter, and processed for components, somatic cell count (SCC), retinol, α-tocopherol, and β-carotene. Serum samples were collected on d -35, −7, +3, +9, +21 and processed for NEFA, BHBA, haptaglobin, and thiobarbituric acid reactive species (TBARS). Peripheral blood mononuclear cells (PBMC) were also isolated on d +7. Real time qPCR gene analysis for intercellular adhesion molecule (*ICAM-1*), interleukin (*IL*) 1β and 6, and tumor necrosis factor-α (*TNF-α*) were performed on PBMC. Significance of treatments was declared at $P \leq 0.05$. Results indicated vitamin A reduced ($P = 0.05$) milk SCC with no effect on milk yield or composition, DM intake both pre- and postpartum. An effect of CP × monensin on milk retinol concentration was observed (2.19, 1.72, 2.12, and 2.35 ± 0.16 µg/mL for low CP + monensin, low CP– monensin, high CP + monensin, and high CP– monensin, respectively; $P = 0.03$), but no differences in milk α-tocopherol and β-carotene were found. Furthermore, serum haptoglobin was lower ($P = 0.03$) with greater dietary CP. Also, cows that received monensin had lower ($P = 0.013$) serum haptoglobin postpartum compared with the prepartum concentrations observed. No differences in serum NEFA, BHBA, or TBARS were detected. Cows that received greater CP had increased gene expression of *TNF*-α ($P = 0.04$) in PBMC, but not effect on gene expression of *ICAM-1*, *IL-1β*, and *IL-6* was found. Overall, these observations show that dietary vitamin A, monensin and protein affect retinol and SCC in milk without affecting performance measures. Further studies are needed to fully understand the retinoid metabolism in the transition dairy cow.

Key Words: transition cows, retinoids, gene expression

0344 Reproductive performance of timed artificial insemination and activity-based estrus detection.

K. A. Dolecheck*, W. J. Silvia, G. Heersche Jr., and J. M. Bewley, *University of Kentucky, Lexington*.

A study comparing reproductive management programs without visual estrus detection was conducted using 268 cows from 2 commercial dairy herds in Kentucky between October 2012 and November 2013. Before enrollment, resumption of ovarian activity was confirmed and BCS was evaluated. Eligible cows (BCS ≥ 2.5) were balanced for parity and predicted milk yield then randomly assigned to 1 of 2 treatments: TAI or activity. Ovulation synchronization using G7G/Ovsynch and Resynch occurred up to 3 times for all cows assigned to the TAI treatment. Cows assigned to the activity treatment received a leg-mounted accelerometer (AfiTag Pedometer Plus, S.A.E. afimilk, Kibbutz Afikim, Israel) and were bred according to estrus alerts created by the system algorithm for up to 90 d after the voluntary waiting period (VWP). Pregnancy diagnosis via ultrasound occurred 33 to 46 d after insemination and pregnancy loss was determined between 60 and 74 d bred. The GLM procedure of SAS (SAS Institute, Inc., Cary, NC) was used to evaluate the effects of treatment (TAI or activity), herd (1 or 2), temperature humidity index (THI), parity (primiparous or multiparous), BCS (≤ 2.75 or ≥ 3.00), summit milk, and their interactions on days to first service, first service conception rate (CR1), repeat service conception rate (≥ 2CR), days open (DO), pregnancy loss (PL), and percent pregnant at the end of the 90 d study period (%P90). Stepwise backward elimination removed all nonsignificant interactions ($P \geq 0.05$). Main effects remained in each model regardless of significance. Days to first service was lower ($P < 0.01$) for the TAI group than for the activity group (6.21 ± 0.98 vs. 18.30 ± 0.99 d after the VWP, respectively). Treatment was not a predictor of CR1 (TAI: 46.89 ± 4.43% vs. activity: 43.78 ± 4.47%, $P = 0.61$), ≥ 2CR (TAI: 41.15 ± 4.88% vs. activity: 39.92 ± 4.95%, $P = 0.86$), DO (TAI: 33.16 ± 3.09 vs. activity: 33.08 ± 3.02 d after the VWP, $P = 0.98$), PL (TAI: 16.97 ± 3.33% vs. activity: 10.77 ± 3.43%, $P = 0.14$), and %P90 (TAI: 65.54 ± 4.57% vs. activity: 66.11 ± 4.43%, $P = 0.92$). These

results indicate that continuous activity monitoring can produce similar reproductive performance to TAI.

Key Words: activity monitoring, timed artificial insemination, estrus detection

0345 Energy content of reduced-fat distillers grains for lactating dairy cows. A. Foth*[1], G. Garcia Gomez[1], T. Brown-Brandl[2], H. C. Freetly[3], and P. J. Kononoff[1], *[1]University of Nebraska, Lincoln, [2]ARS-USDA, Clay Center, NE, [3]USDA, ARS, US MARC, Clay Center, NE.*

The corn-ethanol industry has started to produce distillers grains and solubles that contain a reduced concentration of fat (RFDDGS), but the impact of this feed on the supply of energy to the cow has not been studied in depth. Eight Holstein and 8 Jersey multiparous, lactating cows were used to complete 56 energy balances to determine the energy content of rations containing RFDDGS. A repeated switchback design was used to compare treatments with and without RFDDGS. On a DM basis, treatments consisted of 24.2% corn silage, 18.4% alfalfa hay, 6.94% brome hay with either 22.9% rolled corn and 14.8% soybean meal, or 4.51% rolled corn, 14.5% RFDDGS, and 0% soybean meal (DM basis). The inclusion of RFDDGS increased DMI from 21.7 ± 0.70 kg/d to 23.3 ± 0.68 kg/d ($P < 0.01$) but did not affect milk production (30.4 ± 1.46 kg/d; $P = 0.11$). However, 3.5% FCM tended ($P = 0.10$) to be different (33.0 ± 1.27 and 34.2 ± 1.25 kg/d for Control and RFDDGS treatment, respectively). Milk energies were 1.44 ± 0.50 Mcal/d higher with RFDDGS ($P = 0.01$). Energy lost as methane was reduced ($P = 0.01$) by 0.28 Mcal/d with the addition of RFDDGS. Heat loss averaged 30.4 ± 0.55 Mcal/d and did not differ by treatment ($P = 0.94$). Energy retained as tissue energy was found to be -0.22 ± 1.48 Mcal/d for the Control and 6.78 ± 1.43 Mcal/d for the RFDDGS treatment ($P < 0.01$). Intakes of digestible and metabolizable energies were lower ($P < 0.01$) for the Control (2.70 and 2.36 ± 0.05 Mcal/kg DM, respectively) compared to RFDDGS (2.86 and 2.54 ± 0.05 Mcal/kg DM). There was also a treatment by breed interaction for digestible, metabolizable and lactational net energies ($P < 0.01$) with a greater difference between treatments with Holstein cows than Jersey cows. Differences between treatments in Holsteins were 12.0 ± 2.09, 11.7 ± 1.98 and 11.3 ± 1.90 Mcal/d ($P < 0.01$), and Jerseys were 4.16 ± 2.14, 4.32 ± 2.04 and 5.47 ± 1.96 Mcal/d ($P = 0.06$, 0.04 and 0.01), for digestible, metabolizable and lactational net energies, respectively. These energy estimates suggest higher energy content of diets containing RFDDGS than diets containing a mixture of corn and soybean meal in lactating dairy cows.

Key Words: reduced-fat distillers grains with solubles, energy balance, methane

0346 Relationship between digestibility and residual feed intake in lactating Holstein cows fed high and low starch diets. S. E. Burczynski*, J. P. Boerman, A. L. Lock, M. S. Allen, and M. J. VandeHaar, *Michigan State University, East Lansing.*

We determined if differences in digestibility among cows explained variation in residual feed intake (RFI) in 3 crossover design experiments. Lactating Holstein cows ($n = 89$; 107 ± 27 DIM) were fed diets high (HI) or low (LO) in starch. LO diets were ~38% NDF and ~14% starch; HI diets were ~26% NDF and ~32% starch. Each experiment consisted of two 28-d treatment periods, with digestibility measured during the last 5 d. Individual DMI and milk yield were recorded daily, BW was measured 3−5 times per wk, and milk components were analyzed twice weekly. DMI was modeled as a function of milk energy output, metabolic BW, body energy gain, and fixed effects of parity and cohort, with the residual being RFI. High RFI cows are less efficient because they eat more than expected for a given multiple of maintenance based on requirements. RFI was negatively correlated with digestibility of starch for both HI ($r = -0.25$; $P = 0.02$) and LO diets ($r = -0.20$; $P = 0.07$), and with digestibility of DM ($r = -0.30$; $P < 0.01$) and NDF ($r = -0.24$; $P = 0.03$) for LO diets but not HI diets ($P > 0.4$). Cows with the highest RFI (HiRFI) and the lowest RFI (LoRFI) were those greater or less than 1 SD of the mean for each cohort. For HI diets, LoRFI cows tended to have greater starch digestibility than HiRFI (96 vs. 94%; $P = 0.08$), but similar digestibilities ($P > 0.2$) of DM (67%) and NDF (37%). For LO diets, LoRFI cows tended to have greater DM digestibility (66 vs. 64%; $P = 0.08$), but similar starch (95%; $P > 0.2$) and NDF (50%; $P > 0.3$) digestibilities. Apparent NE_L concentrations for HI and LO diets, based on cow performance, were 21 and 12% greater ($P < 0.01$), respectively, for LoRFI cows than HiRFI cows. LoRFI cows had 3% greater DM digestibility than HiRFI cows for LO diets, which accounted for 25% of their greater ability to extract NE_L from the same diet. Although digestibility differed for LoRFI and HiRFI cows, some of the differences were expected because high RFI cows eat at a higher multiple of maintenance, which should depress digestibility. Based on these data, we conclude that a cow's digestive ability explains none of the variation in RFI for cows eating high starch diets but may explain as much as 25% of the variation in RFI among cows eating low starch diets.

Key Words: residual feed intake, digestibility, dietary starch

0347 Evaluation of the effects of vitamin D and toll-like receptor signaling pathways on expression of antibacterial β-defensin genes in bovine neutrophils and mammary epithelial cells.

K. E. Merriman* and C. D. Nelson, *Department of Animal Sciences, University of Florida, Gainesville.*

Bacterial infection in the udder stimulates synthesis of 1,25-dihydroxyvitamin D_3 ($1,25(OH)_2D_3$) from 25-dihydroxyvitamin D_3 in macrophages that are in the mammary glands. The $1,25(OH)_2D_3$, along with toll-like receptor (TLR) recognition of pathogen associated molecules, enhances the expression of β-defensin 3 (*DEFB3*), *DEFB6, DEFB7,* and *DEFB10* genes in bovine macrophages. The β-defensin genes encode for small cationic peptides that have potent bactericidal and immunomodulatory activity. Neutrophils and mammary epithelial cells (MEC) are additional sources of β-defensin peptides in the udder. It was hypothesized that $1,25(OH)_2D_3$ and TLR agonists also would promote expression of the β-defensins in neutrophils and MEC. Therefore, the objective of this study was to determine the contribution of vitamin D and TLR signaling pathways on expression of *DEFB3, DEFB4, DEFB6, DEFB7*, and *DEFB10* genes in bovine neutrophils and MEC. Peripheral blood neutrophils from cattle and primary bovine MEC cultures were treated with 0 or 1 μg/mL lipopolysaccharide (LPS) in combination with 0 or 10 nM $1,25(OH)_2D_3$. The mRNA transcripts of *DEFB3, DEFB4, DEFB6, DEFB7,* and *DEFB10* genes were quantified by real-time PCR. The threshold cycle (Ct) for each gene was normalized to ribosomal protein S9 transcript abundance and the normalized Ct values for each treatment were analyzed with a general linear model to test for effects of $1,25(OH)_2D_3$ and LPS treatments. In contrast to macrophages, $1,25(OH)_2D_3$ did not upregulate expression of the *DEFB3, DEFB6, DEFB7,* or *DEFB10* genes in either non-stimulated or LPS-stimulated neutrophils or MEC ($P > 0.05$). However, the $1,25(OH)_2D_3$ treatment increased *DEFB4* gene expression 5 ± 1-fold ($P < 0.05$) in MEC not treated with LPS, and 3 ± 1-fold ($P < 0.05$) in MEC treated with LPS. Furthermore, LPS combined with $1,25(OH)_2D_3$ upregulated *DEFB4* 30-fold ($P < 0.05$) compared to MEC cultured in the absence of LPS and $1,25(OH)_2D_3$. The LPS treatment alone upregulated *DEFB3, DEFB4*, and *DEFB7* in MEC ($P < 0.05$; 3 ± 1, 11 ± 3, and 8 ± threefold change ± SE, respectively), and *DEFB3, DEFB4, DEFB6, DEFB7*, and *DEFB10* in neutrophils ($P < 0.05$; 121 ± 44, 10 ± 7, 144 ± 85, 112 ± 51, and 56 ± 22, fold change ± SE, respectively). In conclusion, $1,25(OH)_2D_3$ does not enhance β-defensin gene expression in bovine MEC or neutrophils as it does in macrophages. However, LPS does strongly enhance several of the β-defensins in MEC and neutrophils. Therefore, activation of the TLR pathway in neutrophils and MEC, combined with activation of the vitamin D pathway in macrophages, may serve to boost the innate defense system of the udder.

Key Words: vitamin D, innate immunity, mammary

GRADUATE STUDENT COMPETITION: ADSA PRODUCTION ORAL COMPETITION, PhD

0348 Antioxidant activity after in vitro gastrointestinal digestion of cheese containing catechins encapsulated within liposomes. A. Rashidinejad*[1,2], D. Everett[1,2], J. Birch[1], and D. Sun-Waterhouse[3], [1]*University of Otago, Dunedin, New Zealand,* [2]*Riddet Institute, Palmerston North, New Zealand,* [3]*Plant and Food Research, Auckland, New Zealand.*

Two important green tea phenolic compounds, (+)-catechin and (−)-epigallocatechin gallate (EGCG) were first encapsulated in soy lecithin liposomes and then incorporated into a low-fat hard cheese to determine the effect of cheese ripening and simulated digestion on the antioxidant activity and recovery of incorporated catechins. The total antioxidant activity (TAA) was measured after in vitro gastrointestinal digestion of cheese that was ripened over 90 d at 8°C to evaluate the efficacy of added antioxidants. Total phenolic content (TPC) was measured using the Folin-Ciocalteu assay, while TAA by both ferric reducing antioxidant power (FRAP) and oxygen radical absorbance capacity (ORAC) assays. The correlation coefficients among the TPC and TAA assays, and the recovery of the encapsulated phenolics for cheese fortification (measured by HPLC), were calculated. Fortification of low-fat cheese with either catechin or EGCG encapsulated in liposomes, led to a significant increase ($p < 0.01$) in TPC, FRAP, and ORAC values measured within the digesta matrix, with no significant impact on cheese composition, pH, and yield. Catechin and EGCG were not detected in the cheese whey, indicating their complete retention in the cheese curd. The phenolic recovery from the digesta was about half of the initial concentration for catechin, i.e., 51.3, 53.9, and 46.0% for the fresh (Day 0) cheese and cheese ripened for 30 and 90 d (Day 30 and 90 cheese), respectively, and more than one third for EGCG, i.e., 38.8, 33.7, and 33.5% for Day 0, 30, and 90 cheese, respectively. TPC values were highly correlated with both the FRAP values (i.e., correlation coefficient was 0.97, 0.98, and 0.96 for Day 0, 30, and 90 cheese, respectively) and ORAC values (i.e., correlation coefficient was 0.98, 0.98, and, 0.97 for Day 0, 30, and 90 cheese, respectively). Moreover, the corresponding FRAP and ORAC values were also highly correlated with the coefficients being 0.98, 0.97, and 0.98 for Day 0, 30, and 90 cheese, respectively, suggesting the suitability of these assays for evaluating the TAA of fortified cheese. Thus, the manufacture of a low-fat hard cheese fortified with encapsulated catechin and epigallocatechin gallate in liposomes is feasible with good retention of phenolics and high antioxidant activity. Further investigations on aspects such as bioavailability of fortified phenolics, dose for phenolic consumption, and sensory attributes of fortified cheese are still required before product commercialization.

0349 Effects of mineral salts and calcium chelating agents on the functionalities of milk protein concentrate prepared by ultrafiltration. X. Luo*, L. Ramchandran, and T. Vasiljevic, *Victoria University, Melbourne, Australia*.

Functionality of milk protein concentrates can be tailored by modifying state of casein micelles through manipulation of processing conditions including temperature, pH and/or addition of calcium chelators. The objective of this study was to investigate the effect of calcium and calcium chelating agents (EDTA and citrate) on the performance of membrane ultrafiltration (UF) process and the functionalities of resulting milk protein concentrates (MPC). Skim milk adjusted to pH 5.9 was pre-treated with EDTA or citric acid (10, 20 or 30 mmol) and ultrafiltered using a polyethersulfone (PES) membrane at 15°C to five times concentration factor. The membrane performance was measured by the permeate flux during UF process. Used membranes were examined using scanning electron microscopy (SEM). The MPC samples were freeze dried and powders were assessed for physical functionalities including solubility, heat stability and emulsification. Addition of chilators led to a shift in a protein-mineral equilibrium and calcium dissociation from the casein micelle. The total calcium in the final MPC was reduced ($p < 0.05$) from 191 (control) to 131 mM or 135 mM for skim milk pre-treated with 30 mmol of EDTA or citrate, respectively. The casein micelle particle size was subsequently reduced ($p < 0.05$) from 200 nm (control) to 28 nm or 24 nm for the milk pre-treated with EDTA or citrate at concentrations equal to or greater than 20 mmol. Consequently, solubility of the MPC increased ($p < 0.05$) from 92% (control) to 98% (ETDA, $\geq$ 20 mmol) or 98.9% (citrate, 30 mmol); heat stability was also enhanced ($p < 0.05$) from 78% (control) to 83% (EDTA, 20 mmol) or 87% (citrate, $\geq$ 20 mmol). The emulsion capacity has increased from 1170 (control) to 1392 or 1459 (g oil/g protein) ($p < 0.05$) when 30 mmol of EDTA or citrate were added, respectively. Addition of EDTA or citrate hindered the membrane performance as observed by reduced permeate flux from 10.5 kg/h.m^2 (control) to 7.9 kg/h.m^2 (EDTA, $\geq$ 20 mmol) and 8.6 kg/h.m^2(citrate, $\geq$ 20 mmol) at the start of UF. Consequently UF processing time increased from 5 h (control) to 7 h (EDTA) or 6 h (citrate). This work has provided new insights into the relationship between calcium, calcium chelators and their influence on the casein micelle size and the physicochemical properties of MPC produced using UF, and also demonstrated the potential of using EDTA and citrate acid to manipulate MPC product functionality using UF.

Key Words: milk protein concentrate (MPC), functionality, ultrafiltration (UF), membrane, calcium chelator, casein micelle

0350 Effects of slow-release urea, rumen-protected methionine, and histidine on performance of dairy cows fed metabolizable protein-deficient diets.
F. Giallongo*[1], J. Oh[1], T. Frederick[1], H. Weeks[1], A. N. Hristov[1], H. Lapierre[2], R. A. Patton[3], A. Gehman[4], and C. Parys[5], *[1]Department of Animal Science, The Pennsylvania State University, University Park, [2]Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, [3]Nittany Dairy Nutrition Inc., Mifflinburg, PA, [4]Alltech Inc., Nicholasville, KY, [5]Evonik Industries AG, Hanau, Germany.*

The main objective of this experiment was to investigate the effects of slow-release urea and rumen-protected (RP) Met and His supplementation of a metabolizable protein (MP)-deficient diet on lactation performance of dairy cows. Sixty Holstein cows (DIM, 87 ± 40 and BW, 640 ± 70 kg) were used in a 10-wk randomized complete block design trial. After a 2-wk covariate period, cows were blocked by parity, DIM, and milk yield, and randomly assigned to 1 of 5 dietary treatments: MP-adequate diet [AMP; 107% of MP requirements (NRC, 2001)]; MP-deficient diet [DMP; 95% of MP requirements]; DMP supplemented with slow-release urea as Optigen (Alltech Inc.; DMPO); DMPO supplemented with RPMet as Mepron (Evonik Industries AG; DMPOM); and DMPOM supplemented with RPHis (Balchem Corp.; DMPOMH). The basal diet consisted of (DM basis): 43% corn silage, 8% grass hay, 4% cottonseed hulls, and 45% concentrate and contained 16.7, 15.8, and 14.8% CP for AMP, DMPO, and DMP, respectively. Total-tract apparent digestibility of nutrients, and urinary N and urea excretions were decreased ($P < 0.01$) by DMP compared with AMP. Relative to AMP, milk N secretion as a proportion of N intake tended to be higher ($P = 0.07$) for DMP. DMI was not affected by MP level but tended to be higher ($P = 0.09$) for the DMPOMH (28.4 kg/d) compared with DMPOM (27.0 kg/d). Yields of milk and milk fat were not affected by treatment, averaging 44.0 kg/d and 1.56 kg/d, respectively; milk fat content tended to be lower ($P = 0.06$) for DMPOMH (3.36%) than DMPOM (3.78%). Milk true protein content was increased (3.26 vs. 3.16%, $P = 0.04$) and milk protein yield was numerically increased (1.49 vs. 1.39 kg/d, $P = 0.14$) by DMPOMH, compared with DMPOM. Cows fed DMP gained 14 g/d BW whereas cows on all other treatments gained on average 267 g/d ($P \leq 0.10$). Supplementation of the DMPO diet with RPAA increased ($P = 0.03$) plasma glucose and numerically increased ($P = 0.12$) plasma insulin. In conclusion, feeding a 5% MP-deficient diet did not decrease DMI and yields of milk and milk components, despite the reduction in nutrient digestibility. Supplementation of the DMPOM diet with RPHis tended to increase DMI and increased milk protein content. These results confirm previous data and suggest that His may have a positive effect on voluntary feed intake in high-yielding dairy cows.

Key Words: metabolizable protein, slow-release urea, rumen-protected methionine, rumen-protected histidine

0351 Effect of dietary phosphorus on intestinal P absorption in growing Holstein steers.
X. Feng*, E. T. Ronk, H. H. Schramm, M. D. Hanigan, M. A. McCann, and K. F. Knowlton, *Virginia Polytechnic Institute and State University, Blacksburg.*

The effect of dietary phosphorus (P) intake on intestinal P absorption was evaluated in growing steers. Diets varying in P content (0.15%, 0.27%, 0.36% and 0.45%, DM basis) were fed to 8 growing Holstein steers (174 ± 10kg BW) fitted with permanent duodenal and ileal cannulas in a replicated 4 × 4 Latin square with 14 d periods. Ytterbium-labeled corn silage and cobalt-EDTA were used as particulate and liquid phase markers, respectively, to measure digesta flow. Duodenal and ileal samples and spot samples of urine were collected every 9 h from d 11 to 14. Total fecal collection was conducted on d 11 to 14 with fecal bags. Blood samples were collected from the coccygeal vessel on d 14. Feed, digesta, and fecal samples were analyzed for total P and Pi using the molybdovanadate yellow method and blue method, respectively. Data were analyzed using PROC GLIMMIX in SAS with a model including treatment, square, period and interaction of treatment and square. Preplanned contrasts were used to evaluate linear and quadratic treatment effects. Results are reported as least square means. Dry matter intake (mean = 4.90 kg/d, 2.8% of BW) and apparent DM digestibility (mean = 78.1%) were unaffected by treatment. Duodenal and ileal flow of total P increased linearly with increasing P intake (13.4, 18.5, 23.0 and 27.4 g/d, $P < 0.01$; 6.80, 7.87, 8.42, and 10.4 g/d, $P < 0.05$). Increasing P intake linearly increased the quantity of P absorbed from the small intestine (6.96, 11.1, 14.6 and 17.2 g/d, $P < 0.01$) but absorption efficiency was unchanged (mean = 59.6%). Phosphorus was absorbed on a net basis from the large intestine, but this was not affected by treatment and was a small percentage of total P absorption. Blood Pi increased linearly with increased dietary P (4.36, 6.31, 7.68, and 8.5 mg/dL, $P < 0.01$) and salivary P secretion was unchanged (mean = 5.79 g/d) suggesting that rumen function was prioritized during short-term P deficiency. The absence of change in absorption efficiency and salivary P secretion in the face of short term P deficiency may be used to improve published models of P digestion, absorption, and metabolism.

Key Words: phosphorus, absorption, growing steers

0352 A survey of calving and colostrum management practices on Irish dairy farms.
C. Cummins*[1,2], R. Sayers[1], I. Lorenz[2], and E. Kennedy[1], *[1]Teagasc, Animal and Grassland Research and Innovation Center, Moorepark, Fermoy, Co. Cork, Ireland, [2]School of Agriculture, Food Science & Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland.*

This study aimed to identify calving and colostrum management practices on Irish dairy farms that may compromise neonatal

calf health. The study population was randomly selected from the Irish Cattle Breeding Federation (ICBF) HerdPlus group (n = 320) and balanced for herd size and geographical location. The survey consisted of four sections: cow management, calving management, colostrum management and calf management (calving and colostrum are described here). Questions related to hygiene, type of calving pens used, and colostrum collection, storage, and feeding management. Surveys were mailed between 11 July and 15 August 2013. Responses were entered onto the online package SurveyMonkey (www.surveymonkey.com). Coded responses were downloaded to one file and data were collated using Microsoft Excel. A univariable chi-square analysis (significance $P < 0.05$) was performed using 'PROC FREQ' in SAS (v9.3), with two independent variables: milk production (MP), and enterprise. Milk production category one (MP1) included suppliers with a milk production limit (quota) of $\leq$ 380,000L; MP2 > 380,000L and < 600,000L; and MP3 $\geq$ 600,000L. Enterprise was divided into specialist dairy farms (SD) and dairy farms with another enterprise (DO). The final response rate was 85%. On univariable analysis, group calving pens were more common among MP3 (60%) than MP1 (37%; $P < 0.05$), who tended to use individual pens (24% MP3; 47% MP1; $P < 0.05$). Cleaning of calving pens was infrequent across all study herds (42% $\leq$ 1 × month), while 81% left calves in calving pens for $\geq$ 2 h after birth. Regarding colostrum, MP3 respondents more commonly collected colostrum at first herd milking post-calving compared to MP1 and MP2, the majority of which collected within 2 h ($P < 0.05$). Most SD herds collected colostrum at the first scheduled milking post-calving compared to DO herds (43% SD; 26% DO; $P < 0.01$). More MP1 herds allowed calves to consume own dam colostrum (79%), compared to MP2 (56%) and MP3 (44%), however they also allowed calves suckle their dam (48% MP1 vs. 40% MP2 and 32% MP3). Consequently, MP1 calves received colostrum earlier compared to MP3 (45% MP1 vs. 35% MP3 within 1 h; $P < 0.05$). Of farms not feeding calves colostrum from their own dam, 32% of MP3 used pooled colostrum for the calf's first feed compared to MP1 (13%) and MP2 (15%). The most common storage method was freezing (46%), mainly for 1−6 mo (44%). This study indicates that calving and colostrum management practices on many Irish dairy farms are suboptimal and may lead to compromised calf health.

Key Words: colostrum, calving, survey

0353 Effects of supplementing lipid-encapsulated echium oil on lactational responses and milk fatty acid composition.

M. Bainbridge*[1], A. L. Lock[2], and J. Kraft[3], [1]*University of Vermont, Burlington,* [2]*Michigan State University, East Lansing,* [3]*Department of Animal Science, University of Vermont, Burlington.*

Echium oil is a terrestrial source of n-3 fatty acids (FA) that is particularly high in the n-3 FA stearidonic acid (SDA; 18:4 6c,9c,12c,15c) which bypasses the rate limiting step of delta-6-desaturase in conversion to eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) in mammalian tissues. The objective of this study was to evaluate the impact of feeding a lipid-encapsulated echium oil (EO) supplement on animal production and milk fatty acid concentrations. Twelve Holstein dairy cattle (229 ± 62 d in milk) were assigned randomly to treatment sequence in a 3 × 3 Latin Square design. Treatments were a control diet (CON; no added EO), 1.5% EO (1.5% EO), or 3.0% diet dry matter (DM) added EO (3.0% EO). Treatment periods were 14 d with the final 4 d used for sample and data collection. The statistical model included the random effect of cow nested within square and the fixed effects of treatment and period. Compared with CON, EO treatments had no effect on dry matter intake (26.6 kg/day; $P = 0.93$), milk yield (30.5 kg/day; $P = 0.34$), or milk protein yield (1.1 kg/day; $P = 0.84$). Increasing EO supplementation increased milk fat concentration (4.1, 4.2, 4.3%; $P < 0.05$) and fat yield (1.24, 1.27, 1.32 kg/day; $P < 0.05$) but decreased milk protein concentration (3.56, 3.54, 3.47%; $P < 0.01$) for CON, 1.5% EO, and 3.0% EO, respectively. Compared with CON, the concentration of total saturated FA in milk fat decreased with increasing EO supplementation (73.7, 72.4, and 71.1 g/100 g FA, $P < 0.0001$). Increasing EO supplementation increased milk fat concentration of total n-3 FA (0.49, 0.65, 0.81 g/100 g FA, $P < 0.0001$), α-Linolenic acid (18:3 n-3) (0.38, 0.47, 0.58 g/100 g FA, $P < 0.0001$), and SDA (0.02, 0.06, 0.09 g/100 g FA, $P < 0.001$) for CON, 1.5% EO, 3.0% EO, respectively. For 1.5% EO and 3.0% EO milk fat concentration of EPA was 0.05 g/100 g FA vs. 0.03 g/100 g FA for CON ($P < 0.0001$). DHA was not detected in milk fat. Transfer of SDA from the EO supplement into milk fat was 3.4% and 3.2% for the 1.5% and 3% EO treatments, respectively. In conclusion, supplementation with a lipid-encapsulated EO did not negatively impact lactational responses and increased the concentration of n-3 FA in milk fat. The concentration of n-3 FA in milk fat however, was still a minor component of total milk FA.

Key Words: n-3 fatty acid, milk fat, echium oil

0354 Effects of dietary crude protein level on nitrogen use efficiency and urinary nitrogen excretion during a twelve-week period in late lactation dairy cows.

T. Barros*[1], M. A. Quaassdorff[1], J. J. Olmos Colmenero[2], M. J. Aguerre[1], S. J. Bertics[1], and M. A. Wattiaux[1], [1]*University of Wisconsin, Madison,* [2]*University of Guadalajara, Tepatilan, Mexico.*

Our objectives were to determine the impact of decreasing levels of dietary CP and whether there was a treatment by week interaction on intake-N, milk-N (DHI true protein), N use efficiency (NUE, milk-N/intake-N), MUN, and responses related to urinary excretion in late lactation cows. One hundred twenty-eight Holstein cows (means ± SD; 736 ± 18 kg BW; 224 ± 54 DIM) were used in a 16-pen study with 8 cows

per pen, and fed a TMR once per day (at 8:00 am) for 12 wk (pen = experimental unit). Treatments which included diets of 11.8, 13.1, 14.6, or 16.2% CP (DM basis) were randomly allocated to pen for the entirety of the experiment. Rations consisted of approximately 67% forage (half corn silage; half alfalfa silage); soy hulls replaced soybean meal to achieve the desired dietary CP levels for each treatment. Urine volume was estimated using creatinine concentration in spot urine samples collected 6 h before feeding for a group of four randomly selected cows in each pen. This protocol was repeated 6 h after feeding. LS-means of pen-level data presented in the table were obtained on week 2, 8, and 12. Except for urine volume, there was a linear effect for all responses but there were no quadratic effects. There was a treatment by week interaction for most responses. Regardless of treatment, NUE was high and urinary urea-N excretion was low. Under the conditions of this experiment, the 14.6% CP diet allowed for a reduction in urinary urea-N without affecting milk-N.

Key Words: protein nutrition, MUN, urinary urea

Table 0354. Effect of dietary CP on measured responses

	Dietary CP (DM basis)					*P*-value[1]	
Item	11.8	13.1	14.6	16.2	SEM	L	Trt*wk
Intake-N, g/d	410[d]	505[c]	551[b]	614[a]	9.0	< 0.01	< 0.01
Milk-N, g/d	128[c]	149[b]	163.4[ab]	172.4[a]	5.04	< 0.01	< 0.01
Milk-N/ Intake-N, %	31.1[b]	29.4[ab]	29.6[ab]	28.0[a]	0.006	< 0.01	0.25
MUN, g/dL	6.3[d]	8.6[c]	10.9[b]	13.47[a]	0.34	< 0.01	0.06
Urine volume, L/d	17.5	18.2	16.8	17.8	0.93	0.95	0.04
Urinary-N, g/L	5.1[d]	6.4[c]	7.7[b]	8.5[a]	0.24	< 0.01	0.74
Urinary-N, g/d	88[c]	115[b]	127[ab]	150[a]	6.3	< 0.01	< 0.01
Urinary Urea-N, g/L	2.9[d]	4.6[c]	5.8[b]	6.9[a]	0.29	< 0.01	0.59
Urinary Urea-N, g/d	50[d]	83[c]	99[b]	122[a]	3.2	< 0.01	< 0.01
Urinary-N/ Intake-N, %	21.6	23.1	23.2	24.4	1.56	0.29	< 0.01

[a–d] Least squares means within the same row with different superscripts differ ($P < 0.05$).
[1] Linear (L) effect of CP% level in the diet or interaction treatment by week (Trt*wk).

0355 Evaluation of a handheld device for the detection of β-hydroxybutyrate pre-calving in dairy cattle.

E. H. Tatone*, J. L. Gordon, S. J. LeBlanc, and T. F. Duffield, *University of Guelph, Guelph, ON, Canada.*

Individual and herd ketone levels are commonly monitored in dairy cattle post-partum to identify individuals at-risk of metabolic disease and to identify potential improvements to management factors. The Precision Xtra handheld meter has been validated for use in β-hydroxybutyrate (BHBA) measurements post-calving as a convenient cow-side test for ketonemia. Recent research has identified BHBA cut points pre-partum associated with increased risk of post-partum disease, but at much lower cut-offs than those indicating hyperketonia after calving: 0.6 to 0.8 mmol/L in comparison to 1.0 to 1.4 mmol/L. The objective of the current research is to validate the handheld device, Precision Xtra, in the measurement of BHBA in whole blood against the gold standard method, laboratory evaluation of serum, to assess its diagnostic accuracy in detecting BHBA pre-calving in the range of 0.6 to 0.8 mmol/L. As part of a larger study, 212 cows in 6 herds across southern Ontario were sampled between 3 and 9 d before the expected calving date. Blood was collected and tested on-site with the Precision Xtra device. The serum portion of the sample was separated and sent to a laboratory for measurement of BHBA and non-esterified fatty acid (NEFA) concentrations. The results of the two BHBA measurement methods were compared and evaluated with concordance coefficients. The sensitivity and specificity of the Precision Xtra were determined with receiver operator characteristic curves at cut points of 0.6, 0.7 and 0.8 mmol/L. The two tests had a moderate concordance correlation of 0.77 ± 0.03 (CI_{95}: 0.72 − 0.83) and the area under the curve for each cut point was high with values between 0.90 and 0.93. The Precision Xtra had sensitivities of 85 to 93% and specificities of 76 to 87% depending on the cut point tested. The level of agreement between Precision Xtra cut points and at-risk pre-calving NEFA concentrations of 0.4 and 0.5 mEq/L was calculated. The level of agreement between Precision Xtra BHBA concentrations ≥ 0.8 mmol/L and NEFA concentrations ≥ 0.5 mEq/L was substantial, with a kappa of 0.64. Based on the moderate level of correlation and the good level of sensitivity and specificity, the Precision Xtra is a valid tool in the detection of elevated BHBA pre-calving and may be helpful in identifying individuals at risk of metabolic disease.

Key Words: ketosis, β-hydroxybutyrate, diagnostic test evaluation

0356 Effects of dietary nitrate supplementation on enteric methane and nitrous oxide emissions from beef cattle.

C. J. Neumeier*[1], Q. Wang[1], A. R. Castillo[2], Y. Zhao[1], Y. Pan[1], and F. M. Mitloehner[1], *[1]University of California, Davis, [2]University of California Cooperative Extension, Merced.*

Feeding nitrate has been proposed as a means to reduce enteric greenhouse gas emissions from ruminants. Nitrate can compete with methanogens for hydrogen in the rumen and therefore reduce methane from eructation. However, increasing the nitrate concentration in the rumen could induce enteric nitrous oxide emissions, potentially nullifying the greenhouse gas reduction achieved from lowering methane emissions. The present study investigated the effects 2% nitrate (on DM basis) versus an isonitrogenous concentration of urea supplemented to finishing steers on enteric methane and nitrous oxide emissions. Sixteen steers were allocated to nitrate and urea treatments in a randomized complete block design ($n = 8$). Eructated emis-

sions were collected using head chambers for 12 h following the morning feeding. Methane was measured using the TEI 55C direct methane analyzer and nitrous oxide using the 46i nitrous oxide analyzer (both were Thermo Environmental Instruments, Franklin, MA). All data were analyzed using the Proc Mixed Model in SAS. The nitrate versus urea treatment lowered methane production at measurement h 1 and 2 ($P < 0.01$), but did not lower overall methane production during the 12 h measurement period. The nitrate versus urea treatment increased nitrous oxide production at h 1, 2, and 3 ($P < 0.05$) of measurement and the overall 12 h measurement period ($P < 0.0001$). Nitrous oxide was detected in both treatments at each time point, with a sixfold increase in production in the nitrate (~600 mg/12 h) versus urea treatment (~100 mg/12 h). Overall, combined greenhouse gas production expressed as carbon dioxide equivalents was similar between treatments. This study indicates that nitrate supplementation in finishing beef cattle is effective at reducing eructated methane in the time immediately following feeding, and might need to be supplemented at a higher concentration and/or more frequently to achieve more optimal methane reduction. Furthermore, this study suggests that cattle could be a source of the potent greenhouse gas nitrous oxide, which is further stimulated by nitrate supplementation. Additional research is necessary to evaluate more effective means of reducing methane with nitrate in finishing beef cattle and the production of nitrous oxide with and without supplementation of nitrate.

Key Words: greenhouse gas, hydrogen sink, ruminant

0357 Early pair housing influences the feeding behavior and development of dairy calves. J. H. C. Costa*, R. K. Meagher, M. A. von Keyserlingk, and D. M. Weary, *Animal Welfare Program—University of British Columbia, Vancouver, BC, Canada.*

Calves are social and gregarious animals. Pre-weaned calves are typically kept in individual pens but little is known about how individual versus social rearing affects development of feeding behavior. The aim of this study was to assess the effects of early and late pairing feeding behavior and weight gain before and after weaning. Holstein bull calves were reared individually ($n = 8$ calves) or paired with another calf at 3 d of age ($n = 8$ pairs) or 42d of age ($n = 8$ pairs). All calves were fed 8 L of milk/d for 4 wk, 6 L/d from 4 to 6 wk and weaned at 8 wk of age. Calves were provided ad libitum access to calf starter and a total mixed ration (TMR). Body weight and feed consumption were followed weekly from 6 wk until 10 wk of age. At 6 wk, intake of TMR averaged (± SEM) 0.25 ± 0.05 Kg/d, 0.41 ± 0.12 Kg/d, 0.32 ± 0.09 Kg/d, for individual, and early paired late paired housed calves, respectively. Starter intake was similar for the individually reared and late-paired calves (0.09 ± 0.03 Kg/d and 0.04 ± 0.01 Kg/d) but higher for the early-paired calves (0.23 ± 0.07 Kg/d). Consumption increased after weaning in all treatments, but this increase was greatest for the early-paired calves. At 10 wk of age, TMR intake averaged 2.89 ± 0.54 Kg/d, 3.27 ± 0.72 Kg/d and 3.08 ± 0.46 Kg/d for individual, early paired and late paired housed calves, respectively. Starter intake averaged 1.26 ± 0.33 Kg/d, 2.20 ± 0.22 Kg/d and 1.09 ± 0.25 Kg/d for the same three treatments. Calves in the early pair treatment showed higher average daily gains (1.13 ± 0.05 Kg/d versus 0.92 ± 0.04 Kg/d and 0.84 ± 0.05 Kg/d for the individual and late-paired calves). Pair housing soon after birth increased calf feed intake and weight gains in comparison with late pairing and individual housing.

Key Words: feeding behavior, group housing, dietary transition

---

0358 Epigenetic differences of cows classified with biased antibody and cell mediated immune response traits. M. A. Paibomesai*[1] and B. Mallard[2], [1]*University of Guelph, Guelph, ON, Canada,* [2]*Dept Pathobiology, University of Guelph, Guelph, ON, Canada.*

The identification of cattle that are better able to respond immunologically to pathogens would be useful to reduce the incidence of disease on commercial dairy farms. High Immune Response (HIR) technology provides a unique tool to rank animals based on their ability to respond to test antigens, and high ranking dairy cows have been shown to have a lower incidence of disease. HIR evaluates two branches of the adaptive immune response: the antibody mediated immune response (AMIR, prominent IL-4 production) which responds primarily to extracellular pathogens, and the cell mediated immune response (CMIR, prominent IFN-g production), which responds primarily to intracellular pathogens. Genetic control of the immune response has been well studied in past years, but epigenetic influences on phenotype remain to be defined. Epigenetics is defined as modifications to DNA that control gene expression without changing the DNA sequence. Specifically, DNA methylation, an epigenetic modification, is associated with a decrease in gene transcription, while the lack of DNA methylation is associated with increased gene expression. CD4+ helper T cells are mediators of AMIR and CMIR, producing cytokines, such as IL-4 and IFN-γ, for the direction of an appropriate response. Biased immune responder cattle respond strongly with either high AMIR (H-AMIR) or high CMIR (H-CMIR) to test antigens. Cows with H-AMIR/L-CMIR (H-AMIR; $n = 10$) and H-CMIR/L-AMIR (H-CMIR; $n = 11$) phenotypes were used to investigate mechanisms of immune response variation and the role of epigenetics in cattle immune response traits. Isolated CD4+ helper T cells from H-CMIR and H-AMIR cows were stimulated with a T cell mitogen (ConA) and cell culture supernatants were harvested at 24 h to quantify IL-4 and IFNγ by ELISA. DNA was extracted from unstimulated and stimulated cells and bisulfite pyrosequencing was used to quantify DNA methylation for both IL-4 and IFNγ promoters. CD4+ T cells from H-CMIR cows pro-

duced more IFN-γ ($P = 0.059$), and significantly more IL-4 ($P = 0.02$) than T cells from H-AMIR cows, when sampled 21 d into lactation. In H-CMIR cows higher secretion of IFN-γ was associated with decreased methylation in the promoter region of the IFNγ gene compared to H-AMIR cows ($P = 0.01$). In contrast, there was no difference in DNA methylation at the IL-4 promoter observed between the two immune response phenotypes. This study is the first to show an association between DNA methylation and specific phenotypes.

Key Words: immune response, epigenetics, dairy cows

GRADUATE STUDENT COMPETITION: ADSA SOUTHERN SECTION ORAL

0359 Changes in activity and milk components around onset of clinical mastitis. A. S. Griffith*, M. L. McGilliard, and C. S. Petersson-Wolfe, *Virginia Tech University, Blacksburg.*

The objectives of the current study were to identify early indicators of naturally-occurring clinical mastitis in the first 30 DIM using peripartum daily activity, postpartum milk components, and milk yield data. A total of 200 cows that consisted of 136 Holstein (60 primiparous, 76 multiparous), 59 Jersey (24 primiparous, 35 multiparous), and 5 Crossbred (5 multiparous) animals were followed from January 2013 through September 2013. Daily activity was collected from 21 d prepartum to 30 d postpartum for all animals with a behavioral monitoring system (Afi PedometerPlus, S.A.E. Afikim, Israel), which collected rest bouts, rest duration, rest time and step activity. Daily milk lactose % and fat:protein ratio were collected from 4 to 30 DIM for all animals, using an in-line milk analysis system (AfiLab, S.A.E. Afikim, Israel) and daily yield was collected from the milk meter. Mastitis was defined as visual changes in milk appearance (flakes, chunks, or color) in one or more quarters as detected by the milk harvesters at the time of milking. Controls were defined as any animal in the same group, parity (1 or $\geq$ 2), and breed on the same date as the diseased cow, that did not experience any disease within the first 30 DIM. Differences between diseased and controls from d -7 to d 7 relative to disease, were examined using PROC GLIMMIX in SAS (Cary, NC). Lactation number, day relative to disease, disease status, and their interactions were included in the model. Significance was determined at $P \leq 0.05$. Animals that experienced mastitis ($n = 15$) showed more daily steps from d -5 to 0 and fewer daily rest bouts on d -1 and 0 relative to disease, compared to controls. Additionally, diseased cows showed reduced milk lactose % compared to controls from d -1 to 2 relative to disease and daily yield was decreased from d -2 to 1. Finally, no differences were found in daily rest time, rest duration or fat:protein ratio. This is the first study to show changes in activity and milk components before the onset of naturally-occurring clinical mastitis in early lactation. The identification of animals at risk for periparturient disease may allow producers to implement a proactive strategy for disease treatment, improve animal well-being and alleviate the economic losses associated with health problems during the transition period.

Key Words: mastitis, daily activity, milk components

0360 Predicting impending calving using automatically collected measures of activity and rumination in dairy cattle. M. R. Borchers*, A. E. Sterrett, B. A. Wadsworth, and J. M. Bewley, *University of Kentucky, Lexington*.

The objective of this study was to monitor behavioral changes in prepartum dairy cattle and predict impending calvings through the automated observation of activity and rumination. Data collection for 29 primiparous and 46 multiparous Holstein dairy cattle occurred from September 13, 2011 through May 16, 2013 at the University of Kentucky Coldstream Dairy. The HR Tag (SCR Engineers, Ltd., Israel) was used to automatically collect neck activity and rumination data in 2-hour increments. The IceQube (IceRobotics, Ltd., Scotland) collected hourly step number, hours lying, hours standing, lying bouts, and total motion data. Data collection occurred for 7 wk prepartum and retrospective data analysis was performed using SAS (Cary, NC). Data summed by day for each cow was included in the calculation of a 7-d backward moving average and standard deviation to establish each cow's baseline values. Least-squares means were calculated from moving averages using the MIXED procedure of SAS. Parameters exhibiting significant differences ($P < 0.05$; mean ± SE) on the day of calving (DAY^0) versus the day before (DAY^{-1}) included: hours lying (DAY^0: 10.15 ± 0.25 vs. DAY^{-1}: 10.50 ± 0.25), hours standing (DAY^0: 13.79 ± 0.25 vs. DAY^{-1}: 13.47 ± 0.25), lying bouts (DAY^0: 11.36 ± 0.38 vs. DAY^{-1}: 9.86 ± 0.38), and minutes ruminating (DAY^0: 319.29 ± 12.01 vs. DAY^{-1}: 336.86 ± 12.01). Neck activity, step number and total motion showed no significant differences between DAY^0 and DAY^{-1}. Z-scores were calculated using data summed by day for each cow, moving averages, and moving standard deviations. Deviations $\geq$ 1.5 from the mean dictated alert creation. The percent of cows ($n = 61$) showing an alert by parameter on DAY^0 was: lying bouts (75.4%), minutes ruminating (45.9%), step number (39.3%), total motion (39.3%), hours standing (32.8%), hours lying (31.1%), and neck activity (21.3%). In comparison, the percent of cows ($n = 57$) showing an alert by parameter on DAY^{-1} was: lying bouts (15.8%), minutes ruminating (15.8%), step number (17.5%), total motion (15.8%), hours standing (28.1%), hours lying (28.1%), and neck activity (12.3%). Changes in least-squares means and alerts relative to calving indicate that these measures may be useful in predicting impending calvings without adding new technologies or parameters, but further research is necessary.

Key Words: calving prediction, days before calving, activity and rumination

GRADUATE STUDENT COMPETITION: ADSA-ASAS NORTHEAST SECTION ORAL: ADSA/ASAS NORTHEAST BRANCH GRADUATE STUDENT COMPETITION

0361 Glucose metabolism by bovine neutrophils characterized by mass spectrometry and [$^{13}C_6$] glucose. Y. Qu*[1], B. J. Bequette[1], T. H. Elsasser[2] and K. M. Moyes[1], [1]*Department of Animal and Avian Sciences, University of Maryland, College Park,* [2]*USDA/ARS Growth Biology Lab, Beltsville, MD.*

At the present time, the metabolic priority for and subsequent pathway fate of glucose by bovine blood neutrophils (BBN) is unknown. During early lactation, glucose availability is low. Consequently, a resulting energy-compromised state may partly explain the lack of robust immune response observed at this time. The objective of this study was to characterize the metabolic utilization of glucose by BBN from dairy cows in early and mid-lactation by incubation of BBN with [$^{13}C_6$] glucose followed by gas chromatography–mass spectrometry (GC–MS). Jugular blood (~150 mL) was collected from 4 healthy multiparous dairy cows in early (n = 2; < 21 d in milk) and mid-lactation (n = 2; > 90 d in milk). The BBN were isolated and adjusted to a final concentration of 6×10^6 cells/mL using RPMI/5% fetal bovine serum containing 4 mM of a 50:50 mix of unlabeled and ^{13}C-labeled glucose. Cells were incubated for 2 h at 37°C, 95% humidity, and 5% CO_2. Nonessential AA in metabolic equilibrium with Krebs cycle intermediates and lactate in BBN were monitored by GC–MS. Data were analyzed by the student's t test for unpaired comparison. Significance was declared at $P \leq 0.05$. No stage of lactation effect was observed. Although 43% of the pyruvate pool derived from glucose, a small proportion of this pool entered the Krebs cycle. Our results suggest that the pyruvate carboxylase flux was minimal and only 5% of the acetyl-CoA pool was derived from the pyruvate pool. In conclusion, although BBN exhibit high rates of glycolysis, glucose is not the main substrate oxidized for energy in the Krebs cycle, and perhaps other extracellular substrates (e.g., fatty acids, glutamine, aspartate) are preferred. Future studies are needed to examine the metabolic utilization of other substrates and their influence on the function of BBN.

Key Words: cow, glucose, neutrophil

0362 Exploring the Molecular diversity and density of the rumen microbiome within the impala (*Aepyceros melampus melampus*) from Pongola, South Africa. L. M. Cersosimo*[1], B. St-Pierre[1], W. van Hoven[2], and A. D. G. Wright[1], [1]*The University of Vermont, Burlington,* [2]*University of Pretoria, Pretoria, South Africa.*

The rumen microbiome of domesticated ruminants has been studied extensively, but few studies have explored the microbiome of wild ruminants and no studies have used a metagenomic approach to examine the rumen microbiota within the impala (*Aepyceros melampus melampus*). Impala, like all domesticated ruminants, have a consortium of anaerobic microorganisms inhabiting their foregut (i.e., the rumen) that contribute to the feed efficiency of the animal, as well as greenhouse gas emissions. The present investigation seeks to expand our knowledge about the rumen microbial community of the impala while drawing comparisons to their domesticated relatives that could lead to advances in both feed efficiency and methane mitigation strategies. The rumen contents from 4 male impala culled in the Kwazulu-Natal province of Pongola, South Africa, were collected postmortem. Once bacterial and archaeal amplicons were generated, next-generation sequencing techniques (i.e., Roche 454-pyrosequencing) were used to identify the diversity of bacterial and methanogenic archaeal (i.e., methanogens) 16S rRNA gene sequences. Real-time PCR amplification of the 16S rRNA gene was used to estimate the density of the bacterial population (R^2 = 0.997), while the mcrA (methyl coenzyme-M reductase) gene was used to estimate the density of the methanogen population (R^2 = 0.997). Using the bioinformatic platform, MOTHUR, a total of 20,124 methanogen sequence reads were assigned to 344 operational taxonomic units (OTUs) using a sequence identity cutoff of 3%. A high sampling efficiency was observed with OTU coverages > 99% for each individual impala, along with similar Shannon indices of 1.90 ± 0.003. The Ribosomal Database Project (RDP) Classifier classified 94.3% of the reads to the genus *Methanobrevibacter,* 4.2% of the reads to the genus *Methanosphaera*, with the remaining 1.5% of the reads being unclassified. Most notably was the abundance of *Methanobrevibacter thaueri*-related methanogen sequence reads in all 4 impala samples, representing > 30% of each animal's total sequences. This high abundance of *Methanobrevibacter thaueri*-related methanogen sequences has not been observed in previous studies of domesticated or wild ruminants, suggesting that either the diet and/or the rumen physiology of the impala may differ from previously studied ruminants. The diversity of the rumen bacteria will also be elucidated and discussed. Future studies to look at other factors that affect the rumen environment, like gender, should be performed to see if these findings are consistent.

Key Words: methanogens, bacteria, impala, rumen, *Methanobrevibacter*, operational taxonomic units

0363 Effects of ground flaxseed on milk production, milk composition, and methane emissions in organically-managed Jersey cows during the grazing season. B. J. Isenberg*[1], A. F. Brito[1], A. B. D. Pereira[1], N. L. Whitehouse[1], R. B. Standish[1] and K. J. Soder[2], *[1]University of New Hampshire, Durham, [2]USDA-Agricultural Research Service, University Park, PA*

Our previous research feeding incremental levels of ground flaxseed (GFLAX; 0, 5, 10, or 15% of diet DM) to organically-managed Jersey cows linearly reduced yields of milk and milk components, DMI, and enteric CH_4 emissions. While milk yield did not differ significantly between 0 and 10%, 10% GFLAX significantly increased n-3 fatty acids and conjugated linoleic acid. Flaxseed is rich in n-3 fatty acids and energy; energy is a limiting factor to milk production in pasture-based diets. This study evaluated impacts of supplementing pasture with 10% of diet DM as GFLAX to Jersey cows on milk production and composition, and enteric CH_4 emissions. Twenty multiparous lactating organically managed Jersey cows, averaging 408 kg BW and 112 d in milk (DIM), were blocked by milk production and DIM and randomly assigned to 1 of 2 treatments: (1) control (soybean meal and ground corn grain mix as 10% of total DMI) or (2) ground flaxseed as 10% of total DMI. Treatments were top-dressed onto a 25% mixed grass-legume baleage, 23% grain meal, and 2% liquid molasses TMR (% of diet DM); pasture composed the remaining 40% DMI. The study extended from June 8 to September 27, 2013 with four 28-d periods, with the last 7 d used for data and sample collection. Data were analyzed using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) with repeated measures over time; no treatment × period interaction was observed. Cows had access to mixed grass-legume pastures for about 16 h daily in a rotational strip grazing system. Cows were milked twice daily with milk production recorded each time. Milk samples were collected for 2 consecutive days and analyzed for fat and protein. A portable automated head chamber system was used for assessing CH_4 fluxes. Milk production did not differ significantly in cows supplemented (17.6 kg/d) or not (18.2 kg/d) with GFLAX. Similarly, concentration and yield of milk components did not differ significantly, averaging 4.20% and 0.76 kg/d for milk fat and 3.45% and 0.61 kg/d for milk protein. Intake of TMR was lower ($P < 0.01$) in cows with (10.5 kg/d) or without (10.8 kg/d) GFLAX supplementation. Methane emissions did not differ significantly, averaging 299 g cow^{-1} d^{-1} (control diet) and 295 g cow^{-1} d^{-1} (GFLAX diet). Feeding 10% of total DMI as GFLAX to grazing dairy cows had no negative impact on milk production and composition, but did not mitigate CH_4emissions under conditions of the current experiment.

Key Words: pasture, ground flaxseed, methane

0364 Farm-level evaluation of implementing feeding best management practices (BMP) on Pennsylvania dairy farms. H. L. Weeks*, T. W. Frederick, L. M. Hagan, K. S. Heyler, and A. N. Hristov, *Department of Animal Science, The Pennsylvania State University, University Park, PA*

Feeding best management practices (BMP) can have a significant impact on the environmental footprint of dairy farms. The objective of this study was to evaluate the environmental and productive effects of implementing feeding BMP on commercial dairy farms in Pennsylvania. Fifteen farms (124.8 ± 20.5 ha, 169 ± 39 cows, and 31.4 ± 0.2 kg cow^{-1} d^{-1} milk production) in central and southeast Pennsylvania participated in the study. A set of 4 background total mixed ration (TMR), forage, milk, feces, urine samples, as well as feed intake and production data, were collected from each cooperator farm biweekly between January and March of 2013 (preBMP period). Following the implementation of applicable feeding BMP, chosen by the producer, including reduction of dietary crude protein (CP; $n = 9$) and P ($n = 5$), adjusting rations for changes in forage dry matter ($n = 10$), and group feeding of the lactating herd ($n = 2$), another set of 4 sampling and data collection events took place between June and August of 2013 (postBMP period). Data were analyzed using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) with farm as a random effect. On farms in which dietary CP was reduced (from 17.2 to 15.9%; $P < 0.01$), fecal N (FN; 2.78 vs. 2.63%; $P = 0.01$), total urinary N (UN; 0.071 vs. 0.055%; $P < 0.01$), urinary urea N (UUN; 52.2 vs. 44.4mg/dL; $P < 0.01$), and milk urea N (MUN; 16.9 vs. 13.9 mg/dL; $P < 0.01$) decreased (pre- vs. postBMP, respectively). Only 3 farms successfully decreased dietary P (from 0.42 to 0.40; $P < 0.01$), which resulted in decreased fecal P concentration (0.85 vs. 0.69; $P < 0.01$). Group feeding was implemented on 2 farms. The average CP of the rations fed on these farms decreased from 15.7 to 14.4% ($P = 0.03$), which resulted in decreased, UN (0.077 vs. 0.048%; $P < 0.01$), UUN (56.1 vs. 36.9 mg/dL; $P < 0.01$), and MUN (17.4 vs. 13.7 mg/dL; $P = 0.03$). Milk production and DMI were not affected by BMP implementation. Bulk tank milk fat (3.91 vs. 3.56%; $P < 0.01$) and milk protein (3.13 vs. 2.98%; $P < 0.01$) decreased from pre- to postBMP on all farms, perhaps due to seasonal effects. In conclusion, reduced dietary CP decreased N concentrations in urine and feces and reduced dietary P decreased fecal P concentration on commercial dairy farms.

Key Words: dairy farm, dietary protein, dietary phosphorus

0365 The impact of dairy advisory teams on farm improvement in Pennsylvania dairies. M. H. Buza*, L. Holden, and R. C. Goodling, *The Pennsylvania State University, University Park, PA*

Dairy producers continuously seek ways to improve their farm, and many choose to form a dairy advisory team (DAT) to improve management. The objectives were: (1) to compare key measures before and after the team to determine if the use of a DAT was effective, and (2) to compare a group of 20 herds with a DAT to Pennsylvania (PA) averages for key measures. Teams were formed between May 2008 and January 2013. The range for herd size was 42 to 694 ± 139 cows. Herd size, milk yield, somatic cell score (SCS), peak milk yield, age at first calving (AFC), days in milk (DIM), pregnancy rate, and cull and mortality rate were key measures analyzed. The changes in key measures, after using DAT for at least 1 yr, were analyzed using a paired *t* test. After DAT use, herds had higher ($P < 0.01$) herd sizes (187 vs. 177 cows) and higher ($P = 0.066$) milk yields of 31.3 vs. 32.1 kg, as well as lower ($P = 0.077$) AFC of 24.9 vs. 25.4 mo and lower ($P = 0.054$) percent of herd with SCS $\geq$ 4 of 21.7 vs. 23.9%. The DAT herds' January Dairy Herd Improvement Association (DHIA) test data were compared with Dairy Metric's PA average for January 2014 using a 1-sample *t* test. Farms with DAT had significantly ($P < 0.05$) higher milk yield of 33.9 vs. 31.9 kg and peak milk yield for lactation 1 with 36.1 vs. 33.9 kg. There was no significant difference between the averages for DAT herds and PA herds for peak milk yield in older cows, but DAT herds had numerically higher peaks (44.3 vs. 42.7 kg and 47.4 vs. 45.9 kg for second and third lactation, respectively) in older cows. Herds with DAT had significantly ($P < 0.001$) lower AFC of 24.4 vs. 25.6 mo and lower percentage of herd with SCS $\geq$ 4 with 20.15 vs. 26.6%. There were no differences for pregnancy rate, DIM, or cull or mortality rate. Use of DAT led to larger herd size, greater milk yield, lower AFC, and better SCS. Herds with DAT had higher milk yield, lower AFC, and better SCS compared with PA averages. Use of a DAT was beneficial to dairy farms.

Key Words: dairy advisory team, dairy herd improvement, dairy herd key measures

0366 Plant-derived compounds, trans-cinnamaldehyde and eugenol, reduce adhesion and invasion of *Staphylococcus aureus* in bovine mammary epithelial cells in vitro. D. Jaganathan*[1], A. Kollanoor-Johny[1], K. Vekitanarayanan[1], G. W. Kazmer[1], L. Kuo[2], Y. B. Wang[2], and K. E. Govoni[1], *[1]Department of Animal Science, University of Connecticut, Storrs, [2]Department of Statistics, University of Connecticut, Storrs.*

Staphylococcus aureus is 1 of the major bacterial pathogens involved in ruminant mastitis globally. The disease has major impacts on animal health and milk quality leading to severe economic losses to the dairy industry. *S. aureus* adhesion to and invasion of mammary epithelial cells (MEC) is critical for the establishment of the disease. We hypothesized that 2 plant-derived antimicrobials, *trans*-cinnamaldehyde (TC) and eugenol (EG), would reduce *S. aureus* adhesion to and invasion of primary bovine MEC in vitro. Mammary epithelial cells were isolated from mammary glands of lactating cows postslaughter and were characterized using multicytokeratin immunostaining. Confluent MEC monolayers were inoculated with 4 *S. aureus* strains (Strain ST 35, Thorn 17, 15, and M9175) at mid-log phase separately (multiplicity of infection– 100:1) either in the presence or absence (control) of subinhibitory concentrations (SICs: greatest concentration that did not inhibit bacterial growth) of TC (0.006%) and EG (0.03%), and incubated for 2 h for bacterial adhesion. Infected cells were treated with gentamicin (100 µg/mL) for 1 h at 37°C for enumerating invaded bacteria. All experiments included duplicate samples and were repeated 3 times. Data were analyzed using PROC ANOVA and significance determined at $P < 0.05$. For strain Thorn 17, pre-exposure of *S. aureus* (5 h) and MEC (12 h) to EG reduced *S. aureus* adhesion to and invasion of MEC by ~1.6 ± 0.01 $\log_{10}$ CFU/mL (control = 6.67 ± 0.01 $\log_{10}$ CFU/mL; $P < 0.0001$) and 2.8 ± 0.11 $\log_{10}$ CFU/mL (control = 3.9 ± 0.02 $\log_{10}$ CFU/mL; $P < 0.0001$), respectively. Preexposure of *S. aureus* and MEC to TC reduced *S. aureus* adhesion to and invasion of MEC by ~2.2 ± 0.02 $\log_{10}$ CFU/mL (control = 6.7 ± 0.02 $\log_{10}$ CFU/mL; $P < 0.0001$) and 2.85 ± 0.08 $\log_{10}$ CFU/mL (control = 3.94 ± 0.01 $\log_{10}$ CFU/mL $P < 0.0001$), respectively. Similar results were observed with strains ST 35, M9175 and Thorn 15. In conclusion, SICs of TC and EG reduced *S. aureus* adhesion to and invasion of MEC. In vivo studies using a mammalian model to validate these results are warranted.

Key Words: mammary epithelial cells, plant compound, *Staphylococcus aureus*

0367 Effect of dietary supplementation of *Capsicum* extract on feed intake, milk production and composition, rumen fermentation, and rumen microbial populations in dairy cows. J. Oh*[1], F. Giallongo[1], H. L. Weeks[1], T. W. Frederick[1], A. N. Hristov[1], and E. H. Wall[2], *[1]Department of Animal Science, The Pennsylvania State University, University Park, PA, [2]Pancosma, Geneva, Switzerland*.

Dietary supplementation of *Capsicum* extract (CE) has been reported to increase feed intake and modify ruminal fermentation in cattle. The objective of this experiment was to investigate the effects of CE on feed intake, digestibility, N utilization, milk performance, ruminal fermentation, and ruminal microbial diversity in lactating dairy cows. Eight multiparous Holstein cows (days in milk, 50 ± 9.6 d; BW, 591 ± 32.6 kg), including 3 ruminally-cannulated, were used in a replicated 4

× 4 incomplete Latin square design with 25-d periods. Treatments were 0 (CON), 250, 500, and 1000 mg CE cow^{-1} d^{-1}. The CE was mixed with a small portion of the TMR and top-dressed. Apparent total tract digestibility was not affected by treatment. Treatments also had no effect on urinary-N, urea-N, urinary purine derivatives, and fecal-N excretions. Milk yield tended to quadratically increase (P = 0.08, SEM = 0.86) with CE: 50.5, 51.9, 51.5, and 50.3 kg/d, respectively. Dry matter intake was not affected by CE (27.0 ± 0.64 kg/d). Feed efficiency tended to increase quadratically (P = 0.08; SEM = 0.047) with CE supplementation: 1.90, 1.93, 2.02, and 1.96 kg/kg, respectively. Milk fat yield increased (P = 0.05) for CE treatments compared with CON (1.58 vs. 1.46 kg/d, respectively). Relative to CON, CE increased (P = 0.04) 4% FCM and tended to increase (P = 0.06) energy corrected milk yields. Concentration of milk lactose was decreased (P = 0.01) by CE. Compared with CON, concentration of β-hydroxybutyrate (BHBA) in blood plasma tended to be higher (P = 0.07) for CE and quadratically responded (P = 0.02) to CE supplementation level. Plasma NEFA was not affected by CE. Ruminal pH tended to be decreased (P = 0.06) by CE compared with CON. Ruminal ammonia and VFA concentrations were not affected by treatment, although acetate tended to linearly decrease (P = 0.11) with CE. Predominant bacteria in rumen contents were *Ruminococcaceae* spp. and *Prevotella* spp. (10.8 to 22.6% of the total population). Compared with CON, *Prevotella* spp., *Butyrivibrio* spp., and *Roseburia* spp. were decreased ($P \leq$ 0.05) by CE. In conclusion, feed intake, total tract digestibility of nutrients, and N utilization were not affected by dietary CE supplementation. However, CE increased milk production, milk fat yield, and plasma BHBA concentration. Collectively, these results suggest that CE may increase lipid mobilization for milk fat synthesis in dairy cows.

Key Words: capsicum extract, feed intake, milk production

0368 The effects of CO_2 and HEPES buffer on in-vitro chemotaxis assays of bovine neutrophils.

A. M. Barnard*, R. Nebenhaus, R. M. Dyer, and T. F. Gressley, *University of Delaware, Newark.*

Neutrophil (PMN) chemotaxis can be measured in vitro with or without 5% CO_2. The production of carbonic acid during incubation with 5% CO_2 may reduce pH, possibly affecting cellular migratory function. The goals of this study were to determine whether incubation with 5% CO_2 impacts PMN chemotactic function, and if the addition of HEPES buffer affects response to CO_2. Neutrophils were isolated from 12 lactating cows over 5 different test dates and cell concentration adjusted to 2 × 10^6 cells/mL. Media consisted of HBSS containing 5% FBS with or without the addition of 10 mM HEPES. The bottom wells of a 48-well chemotaxis chamber (Neuro Probe Inc., Gaithersburg, MD) contained 28 µL of media supplemented with 50 ng/mL of complement component 5a (C5a) or 100 ng/mL of Interleukin-8 (IL-8). A 5 µm polycarbonate membrane separated the top and bottom wells. Neutrophil suspension (50 µL) was added to the top wells, and the chambers were incubated at 37°C for 1 h, in the presence or absence of 5% CO_2. Negative controls did not contain chemoattractant in either well while positive controls contained 50 ng/mL C5a in both top and bottom wells. Raw adherence (RawAd) was determined by counting PMN adhered to the bottom of the membrane in 5 microscope fields per well. Relative adherence (RelAd) was calculated as (RawAd test well)/(RawAd negative control well) × 100%. Data were analyzed using the Glimmix procedure of SAS (SAS Inst. Inc., Cary, NC) with the fixed effects of HEPES, CO_2, chemoattractant and all interactions and random effects of date and cow within date. RawAd and RelAd were both affected by CO_2 (P = 0.03; 0.002, respectively) and chemoattractant (P = < 0.0001 and 0.0002, respectively). The presence of CO_2 caused a decrease in both RawAd and RelAd. For both RawAd and RelAd, chemotaxis towards C5a or IL-8 did not differ but both were greater than chemotaxis to controls. RawAd was also affected by CO_2 × chemoattractant (P = 0.02) and HEPES × CO_2 (P = 0.0001). RawAd for C5a or IL-8 wells was approximately twice that of control wells in the absence of CO_2, but was not significantly different from controls in the presence of CO_2. RawAd decreased in the presence of CO_2 when HEPES was not present, but was unaffected by CO_2 in the presence of HEPES. These results suggest that incubating PMN with CO_2 reduces the chemotactic response and that HEPES partially ameliorated this effect.

Key Words: neutrophils, chemotaxis, bovine

0369 The 2001 Dairy NRC Ration Evaluation Software effectively predicts dietary strong ion and DCAD concentrations in lactating dairy cow diets.

M. E. Iwaniuk* and R. A. Erdman, *University of Maryland, College Park*.

Recent research suggests that increasing DCAD concentration using buffers in lactating dairy cow diets results in increased milk yield and milk fat percentage. Dietary buffers, such as $NaHCO_3$ and K_2CO_3, alter DCAD concentration and have been used in lactating dairy cow diets for decades. However, most of the published work on buffer supplementation was conducted before the development of the DCAD concept. Thus, these data have not been included in previous metaanalyses of DCAD effects on dairy cow performance. One problem with the use of these data is the lack of measured concentrations for each of the minerals required for calculation of DCAD (Na + K– Cl, meq/kg DM). To overcome this obstacle, a study was conducted to determine if the 2001 Dairy NRC Ration Evaluation Software could be used to estimate missing dietary ion concentrations. Data from 44 journal articles on the effects of buffers and DCAD that were published from 1965 to 2011 were used in the study. Experimental diets where Na, K, and Cl concentrations were analyzed were used as test ob-

servations. Ingredient information for each diet was extracted from each article and entered into the 2001 NRC software to estimate dietary mineral concentrations. The NRC predicted Na, K, Cl, and DCAD were regressed on the respective measured concentrations and the regression statistics are reported. The root mean prediction square error (RMPSE) expressed as a fraction of the mean concentration was small. Chloride data were clustered in 2 distinct populations (0.25 to 0.5 and > 1.0%) which may have resulted in slope confidence intervals different from 1. However, the regression slopes for Na, K, and DCAD were not different from 1 ($P > 0.05$). Intercept values when significant (Na and Cl) were small compared with the mean concentration for each mineral. Residual plots indicated no mean or linear bias. In conclusion, the NRC software accurately estimated mineral and DCAD concentrations and could be used to estimate missing ion concentrations in future metaanalyses of DCAD experiments.

Key Words: DCAD, NRC Software, dairy cows

Table 0369.

Item	Obs	Mean	SD	Slope	95% CI	Int	$P <$	R^2	RMPSE
Na, %	129	0.39	0.18	0.98	± 0.065	0.04	0.003	0.88	0.06
K, %	137	1.45	0.52	0.96	± 0.072	0.04	0.511	0.84	0.21
Cl, %	84	0.71	0.40	0.86	± 0.091	0.12	0.002	0.81	0.17
DCAD, meq/kg	60	343.9	143.9	0.96	± 0.102	-23.4	0.266	0.86	54.7

GROWTH & DEVELOPMENT

0370 Whole or ground oats in calf starters: Effects on rumen fermentation and rumen development.
F. X. Suarez-Mena*[1], A. J. Heinrichs[1], C. M. Jones[1], T. M. Hill[2], and J. D. Quigley[2], [1]*The Pennsylvania State University, University Park,* [2]*Provimi North America, Brookville, OH.*

A series of 3 trials were conducted to determine effects of whole or ground oats in starter grain on rumen fermentation and development of preweaned calves. Male Holstein calves (43.1 ± 2.3 kg BW at birth; n = 8, 9, and 7 for trials 1, 2, and 3 respectively) were housed in individual pens in a heated facility; bedding was covered with landscape fabric to avoid any consumption of bedding. In trials 1 and 2 only, calves were fitted with a rumen cannula by wk 2 of life. Water was offered free choice, and milk replacer was fed to 12% of birth BW. In all trials, a fixed amount of starter (containing 25% oats either ground and in the pellet or whole; 18.7% CP, 12.7% NDF) was offered daily based on average intakes of calves on similar milk replacer diets; orts were fed through the cannula in Trials 1 and 2. Calves were randomly assigned to all pelleted starter (Ground, n = 11) or pellets plus whole oats (Whole, n = 13). Rumen contents (Trials 1 and 2) were sampled weekly at −8, −4, 0, 2, 4, 8, and 12 h after grain feeding for pH and VFA determination. Calves were euthanized 3 wk (Trial 1) or 4 wk (Trials 2 and 3) after grain was offered; organs were harvested, emptied, rinsed, and weighed to gauge digestive organ development. Experimental design was complete randomized block. Starter intake was not different between treatments by design (P > 0.05); weekly intakes were 481 ± 24, 1575 ± 30, 3176 ± 48, 4656 ± 143 g for wk 1 to 4 of grain feeding. Weekly measurements of rumen digesta pH and molar proportion of individual VFA did not change with diet. Molar proportion of butyrate and pH linearly decreased with age, while acetate proportion increased. Reticulorumen weight (569 ground vs. 503 whole ± 24 g) and papillae length (0.75 ground vs. 0.68 whole ± 0.03 mm) tended to be greater for ground (P < 0.1) while abomasum weight (240 ground vs. 274 whole ± 9 g) was greater for whole (P < 0.05). Liver and omasum weights were not different. Under the conditions of this study, physical form of oats in starter grain did not affect rumen fermentation parameters; greater rumen weight and papillae length in Ground may be a result of greater nutrient availability of ground oats.

Key Words: rumen-development, oats

0371 Rumen epithelial gene expression in periruminant holstein bull calves fed a fermentation extract of *Aspergillus oryzae*.
T. T. Yohe*, K. M. O'Diam, and K. M. Daniels, *Department of Animal Sciences, The Ohio State University, Wooster.*

A fermentation extract of *Aspergillus oryzae* has previously been utilized as a direct fed microbial (DFM) to promote starter intake and feed efficiency in calves. Potential effects of this DFM on rumen epithelial gene expression are unknown, and may help explain some benefits of supplementation. The objective was to determine if age and dietary inclusion of an extract of *A. oryzae* alter relative abundance of select rumen epithelial genes in periruminant Holstein bull calves. The genes investigated encode proteins that specialize in: VFA transport (*MCT1*, *MCT2*, *MCT4*), intracellular regulation of pH (*NHE1, NHE2, NHE3, DRA, PAT1*), and epithelial barrier function (*GJA1, CLDN1*). Individual calves (n = 52) were randomly assigned to a slaughter age, 4 wk (n = 16) or 8 wk (n = 36), and treatment, control (CON; n = 27) or direct fed microbial (DFM; n = 25). Calves were housed with no bedding and fed individually. Liquid DFM was delivered in milk replacer (2 g per day) for the first 4 wk of the trial; solid DFM (2 g per day) was top-dressed on grain thereafter. Calves were fed nonmedicated milk replacer twice daily (22.0% CP, 20.0% fat DM basis; 680 g/d) and had ad libitum access to texturized grain (20% CP, 2.0% fat) and water. At slaughter, rumen tissue was obtained from the cranial ventral region of each calf; the epithelial portion was separated and preserved for later RNA extraction and cDNA synthesis. cDNA was used in quantitative reverse transcription PCR assays. *UXT, RPS9, RPS15, and RPS26* were endogenous control genes. All transcripts were detectable in all calves. Relative mRNA abundance of *NHE3* was shown to decrease with age (P < 0.05); no other genes were affected by age or treatment. In summary, dietary inclusion (2 g/d) of an extract of *A. oryzae* did not result in altered rumen epithelial gene expression when supplemented animals were compared with cohorts not fed DFM. More differences were expected due to age, as selected genes are related to metabolic development of the rumen, but it is important to point out that gene level data do not always correlate with protein abundance. Further, it is possible that the dose used here was not high enough to elicit treatment effects. Regardless, we provide new data about ruminal gene expression in periruminant dairy calves.

Key Words: dairy calf, rumen, gene expression

0372 Performance and rumen development of artificially reared calves to dietary butyrate supplementation. A. K. Kelly[1], J. V. O'Doherty[1], D. A. Kenny[2], T. M. Boland[3], and K. M. Pierce*[3], *[1]School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, [2]Teagasc Grange, Meath, Ireland, [3]School of Agriculture and Food Science, University College Dublin, Dublin 4, Ireland*.

Recently, there has been increased interest in the potential of certain diet-derived chemicals to enhance immune response, gastrointestinal health, and growth potential of young livestock. Of those evaluated thus far, the short-chain fatty acid butyrate has shown significant potential as an antipathogenic immune stimulant. The aim of this study was to determine the effect of sodium butyrate supplementation on calf performance, intestinal development, and volatile fatty acids profiles in preweaned calves. Forty-four Holstein Fresian male calves with a mean age of 13 ± 5 d were divided into 2 equal groups and fed milk replacer supplemented with 4 g of coated sodium butyrate (SB)/d or with no-coated sodium butyrate (CON). Calves were allocated to a standard 56 d calf rearing requiem: Milk offered at 6 L/d (125 g/L) for 10 to 49 d and weaning over 7 d (49 to 56 d) by gradually reducing the allowance. Concentrate and water was offered to calves on an ad libitum basis thoughout the trial period. Milk replacer and concentrate intake was recorded daily using a computerized calf rearing system (Forster Technik, Germany). Bodyweight was measured weekly. Respiration rate, rectal temperature, and fecal scores were recorded daily. At weaning (d 56), 8 animals from each treatment (SB vs. CON) were euthanized. Rumen digesta and tissue was harvested for VFA and rumen development analysis. Calves supplemented with SB tended ($P = 0.08$) to have higher preweaning growth rates compared with CON (0.69 vs. 0.59 kg/d). At weaning, SB calves (80.2 kg) were 3.2 kg heavier than the CON group (76.9 kg), with bodyweight difference detected from d 42 to weaning. Bodyweight differences between treatments were not evident before this ($P > 0.10$). Total DMI was not different between dietary treatments, but preweaning SB supplementation tended ($P = 0.08$) to improve feed conversion rate of the calves. There were no significant differences on rectal temperature, respiration rate, and fecal score between the treatments. Rumen papillae length, width, and perimeter were not affected by SB supplementation of milk replacer. Similarly, rumen concentrations of total VFAs were not altered by dietary treatments. In conclusion, the supplementation of milk replacer with coated sodium butyrate could improve preweaning performance of dairy calves.

Key Words: butyrate, dairy calf, rumen development

0373 Nongenomic effects of trenbolone acetate on bovine satellite cell proliferation. K. J. Thornton*, E. Kamanga-Sollo, M. E. White, and W. R. Dayton, *University of Minnesota, Saint Paul.*

Androgen treatment improves skeletal muscle growth in a number of species; however, the mechanism responsible for this improved muscle growth has not been fully elucidated. Trenbolone acetate (TBA), a testosterone analog that does not undergo aromatization to estradiol, has been shown to increase proliferation and protein synthesis rates and decrease protein degradation rate in bovine satellite cell (BSC) cultures. This is particularly significant because satellite cells are the source of nuclei needed to support postnatal muscle fiber hypertrophy and are thus crucial in determining the rate and extent of muscle growth, although the mechanism responsible for these effects of TBA on BSC has not been fully determined. The classical genomic actions of testosterone in which the androgen receptor acts as a ligand inducible transcription factor modulating target gene transcription has been well characterized. However, our recent studies have indicated that TBA may also initiate a quicker, nongenomic response that involves release of membrane-bound heparin-binding epidermal growth factor-like growth factor (hbEGF), which then binds to and activates the epidermal growth factor receptor (EGFR). To determine whether this nongenomic pathway is involved in TBA-stimulated BSC proliferation, we analyzed the effects of treating BSC with AG1478, a specific EGFR tyrosine kinase inhibitor, and CRM197, a specific inhibitor of hbEGF, on TBA-stimulated proliferation rate (3H-thymidine incorporation). As expected, BSC cultures treated with 10 nm TBA showed significantly ($P < 0.05$) increased proliferation rate when compared with control cultures. Additionally, treatment with 5 ng hbEGF/mL stimulated proliferation in BSC cultures ($P < 0.05$). Treatment with AG1478 significantly ($P < 0.05$) suppressed TBA-induced increases in proliferation. Additionally, in the presence of CRM197, TBA induced increases in proliferation were significantly ($P < 0.05$) decreased. These data indicate that hbEGF and the EGFR may play a role in TBA-mediated increases in BSC proliferation. Further, these findings demonstrate that testosterone and/or TBA may stimulate increases in skeletal muscle growth utilizing a nongenomic mechanism.

Key Words: epidermal growth factor receptor, satellite cells, trenbolone acetate

0374 Effects of recombinant bovine somatotropin on performance and biological activity of skeletal muscle over the finishing phase of feedlot heifers.
J. E. Hergenreder*[1], J. O. Baggerman[1], A. J. Thompson[1], M. A. Jennings[1], K. S. Spivey[1], W. C. Burson[1], A. J. Laurent[1], G. J. Vogel[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Elanco Animal Health, Greenfield, IN.*

Our objective was to determine if recombinant bovine somatotropin (rBST) enhanced performance and biological activity in skeletal muscle over the finishing phase of feedlot heifers. Heifers (n = 16; initial BW = 457 ± 3 kg) were randomly assigned to pens (4 pens/treatment; 2 heifers/pen) and treatment: (1) no rBST (control); (2) 500 mg/animal of sometribove zinc at d 0 and 14 (rBST; Posilac, Elanco Animal Health). Upon arrival, heifers were acclimated for 14 d. *Longissimus* muscle biopsies for gene expression and protein abundance were performed on d 0, 14, 28, 42, and 56. On d 88 (102 d on feed) heifers were harvested and carcass data were collected. Average daily gain, DMI, and G:F were not affected by treatment ($P > 0.05$). There was no change in final BW, HCW, or dressing percentage (DP; $P > 0.05$); however, there was a tendency for control cattle to have greater marbling and decreased KPH ($P \leq 0.08$). Loin muscle area, fat thickness, and yield grade did not differ ($P > 0.05$). Using quantitative reverse transcription PCR, genes of interest were quantified: AMPKα, β_1AR, β_2AR, β_3AR, MHC-I, MHC-IIA, MHC-IIX, IGF-I, GPR43, GPR41, Glut4, SCD, CEBPβ, and PPARγ. The rBST cattle had the greatest quantity of AMPKα mRNA ($P < 0.05$) on d 0. There was a day effect on MHC-IIA, MHC-IIX, β_2AR, PPARγ, and SCD ($P < 0.05$). All cattle had the greatest concentration of MHC-IIA mRNA on d 56 and the greatest concentration of MHC-IIX mRNA on d 14, 28, and 42 ($P < 0.05$). Concentration of β_2AR mRNA were the greatest on d 56 ($P < 0.05$), while the greatest concentration of PPARγ and SCD mRNA were on d 0 and 56 ($P < 0.05$). No differences ($P > 0.05$) were observed in mRNA between treatments for MHC-I, β_3AR, GPR41, or Glut4. Protein quantification was performed utilizing western blotting procedures to assess the abundance of β_1AR, β_2AR, and β_3AR. There was a day effect on protein abundance ($P < 0.05$). The βAR were quantified at their greatest abundance on d 0 for β_1AR, d 0 and 42 for β_2AR, and d 0 and 28 for β_3AR ($P < 0.05$). These data indicate that as days on feed increase, the effects of skeletal muscle biological activity may not be solely dependent on rBST administration. However, further investigation is needed to elucidate interactions that effect muscle metabolism during the finishing period.

Key Words: β-adrenergic receptor, myosin heavy chain, recombinant bovine somatotropin

0375 Identification of potential serum biomarkers for feed efficiency in young pigs.
J. K. Grubbs*, S. M. Lonergan, J. C. M. Dekkers, and C. K. Tuggle, *Iowa State University, Ames.*

Identification of biomarkers for feed efficiency is important for increasing overall productivity of animal production. Early indicators of feed efficiency would be of particular value. The purpose of this project was to establish serum biomarkers for feed efficiency in young pigs. Serum was collected from 5-wk-old pigs from generation 8 of the Iowa State Residual Feed Intake (RFI) project. The pigs were then finished on either a high energy, low fiber diet or low energy, high fiber diet. The RFI was calculated using feed intake data from FIRE Performance Testing System (Osborne Industries, Osborne, KS). Serum protein samples were analyzed using 2D Difference in Gel Electrophoresis (2D-DIGE). Separate 2D-DIGE experiments were carried for each diet using pigs from the more efficient low RFI line (n = 8) or the less efficient high RFI line (n = 8). Selected proteins were identified through mass spectrometry. Both 2D-DIGE comparisons yielded several potential protein biomarkers for feed efficiency including gelsolin, vitronectin, serpinA3–6, and serpinA3–8. Gelsolin and vitronectin were significantly increased (13 to 57%) in abundance in the low RFI line. SerpinA3–6 and A3–8 were identified in 14 protein spots, and the protein abundance in most of these SerpinA3–6 or A3–8 spots was > 100% higher in the low RFI line as compared with the high RFI line pigs. These differences were consistent between the diet comparisons. SerpinA3 is a serine protease inhibitor that has promise as a biomarker to many disease states. In young pigs, an increase in serine protease inhibition could result in lower protein turnover. A decrease in protein turnover indicates less metabolic energy is being used for cellular repair and replacement. These data indicate further investigation is needed into serpinA3 as a biomarker for feed efficiency. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30336 from the USDA National Institute of Food and Agriculture.

Key Words: 2D-DIGE, residual feed intake, SerpinA3

0376 Enhanced protein accretion and vital organ growth with intermittent bolus compared with continuous feeding in neonatal pigs.

S. W. El-Kadi*[1,2], C. Boutry[1], A. Suryawan[1], M. C. Gazzaneo[1], R. A. Orellana[1], N. Srivastava[1], H. V. Nguyen[1], S. R. Kimball[3], M. L. Fiorotto[1], and T. A. Davis[1], *[1]USDA/ARS–Children's Nutrition Research Center, Baylor College of Medicine, Houston, TX, [2]Animal and Poultry Sciences, Virginia Tech, Blacksburg, [3]Cellular and Molecular Physiology, Penn State College of Medicine, Hershey, PA*.

Enhancing the efficiency of protein utilization through dietary interventions may provide new avenues for improving profitability in farm animals. In addition, neonatal pigs can serve as dual-use models for nutrition research in animal agriculture and biomedical fields. Recently, we showed that intermittent compared with continuous feeding enhances lean tissue accretion by increasing muscle protein synthesis in neonatal pigs. The aim of this study was to determine if these feeding modalities affect vital organ protein accretion and growth. Neonatal pigs (n = 6/treatment, 6 d old) were fed the same diet in equivalent amounts continuously (CON) or intermittently (INT; meal every 4 h) for 21 d. Plasma branched-chain AA and insulin and fractional protein synthesis rates in liver, kidney, jejunum, and ileum were determined on the last day of feeding. Fractional rate of protein synthesis in organs was measured using the flooding dose method, and activation of translation initiation factors was determined by PAGE. Weight gain was greater ($P < 0.05$) for INT than for CON pigs and resulted in heavier body weights from 9 d of feeding onward. Arterial branched-chain AA and insulin concentrations measured on the last day of feeding were greater for INT after the meal than for CON pigs ($P < 0.05$). Phosphorylation of ribosomal protein S6 kinase were higher in ileum and liver in INT compared with CON fed pigs, indicating increased translation initiation signaling ($P < 0.05$). The proportion of rpS8 mRNA associated with polysomes in liver was greater in the INT compared with CON fed group ($P < 0.05$). Protein synthesis increased by 14% in jejunum, 48% in ileum, and 22% in liver ($P < 0.05$), while for the kidneys the increase was only modest. Jejunum, ileum, liver, and kidneys were 41, 36, 73, and 55% heavier for pigs in the INT as compared with the CON group ($P < 0.05$). These results suggest that intermittent feeding, as compared with continuous feeding, enhances protein accretion in vital organ growth by up-regulating protein synthesis. Supported by NIH AR444474 and USDA/ARS 6250–51000–055.

Key Words: branched-chain amino acids, protein synthesis, insulin

GROWTH AND DEVELOPMENT: JOINT MEAT SCIENCE & MUSCLE BIOLOGY, AND GROWTH & DEVELOPMENT— APPLICATIONS OF PROTEOMICS IN ANIMAL PRODUCTION

0377 Proteomics in animal science. J. Lippolis*, *National Animal Disease Center, Ruminant Disease of Cattle Research Unit , Ames, IA.*

The ultimate goal of proteomics is to detect and quantify the tens of thousands of proteins from a specific cell, tissue, or fluid. To observe protein expression, location, interaction, and modification under different experimental conditions would aid the understanding of the molecular mechanisms critical for cellular functions. In the context of animal health, better understanding of cellular functions would be the basis for rational therapeutic designs to target pathogens and correct disease conditions. The unique advantage of this technology is that a fairly large number of proteins can be identified and quantitated at one time, without any prior knowledge that any specific protein might exist in a sample. Analyzing a proteomic dataset can often lead to surprising results, and the unexpected may be the most interesting observation. In fact, most shotgun proteomic experiments are not typical "hypothesis driven" experiments, but may be better described as experiments designed to find a hypothesis. In these experiments hundreds if not thousands of proteins can be identified whose expression is altered by a defined experimental condition. Some changes in protein expression observed in a proteomics experiment may be expected and even well characterized. However, some may be unexpected or unknown and lead to new hypothesis for the connections between protein expression and cellular processes. Utilization of this technology with its potential for discovery, balanced with its limitations, is a useful tool in animal health research.

0378 Functional proteomics: Elucidation of molecular mechanisms of physiological variations of fat depots in beef cattle. J. M. Romao[1], M. He[2], T. McAllister[2], and L. L. Guan[1]*, *[1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Alberta, Canada, [2]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada.*

Adipose tissue plays an important role in energetics, meat quality and animal productivity, but the factors that regulate fat metabolism in beef cattle are unclear. Recent transcriptomics has identified hundreds of genes that may influence fat deposition in bovine adipocytes, but the phenotypic traits of fat are ultimately determined by the functional proteins that regulate adipogenesis and lipolysis. It is evident that gene expression does not always correspond to the levels of functional proteins produced due to differences in translation efficiency and post-translational modification. Using high throughput Label Free Quantification (LC-MS/MS), we have attempted to identify the global changes in protein expression in bovine subcutaneous and visceral fat depots of steers fed different diets at different stages of physiological maturity. Our results revealed that the proteomic profile of bovine adipocytes differs among fat depots, reflecting functional and physiological differences such as the higher metabolic activity of visceral fat. Changes in lipid profiles in the diet, altered proteomic profiles in subcutaneous fat and provide insight into mechanisms whereby the fatty acid composition of adipose tissue may be favourable altered. Moreover, proteomic changes in subcutaneous adipose tissue of feedlot cattle between 12and 15 months reflected increased adipocyte growth and proliferation, but fatty acid synthesis declined as steers approached finishing weight. These findings suggest that the rate of fatty acids synthesis is not static during growth, revealing a coordinated balance between subcutaneous fat mass and the cellular abundance of lipogenic proteins which regulate the rate and degree of fat deposition in beef cattle. Additional work suggested that miRNAs within bovine adipose tissue may play an important role in the controlling the expression of regulatory proteins within fat depots. Consequently, proteins and miRNAs may serve as markers for future selection of cattle based on their ability to generate favourable levels of adipose tissue with desirable fatty acid profiles within beef meat.

0379 Use of proteomics in animal health and disease research. P. D. Eckersall*, *Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Bearsden Rd, Glasgow, G61 1QH, UK.*

Proteomics is the application of advanced protein analytical methods to determine the individual protein components in a biological sample from cells, tissue or fluid. These technologies have application wherever proteins are investigated and are essential for a full systems biology approach for integration of omic technologies to address myriad research questions. While there have been great strides made in the applications of proteomics in research into human disease and for in vitro study there has been relatively limited application in farm animal health and disease. However the value of proteomic investigation is being recognized in animal research. The combination of two dimension electrophoresis and mass spectrometry was the initial approach to proteomic investigation and remains a powerful technology for proteome characterisation and biomarker discovery. In our laboratory, investigation of bovine nasal secretion to assess its value as a non-invasive medium for diagnosis of bovine respiratory disease has revealed the presence of glutathione S-transferase as a significant component of the secretion. γ-Glutamyl trans-

ferase and alkaline phosphatase have also been identified in nasal secretion with active host defence mechanisms being suggested. Recently non-gel based proteomics combining liquid chromatography with mass spectrometry have seen major application in farm animal research. Quantitative proteomics shows great promise in providing multiplexed assay systems for the simultaneous assay of numerous low abundance protein biomarkers. For example, it has been shown that the concentrations of cytokines, acute phase proteins and bioactive peptides can be monitored in the same micro-litre volume of milk during bovine mastitis, using standards of specific peptides derived from the respective proteins with great potential for research into this important disease (Bislev et al., 2012 J Prot Res 11:1832). Undoubtedly, the use of proteomics will become an established and valuable tool for animal health and disease research in the near future.

0380 Use of proteomics for livestock improvement.

E. Huff-Lonergan, S. M. Lonergan, S. Cruzen, K. Grubbs, J. Dekkers, N. Gabler, J. Selsby, and L. Baumgard, *Department of Animal Science, Iowa State University, Ames.*

Proteomics is a very broad term that includes a wide variety of techniques to characterize the entire protein profile of the cell or tissue (referred to as the proteome). Proteomic tools provide insight into the relative abundance of specific proteins, protein modifications (including proteolysis, phosphorylation, glycosolation, etc.), subcellular localization of specific proteins, interaction partners and protein sequence information. One of the challenges that face researchers is that differences that are noted are all with respect to a particular point in time. The very nature of the proteome dictates this because the proteome is dynamic, especially in respect to posttranslational modifications. Proteomics is very powerful in helping understand the role of proteins in various tissues/cells, it is however a challenging tool to use if the desired outcome is truly to identify the entire complement of proteins in a cell. Investigators should focus first on their research question before commencing any experiment, but this might be even more important in the "global" experiments that utilize any of the new integrated "omics" approaches. Often, researchers will choose to narrow their focus and look more specifically at a particular organelle or subcellular fraction. This decision cannot be made lightly, and interpretation of the results must take into consideration the techniques employed as well as all of the steps involved in sample preparation. The creative use of appropriate proteomics techniques has the potential to reveal many subtle changes in protein profiles that can aid in characterizing the physiological response to a wide variety of stressors to identify factors impact animals' ability to cope. In addition, proteomic techniques can be a valuable adjunct to studies that seek to understand innate differences in production characteristics.

HORSE SPECIES: **ADVANCES IN EQUINE STEM CELL BIOLOGY**

0382 Developmental progenitor cells of articular chondrocytes. J. N. MacLeod*, *University of Kentucky, Lexington.*

Articular cartilage lesions frequently compromise diarthrodial joint function and limit the performance potential of equine athletes. Cartilage is a tissue with poor intrinsic repair capabilities, a primary reason why degenerative joint disease is often progressive. New cell-based therapeutic strategies for equine joint surface injuries are generating a high level of interest. Unfortunately, fibrocartilage formation and poor anchoring of the repair tissue into the surrounding healthy tissue continue to be major challenges. Based on structural and molecular comparisons of different cartilaginous tissues and studies using primary chondrocyte cultures, it is clear that not all chondrocytes are equivalent on a cell biology level. We are trying to advance cell-based therapies for joint surface lesions by considering the unique phenotype that defines normal articular chondrocytes relative to other chondrocyte cell types, as well as the developmental processes that generate these cells. During limb formation, a morphologically distinct zone of cells in the prechondrogenic mesenchyme initiates synovial joint formation. This mesenchymal tissue is known as the "interzone" and appears as a flattened layer of cells connected by gap junctions. Interzone cells exist during early fetal development in all mammals including horses, but are present only transiently before joint space cavitation. In a developmental biology context, the interzone is the normal progenitor of all synovial joint tissues including articular cartilage. Using an amphibian model system, we have demonstrated that interzone tissue can facilitate a remarkable repair of large articular cartilage defects and even generate an entirely new diarthrodial joint *de novo*. More recently, we have been able to characterize interzone tissue in early equine fetuses and isolate primary horse interzone cells that can be expanded in culture. Experiments are being conducted to compare gene expression profiles of interzone cells to different types of chondrocytes on a transcriptome level, while also studying their response to differentiation stimuli. We believe that interzone tissue represents a cell population already developmentally positioned to form articular cartilage– true progenitor cells of articular chondrocytes. As such, they may represent a far superior cell type to focus on for optimizing cell-based therapies to repair articular cartilage defects in the horse.

Key Words: horse, cartilage, interzone

0383 Understanding the link between inflammation and muscle satellite cells in the horse. *S. A. Reed*, Department of Animal Science, University of Connecticut, Storrs.*

As an athletic animal, the horse performs a variety of activities throughout its life. With improvements in care, the equine population is living longer and remaining active and competing at increasingly older ages. Both advancing age and exercise result in increased concentrations of circulating and local cytokines, including interleukin (IL)-1β, IL-6, IL-8, interferon (IFN)-γ, and tumor necrosis factor (TNF)-α. Athletic endeavors in the aged horse may further increase the pro-inflammatory environment in the muscle, decreasing the ability to react appropriately to exercise. Poor response to exercise limits the athletic ability of geriatric horses, thus reducing their useful life span and potentially increasing the risk of injury. Satellite cells are muscle stem cells that reside adjacent to muscle fibers in skeletal muscle and are at least partially responsible for both maintenance of muscle mass and muscle hypertrophy. Normally, these cells exist in a quiescent state, becoming active, proliferating and differentiating in response to specific stimuli. Growth factors and cytokines present during hypertrophy and following exercise affect satellite cell activity. While the specific effects of cytokines on satellite cells are not well established, cytokines can both positively and negatively influence satellite cell and myoblast proliferation and differentiation. Equine satellite cells are comparable to satellite cells isolated from other species, exhibiting a fibroblast-like morphology in culture after activation and expressing desmin, an intermediate filament protein specific to muscle cells. Further, they differentiate into multinucleated myotubes which express myosin heavy chain, a fundamental property of myogenic cells. Understanding the effect of cytokines on equine satellite cell function will allow us to determine the mechanisms responsible for the poor response to exercise. Preliminary data indicates that the pro-inflammatory cytokines IL-1β and IL-6 inhibit myogenesis. C2C12 myoblasts cultured with 1.0 ng/mL IL-1β exhibit impaired fusion compared with controls ($P < 0.01$). Further, C2C12 myoblasts cultured with 10 ng/mL IL-6 exhibit decreased proliferation and decreased fusion compared with controls ($P < 0.01$). Ongoing work is examining the effects of these cytokines on satellite cells from young and adult horses. The pro-inflammatory environment in aged horses may inhibit exercise induced satellite cell activity, thereby diminishing exercise induced hypertrophy. As more horses are surviving and competing into their 20's, more research is required to understand the response of these animals to exercise during normal aging.

Key Words: cytokines, horse, satellite cells

0384 Use of mesenchymal stem cells in bone repair.

K. E. Govoni*, *Department of Animal Science, University of Connecticut, Storrs.*

Equine bone fractures are often catastrophic, potentially fatal, and costly to repair. Traditional methods of healing fractures have limited success, long recovery periods, and a high rate of re-injury. Current research in the equine industry has demonstrated that stem cell therapy is a promising novel therapy to improve fracture healing and reduce the incidence of re-injury; however reports of success in horses have been variable and limited. Stem cells can be derived from embryonic, fetal and adult tissue. However, based on the ease of collection, opportunity for autologous cells, and proven success in other models, adipose or bone marrow derived mesenchymal stem cells (MSC) are often used in equine therapies. Methods for isolation, proliferation, and differentiation of MSC are well established in rodent and human models but are not well characterized in horses. There is recent evidence that equine bone marrow MSC are able to proliferate in culture for several passages in the presence of autologous and fetal bovine serum which is important for expansion of cells. Mesenchymal stem cells are able to differentiate into osteoblasts, the bone forming cells, and this complex process is regulated by a number of transcription factors including, runt-related transcription factor 2 (Runx2) and osterix (Osx). However, it has not been well established if equine MSC are regulated in a similar manner. In the presence of L-ascorbic acid-2-phosphate, glycerol-2-phosphate, and dexamethasone, equine bone marrow MSC are able to differentiate into osteoblasts in culture as demonstrated by increased alkaline phosphatase activity and mineralization ($P < 0.05$). In addition, similar to rodent and human models, in equine bone marrow MSC, *Runx2* expression increased threefold ($P < 0.001$) during early differentiation and *Osx* expression increased ninefold ($P < 0.05$) during late differentiation. Further, expression of a novel transcription factor, *T-box3,* which is required for proliferation of mouse osteoblast cells and inhibits differentiation of osteoblasts, was reduced fourfold ($P < 0.01$) during differentiation of equine bone marrow MSC. These data demonstrate that equine bone marrow MSC may be regulated similar to rodent and human cells during osteoblast differentiation. Stem cell therapy is promising in equine bone repair, however additional research is need to identify optimal methods for reintroduction and potential manipulations to improve their ability to form new bone.

Key Words: bone, equine, mesenchymal stem cells

HORSE SPECIES

0385 Effects of high starch and sugar diets on postprandial inflammatory proteins in horses.

J. K. Suagee*[1], R. K. Splan[2], K. L. Swyers[3], R. J. Geor[4], and B. A. Corl[5], [1]*Ohio State, Wooster,* [2]*Virginia Tech, Middleburg,* [3]*Ranch-Way Feeds, Fort Collins, CO,* [4]*Michigan State University, East Lansing,* [5]*Virginia Tech, Blacksburg.*

Diets high in starches and sugars (HS) are linked to metabolic disorders in horses. Further, overconsumption of starch can result in digestive disturbances and laminitis. We hypothesize that high starch intake reduces intestinal pH and thus the integrity of the epithelial tight junctions, enabling lipopolysaccharide (LPS) to cross into the blood stream. For this experiment, plasma samples were obtained from mares ($n = 6$) consuming a diet high (HS) low (LS) in starch and sugar (Table 0385). Horses consumed 20% of their DE requirement as concentrate and 80% as mixed grass/legume hay (Table 0385). Concentrate was offered individually in 2 equal feedings (0800 and 1400 h) while hay was group fed in 2 equal feedings following concentrate consumption. Samples were collected on d 1 and on d 90 at 0, 1, 2, 3, and 4 h postconsumption of the assigned diet (0800 feeding), as part of a larger study that investigated postprandial starch responses. Plasma samples were then analyzed for LPS, tumor necrosis factor-α (TNF), interleukin (IL)-6, and IL1β. Lipopolysaccharide was analyzed using a commercial colorimetric assay, TNF and IL1β were analyzed using commercial ELISAs, and IL6 was analyzed using individual antibodies and a previously validated method. Each plasma factor was analyzed using repeated measures (SAS v. 9.3, SAS Inst. Inc., Cary, NC) for fixed effects and interactions of hour, day, and diet, with h 0 values as a covariate. Lipopolysaccharide concentrations were lower in HS horses on d 90 than on d1 ($P < 0.02$) but were otherwise unchanged. IL1β concentrations increased in HS horses 1 h postfeeding compared with LS horses ($P < 0.03$), without any differences between diets at other hours ($P > 0.55$). IL6 concentrations were influenced by hour ($P < 0.01$) but not diet ($P > 0.78$), whereby all horses had elevated IL6 concentrations 1 h postfeeding compared with h 0 ($P < 0.01$). TNF tended to be higher in HS horses than LS horses ($P = 0.07$) but was not influenced by day of study or hours postfeeding ($P > 0.51$). Consuming a high starch and sugar diet briefly elevates plasma IL1β, but this is most likely not due to elevated LPS concentrations. Of further interest was the finding that all horses, regardless of diet, had elevated postprandial IL6 concentrations.

Key Words: interleukin-1β, high-starch diet, horse, inflammation

Table 0385. Diet composition

Nutrient, %DM basis	LS	HS	Hay
Water soluble carbohydrates	6.8	8.4	6.7
Starch	3.0	50.6	2.2

0386 Evaluation of conjugated linoleic acid supplementation on markers of joint inflammation and metabolism in young horses challenged with lipopolysaccharide.

A. N. Bradbery*[1], J. Coverdale[1], K. L. Vernon[2], J. L. Lucia[3], C. E. Arnold[1], R. A. Dabareiner[1], M. K. Kahn[1], A. A. Millican[2], and T. H. Welsh, Jr.[4], [1]*Texas A&M University, College Station,* [2]*Clemson University, Clemson, SC,* [3]*Sam Houston State University, Huntsville, TX,* [4]*Department of Animal Science, Texas A&M University, College Station.*

Seventeen yearling Quarter horses were used in a randomized complete block design to evaluate potential of dietary CLA to mitigate intra-articular inflammation and cartilage metabolism following a single inflammatory insult. Horses were blocked by age, BW, and sex and randomly assigned to treatment for a 56-d trial. Treatments consisted of a commercial concentrate offered at 1% BW (as-fed) supplemented with either 1% soybean oil (CON; $n = 6$), 0.5% soybean oil and 0.5% CLA (LOW; $n = 5$; Lutalin, BASF Corp.), or 1% CLA (HIGH; $n = 6$; 55% purity) top-dressed daily. Horses were fed individually at 12-h intervals and offered 1% BW daily (as-fed) coastal bermudagrass (*Cynodon dactylon*) hay. On d 42, a lipopolysaccharide (LPS) challenge was conducted. Carpal joints were randomly assigned to receive intra-articular injections of 0.5 ng LPS derived from *Escherichia coli* 055:B5 or sterile lactated Ringer's solution as a contralateral control. Synovial fluid samples were taken via arthrocentesis at preinjection h 0 and 6, 12, 24, 168, and 336 h postinjection, and were analyzed for prostaglandin E_2 (PGE_2), carboxypeptide of type II collagen (CPII), and collagenase cleavage neopeptide (C2C) using commercial ELISA kits. Vitals, including heart rate, rectal temperature, and respiration rate were monitored at 0, 6, 12, and 24 h; and carpal circumference and surface temperatures were also recorded. Data were analyzed using PROC MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). Vitals were not significantly different across treatments ($P \geq 0.13$) and remained within normal ranges throughout the LPS challenge. Synovial PGE_2 concentrations were not influenced by dietary treatment ($P = 0.15$). Synovial C2C concentrations were influenced by treatment ($P = 0.05$) with LOW and HIGH horses having lesser C2C than CON. Across all treatments C2C concentrations varied over time ($P < 0.01$) with values decreasing from 0 to 6 h, peaking at 12 h and decreasing to 336 h. Levels of synovial CPII tended to be influenced by treatment ($P = 0.10$) with LOW and HIGH horses having greater concentrations compared with CON. Regardless of diet, CPII concentrations increased over time ($P < 0.01$) with levels peaking at 24 h and decreasing to 336 h. In

conclusion, CLA supplementation did not influence PGE_2 concentrations following the LPS challenge; however, horses receiving CLA had lesser C2C and greater CPII concentrations, indicating less degradation and greater synthesis of cartilage in response to acute inflammation.

Key Words: conjugated linoleic acid, synovial, lipopolysaccharide, cartilage

---

0387 Age-related effects on markers of inflammation and cartilage metabolism in response to an intra-articular lipopolysaccharide challenge.

M. K. Kahn*[1], J. Coverdale[1], J. L. Lucia[2], C. E. Arnold[1], R. A. Dabareiner[1], A. Bradbery[1], A. A. Millican[3], and T. H. Welsh[4], *[1]Texas A&M University, College Station, [2]Sam Houston State University, Huntsville, TX, [3]Clemson University, Clemson, SC, [4]Department of Animal Science, Texas A&M University, College Station.*

Eighteen Quarter horses were utilized in a randomized complete design to evaluate age-related effects on inflammation and cartilage turnover after induction of a single inflammatory insult using lipopolysaccharide (LPS). Treatments consisted of age with yearlings ($n = 3$ males, $n = 3$ females), 2 and 3 yr olds ($n = 2$ males, $n = 4$ females), or mature 5 to 8 yr olds ($n = 2$ males, $n = 4$ females) for a 14-d experiment. For 14 d before the start of the experiment, all horses were housed in individual stalls and fed diets that met or exceeded NRC (2007) requirements. On d 0, horses were challenged with an intra-articular injection of LPS. Radial carpal joints were randomly assigned to receive LPS using 0.5 ng LPS solution obtained from *Escherichia coli* O55:B5, or sterile lactated Ringer's solution as a contralateral control. Synovial fluid was collected before LPS injection (0 h) and 6, 12, 24, 168, and 336 h postinjection. Samples were later analyzed using commercial ELISA kits for prostaglandin E_2 (PGE_2), collagenase cleavage neoepitope (C2C), and carboxypeptide of type II collagen (CPII). Rectal temperature (RT), heart rate (HR), and respiratory rate (RR) were monitored before sample collection over the first 24 h, and carpal circumference and joint surface temperature were recorded. Data were analyzed using PROC MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). All values for RT, HR, and RR were within normal range and unaffected by treatment ($P \leq 0.21$). Joint circumference was not influenced by treatment ($P = 0.84$), but circumference and surface temperature increased ($P \leq 0.01$) across all treatments in response to intra-articular LPS. Synovial PGE_2 levels were influenced by age with yearlings tending to have lesser ($P = 0.09$) values than 2 and 3 yr olds and mature horses. This was particularly evident at 12 h, when PGE_2 values peaked for all horses and yearlings had lesser values ($P \leq 0.01$) than mature horses. Synovial C2C was influenced by treatment, with yearlings and 2 and 3 yr olds having lesser ($P \leq 0.01$) concentrations than mature horses. Synovial CPII was influenced by treatment at 24, 168, and 336 h, with yearlings having lesser concentrations ($P \leq 0.01$, $P \leq 0.06$, and $P \leq 0.03$, respectively) compared with 2 and 3 yr olds and mature horses. These results indicate that inflammation and corresponding cartilage turnover in response to LPS administration vary with age.

Key Words: lipopolysaccharide, horse, synovial fluid, prostaglandin E_2, type II collagen, collagenase cleavage neoepitope

---

0388 The effect of restricted diet and slow-feed hay nets on body weight and morphometric measurements in adult horses.

E. Glunk*, A. M. Grev, W. J. Weber, M. Hathaway, and K. L. Martinson, *University of Minnesota, Saint Paul.*

Horses evolved to consume several small, frequent meals throughout the day. However, modern horse care has resulted in many horses being stalled for large portions of the day, and meal fed, therefore decreasing their ability to forage. This management scheme has likely contributed to the increase in obesity in the equine population. The use of slow-feed hay nets represents an opportunity to extend foraging time while restricting forage intake. Therefore, the objective of this study was to determine if restricted feeding, coupled with increased time to forage, would lead to weight loss in overweight adult horses. Eight adult Quarter horses (BW 562 kg ± 2 kg) were used in a completely randomized design, with 4 horses assigned to a control (C) of feeding hay off the stall floor, and 4 horses assigned to feeding from a slow feed (3.2-cm openings) hay net (SN). Horses were fed at 1.08% BW, split evenly between 2 meals. A ration balancer was fed at recommended levels during the morning feeding. Body weight, via a livestock scale, and BCS were measured on d 0, 7, 14, 21, 28, and 35. Morphometric measurements, including neck and girth circumference and cresty neck score, a system developed to estimate the level of adiposity on the crest of the neck using a 0 to 5 scale, were taken on d 0, 14, 21, and 35. Ultrasound measurements of average rump fat, longissimus dorsi (LD) depth, and LD thickness were taken on d 0, 21, and 35. Data were analyzed using the Proc Mixed procedure of SAS (SAS Inst. Inc., Cary, NC). All horses lost weight over the 35-d period ($P < 0.0001$); however, no difference was observed between the SN and control. Horses on the SN lost an average of 40 kg, while horses on the C lost an average of 32 kg. There was no difference observed in BCS, neck and girth circumference, or cresty neck score during the study or between treatments ($P \geq 0.25$). Additionally, no differences were observed in rump fat, LD depth, or LD thickness during the study or between the treatments ($P \geq 0.32$). While all horses lost weight on the restricted diet, the use of a slow feed hay net did not have an effect on weight loss or morphometric measurements during the 35-d study.

Key Words: restricted diet, weight loss, slow-feed hay net

0389 Influence of diet fortification on mature horses at maintenance: Performance characteristics.

J. L. Lucia*[1], D. L. Parker[1], M. J. Anderson[1], K. J. Stutts[1], M. M. Beverly[1], S. F. Kelley[1], and E. D. Lamprecht[2], [1]*Sam Houston State University, Huntsville, TX,* [2]*Cargill Incorporated, Elk River, MN.*

Twenty mature horses (413 to 551 kg and 5 to 10 yr) were utilized in a randomized complete block design to evaluate the effect of dietary fortification on performance variables and immune status in mature horses. Horses were blocked by BW, with BCS, age, and sex randomly assigned and evenly distributed across treatments for a 154-d trial. Dietary treatments consisted of a pellet meeting NRC 2007 requirements (Control; $n = 10$), or the same pellet (Fortified; $n = 10$) including: enhanced AA, increased vitamin E, complexed trace minerals, prebiotic (140 g per d dehydrated *Saccharomyces cerevisiae* yeast fermentation product), and probiotic (min 2.3 million CFU/kg each of *Lactobacillus acidophilus, L. casei, Bifido bacterium bifidium,* and *Enterococcus faecium*) fermentation products dehydrated. Dietary treatments were offered individually at 0.25% BW at 12-h intervals. Horses were housed by block and maintained in adjacent dry lots with ad libitium access to coastal Bermudagrass (*Cynodon dactylon*) hay. Body weight and BCS were obtained every 14 d, with concentrate adjusted accordingly. Ultrasound images were obtained every 28 d to determine rump fat (RF), longissimus dorsi area (LDA), and longissimus dorsi fat thickness (LDF). Blood samples were also collected at 28-d intervals to determine circulating white blood cell counts (WBC) utilizing a Celdyne 3700 cell counter (Abbott Industries, Abbott Park, IL). Data were analyzed using the PROC MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). Body weight and BCS were not influenced ($P = 0.11$ and $P = 0.25$, respectively) by dietary treatment. However, all horses gained BW and BCS throughout the trial ($P \leq 0.01$). Longissimus dorsi area and LDF were greater ($P \leq 0.01$) for horses fed Fortified pellets compared with Control. Similarly, RF measurements increased ($P \leq 0.01$) in the Fortified diet beginning at d 56 of the trial. Whole blood WBC was greater ($P \leq 0.01$) in the Fortified diet when compared with Control. These results indicate the addition of fortification may improve the ability of horses to mount an immune response as well as increase muscling and rump fat when fed to mature horses.

Key Words: organic trace mineral, amino acid probiotic, horse, immune response

0390 The effect of small-square feeder design on hay waste, herd weight change, and economics during outdoor feeding of adult horses.

A. M. Grev*, E. Glunk, M. Hathaway, W. Lazarus, and K. L. Martinson, *University of Minnesota, Saint Paul.*

Hay waste during feeding represents a costly expense for horse owners. Researchers have investigated hay waste associated with feeding round-bales and small-square bales in boxstalls, but none have investigated the waste of small square-bales fed outdoors. The objectives of this study were to determine hay waste, herd weight change, and economics of small square-bale feeders when used in outdoor feeding of adult horses. Feeder designs included a hayrack ($280), slat feeder ($349), basket feeder ($372), and a no-feeder control. Two feeders of each type were placed in 4 separate, outdoor, dirt paddocks. Twelve adult mares (BW 503 ± 36 kg) were divided into 4 similar groups each containing 3 mares. Groups were rotated through the 4 paddocks in a Latin Square design. Herds remained in each paddock for 7 d, including 2 d of acclimation and 5 d of data collection. Horses were weighed immediately before and after the 5 d data collection period; the difference was herd weight change. Horses were fed grass hay at 2.5% of the herd body weight split evenly at 0800 and 1600 h. Waste hay on the ground was collected daily before each feeding, dried, and weighed. Any hay remaining inside the feeder was collected, dried, weighed, and subtracted from the amount fed. The daily amount of hay removed from the ground was considered waste. The number of months to repay the feeder cost (payback) was calculated using hay valued at $250/t, and improved efficiency over the control. Mean hay waste was 13, 5, 2, and 1%, for the control, hayrack, basket feeder, and slat feeder, respectively. All feeders resulted in less hay waste compared with the control ($P \leq 0.0001$), and a difference was measured between the hayrack and slat feeder ($P = 0.0175$). Herd weight change was different among all feeders ($P \leq 0.0074$). Herds gained 10 and 7 kg when feeding from the basket feeder and hayrack, and lost 3 and 11 kg when feeding from the slat feeder and control. The basket feeder, hayrack, and slat feeder paid for themselves in 11, 11, and 9 mo, respectively, with the slat feeder resulting in a shorter payback ($P \leq 0.0140$). Use of a small square-bale feeder resulted in less hay waste compared with the control, and all feeders paid for themselves within 11 mo. This information will aid horse owners when purchasing small square-bale feeders.

Key Words: hay waste, hay feeder, payback

0391 Influence of ambient temperature and relative humidity on recovery from exercise in young horses. J. L. Lucia*[1], K. S. Carlson[1], M. J. Anderson[1], K. W. Walter[2], K. J. Stutts[1], M. M. Beverly[1], and S. F. Kelley[1], *[1]Sam Houston State University, Huntsville, TX, [2]Truman State University, Kirksville, MO.*

Heat stress affects many livestock species, but horses are a particular concern due to the regular exercise they receive. To determine the influence of ambient temperature on exercise recovery in young horses, fourteen Quarter horses (2 to 5 yr; 338 to 540 kg) were utilized in a randomized complete block design. Horses were blocked by BW, age, and sex, and randomly assigned to 1 of 2 groups that included horses performing a 25-min standardized exercise test at either 0600 h (AM; $n = 7$) or 1300 h (PM; $n = 7$). The ambient temperature for the AM was 23.31°C (83.9% relative humidity), while the ambient temperature for the PM was 34.70°C (40.8% relative humidity). Whole blood lactate (LAC), total plasma protein (TP), heart rate (HR), respiration rate (RR), rectal temperature (RT), and ocular temperature (OT) were obtained immediately following (0 min) exercise, and during a recovery period (5, 15, and 30 min post-exercise). Differences in parameters measured were determined using the PROC MIXED procedure in SAS (SAS Inst. Inc., Cary, NC). Clinical parameters, including HR, RR, and RT, were greater ($P = 0.03$) in the PM beginning at 5 min of recovery and remained elevated at 30 min postexercise when compared with the AM. Additionally, OT was higher ($P \leq 0.01$) in the PM at 0 min, and values remained higher through 30 min postexercise. Similar to OT, LAC was greater ($P \leq 0.01$) at 0 min in the PM (12.72 ± 1.84 mmol/L) compared with the AM (4.94 ± 1.84 mmol/L), with lactate values in the PM (8.79 ± 1.13 mmol/L) continuing to be greater than the AM (2.25 ± 1.13 mmol/L) at 30 min following exercise. No differences were detected in TP ($P = 0.18$) between exercise groups, suggesting the exercise intensity did not alter extracellular fluid loss within plasma. Respiration rate, OT, and RT remained elevated through recovery, demonstrating an impaired ability to dissipate heat due to the higher ambient temperature during exercise. Lactate values in the PM illustrated that horses exercising at a higher ambient temperature required an increased recovery time due to the increased demands of anaerobic metabolism. Understanding the physiological responses during recovery of exercise at different temperatures may enable industry professionals to adapt daily exercise regimens to better prepare the equine athlete to perform at their full potential.

Key Words: heat stress, exercise, equine

0392 Commercial application of the follicular ablation technique in mares. S. E. Buist*, A. K. Sexten, D. M. Grieger, C. A. Blevins, J. S. Stevenson, and J. M. Kouba, *Kansas State University, Manhattan.*

Two experiments were conducted to determine the practicality of utilizing ultrasound-guided follicular ablation in a commercial setting. The objective of the initial experiment was to investigate the efficacy of follicular ablation as a technique for ovulation synchronization when compared with a standard progesterone and estrogen (P&E) protocol. Twenty nonpregnant mares were assigned to an ablation (AB) or P&E group. Briefly, AB mares ($n = 10$) were subjected to ablation for removal of all follicles larger than 10 mm on d 0 and administered PGF2α twice on d 5. Mares were administered hCG on d 11 and subjected to ultrasound twice per day until ovulation was detected. Mares in the P&E group ($n = 10$) were scanned at initiation of the protocol and received P&E IM once a day for 10 d. On d 10, mares received PGF2α and ultrasound monitoring began on d 15. On d 18, mares were administered hCG and evaluated twice per day until ovulation was detected. The interval from initiation of synchronization to ovulation (10.4 vs. 19.1 d, $P < 0.0001$) and the interval from hCG administration (1.2 vs. 2.3, $P < 0.0001$) was shortened in the AB group. Ablation may be an acceptable nonsteroidal alternative to the conventional P&E protocol. The objective of the second experiment was to determine if ablation could lengthen the postpartum interval to ovulation to increase the chance of conception postfoaling. Eighteen postpartum mares were assigned to an AB or control (CON) group. On d 6 postpartum, AB mares ($n = 9$) were subjected to follicular ablation for removal of all follicles larger than 10 mm. Mares were administered PGF2α twice on D11 and monitored via ultrasound once per day until a follicle $\geq$ 35 mm was detected, at which time they received hCG. Following hCG, mares were monitored twice per day until ovulation was detected. The CON mares were evaluated using ultrasound, beginning d 4 postpartum and continuing every other day until a follicle $\geq$ 30 mm was detected, and scanning frequency increased to once per day. When a follicle $\geq$ 35 mm was identified, mares were administered hCG and monitored twice per day until ovulation was detected. Ablation lengthened the interval from foaling to ovulation (15.9 vs. 10.0, $P = 0.003$). Increasing the interval from foaling to ovulation is known to increase conception rates; therefore, the application of this procedure could be utilized to optimize the timing of breeding to improve conception outcomes. These experiments demonstrate commercial application of follicular ablation and are evidence for incorporating this procedure in a commercial setting.

Key Words: mares, follicle ablation, postpartum ovulation

HORSE SPECIES: **DEVELOPMENTAL PROGRAMMING: APPLICATIONS IN THE HORSE**

0393 Developmental programming in agriculturally relevant species: An overview. K. A. Vonnahme*, *North Dakota State University, Fargo.*

Postnatal growth and development of offspring can be influenced by stressors that their parents experienced before their conception, during their gestation, or during lactation. This phenomenon is known as developmental programming. Developmental programming has been shown to influence many of our large domesticated animals and may impact livestock production. An important component to developmental programming is that placental function can be influenced by many factors impacting nutrient transport. Not only does nutritional stress, such as nutrient restriction, impact fetal and placental growth, but other stressors such as transportation, extreme temperatures, and social environments influence the offspring in utero, at birth, and after weaning. Understanding the mechanisms of how these stressors impact nutrient availability to the developing offspring will help in determining potential management strategies and therapeutics that could be implemented to reduce negative consequences. This overview of developmental programming will preface equine specific presentations on how the horse is impacted by the maternal environment and the potential impact on the equine industry.

Key Words: developmental programming, livestock, placenta

0394 Glucorticoid programming of development during early life. A. Fowden*, O. A. Valenzuela, J. K. Jellyman, N. B. Holdstock, and A. J. Forhead, *University of Cambridge, Cambridge, UK.*

Human epidemiological studies have shown that low birth weight is associated with an increased incidence of adult metabolic disease. Similarly, in experimental animals, induction of fetal growth restriction alters adult metabolic phenotype. Collectively, these studies have led to the concept that suboptimal environmental conditions during early development program later metabolic dysfunction. Glucocorticoid stress hormones may mediate many of these environmental programming effects, as they inhibit fetal growth and their maternal administration is known to alter metabolic and endocrine function of the adult offspring in several species. Normally, glucocorticoids only act as prepartum maturational signals but, earlier in development, they can also act as signals of environmental adversity. However, relatively little is known about the programming effects of neonatal glucocorticoid overexposure when tissues are particularly glucocorticoid-sensitive. In horses, unlike other species, the fetal hypothalamic-pituitary-adrenal (HPA) axis develops late in gestation, with the main cortisol increment after, not before, birth. Indeed, in preterm and dysmature foals, cortisol concentrations can be high for several days after birth. Thus, horses may be more susceptible to glucocorticoid programming in the neonatal rather than fetal period of development. Administration of synthetic glucocorticoids to pregnant mares near term ($\geq$ 300 d) causes both stillbirth and early delivery of viable foals, depending on the exact gestational age at treatment (4). In ponies in late gestation ($\geq$ 270 d), this treatment causes maternal hyperinsulinaemia and hyperglycaemia, indicative of insulin resistance, but has little effect on gestational length or foal birth weight and size, although it does have minor actions on foal HPA function in the first 2 to 3 wk after birth. In contrast, raising cortisol concentrations endogenously in the foal for 5 d after birth by ACTH administration had little effect on HPA function in the young foal ($\leq$ 15 wk), but did alter basal ACTH concentrations and hypoglycaemia-induced ACTH secretion in the adult ponies at 1 and 2 yr of age, in association with sex-linked differences in adreno-cortical growth at 2 yr. In addition, neonatal cortisol overexposure reduced glucose-stimulated insulin secretion in the young foals but not in the adults, while increasing insulin sensitivity in the young foals and yearlings but not in the 2 yr olds. However, the extent to which these changes persist, resolve, or exacerbate with increasing age remains unknown. Cortisol overexposure of equine neonates, therefore, programs their subsequent endocrine and metabolic phenotype, with implications for their adult health and potential athletic performance.

Key Words: glucocorticoid programming

0395 Nutritional programming and the impact on mare and foal performance. J. Coverdale*[1], C. J. Hammer[2], and K. W. Walter[3], *[1]Texas A&M University, College Station, TX, [2]North Dakota State University, Fargo, [3]Truman State University, Kirksville, MO.*

Many environmental factors can alter phenotype of offspring when applied during critical periods of early development. In most domestic species, maternal nutrition influences fetal development, and the fetus is sensitive to nutrition of the dam during pregnancy. Large numbers of techniques have been explored including both under- and overnutrition of the dam. Both nutritional strategies have yielded potential consequences, including: altered glucose tolerance, pancreatic endocrine function, insulin sensitivity, body composition, and colostrum quality. While the impact of maternal nutrition on fetal development in the equine has not been thoroughly investigated, overnutrition is a common occurrence in the industry. Work in our laboratory has focused on effects of

maternal overnutrition on mare and foal performance, mare intake, mare hormone concentrations, foaling parameters, colostrum quality, passive transfer of immunity, and glucose and insulin dynamics. Over several trials, mares were fed either 100 or 140% of NRC requirements for DE, and supplemental Se and arginine were added to diets in an attempt to mitigate potential intrauterine growth retardation resulting from dams overfed during the last third of pregnancy. As expected, when mares were overfed, BW, BCS, and rump fat values increased. Despite this change in mare body composition, foaling parameters such as time to stand and time to nurse were unaffected. Foal growth over 150 d was also not influenced. Maternal nutrition did not alter colostrum volume, but influenced colostrum quality. Maternal overnutrition resulted in lower colostrum IgG concentrations, but did not cause failure of passive transfer in foals. Supplemental Se and arginine were unable to mitigate this reduction in colostrum IgG. Additionally, mare and foal glucose and insulin dynamics were influenced by maternal nutrition. Mare glucose and insulin area under the curve (AUC) increased with increased concentrate supplementation, and in a subsequent trial supplemental arginine was able to decrease mare insulin AUC. Foal insulin AUC and peak insulin concentrations were increased when mares were fed concentrate during the last third of pregnancy, and in a later trial, foal peak glucose values were reduced with arginine supplementation of the mare. This influence of maternal nutrition on glucose and insulin dynamics warrants further investigation, as it may be related to athletic performance and metabolic disease in the adult. Further studies will be necessary to fully elucidate the influence of mare nutrition during pregnancy on performance of the mare and resulting foal, as well as long-term consequences of developmental programming.

Key Words: horse, nutrition, foal, developmental programming

INTERNATIONAL ANIMAL AGRICULTURE: **INTERNATIONAL ANIMAL PRODUCTION**

0396 Effect of high nutrient density diets on growth performance, feed efficiency, age at puberty, and feeding economics in Nili-Ravi buffalo heifers.
M. Abdullah*[1], K. Javed[1], Z. M. Iqbal[1], M. Saadullah[1], M. A. Jabbar[1], and A. U. Haque[2], *[1]University of Veterinary and Animal Sciences, Lahore, Pakistan, [2]Buffalo Research Institute, Pattoki, Pakistan*.

Traditional buffalo raising becomes uneconomical due to poor growth and delayed age at puberty. The feeding trial was conducted to evaluate the feeding diets with varying nutrient density on dry matter intake, growth rate, age at puberty, feed efficency, and feeding economics in Nili-Ravi buffalo heifers. Thirty Nili-Ravi buffalo heifer calves between the age of 5 and 7 mo and approximately of 95 kg body weight were assigned to 3 different treatments: (A) Control (CP and ME at NRC, 2001), (B) CP and ME contents at 20% above, and (C) CP and ME 40% above NRC recommendations. The experiment continued until manifestation of puberty signs (mucous discharge) in all 3 treatment groups. The data were analyzed using SAS 9.1 (SAS Inst. Inc., Cary, NC). Dry matter intake was different ($P < 0.05$) among the treatment groups: $6.71^{a} \pm 2.69$, $7.99^{b} \pm 3.28$, and $9.11^{c} \pm 3.90$ kg for Treatments A, B, and C, respectively. The average daily CP and ME intake was also different ($P < 0.05$): $876.03^{a} \pm 348.38$, $1094.43^{b} \pm 445.84$, and $1285.98^{c} \pm 546.62$ g CP, and $15.36^{a} \pm 6.12$, $18.83^{b} \pm 7.69$, and $21.85^{c} \pm 9.31$ Mcal/kg ME for Treaments A, B, and C, respectively. There was no difference in the average daily gain of Treatments A and B ($525.88^{a} \pm 292.92$, 551.98^{a} g), while Treatment C ($612.99^{b} \pm 350.17$ g) gained higher as compared with other 2 treatment groups. The feed efficiency of Treatment A ($0.093^{a} \pm 0.06$) was higher as compared with Treatments B and C ($0.081^{b} \pm 0.05$ and $0.081^{b} \pm 0.05$). The mean body length ($111.98^{a} \pm 12.79$ and $111.35^{a} \pm 13.61$ cm) and heart girth ($142.22^{a} \pm 21.27$ and $142.89^{a} \pm 22.71$ cm) was same in Treatments A and B, while different in Treatment C ($113.07^{b} \pm 14.29$ cm) and ($144.39^{b} \pm 23.71$ cm). The height at wither was higher in Treatment C ($116.20^{b} \pm 13.18$ cm) as compared with Treatment A, whereas it was similar between Treatments A and B, and B and C ($117.07^{a} \pm 12.61$ and $116.68^{ab} \pm 12.99$ cm for Treatments A and B, respectively). There was no difference in the mean age at puberty of all the 3 treatment groups ($733.11^{a} \pm 50.55$, $716.78^{a} \pm 33.65$, and $723.50^{a} \pm 26.31$ d) while weight at puberty was same for Treatments A and B ($384.87^{a} \pm 30.47$ and $398.40^{ab} \pm 35.92$ kg) and between B and C ($423.90^{b} \pm 30.12$ kg). The averaged daily feeding cost was lower in Treatment A (Rs. 139.93a ± 28.27) as compared with Treatments B (Rs. $195.12^{b} \pm 41.92$) and C (Rs. $246.25^{c} \pm 56.39$). Buffalo heifers were found to be efficient converters and economical to raise on low-nutrient-density diet without affecting their age at puberty.

Key Words: Nili-Ravi buffaloes, age at puberty, nutrient density

0397 Environment concerns and waste management strategies of pig production in China.
J. Peng*[1], L. Liu[2], and L. Huang[1], *[1]Jiangxi Agricultural University, Nanchang, China, [2]Jiangxi Department of Agriculture, Nanchang, China.*

With the largest population in the world, the Chinese government continues to stimulate pork production to meet the increased demand for protein consumption. However, the increases in hog population and density have created various environmental problems in China. One of the issues is that it can cause water and land contamination when farm wastes being handled incorrectly. Most recently, China published the most updated waste management regulation for animal industry, effective from January 1, 2014. Waste management has become an important focus for swine industry in China. The objective of this study was designed to assess waste streams in pig production under the most current situation in China. Commercial pig farms ($n = 50$) were chosen from 11 different provinces, representing the major area of swine production in China. The size of the pig farm ranges from small, medium, and large. Data was collected through farm visit (and/or farm inspection), personal interview, focus group, meeting discussion, survey questionnaire, and farm document review. A group of Chinese swine experts, including central and local government officers, as well as educators and researchers from different universities and institutes, was selected to verify data and acquire data consensus. This study finds that daily manually scraping of pig pens, along with floor water-line flushing is a common method for solid manure collection and pen hygiene. However, the continuously increasing human labor cost in pig production has forced the solid manure collection method to change from manual to automatic. In addition, the usage of concrete slatted floors to avoid daily manually scraping and flushing is becoming more accepted. Moreover, to reduce the volume of farm slurry, newly designed farms commonly utilize underground pipe for slurry collection and to avoid mixing rainwater. This study also finds the currently government-sponsored anaerobic digester project, promoted as a method of treating slurry, is rarely found to be successful at large-scale intensive pig farms. Consequently, the Chinese government should take serious actions to enforce the disposing of farm waste in a more sustainable and environmentally friendly approach, such as compost and use in an organic fertilizer plant. In conclusion, waste water increases manure volume, which in turn may increase the cost of manure storage and distribution or increase the cost of treatment if to meet the emission standards. Therefore, pig farms should adopt new equipment and innovative technology to avoid wa-

ter wastage, as well as implement novel waste management methods to support sustainability.

Key Words: environment concerns, waste management, sustainability

---

0398 Identification of barriers of Bahamian agriculture production: An assessment of stakeholder needs.

S. J. Trojan*[1], M. T. Brashears[2], S. Morales[2], A. Echeverry[1], and M. Brashears[1], *[1]Texas Tech University, Department of Animal and Food Sciences, Lubbock, [2]Texas Tech University, Department of Agriculture Education and Communications, Lubbock*.

Land available for agriculture production in the Bahamas is roughly 191,000 acres; however, approximately 10% of production capacity is realized. To assist with augmenting Bahamian agriculture production, a team of Texas Tech University researchers worked with the Inter-American Institute for Cooperation on Agriculture (IICA) to evaluate the Bahamian food system from farm to fork to determine stakeholder needs. The team traveled to several islands; visited multiple farms, governmental agencies, a feed mill, an abattoir, a resort butcher department, and met with the Minister of Agriculture. At each stakeholder meeting, barriers to the food production and consumption system were identified. The following themes emerged within respective segments. Issues producers faced included: (1) lack of product standards and certification; (2) theft and feral dogs; (3) inconsistent availability and price of inputs; (4) land availability; and (5) unfair trade regulations. Processors indicated the following barriers: (1) lack of access to employee training; (2) equipment availability and cost; (3) consistency of governmental support; and (4) facility security. The team also conducted a workshop for livestock producers and administered an instrument to help identify audience demographics and major concerns with Bahamian agriculture production. Of the 25 individuals that responded, 50% indicated that agriculture represented 50% of household income, whereas 10 individuals indicated agriculture was the sole income source. For such households, challenges within the agriculture system can lead to significant levels of food insecurity. The instrument also identified the following challenges within the agriculture industry: lack of education in food safety, governmental challenges, lack of marketing infrastructure, and a need for new technologies and methodologies for improving agriculture productivity, transportation and handling, and animal welfare. The needs assessment conducted by the research team was the initial step in communicating barriers the country faces in becoming more food secure to IICA. Researchers made several recommendations to IICA to focus stakeholder resources. Educational efforts must be coordinated through IICA and governmental agencies to provide effective training programs and eliminate redundancy. Communication at all levels of government related to food production and consumption should be improved. The single abattoir on the island of New Providence should be evaluated for feasibility of continued operations or elimination. Alternatives for providing humane animal slaughter in multiple locations were proposed with the goal of improving processing quality to World Trade Organization food safety guidelines. Efforts to open an agricultural branch of the College of the Bahamas on Andros Island should be strongly supported.

Key Words: Bahamas, food security, needs assessment

0399 Diet-induced shifts in the rumen microbiome of Mehshana buffalo (*Bubalus bubalis*).

D. W. Pitta[1], S. Kumar*[1], B. Veiccharelli[1], N. Parmar[2], and C. Joshi[2], *[1]University of Pennsylvania, Kennett Square, PA, [2]Anand Agriculture University, Anand, India*

We investigated the diet-induced shifts in the microbiome of both solid and liquid ruminal fractions retrieved from water buffalo utilizing 16S rRNA pyrosequencing technology. The depth of coverage of metabolically active bacteria in a community using different primer pairs was also determined. To assess reproducibility, interanimal variation was considered in all phylogenetic and community comparisons. The experiment included 4 nonlactating water buffaloes fed 3 different diets for 6 wk each; diets were M1 (50% concentrate: 50% dry roughage), M2 (25% concentrate: 75% dry roughage), and M3 (100% dry roughage). A total of 333,851 pyrotags were analysed in this study. Phylogenetic analysis revealed significant differences in the rumen microbiome mediated by primer and diet ($P < 0.05$). Differences in community composition due to primer, diet, fraction, and animal were compared using unweighted and weighted UniFrac analysis. Clustering of communities was largely explained by primer differences in both weighted and unweighted UniFrac analyses ($P < 0.001$). In the weighted analysis, communities clustered by diets ($P < 0.05$) and fractions ($P < 0.08$) while no interanimal variation was observed. The identified repertoire of bacterial populations was dependent on the primer pair, as targeting the V4-V5 region resulted in greater diversity profiles of the microbiome. Within each primer pair, dietary changes altered the community composition with noticeable shifts at the genus level. Genera such as *Ruminococcus* and *Fibrobacter* ($P < 0.05$) were higher in abundance on M3 diet, while *Prevotella* dominated ($P < 0.05$) on the M1 diet.

Key Words: rumen bacterial community, hypervariable regions, UniFrac analyses

INTERNATIONAL ANIMAL AGRICULTURE: GLOBAL PROSPECTIVE OF LIVESTOCK PRODUCTION SYSTEMS TO MEET THE GROWING NEED FOR ANIMAL PROTEIN IN HUMAN DIETS: IMPACTS ON PRODUCTION AND HUMAN HEALTH

0402 Parallel comparisons of intensive meat production in developed and developing countries. What can we learn from each other's systems?.

R. Barajas Cruz*, *Universidad de Sinaloa, Culiacan, Mexico.*

The world in the short future will confront 2 important facts: the population is increasing and meat consumption by people has been increasing. The challenge will then be: how will we produce enough meat to supply this growing meat demand? It is time to review the intensive meat production strategies conducted in different regions of the world and to learn from each other. In the developed countries, meat production is based in obtaining food energy from cereal grains, and the use of extensively processed grains is the main starch source. In developing countries, food energy sources come from crop residues, grain process byproducts, high-sugar-content byproducts, low-processed grains, and alternative feedstuffs regionally available. The concept of meat quality is different, too. Lean meat is the goal in pork production; while in beef production, it is different. In several developed countries such as in the United States and Japan, meat quality has a high relationship with tenderness and marbling. In most developing countries, lean beef is well accepted and tenderness is not necessarily a condition for sale. Geographical location imposes limitations on cattle breed, age to placement in feedlots, and finishing weight. This presentation will explore what we can learn from these production systems, drawing a parallel comparison of intensive meat production in developed and developing countries.

Key Words: meat production, population

0403 Methods to improve nutrient intake in grazing cattle: Pasture management and supplementation.

F. A. P. Santos*, J. R. R. Dórea, F. Batistel, and D. F. A. Costa, *University of São Paulo, Piracicaba, Brazil.*

Most of the grassland areas in Brazil are covered with tropical grasses. The majority of the milk (Stock et al., 2011) and beef (Millen et al., 2009) are produced on pasture-based systems. In intensive grazing systems during the hot rainy season, stocking rates of 6 to 10 AU/ha (1 AU = 450 kg BW) can be achieved (Santos et al., 2014). Despite the high stock capacity, the ADG and milk production are lower than the animals' genetic potential, and this is attributed to the limited energy intake. Some of the major factors imposing limitations to energy intake by the animals in tropical grazing systems are: (a) low efficiency of the grazing process because of sward structure, and (b) rumen fill. During the last 2 decades, a considerable amount of information has been published related to new management practices of tropical pastures. The adoption of the start grazing point, based on the 95% light interception criterion, has successfully resulted in a more favorable sward structure which allows the animal to harvest a greater daily amount of forage in a shorter grazing period. However, even when all the available technology on tropical pasture management is applied, forage intake is still limited because of rumen fill. The quality of the tropical forage NDF (IVNDFD) is greater than alfalfa. However, the NDF content (51 to 65%) and its low cell fragility cause rumen fill, and they limit energy intake. Studies related on cell fragility of tropical grasses are limited, and this topic deserves more attention. Supplementing high energy concentrates for grazing cattle is, at the same time, an efficient strategy to increase energy intake and to decrease the energy expended with the grazing activity. The substitution effect observed when concentrate is fed to grazing cattle is related not only to the amount of concentrate fed, but it is also related to the pasture management practices.

Key Words: grazing, nutrient intake, efficiency

LACTATION BIOLOGY I

0404 Temporary alterations to milking frequency, immediately postpartum, modifies expression of milk synthesis and apoptosis genes in the mammary glands of grazing dairy cows.

T. M. Grala[1], J. K. Kay[2], J. R. Roche[2], A. G. Rius[3], and C. V. Phyn*[2], *[1]DairyNZ, Auckland, NZ, [2]DairyNZ, Hamilton, NZ, [3]University of Tennessee, Knoxville.*

Temporary changes to postpartum milking frequency can elicit lactation-long changes in milk production. The hypothesis tested in this experiment was that the immediate and long-term milk yield response to altered milking frequency would correspond to gene expression changes associated with mammary cell secretory activity and/or number. Multiparous, grazing Holstein-Friesian cows (n = 150) were randomly assigned to 1 of 5 groups at calving: milked once daily (1×) for 3 or 6 wk and twice daily (2×) thereafter; milked 2× for the entire lactation (control); or milked thrice daily (3×) for 3 or 6 wk and 2× thereafter. Milk yields were recorded daily and milk composition weekly. Mammary tissue was collected at 3, 6, and 9 wk postpartum (n = 12 cows/treatment), and gene expression measured using quantitative reverse transcription PCR. Data were analyzed using mixed models fitted with REML (Restricted Maximum Likelihood) in GenStat, including: treatment and contrasts to test milking frequency (1×, 2×, 3×), duration (3 wk, 6 wk), and their interaction as fixed effects, and cow as a random effect. Immediate ($P < 0.001$) and lactation-long ($P < 0.01$) decreases in milk and energy-corrected (ECM) production were recorded in cows milked 1× postpartum relative to 2×; however, cows milked 3× only produced greater ($P < 0.05$) milk volumes during the treatment period and did not differ ($P > 0.05$) in ECM production. Transcript levels from genes involved in milk fat (*ACACA*, *FASN*), protein (*CSN1S1*, *CSN2*), and lactose (*LALBA*, *B4GALT1*) synthesis were not altered in cows milked 3×, but were downregulated ($P < 0.05$) at 3 and 6 wk postpartum in cows milked 1×. Decreased ($P < 0.05$) expression of these genes was maintained after 1× cows were switched to 2× milking. Furthermore, at 9 wk postpartum, cows milked 1× for 3 wk had lower ($P < 0.05$) expression of genes involved in fat and lactose synthesis than cows milked 1× for 6 wk. In contrast, apoptotic genes (*PYCARD*, *FAS*) were up-regulated ($P < 0.05$) in cows milked 1×. This effect was still apparent at 9 wk ($P < 0.01$), indicating that greater mammary cell death was maintained post-treatment. In conclusion, greater milk volumes during 3× milking were not associated with altered expression of genes involved in milk synthesis or mammary cell death. However, changes in expression of genes involved in these processes may underpin the long-term reduction in milk and ECM yields in cows milked 1× postpartum.

Key Words: milking frequency, mammary apoptosis, gene expression

0405 Dietary anion-cation difference and daylength differently affect milk calcium secretion pathways.

M. Boutinaud*[1], A. Bondon[1], A. Narcy[2], C. Hurtaud[1], M. Johan[1], J. Couedon[1], and P. Lamberton[3], *[1]INRA, Saint Gilles, France, [2]INRA, Nouzilly, France, [3]INRA, Le Rheu, France.*

Milk is an important source of Ca for growth and development of children. However, it has been recently shown that dairy milk Ca content decreases with long-day photoperiod and varies according to the type of diet. Many proteins are involved in the secretion of Ca into milk by the mammary epithelial cell (MEC). The aim of this study was to identify the role of gene expression of these proteins in the regulation of milk Ca content. A trial was performed according to a Latin square design using 8 dairy cows averaging 103 ± 44 d in milk, with 2 treatments in a factorial arrangement with 4 periods of 14 d. The cows received 2 levels of dietary anion-cation differences (DCAD; 0 mEq/kg DM for d 0 and 400 mEq/kg for d 400) and 2 daylengths (8 h of light/d for short days and 16 h/d for long days). The DCAD treatments were conceived to mimic diets based either on corn silage or on herbage. The cows were exposed to solarium lights providing UVA and UVB. Once per period, MEC were prepared after milk centrifugation by purification using an anti-cytoketatin antibody bound to magnetic beads to study by real-time RT-PCR the mRNA level of genes involved in Ca secretion expressed related to RPLP0 housekeeping gene. Data were analyzed using Mixed procedure. There was no significant interaction between daylength and DCAD level. Milk and Ca yields did not vary with any treatments, averaging 32.7 kg/d and 41.1 g/d, respectively. With d 400 compared with d 0, milk Ca content increased ($P < 0.01$) with no link with casein content. No significant variation was observed on gene expression with DCAD treatment and on kappa casein and a-lactalbumin mRNA levels with any treatments. Milk Ca and casein content were lower with long days compared with short days ($P < 0.05$). The lower Ca secretion was associated with lower mRNA levels for SPCA1, ITPR1, and PMCA1, 3 Ca transporters in milk purified MEC ($P < 0.05$). This work suggests that Ca secretion pathways may be downregulated with long photoperiod, and that could explain a part of the seasonal decrease of milk Ca content during summer. In contrast, no significant variation of gene expression could explain the increase in milk Ca content with d 400.

Key Words: milk calcium, mammary epithelial cell, photoperid, feeding

0406 Infusion of a 5-hydroxy-L-tryptophan (5-HTP) to late-lactation cows impacts circulating calcium and glucose concentrations. J. Laporta*[1], S. A. E. Moore[1], A. P. Prichard[1], M. Olsen[1], B. P. Schnell[1], S. R. Weaver[1], C. R. Cronick[1], R. M. Bruckmaier[2], and L. L. Hernandez[1], [1]*University of Wisconsin-Madison, Madison,* [2]*Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland.*

Supplementation of 5-hydroxy-L-tryptophan (5-HTP) improved Ca and glucose status in lactating rodents, and serotonin was shown to be an indicator of positive Ca and glucose status in lactating dairy cows. Here, we examined the effect of intravenous infusion of 5-HTP on circulating Ca and glucose concentrations. Using a 4 × 4 latin square design, multiparous Holstein cows (avg. lactation = 3; avg. d in milk = 333 d) were infused with a sterile saline control (CON) or 1 of 3 doses of 5-HTP (TRT; 0.5, 1.0 and 1.5 mg/kg). Infusion periods were 4 d, with a 5-d washout between periods. Cows were infused at a constant rate for 1 h, and blood samples were collected at 0 min (preinfusion), and 5, 10, 30, 60, 90, and 120 min postinfusion. Heart rate (HR), respiration rate (RR), and rectal temperature (TEMP) were recorded every 15 min during infusion and 15 min postinfusion; milk yield (MY) was recorded daily, and manure score (0 to 4, MS) and frequency were recorded during infusions. Data were analyzed using PROC MIXED in SAS (SAS Inst. Inc., Cary, NC). Heart rate, RR, TEMP, and MY were not different between CON and TRT at any dose ($P > 0.05$) and MS was affected by TRT ($P = 0.013$). The MS was similar between CON and 0.5 mg/kg TRT, but different between CON and 1.0 and 1.5 mg/kg TRT (0.44 vs. 1.69 and 2.06 ± 0.33, respectively). Serum Ca and plasma glucose concentrations were measured and area under the curve (AUC) was calculated using the trapezoidal model. For Ca, all 5-HTP doses significantly decreased AUC compared with CON ($P < 0.001$), decreasing the first 30 min postinfusion, increasing and reaching initial Ca concentrations 120 m postinfusion. Mean Ca was greater for CON compared with all TRT doses (1.70 vs. 1.56, 1.60 and 1.59 ± 0.05 m*M*, respectively) and the same was observed for minimum Ca. Glucose AUC was greater for 1.0 and 1.5 mg/kg TRT compared with CON and 0.5 mg/kg TRT ($P = 0.02$). Mean glucose was greater for 1.0 mg/kg TRT compared with CON and 0.5 mg/kg TRT only at 90 m postinfusion ($P < 0.04$). These results demonstrate that 5-HTP stimulates a decrease in circulating Ca, and only the 2 higher doses of 5-HTP increased circulating glucose. In conclusion, 5-HTP differentially affects circulating Ca and glucose concentrations in dairy cattle, suggesting significant impacts on Ca and glucose metabolism during lactation.

Key Words: 5-hydroxytryptophan, calcium, glucose

0407 The dopamine antagonist domperidone increases prolactin concentration and milk production in dairy cows. P. Lacasse* and S. Ollier, *Dairy and Swine R&D Centre, Sherbrooke, QC, Canada.*

In previous studies, we have shown that inhibition of prolactin (PRL) secretion by the dopamine agonist quinagolide reduces milk production of dairy cows (Domest. Anim. Endocrinol. 43:154). The objective of this study was to determine the effects of the administration of a dopamine antagonist and feed restriction on basal and milking-induced PRL concentrations in blood and milk production in dairy cows. Twelve mid-lactation Holstein cows received daily subcutaneous injections of either domperidone (300 mg, DOMP, $n = 6$) or canola oil (CTL, $n = 6$) for 5 wk. During the fifth wk, all cows were fed at 65% of their DMI of the previous wk. Blood samples were collected before morning milking 3 d a wk from d 8 to d 42 (7 d after the last injections). In addition, blood samples were collected during morning milking at d 1 (before the first injection), 2, 29, and 35. Basal PRL concentration was similar among both groups before the start of treatments. Domperidone injection caused a gradual increase ($P < 0.001$) in basal PRL concentration which averaged, on the week prior the feed restriction, 32.2 and 13.9 ± 2.1 ng/mL for DOMP and CTL, respectively. Feed restriction did not affect basal PRL concentration in DOMP cows but reduced it in CTL cows ($P < 0.05$), averaging 28.0 and 7.9 ± 2.4 ng/mL, respectively. Concentration of PRL was still elevated ($P < 0.05$) in DOMP cows 7 d after the last injection, averaging 19.4 and 10.8 ± 2.7 ng/mL for DOMP and CTL, respectively. In CTL cows, the milking-induced PRL above premilking concentration (AUC) was similar at d 1, 2, and 29, but was reduced ($P < 0.05$) during feed restriction (d 35). In DOMP cows, AUC was similar at d 1 and 2, but was reduced ($P < 0.05$) at d 29 and 35. Milk production was similar for both groups before the start of treatments. There was time × TRT interaction ($P < 0.001$) for milk production during the treatment period. Milk production was similar during the first 2 wk of treatments, but was greater ($P < 0.02$) in DOMP cows during the 2 following weeks, averaging 38.0 and 35.0 ± 0.6 kg/d at wk 3 and 38.0 and 35.3 ± 0.7 kg/d at wk 4 for DOMP and CTL, respectively. Milk production declined in both groups during feed restriction but remained greater ($P < 0.05$) in DOMP cows. Milk production of both groups became similar again 5 d after the last injection. Milk composition and DMI were not affected by DOMP. These results support the hypothesis that PRL is galactopoietic in dairy cattle.

Key Words: feed restriction, prolactin

0408 Compensatory feeding of gestating gilts does not affect mammary development of their offspring at puberty. C. Farmer*[1], M. F. Palin[1], and Y. Martel-Kennes[2], [1]*Agriculture and Agri-Food Canada, Dairy and Swine R&D Centre, Sherbrooke, QC,* [2]*La COOP Fédérée, Animal Nutrition Division, St-Romuald, QC, Canada.*

The goal of this project was to determine if feed restriction followed by compensatory feeding of gestating gilts affects mammary development and mammary gene expression of their female offspring at puberty. Gilts were fed a conventional (CTL; $n = 5$) or an experimental (TRT; $n = 3$) dietary regimen. The experimental regimen provided 70% (restriction) and 115% (compensatory) of the protein and DE contents provided by the CTL diet. The restriction diet was given during the first 10 wk of gestation, followed by the compensatory diet until farrowing. Gilts were allowed to farrow, and female offspring from these (11 CTL, 12 TRT) were weighed at birth, weaning (d 20), and puberty (d 211), at which time they were slaughtered and had their mammary glands collected and dissected. Parenchymal tissue samples were collected for molecular biology work and blood samples were obtained the day before slaughter to measure IGF-1 concentrations. The MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) with treatment as main effect and sow as a randomized effect was used for statistical analyses. Piglets from TRT sows tended to weigh less at birth (1.31 vs. 1.53 kg, SEM = 0.05, $P = 0.10$) than piglets from CTL sows, but had similar BW at weaning and puberty ($P > 0.10$). Concentrations of IGF-1 at slaughter tended to be greater in gilts from TRT than in gilts from CTL sows (167 vs. 142 ng/mL, SEM = 9, $P = 0.06$). Amounts of parenchymal (534.9 vs. 542.4 g for TRT and CTL gilts, respectively, SEM = 45.0) and extra-parenchymal tissue as well as composition of parenchymal tissue (DM, protein, fat, and DNA contents) were similar across treatments ($P > 0.10$). There were no differences in mRNA abundance for *IGF1*, *IGF2*, ornithine decarboxylase 1 (*ODC1*), prolactin receptor (*PRLR*), signal transducer and activator of transcription 5A (*STAT5A*) or 5B (*STAT5A*) in mammary parenchyma ($P > 0.10$). In conclusion, feed restriction and subsequent compensatory feeding of gestating gilts had no effects on mammary development or mammary gene expression of their female offspring at puberty.

Key Words: diet deprivation, diet over allowance, gestation, mammary development, offspring, sows

0409 Comparative 2D-DIGE proteomic analysis of mammary epithelial cells during lactation reveals protein signatures for lactation persistency and milk yield. J. Janjanam*, S. Singh, M. K. Jena, J. K. Kaushik, A. K. Dang, and A. K. Mohanty, *National Dairy Research Institute, Karnal, India.*

The mammary gland is made up of a branching network of ducts that end with alveoli which surrounds the lumen. These alveolar mammary epithelial cells (MEC) reflect the milk producing ability of farm animals. In our previous study, we reported the proteome profile of functionally differentiated mammary epithelial cells isolated from milk (Janjanam et al., 2013). In this study, we have used 2-D DIGE and mass spectrometry to identify and relatively quantify protein expression changes in MEC during early, peak, and late stages of lactation and also compared differentially expressed proteins in MEC isolated from high and low milk yielding animals. All the animals selected for these studies were in their third or fourth parity. For the comparative proteomic analysis at different stages of lactations, we selected 4 animals (Sahiwal cows) in each group of immediate early (E, d 15 to 30 postparturition), peak (P, d 75 to 100 postparturition), and late stage (L, d 210 to 250 postparturition) of lactation. For the comparative proteomic analysis of high and low milk yield samples, we selected 4 animals each of indigenous Sahiwal cows with high yielding (Hy, ~15 L/day) and low-yielding (Ly, ~5 L/day) breeds and 4 high-yielding cross bred cows (Karan Fries: KF, ~22 L/d) were selected which were at peak stage of their lactation. We have identified 44 differentially expressed proteins during lactation stages, and 28 proteins in high and low milk yielding animals. Bioinformatics analysis showed, a majority of the differentially expressed proteins are associated in metabolic process, catalytic, and binding activity. The differentially expressed proteins were mapped to the available biological pathways and networks involved in lactation. The proteins up-regulated during late stage of lactation are associated with NF-kB stress induced signaling pathways and whereas Akt, PI3K, and p38/MAPK signaling pathways are associated with high milk production mediated through insulin hormone signaling. The differentially expressed proteins reported in our present study could be potential biomarkers associated with lactation persistency and secretory diminution. The findings reported in the present study could benefit to the field of lactation biology. Reference: Janjanam et al. (2013). Proteome analysis of functionally differentiated bovine (*Bos indicus*) mammary epithelial cells isolated from milk. Proteomics 13:3189–3204.

Key Words: lactation, mammary epithelial cells, proteomics

0410 Milk protein synthesis is regulated by lysine and branched chain amino acid deficiencies in lactating bovine mammary glands. J. Doelman*[1], R. V. Curtis[2], M. Carson[1], J. J. M. Kim[2], J. P. Cant[2], and J. A. Metcalf[1], *[1]Nutreco Canada Agresearch, Guelph, ON, Canada, [2]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

The supply of specific essential AA is tightly regulated by the lactating dairy cow to maintain milk protein production. To determine the effect of essential amino acid (EAA) deficiencies and imbalances on milk protein synthesis and metabolic parameters, early lactation fistulated dairy cows (105 ± 12 d in milk) were abomasally infused with either saline, EAA, EAA less lysine, EAA less leucine, or EAA less the branched-chain amino acids (BCAA; isoleucine, leucine, and valine) in a 5 × 5 Latin square design. Cows were fed a diet to provide an NE_L of 6.9MJ/kg DM and 11.7% crude protein. Compared with EAA, a BCAA deficiency significantly decreased plasma concentration of Leu, Val and total BCAA by 72, 67, and 66%, respectively ($P < 0.001$). In response to a leucine deficiency, plasma concentration of Ile and Val increased 71 and 62%, respectively, while plasma leucine decreased 72% ($P < 0.001$). Omission of lysine from the abomasal infusate resulted in a 72 and 77% decline in plasma lysine and asparagine, respectively ($P < 0.04$). Plasma concentrations of β-hydroxybutrytrate and NEFA were not significantly different between treatments. While no significant treatment differences were observed for daily milk production (30.1 kg/d), milk protein yield increased 18% by the EAA infusion over saline ($P = 0.001$), while the omissions of lysine, leucine, and the BCAA decreased milk yield by 10.2, 21.1, and 12.2%, respectively, compared with EAA ($P < 0.03$). In comparison with EAA, milk protein concentration was 0.23 ($P = 0.057$), 0.3 ($P = 0.01$), and 0.29 ($P = 0.01$), percentage points lower for lysine, leucine, and BCAA deficiencies, respectively. The increase in plasma concentration of Ile and Val in response to Leu deficiency suggests that compensatory measures were initiated to maintain substrate supply for milk protein synthesis. These results indicate that protein synthesis in the mammary gland is sensitive to the supply of Lys, Leu, and the BCAA.

Key Words: mammary gland, milk protein synthesis, essential amino acid

0411 Lysine and branched-chain amino acid deficiencies decrease abundances of S6K and eIF2Bε in the mammary glands of lactating dairy cows. J. Doelman[1], R. V. Curtis*[2], M. Carson[1], J. J. M. Kim[2], J. A. Metcalf[1], and J. P. Cant[2], *[1]Nutreco Canada Agresearch, Guelph, ON, Canada, [2]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada.*

There have been recent investigations into the potential role of mRNA translational control in the regulation of synthesis of milk protein in the lactating bovine mammary gland. An infusion subtraction protocol was used to explore effects on abundance and activity state of regulators of mRNA translation in response to specific essential amino acid (EAA) deficiencies and imbalances. Five lactating cows on a diet of 11.7% protein were infused abomasally for 5 d with saline, 563 g/d of a complete EAA mix (equivalent to EAA in 1 kg casein), or EAA without Lys, Leu, or the branched-chain amino acids (BCAA; Ile, Leu, and Val) in a 5 × 5 Latin square design. Data was analyzed using the MIXED procedure in SAS (SAS Inst. Inc., Cary, NC) where period and treatment were considered classification effects and cow considered a random effect. The translation factors examined in mammary biopsies collected on d 5 of each period were ribosomal protein S6 kinase (S6K) to indicate mTOR (mammalian target of rapamycin) activity, eukaryotic initiation factor 2 α (eIF2α) to indicate uncharged tRNA signalling, and eukaryotic initiation factor 2B epsilon (eIF2Bε) to indicate insulin effects. Milk protein yield increased in response to EAA compared with saline ($P = 0.001$), while Lys, Leu, and BCAA deficiencies depressed milk protein yield compared with EAA ($P < 0.03$). Infusion of the complete EAA mix did not affect mTOR activity ($P = 0.65$), but subtraction of BCAA from the mix decreased phosphorylated S6K abundance ($P = 0.05$) and subtraction of Leu tended to decrease phosphorylated S6K ($P = 0.10$). Similarly, abundance of total eIF2Bε was not affected by infusion of EAA ($P = 0.39$) but decreased when BCAA ($P = 0.04$) or Leu ($P = 0.06$) were subtracted. There was a correlation of 0.58 between abundances of phosphorylated S6K and total eIF2Bε. Lys subtraction had no effect on mammary mTOR/eIF2Bε signalling, but the abundance of total S6K tended to be lower during Lys deficiency compared with saline ($P = 0.06$) and EAA ($P = 0.09$). Phosphorylation state of eIF2α was not increased by any of the imbalances or deficiencies. It was concluded that Lys deficiency may impair milk protein yield through a decline in translational activation capacity, indicated by S6K abundance. The BCAA deficiencies may impair milk protein yields through deactivation of mTOR-mediated up-regulation of eIF2Bε abundance.

Key Words: milk protein synthesis; mRNA translation regulation, essential amino acid

LACTATION BIOLOGY II

0412 Intramammary glucocorticoid during a mammary immune response to lipopolysaccharide modulates the blood-milk barrier. O. Wellnitz*, S. K. Wall, M. Saudenova, and R. M. Bruckmaier, *Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland.*

Glucocorticoids such as prednisolone are frequently used in addition to intramammary antibiotic therapy to increase the cure rate of mastitis in dairy cows. This study aimed to investigate the effects of intramammary administered prednisolone during the mammary immune response to lipopolysaccharide (LPS). Five healthy mid-lactation Holstein dairy cows received 1 of 4 intramammary treatments in each of their 4 quarters: prednisolone (10 mg), LPS (100 μg), LPS (100 μg), and prednisolone (10 mg), or saline control. Milk samples were taken 0, 3, 6, 9, 12, 24, and 36 h after challenge. Somatic cell count (SCC), and concentrations of lactate dehydrogenase (LDH), serum albumin (SA), and tumor necrosis factor-α (TNFα) in milk and mRNA abundance of TNFα, Interleukin (IL)-8, and IL-1β in milk somatic cells were compared at each time point. Differences between quarters were tested by analysis of variance using a MIXED procedure and were considered significant if $P < 0.05$. Control and prednisolone infused quarters did not show changes of SCC, LDH, SA, and TNFα concentrations in milk and mRNA expression of TNFα, IL-1β, and IL-8 in milk somatic cells. Concentrations of SCC and TNFα in milk increased similarly in LPS challenged quarters independent of additional prednisolone application. However, the increase of LDH activity and SA concentration in LPS challenged quarters was diminished by prednisolone ($P = 0.028$ and $P < 0.001$, respectively) from 1352 ± 845 to 264 ± 107 U/L for LDH, and 8.17 ± 0.29 to 2.68 ± 0.30 mg/L for SA at 6 h after challenge, respectively. The mRNA abundance of TNFα, IL-8, and IL-1β in milk somatic cells increased in response to LPS challenge unaffected by prednisolone. In conclusion, the intramammary administration of the glucocorticoid prednisolone does not induce an increase of SCC, changes in concentrations of blood components in milk, and does not change the production of TNFα, IL-8, and IL-1β in milk cells in response to intramammary LPS challenge. However, the intramammary administration of prednisolone clearly reduces the disruption of the blood-milk barrier induced by endotoxin challenge shown by a reduced appearance of blood constituents like SA or LDH in milk. This effect could have an important influence on the severity and on the cure rate of mastitis.

Key Words: prednisolone, blood-milk barrier, mastitis

0413 Milk prolactin response after experimental infection with different coagulase-negative staphylococci in dairy heifers. K. Piccart*[1], S. Piepers[1], J. Verbeke[1], N. Melo de Sousa[2], J. F. Beckers[2], and S. De Vliegher[1], *[1]Ghent University, Ghent, Belgium, [2]University of Liège, Liège, Belgium.*

Coagulase-negative staphylococci (CNS) are the most common group of bacteria involved in subclinical bovine mastitis. Dairy heifers infected with CNS seem to produce more milk than uninfected heifers, but the underlying mechanism is yet unclear. This study investigates the response of prolactin (PRL) in milk as a potential mediator of milk yield (MY) after experimental challenge with different CNS species. Eight Holstein-Friesian heifers in mid-lactation (126 d in milk ± 66) were challenged in a split-udder design with 3 different CNS isolates: 1 *S. fleurettii* isolate from sawdust and 2 phenotypically dissimilar *S. chromogenes* isolates. The first *S. chromogenes* isolate originates from a chronic intramammary infection, while the other is cultured from a teat apex. Three quarters were simultaneously inoculated with 1.0×10^6 colony forming units. The remaining quarter was infused with sterile phosphate-buffered saline and served as a control. Milk samples were obtained for measuring PRL (by radioimmunoassay) at various time points starting 24 h preinoculation until 72 h after challenge. Furthermore, quarter MY was recorded. Milk samples were cultured to evaluate bacterial clearance. A linear mixed regression model, using heifer and quarter as random effects, was built to evaluate the PRL response after infection with sampling time and inoculation type as fixed effects. Preinoculation data were not included in the analysis. None of the quarters developed clinical symptoms and none of the heifers showed signs of illness. Milk culture results revealed that all CNS were eliminated before the end of the trial. Even though this study did not focus on MY, a decreased production was observed in all quarters. The infection status did not have a demonstrable effect on milk PRL concentration: no significant difference was found between infected and control quarters, or between different CNS-isolates ($P = 0.40$). However, milk PRL generally changed over time ($P < 0.05$). These findings suggest that milk PRL is not a likely candidate to explain any potential increase in milk production after a subclinical infection caused by *S. chromogenes* or *S. fleurettii*.

Key Words: prolactin, mastitis, coagulase-negative staphylococci

0414 Regulation of nuclear IGFBP-3 in response to intrinsic apoptotic stress in bovine mammary epithelial cells. A. Agostini-Dreyer, A. E. Jetzt, and W. S. Cohick*, *Rutgers, the State University of New Jersey, New Brunswick.*

Following peak lactation, the number of secretory mammary epithelial cells (MEC) in the bovine gland gradually

decreases due to increased apoptosis, leading to a decrease in lactation persistency. However, the mechanisms that govern apoptosis in the bovine MEC are under-investigated. We have previously shown that anisomycin (ANS), an activator of the intrinsic apoptotic pathway, is a potent inducer of IGFBP-3 production in MAC-T cells, and that knock-down of IGFBP-3 with siRNA attenuates the ability of ANS to activate apoptosis. Interestingly, IGFBP-3 is found in both the nucleus and the conditioned media in response to ANS, indicating a potential for both intra- and extracellular functions. Whether nuclear IGFBP-3 arises from secreted IGFBP-3 is controversial. In the present work, MAC-T cells were transfected with a plasmid expressing GFP-tagged IGFBP-3. Analysis using fluorescent microscopy indicated that IGFBP-3 resided basally in the cytosol and translocated to the nucleus in response to ANS. Since IGFBP-3-GFP is too large to passively diffuse through nuclear pores, this supports a role for active nuclear import. Chemical inhibition of the nuclear transport protein importin-β with importazole reduced ANS-induced nuclear IGFBP-3-GFP, indicating that IGFBP-3 utilizes importin-β for nuclear import. Endoglycosidase-H digestion of nuclear fractions showed that intracellular IGFBP-3 was glycosylated, indicating it had been transported through the secretory pathway. However, inhibition of ER to Golgi transport with Brefeldin A inhibited secretion of IGFBP-3 but increased its nuclear accumulation, indicating that secretion is not required for nuclear localization. In support of these data, inhibition of clathrin-mediated endocytosis with the chemical inhibitor Pitstop2 did not impact nuclear localization of IGFBP-3. In summary, these data show that secretion is not required for ANS-induced nuclear localization of IGFBP-3 and that its nuclear import is a regulated event.

Key Words: mammary gland, lactation, IGFBP-3

0415 Cellular composition of water buffalo mammary gland and its proliferation status during dry and mastitis.

R. K. Choudhary*[1], D. Pathak[2], D. Deka[1], and R. Verma[1], *[1]School of Animal Biotechnology, GADVASU, Ludhiana, Punjab, 141 004, India, [2]Department of Veterinary Anatomy, GADVASU, Ludhiana, Punjab, 141 004, India*

Mammary alveoli, composed of mammary epithelial cells, are the structural and functional units of a mammary gland, which secrete milk into the alveolar lumen. Milk production is directly related to secretory activity and number of alveolar cells. Alternation in cellular composition, in particular alveolar cells, thus has a direct role in volume of milk secretion. We collected mammary tissues of milking water buffalo from a slaughterhouse for the purpose of evaluation of its cellular composition, proliferation status, and identification of myoepithelial cells. Out of 21 buffaloes, ~80% of mammary samples were from the dry animals (evidenced by presence of small nonsecretory epithelial cells and virgin-like state of the gland) and ~20% of samples were from the lactating animals. All the lactating animals were affected with mastitis (suggested by the presence of fibrin clots, cellular debris, and loss of alveolar epithelium), which were also confirmed by a veterinary pathologist. The fraction of total mammary epithelium (large secretory and small nonsecretory cells; mean % ± SE) did not differ in dry vs. lactation period (22.6 ± 1.66 vs. 18.7 ± 3.59; $P > 0.05$). However, number of small nonsecretory epithelium were greater in dry period (22.6 ± 1.66 vs. 10.1 ± 2.97; $P = 0.006$) than the lactation period, likely due to differentiation of nonsecretory cells into secretory cells. Number of myoepithelial cells (identified by vimentin expression in basal layer of epithelium) were greater (23.38 ± 2.89 vs. 5.55 ± 1.10; $P = 0.004$) in mastitis-afflicted than the dry animals. Increased expression of vimentin (also a marker of migrating cells) in the stroma, suggested the role of cell migration in inflammation, tissue regeneration and immune response during mastitis. Thus, mastitis-infected animals had increased number of myoepithelial cells and stromal migratory cells in their mammary glands. A greater number of myoepithelial cells during mastitis was concomitant with increased (5×) expression of Ki-67, a marker of cell proliferation. This study demonstrates cellular composition of buffalo mammary glands as well as supports the idea that infection of mammary gland enhances proliferation of mammary epithelial cells.

Key Words: water buffalo mammary gland, cellular composition, vimentin, proliferation

---

0416 Use of the RatLoft in laboratory conditions decreases pup mortality in lactating mice.

S. R. Weaver*, C. R. Cronick, A. P. Prichard, J. Laporta, N. J. Benevenga, and L. L. Hernandez, *University of Wisconsin-Madison, Madison.*

Mice in laboratory conditions are under considerable stress. Lactating dams may manifest this psychological distress through a decrease in milk yield or increase in pup mortality. The RatLoft (Research Animal Welfare Equipment, LLC, Madison, WI) is a stainless steel tube that hangs over the side of the cage with access to food, allowing the dam time away from her pups. Here, we examined the effect of the RatLoft on milk yield, circulating serotonin (5-HT), pup mortality, and behavioral distress as measured by the Porsolt Forced Swim Test (FST). Pregnant mice deficient for tryptophan hydroxylase-1 ($TPH1^{-/-}$, $n = 10$) and wild-type mice (WT, $n = 10$) were randomly assigned to loft (L; $n = 5$) and no loft (NL; $n = 5$) treatment groups. Milk yield was measured daily for 21 d. The FST was performed on d 10 and pup mortality was recorded throughout the experiment. Blood was collected on d 1, 9, and 21. Data was analyzed using a 2-way ANOVA. Milk yield increased over time in all animals ($P < 0.0001$). Presence or absence of the RatLoft did not affect milk yield ($P > 0.05$). Overall, WT mice had increased milk yield compared with $TPH1^{-/-}$ mice, regardless of the presence of RatLoft ($P < 0.05$).

The FST used to evaluate behavioral distress indicated that the presence or absence of RatLoft was not significant ($P > 0.05$). Serum 5-HT concentrations were increased in WT compared with TPH1$^{-/-}$ mice. Presence or absence of the RatLoft did not affect circulating 5-HT concentrations ($P > 0.05$, 373 vs. 309 ± 55 ng/mL), but 5-HT concentrations decreased throughout lactation (455 vs. 245 ± 65 ng/mL on d 1 and 21, respectively). Serotonin concentrations were increased in TPH1$^{-/-}$ mice with the L ($P < 0.01$; 33 ± 13 ng/mL vs. 13 ± 1.4 ng/mL). The TPH1$^{-/-}$ mice with L had less 5-HT on d 1 and 9 compared with d 21 ($P = 0.005$; 21 and 17 vs. 51 ± 6.5 ng/mL, respectively). The 5-HT levels in TPH1$^{-/-}$ mice with NL did not change over time ($P > 0.05$). Pup mortality was significantly less for dams with L as compared with mice with NL ($P = 0.047$, 0.49 ± 0.16 pups/dam vs. 0.195 ± 0.06). Mortality rates were not different between WT and TPH1$^{-/-}$ mice ($P > 0.05$). These results demonstrate that access to RatLoft during lactation decreases pup mortality rates in all animals, as well as increased 5-HT concentrations in TPH1$^{-/-}$ mice. In conclusion, use of the RatLoft could prove beneficial to researchers working with lactating mouse models to decrease pup mortality rates.

Key Words: serotonin, lactation, RatLoft

0417 Addition of glycerol to lactating cow diets stimulates milk protein yield to a greater extent than addition of corn grain. D. L. Bajramaj*[1], R. V. Curtis[2], J. J. M. Kim[2], V. R. Osborne[1], T. Wright[3], and J. P. Cant[1], *[1]University of Guelph, Guelph, ON, Canada, [2]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [3]University of Guelph/OMAF, Guelph, ON, Canada.*

As the biofuel industry grows and expands, there is an increased availability of the byproduct glycerol, which could be a glucogenic feedstuff for dairy cows. The objective of this study was to determine if the addition of glycerol to the diet of dairy cows would stimulate milk protein yield in the same manner as the addition of corn grain. Twelve lactating dairy cows were assigned at 81 ± 5 d in milk to 3 diets in a repeated 3 × 3 Latin square design. The diets were a 70%-forage diet considered the base diet, the base diet with 19% ground and high-moisture corn replacing forages, and the base diet with 15% refined glycerol and 4% added protein supplements to be isocaloric and isonitrogenous with the corn diet. Diets contained 17.2, 17.9, and 17.3% CP, respectively, and 34, 28, and 30% NDF, respectively. The diets were fed for periods of 28 d each, and milk, feed, and blood samples were collected during the last week of each period for compositional analysis. Treatment differences were evaluated by ANOVA using PROC MIXED of SAS (SAS Inst. Inc., Cary, NC) with cow as a random effect. Dry matter intake increased from 23.7 kg/d on the base diet to 25.8 kg/d on the corn diet ($P = 0.007$) and to 27.2 kg/d on the glycerol diet ($P < 0.001$). There was a tendency for DMI to be higher with glycerol than corn ($P = 0.06$). Milk production increased from 39.2 kg/d on the base diet to 43.8 kg/d on the corn diet ($P < 0.001$) and to 44.2 kg/d on the glycerol diet ($P < 0.001$). There was no difference in milk yield between corn and glycerol diets. Milk protein content was 3.19, 3.33, and 3.44% on the base, corn, and glycerol diets, respectively, and the stimulation by glycerol was greater than the stimulation by corn ($P = 0.037$). Protein yield was increased 197 g/d by the addition of corn and 263 g/d by the addition of glycerol, and the glycerol effect was larger than the corn effect ($P = 0.054$). Efficiency of capture of dietary protein in milk protein, however, was lower on the glycerol diet at 29.5% compared with 32.6% on the corn diet ($P = 0.017$). It was concluded that glycerol stimulated milk protein yield to a greater extent than corn grain.

Key Words: glycerol, milk protein synthesis, dairy cow

0418 Glucose does not stimulate milk protein yield of dairy cows when essential amino acids are in excess supply. K. Nichols*[1], M. Carson[2], J. J. M. Kim[1], J. A. Metcalf[2], J. P. Cant[1], and J. Doelman[2], *[1]Department of Animal and Poultry Science, University of Guelph, Guelph, ON, Canada, [2]Nutreco Canada Agresearch, Guelph, ON, Canada.*

To determine if glucose stimulates milk protein yield when essential amino acids (EAA) are supplied in excess, 5 early-lactation, rumen-fistulated dairy cows (78 ± 13 d in milk) were abomasally infused for 5 d with EAA and glucose solutions in a 5 × 5 Latin square design. The 5 infusion treatments were saline, 844 g/d EAA in the profile of casein, 1126 g/d EAA, 844 g/d EAA + 1000 g/d glucose, or 1126 g/d EAA + 1000 g/d glucose. Cows were fed a diet containing 6.96 MJ/kg NE_L and 12% crude protein on a dry basis. Milk composition and yield during the last 2 d of each period and plasma metabolite concentrations during d 4 of infusion were subjected to ANOVA using PROC MIXED of SAS (SAS Inst. Inc., Cary, NC), where cow was a random effect. EAA infusion increased essential and branched-chain AA concentrations in plasma 3- to fourfold compared with saline ($P < 0.001$). Non-EAA concentrations decreased 11 to 17% during EAA infusions ($P < 0.001$). Addition of glucose to EAA infusates decreased essential and branched AA concentrations in plasma ($P < 0.031$) and had no effect on non-EAA concentrations. Essential amino acid infusion increased concentrations of NEFA ($P = 0.004$) and urea N ($P < 0.001$) in plasma, but had no effect on glucose concentrations. Addition of glucose to EAA infusates increased glucose concentrations in plasma 13 to 19% ($P < 0.001$), decreased NEFA 26 to 32% ($P < 0.001$) and had no effect on urea N. Dry matter intake was not affected by EAA infusion, while daily milk yield increased 16% and milk protein yield increased 27% (for an average of 262 g/d) at the highest level of EAA infusion compared with saline ($P < 0.001$). Milk protein concentration increased from 2.9% with saline to 3.3%

with EAA ($P < 0.001$). The addition of glucose to EAA infusates caused DMI to decrease 0.65 kg/d ($P = 0.040$), tended to increase milk yield ($P = 0.057$), had no effect on milk protein yields ($P = 0.318$), but tended to decrease milk protein concentration ($P = 0.097$) and decreased milk fat concentration ($P < 0.001$). Thus, increased supply of glucose at high levels of EAA supplementation did not improve milk protein yields, but because of the decline in feed intake there was an increased efficiency of capture of dietary protein into milk protein.

Key Words: milk protein, essential amino acids

MEAT SCIENCE & MUSCLE BIOLOGY

0419 Changes to the muscle proteome during acute heat stress are dependent on predominant fiber type. S. M. Cruzen*, K. B. Carlson, S. C. Pearce, L. H. Baumgard, N. K. Gabler, and S. M. Lonergan, *Iowa State University, Ames*.

The objective was to determine acute proteomic changes in muscle caused by heat stress. Crossbred gilts (n = 16) were exposed to either thermal neutral (TN, 20°C, 40% relative humidity) or heat stress (HS, 37°C, 40% relative humidity) conditions for 12 h with ad-libitum feed intake. The semitendinosus was collected, divided into red (RST) and white (WST) portions, and frozen in liquid N. Protein abundance changes due to treatment were determined ($P < 0.15$) in sarcoplasmic extracts of HS and TN animals via 2-dimensional difference in gel electrophoresis (2D-DIGE). Proteins were identified using electrospray ionization mass spectrometry. Compared with TN muscle, heat shock protein (Hsp) 70, mitochondrial Hsp70, Hsp27, Hsp20, and α-B crystallin were increased in abundance in muscle of HS pigs. However, 1 spot identified as α-B crystallin was decreased in abundance in the RST with HS. Several protein spots associated with glycolysis or the TCA cycle were changed in abundance with HS, indicating that muscle energetic metabolism is altered during HS. In the RST, these proteins included aldolase A (decreased, 1 spot), phosphoglycerate kinase 1 (increased, 2 spots), phosphoglycerate mutase 2 (decreased, 1 spot), malate dehydrogenase (increased, 2 spots), succinyl-CoA synthetase (increased, 1 spot), and creatine kinase (increased, 1 spot). In the WST, changes in the proteins aldolase A (increased, 1 spot), glyceraldehyde 3-phosphate dehydrogenase (increased, 1 spot), and creatine kinase (decreased, 1 spot) were identified. In both muscle types, β-enolase (increased, 1 spot), isocitrate dehydrogenase (increased, 1 spot), and malate dehydrogenase (increased, 2 spots) were changed in abundance with HS. Heat stress may also affect cell structure. In the WST, HS altered abundance of proteins involved in microtubule or microfilament structure, including α and β tubulin (decreased, 1 spot each) and cofilin 2 (increased, 1 spot). Finally, abundance of several peroxiredoxins was altered with HS, which may indicate that oxidation regulation is changed during acute HS. In HS pigs, peroxiredoxin 6 was increased in 1 spot in the RST, and peroxiredoxin 1 was decreased in 1 spot in the WST. Peroxiredoxin 2 was decreased in abundance in 2 spots in both muscle types due to HS. These results demonstrate that acute HS may have measurable impacts on muscle metabolism, structure, and antioxidant enzymes, which may contribute to the decreased performance generally observed in HS pigs. Additionally, muscle types may respond and adapt differently to acute HS.

Key Words: heat stress, pigs, fiber type

0420 Relationship of fat quality to meat quality traits of pork. E. D. Testroet*, C. Yoder, C. Bustos, S. M. Lei, D. C. Beitz, and T. J. Baas, *Iowa State University, Ames.*

The objectives of this research were to investigate the relationship of pork fat quality to meat quality, the effect of genetic differences on fat quality, how fat quality and adipocyte cellularity varies amongst anatomical sites, and finally how the 7 breeds performed when compared with one another. Our hypothesis was that measures of pork fat and meat quality vary with different breeds of pigs, and that a relationship exists between fat and pork quality measures. Barrows and gilts (n = 352) of 6 purebred lines and 1 commercial crossbred line were fed commercial swine diets with dried distillers grains with solubles (DDGS) inclusion at 30% of DM. Pigs began the experiment when the pen average pig weight was 31.8 kg and were harvested at a minimal weight of 111.1 kg. At harvest, carcass characteristics were measured, adipose tissue was collected from the back, belly, and jowl, and meat samples were taken from the longissimus muscle for evaluation of fat and meat quality characteristics. Iodine values varied amongst breed within anatomical site and between anatomical sites within each breed, and, therefore, the anatomical site of adipose tissue sampling may be of importance when evaluating iodine values of pork fat. Jowl fat iodine values are significant ($P < 0.0001$) predictors of back and belly fat iodine values (R^2 = 0.2922 and 0.3604 respectively). Backfat iodine values were not significantly correlated with ultimate pork chop muscle pH ($P = 0.0680$) but were significantly negatively correlated with visual color ($P = 0.0002$), visual marbling ($P < 0.0001$), and visual firmness ($P = 0.0346$), indicating that an increase in iodine value of pork fat is related to a decrease in pork quality as perceived by consumers. Finally, adipocyte cellularity was significantly affected by breed when compared within anatomical location across breeds ($P < 0.05$), but significant differences between breeds, within anatomical location, of mean cell size of adipocytes were only found for belly adipose tissues. Overall, these experimental results support our hypothesis that there is a significant relationship between pork fat and pork quality and that pork fat quality and meat quality vary by breed. Additionally, iodine values are a valuable measure of pork quality, and iodine values of jowl fat can be used to predict iodine values of back and belly fat, providing a powerful tool to meat packers for fat quality estimation.

Key Words: iodine value, pork quality, adipocyte cellularity

0421 Effects of dietary level of dried citrus pulp on growth, feed efficiency, carcass merit, and lean quality of finishing pigs. C. M. Strong*, J. H. Brendemuhl, D. D. Johnson, and C. Carr, *University of Florida, Gainesville.*

As feed costs continue to be the largest expense for producers, fibrous feedstuffs such as dried citrus pulp (DCP), previously thought to be of marginal quality, are now being explored for use in swine diets because of their availability and low cost. Previous research has focused on DCP as an energy supplement in cattle diets in Florida, but there have been limited studies investigating the effects of differing dietary levels of DCP on the growth, efficiency, carcass merit, and lean quality of finishing pigs. Pigs (n = 40) were fed 1 of 4 diets for 49 d: a corn soybean meal control diet (CON; n = 10), or the same diet with DCP replacing 15% (15DCP; n = 10), 22.5% (22.5DCP; n = 10), or 30% (30DCP; n = 10) of the total diet DM. Overall, G:F over 49 d was greater in CON and 22.5DCP than 30DCP ($P < 0.02$). Pigs were slaughtered at the University of Florida Meat Laboratory abattoir. Initial pH was taken 60 min postexsanguination from the LM and the semimembranosus (SM). Carcasses were fabricated at 24 h postmortem, where initial meat quality measurements were made at the 10th and 11th rib interface of the LM and the gluteus medius of the ham face. Fat measurements taken at the blade region of the LM received higher L* values ($P < 0.04$) in CON animals compared with 22.5DCP and 30DCP. When evaluated objectively, bellies from CON pigs were firmer ($P < 0.0001$) than all other treatment groups, but both CON and 15DCP garnered higher subjective firmness scores than 22.5DCP and 30DCP ($P \leq 0.04$). Belly thickness at both the blade and flank ends decreased as DCP percentage increased, with CON exhibiting the thickest ($P < 0.03$) and 30DCP having the thinnest ($P \leq 0.02$) measurements. Longissimus muscle chops from 30DCP pigs received higher juiciness scores from panelists than 22.5DCP and CON ($P \leq 0.03$), while 15DCP chops only earned higher values than CON chops ($P = 0.03$). There was no effect of dietary DCP inclusion on muscle pH, lightness, redness, and yellowness values, chroma, or hue angle, drip or purge loss, live or hot carcass weight, dressing percentage, back fat, loin eye area, percentage lean, shear force, cook loss, retail evaluation, or retail lightness, redness, or yellowness values. Though sensory panelists reported increased palatability (juiciness) of chops from pigs receiving 30% DCP, increasing DCP percentage of the total diet DM appeared to be economically detrimental to overall production because of negative impacts on growth performance and pork belly quality.

Key Words: pork, citrus, byproduct

0422 Effects of zilpaterol hydrochloride and implants in beef heifers I: Feedlot performance, carcass characteristics, and intramyocellular lipid accumulation. M. A. Vaughn*, S. M. Ebarb, K. J. Phelps, D. D. Burnett, J. S. Drouillard, and J. M. Gonzalez, *Kansas State University, Manhattan.*

To assess the effects of zilpaterol hydrochloride (ZH) supplementation and implants on feedlot performance, carcass characteristics, and intramyocellular lipid accumulation, 33 crossbred yearling heifers were blocked by initial BW (464 ± 2 kg) and randomly assigned to 3 treatments consisting of no implant or ZH (CON); Component TE-200 implant on d 1 of the study, no ZH (IMP); implant and 8.3 ppm of ZH for 21 d with a 3-d withdrawal period (ZIL). Animals were fed a finishing ration once daily, ad libitum, with bunks managed to leave a minimum amount of unconsumed feed. After a 75-d feeding period, cattle were harvested at a commercial abattoir. At 36 h postmortem, carcass characteristics were collected and boneless strip loins were transported to the Kansas State University Meats Laboratory. To assess intramyocellular lipid content, 13th-rib LM samples were cryopreserved, cut into 5-µm sections, and exposed to BODIPY 493–503 staining. Final BW, DMI, ADG, and KPH were not affected by treatment ($P > 0.30$). The IMP and ZIL heifers had greater G:F compared with CON ($P = 0.04$). The ZIL heifers had greater ($P < 0.01$) HCW than CON heifers and IMP heifers tended to have greater ($P = 0.07$) HCW than CON heifers. The ZIL heifers had greater ($P = 0.03$) dressing percentage (DP) compared with CON heifers, and IMP heifers tended to have a greater ($P = 0.07$) DP than CON heifers. Heifers fed ZIL also had greater LM area ($P = 0.01$) compared with CON heifers, and IMP heifers tended to have greater ($P = 0.06$) LM area than CON heifers. Heifers from the CON treatment had greater ($P = 0.01$) amounts of backfat than ZIL heifers, and CON heifers tended to have more ($P = 0.09$) backfat than IMP heifers. The CON heifers had greater ($P = 0.04$) marbling than IMP heifers, but ZIL carcasses did not differ in marbling between the 2 other treatments ($P > 0.14$). For LM area, backfat, and marbling, ZIL and IMP carcasses did not differ from one another ($P > 0.37$). Additionally, IMP heifers contained a greater ($P = 0.04$) percentage of muscle fibers with intramyocellular lipid droplets than ZIL heifers. The CON heifers tended to have a greater ($P = 0.08$) percentage of muscle fibers that contained intramyocellular lipid droplets than ZIL heifers. These data suggest that implanting cattle and ZH supplementation increase efficiency of lean meat production while decreasing adipose tissue accumulation in all depots except KPH.

Key Words: implants, zilpaterol hydrochloride, intramyocellular lipids

0423 Effects of zilpaterol hydrochloride and implants in beef heifers II: Aging effects on Warner-Bratzler shear force, collagen solubility, and fiber cross-sectional area. S. M. Ebarb*, K. J. Phelps, M. A. Vaughn, J. A. Noel, C. B. Paulk, J. S. Drouillard, and J. M. Gonzalez, *Kansas State University, Manhattan.*

To evaluate the effects of zilpaterol hydrochloride (ZH), implants, and day of aging (DOA) on Warner-Bratzler shear force (WBSF), collagen solubility, and fiber cross-sectional area (CSA), 33 crossbred heifers were blocked by weight and randomly assigned to 1 of 3 treatments: no implant or ZH (CON); Component TE-200 implant on d 1 of the study (IMP); or implant and 8.3 ppm of ZH for 21 d with a 3-d withdrawal period (ZIL). After 75 d of feeding, animals were shipped to a commercial abattoir for harvest, chilled for 36 h, and boneless strip loins were transported to the Kansas State University Meats Laboratory. To assess CSA and myosin heavy chain isoform (MHC), 13th-rib LM samples were cryopreserved, sectioned into 5-µm sections, and immunostained for MHC type I, IIA, and IIX. On d 3, 14, and 21 of aging, a 2.54-cm steak and a 0.64-cm steak were fabricated for WBSF and collagen solubility analyses, respectively. For WBSF, there was a treatment × DOA interaction ($P < 0.01$). On d 3 of aging, CON steaks had decreased WBSF compared with IMP and ZIL steaks ($P < 0.01$). At d 14, CON and IMP steaks did not differ ($P = 0.21$) in WBSF, but ZIL steak WBSF values were greater than those of the other treatments ($P < 0.01$). After 21 d aging, there were no WBSF differences between treatments ($P > 0.13$). There was no treatment × DOA interaction for percent soluble or total collagen ($P > 0.20$). Implants and ZIL increased the percentage of soluble collagen when compared with CON ($P < 0.05$), and solubility of collagen also increased between d 14 and 21 of aging ($P < 0.01$). Treatment or DOA did not affect total collagen content ($P > 0.51$). For type I muscle fibers, CSA was greatest for the IMP group ($P < 0.01$). Type IIA and IIX CSA were greater for ZIL compared with IMP and CON ($P < 0.01$). There were positive correlations between type IIX CSA and WBSF on d 3, 14, and 21 of aging ($R^2 = 0.64$, 0.58, and 0.37, respectively; $P < 0.05$). Increased CSA for type I and type IIA were positively correlated with increased WBSF for d 3 and 14 (type I $R^2 = 0.51$, 0.44, and 0.26; type IIA $R^2 = 0.51$, 0.45, and 0.27, respectively; $P < 0.05$), but not for d 21 ($P > 0.14$). Implants and ZH increase the CSA of muscle fibers, which correlate positively with WBSF values.

Key Words: growth promotants, shear force, cross-sectional area

0424 Effect of zilpaterol hydrochloride on carcass composition, subprimal yield, and meat quality of Nellore heifers. N. R. B. Cônsolo*[1], R. S. Goulart[2], F. Rodriguez[1], M. O. Frasseto[1], R. A. P. Maciel[1], J. F. Penso[1], and L. F. P. Silva[1], [1]*University of São Paulo, São Paulo, Brazil,* [2]*MSD Saúde Animal, Sao Paulo, Brazil.*

The aim of this research was to evaluate the effects of zilpaterol hydrochloride (ZH) on carcass composition, carcass subprimal yield and meat quality of Nellore heifers. Seventy-two animals were fed with ZH (Zilmax, Merck Animal Health, Summit, NJ) during 30 d, allowing for 3 d of product withdrawn before slaughter. The animals were blocked by BW and previous ADG and allocated into 2 groups: Control and Zilpaterol (8.3 mg ZH/kg of diet DM). After 24 h postmortem, left carcasses were processed and the ninth, 10th, and 11th rib sections (HH sample) were removed from the primal rib to determine carcass chemical composition. Four steak samples were collected from the longissimus muscle to determine cooking loss and Warner-Bratzler shear force (WBSF) after 0, 7, 14, and 21 d of aging. The right carcasses were processed into primal cuts, and weighed. Each primal cut was further processed into boneless subprimal cuts, minor cuts, lean trim, fat, and bone. Statistical analyses were conducted using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) considering the fixed effects of treatment and the random effect of block. Treatments had no effect on the protein, fat, or ash content of the carcass, as estimated by water content. Cooking loss was unaffected by ZH supplementation. There was a ZH × Aging interaction for WBSF, with greater WBSF for ZH at 7 and 14 d of aging. Zilpaterol hydrochloride supplementation increased ($P < 0.05$) the weights of most of the meat cuts analyzed, especially the cuts from the hindquarter ($P < 0.01$), including top sirloin cap ($P = 0.01$), striploin ($P = 0.05$), tenderloin ($P < 0.01$), eye of rump ($P < 0.01$), knuckle ($P < 0.001$), inside round ($P < 0.001$), outside round ($P = 0.01$), and eye of round ($P < 0.05$). Additionally, ZH increased by 7.66% of the subprimal yield and by 1.94% of the debone yield of the heifers. In conclusion, ZH supplementation had no effect on chemical carcass composition, decreased meat tenderness after 7 and 14 d of aging, and increased meat cuts weights and carcass subprimal yield.

Key Words: β-agonist, shear force, subprimal yield

0425 Effects of duration of vitamin C supplementation on growth performance, carcass traits, and protein degradation of the longissimus thoracis of steers fed a 0.31 or 0.59% sulfur diet. D. Pogge*, S. M. Lonergan, and S. L. Hansen, *Iowa State University, Ames.*

Angus steers ($n = 42$) were allotted equally to 7 pens with individual feed intake monitoring technology by BW (304 ± 13 kg), and fed 1 of 7 diets: 4, high-S (0.59% S) diets, supple-

mented with 10 g vitamin C (VC)·steer^{-1}·d^{-1} for 0 d (HSCON), 56 d (HSVC56), 90 d (HSVC90), or 127 d (HSVC127), and 3 low-S diets (LS, 0.31% S) supplemented with 10 g VC·steer^{-1}·d^{-1} for 56 d (LSVC56), 90 d (LSVC90), or 127 d (LSVC127). Jugular blood (d 0, 56, 90, 127) and liver (d 121 or 122) were collected from all steers. Steers (n = 40) were harvested on d 128, and carcass data and rib-sections were collected. Steer was the experimental unit and data were analyzed using Proc Mixed. Final BW ($P < 0.01$), ADG ($P < 0.01$), and DMI ($P = 0.09$) were greater in LS steers than HS steers, but G:F was not affected ($P = 0.41$) by treatment. Total ($P = 0.06$) and reduced ($P = 0.03$) plasma glutathione (GSH) concentrations were greater, and the ratio of oxidized-to-reduced liver GSH was lesser ($P < 0.01$), in VC-fed HS steers compared with HS CON. Ribeye area and marbling score were not affected by diet ($P \geq 0.33$), but LS steers had greater ($P = 0.05$) back-fat than HS steers. a* and b* values were greater ($P \leq 0.05$) in LS steaks than HS steaks over 7 d. Steaks from HS steers had greater total ($P = 0.02$), soluble ($P = 0.06$), and insoluble ($P = 0.06$) collagen (d 2) than steaks from LS steers. Steaks (d 2) from steers fed the HS diet had a greater ($P < 0.01$) and lesser ($P = 0.04$) percentage of the 80 kDa and 76 kDa subunit of calpain-1, respectively, than the LS steers. Adding VC to the HS or LS diets linearly decreased the 80 kDa subunit ($P = 0.03$) and 76 kDa subunit ($P = 0.04$) of calpain-1, respectively. Troponin-T (TT) degradation 2 d postmortem tended to be greater ($P = 0.08$) in LS steers than HS steers, while TT 7 d postmortem did not differ ($P \geq 0.55$) by treatment. In conclusion, improved GSH indices in the VC-supplemented HS steers may be supporting increased activation of calpain-1 compared with steers fed HS alone. It appears that high-S diets may negatively affect the rate, but not extent of longissimus thoracis protein degradation.

Key Words: beef cattle, sulfur, vitamin C

0426 Interaction of various inclusion levels of dietary vitamin D2 enriched yeast cell wall with zilpaterol hydrochloride on dry matter intake and postmortem tenderness in feedlot steers.

A. J. Thompson*[1], F. R. B. Ribeiro[1], J. E. Hergenreder[1], W. C. Burson[1], B. J. Ragland[1], A. D. Hosford[1], J. R. Corley[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Lesaffre Feed Additives, Milwaukee, WI.*

The objectives of this study were to examine the impact of various inclusion rates of vitamin D_2 enriched yeast cell wall (YCW) on performance and carcass characteristics of cattle finished with zilpaterol hydrochloride (ZH). Crossbred steers (n = 192; BW = 546 ± 11 kg) were blocked by BW in a randomized block design and randomly assigned to pen (6 pens/block; 4 cattle/pen). Pens within block were assigned to 1 of 6 treatments (8 pens/treatment): (1) negative control (–CON; no ZH, no YCW), (2) positive control (+CON; ZH, no YCW), (3) vitamin D_2 YCW containing 100,000 IU vitamin D_2/gram (2.5 g · animal^{-1} · d^{-1}), (4) vitamin D_2 YCW (5.0 g · animal^{-1} · d^{-1}), (5) vitamin D_2 YCW (10.0 g · animal^{-1} · d^{-1}), (6) YCW C-wall product (2.5 g · animal^{-1} · d^{-1}). Steers were supplemented with respective treatments for the 51 d duration of the trial, of which ZH was supplemented d 28 to 47. Daily DMI was recorded and BW was collected at d 0, 28, and 51. Carcass data was collected on harvest and 10 choice strip loins were randomly collected from each treatment for further analysis. Strips were cut into steaks and assigned to 1 of 4 aging periods (7, 14, 21, 28 d). Tenderness was estimated using Warner-Bratzler shear force (WBSF). Data were analyzed using a randomized block design with the fixed effect of treatment and the random effect of block. Warner-Bratzler shear force values were analyzed using the same model, including aging period as an additional factor. Dry matter intake showed a significant quadratic relationship ($P = 0.01$) for increasing levels of D_2 YCW for the entire feeding period, with the greatest intake in the 10.0-g treatment (10.30, 10.27, and 10.66 kg/d, respectively). All ZH fed treatments had numerically greater WBSF values than negative control, but values among ZH treatments were insignificant across all aging periods. There was a tendency for lower WBSF values in the 10.0 g D_2 YCW treatment when compared with positive control ($P = 0.10$, 0.06, 0.10, and 0.09), and WBSF values of steaks from the 10.0 g YCW treatment ranged from 0.44 kg (d 21) to 0.69 kg (d 7) lower than positive control for all aging periods. Results indicate that yeast cell wall supplementation could increase performance of finishing steers during ZH supplementation, while vitamin D_2 supplementation may have positive effects on tenderness.

Key Words: vitamin D, yeast, zilpaterol hydrochloride

0427 Zinc methionine alters muscle and adipose gene expression and protein concentration of calf-fed Holstein steers fed zilpaterol hydrochloride.

J. E. Hergenreder*[1], J. O. Baggerman[1], M. E. Branine[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, TX, [2]Zinpro Corporation, Eden Prairie, MN.*

Zinc has been shown to have allosteric binding sites on β2-adrenergic receptors (β-AR), enhancing agonist affinity, and inhibiting antagonist binding. Therefore, our objective was to determine the effect of supplementing a Zn methionine complex (ZINPRO, Zinpro Corp., Eden Prairie, MN) during the last 115 d of feed, when zilpaterol hydrochloride (ZH) is fed for the final 20 d, with a 3-d withdrawal before slaughter on muscle and adipose tissue gene expression and protein concentration of calf-fed Holstein steers. Steers (n = 211; initial BW = 468.5 ± 0.5 kg) were blocked by weight and randomly assigned to pens and treatment: (1) Control; $ZnSO_4$ added to provide 90 ppm Zn, and (2) ZINPRO; 720 mg Zn · animal^{-1} · d^{-1} provided by ZINPRO at the time of terminal implant. Steers were harvested at a commercial abattoir, and 20 steers

per treatment were randomly selected for *semimembranosus* muscle and adipose tissue biochemical analysis. Messenger RNA and protein was isolated from the muscle and adipose tissue for quantitative reverse transcription PCR (RT-qPCR), western blotting, and myosin analysis. Using RT-qPCR analysis, genes of interest included AMPKα, β1AR, β2AR, β3AR, MHC-I, MHC-IIA, MHC-IIX, GPR43, GPR41, Glut4, SCD, CEBPβ, and PPARγ. No differences ($P > 0.05$) were detected in muscle tissue mRNA abundance between treatments for AMPKα, MHC-IIA, β2AR, β3AR, GPR43, GPR41, Glut4, and CEBPβ. ZINPRO-fed cattle had an increased quantity of MHC-I mRNA ($P < 0.05$) in muscle tissue. Control cattle had an increased quantity of MHC-IIX, β1AR, PPARγ and SCD mRNA ($P < 0.05$) in muscle tissue. In adipose tissue, Control cattle had an increased quantity of Glut4 mRNA ($P < 0.05$). There were no differences ($P > 0.05$) between treatments for AMPKα, β2AR, GPR43, GPR41, SCD, CEBPβ, and PPARγ mRNA in adipose tissue. Protein quantification for muscle and adipose tissue was performed via western blotting procedures to assess the abundance of the β1AR, β2AR and β3AR; however, no differences ($P > 0.05$) were detected between treatments. Muscle protein was also run on acrylamide gels to separate MHC-I and II; ZINPRO fed cattle had a greater concentration of MHC-II protein ($P > 0.05$). These results indicate that ZINPRO and ZH in combination increases MHC-I, decreases MHC-IIX gene expression, and increases myosin protein concentration in skeletal muscle.

Key Words: myosin heavy chain, zilpaterol hydrochloride, zinc methionine

---

0428 Muscle fiber and color characteristics of different locations within beef *Longissimus lumborum* steaks. K. J. Phelps*, M. A. Vaughn, S. M. Ebarb, D. D. Burnett, J. S. Drouillard, and J. M. Gonzalez, *Kansas State University, Manhattan.*

The objective of this study was to demonstrate the effect that muscle fiber composition differences within anatomical location of beef strip loin steaks elicit on color characteristics over a 7-d simulated retail display. Beef strip loins ($n = 120$) were collected from a commercial abattoir and before aging, steaks were removed from the 13th rib for immunohistochemical analysis of muscle fiber cross-sectional area (CSA) and myosin-heavy chain (MHC) isoform distribution. Sampling locations included medial (MED), mid-lateral (M/L), and lateral (LAT) within each steak. After 14-d of aging, steaks were fabricated, and L*, a*, surface metmyoglobin, and metmyoglobin reducing ability (MRA) were analyzed during a 7-d simulated retail display. There was a day × location interaction for all color characteristics ($P < 0.01$). Initially, LAT was darker and redder than both MED and M/L ($P < 0.04$), and M/L was redder ($P < 0.01$) than MED. On d 7, MED tended to have reduced ($P < 0.05$) L* value than the M/L and LAT area. The MED area was more ($P < 0.05$) red than LAT, while M/L did not differ in redness compared with the other areas ($P > 0.10$). On d 0, all 3 treatments differed in surface metmyoglobin percentage, with the MED possessing greater a percentage than the other locations ($P < 0.01$). At the end of display, all 3 treatments differed, with the LAT possessing 0.83 and1.75% more metmyoglobin than M/L and MED, respectively ($P = 0.01$). All locations had similar MRA on d 0 ($P > 0.10$), but treatments differed in MRA on d 7 ($P < 0.05$). The MED possessed 3.01 and 6.19% greater MRA than LAT and M/L, respectively ($P < 0.05$). Percentage of type IIA fibers was not different between the 3 locations ($P > 0.10$). The MED area tended to possess fewer Type I fibers ($P = 0.10$) than the M/L, and MED possessed less ($P < 0.01$) Type I fibers than LAT. Type I fiber number in LAT and M/L did not differ ($P = 0.25$). The MED area had more ($P = 0.02$) Type IIX fibers than the M/L and LAT ($P < 0.02$), but the M/L and LAT did not differ ($P = 0.94$). The M/L area had larger Type I and IIX fibers than MED and LAT ($P < 0.01$), and MED tended to have larger ($P = 0.08$) Type I fibers than LAT. Also, LAT had smaller ($P < 0.01$) IIA fibers than M/L and MED, but size of IIA fibers in M/L and MED were similar ($P > 0.10$). Based on fiber distribution, expected biochemistry of these locations does not accurately explain color characteristics during simulated retail display.

Key Words: fiber type, color characteristics, sampling location

---

0429 In utero manipulation of muscle development in beef cattle fetuses. M. S. Duarte*[1], M. P. Gionbelli[2], P. Paulino[1], N. V. L. Serão[3], S. E. Facioni[1], S. de Campos Valadares Filho[1], and M. Du[4], *[1]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [2]Instituto Nacional de Ciência e Tecnologia–Ciência Animal, Viçosa, Minas Gerais, Brazil, [3]Iowa State University, Ames, [4]Washington State University, Pullman.*

Fetal programming has been suggested as new tool in the current meat industry to produce animals with a potential to produce high quality beef. Such hypothesis is based on the fact that the main cells that compose the skeletal muscle tissue (myocytes, adipocytes, and fibroblasts) are all derived from a common pool of mesenchymal stem cells and their commitment to one of those lineages can be altered, among other factors, by maternal nutrition during the gestational period. Besides myogenesis and adipogenesis, fibrogenesis is very active during the fetal stage, during which generates connective tissue. The presence of connective tissue, primarily in the form of collagen fibrils, contributes to the background toughness of meat. Therefore, we investigated the effect of maternal nutrition on molecular mechanisms governing the early commitment of mesenchymal stem cells to either myogenic or adipogenic-fibrogenic lineages in beef cattle fetuses. Twenty-three Nellore pregnant cows were randomly assigned into 2 feeding level groups where 12 cows were fed at 1.0 times the maintenance requirement (Control, C) and 11 cows were fed at 1.5

times the maintenance requirement (Obese, OB) to evaluate effects of maternal obesity on fetal skeletal muscle development. The mRNA expression of β-catenin ($P = 0.0844$), MyoD ($P = 0.5623$), myogenin ($P = 0.7048$), and the number of muscle cells ($P = 0.9032$) was not affected by maternal obesity. Conversely, mRNA expression of adipogenic markers ZfP423 ($P < 0.0001$), C/EBPα ($P = 0.0004$), and PPARγ ($P < 0.0001$) was enhanced by maternal obesity. Indeed, mRNA expression of fibrogenic markers TGFβ ($P < 0.0001$), collagen III ($P < 0.0001$), and collagen content ($P = 0.0032$) was enhanced in OB fetuses. These data show that maternal obesity enhances fibrogenesis and likely adipogenesis without compromise myogenesis in fetal skeletal muscle of cattle.

Key Words: development, muscle, Nellore

MULTIDISCIPLINARY AND INTERNATIONAL LEADERSHIP KEYNOTE (MILK) SYMPOSIUM: WATER: CONSIDERATION FOR THE FUTURE OF ANIMAL AND FOOD PRODUCTION AND PROCESSING

0430 Drought: Lessons to learn in agriculture.
K. Matthews*, *ERS-USDA, Washington, DC.*

Drought impacts vary by commodity and region. Drought in 2012 was the most widespread since 1934. Drought has been pervasive in the West and Southern Plains since 2000, while the Midwest has experienced only 3 years of widespread drought in the same period. Most market participants are adversely affected by drought. Drought-reduced yields for commodities often result in higher prices, but higher prices may not offset lower yields and higher costs, so producer profit margins can be adversely affected. Consumers face higher prices for affected commodities and likely higher prices for substitutes for those commodities. Producers unaffected by drought are the only group who benefit from drought-reduced commodity supplies because they likely produce at least near-normal quantities of products and have access to higher prices for their products, which can boost their profit margins.

Key Words: drought, water, agriculture

0431 Water sources and chemical quality considerations for animal production and food processing.
A. M. Dietrich*, *Virginia Tech, Blacksburg.*

This presentation will focus on the varying qualities of water required for livestock consumption and food processing operations; also to be discussed are implications for changes to water quality due to natural situations (e.g., drought), engineered water treatment, and industrial activity. Quantity and quality of water are the most critical dietary elements for livestock as water directly or indirectly affects physiologic processes. Chemical water quality parameters that are important for livestock and food processing include presence of macrominerals (e.g., total dissolved solids, hardness, sodium, calcium, magnesium, chloride, nitrate, and sulfate), microminerals (iron, copper, manganese, chromium, arsenic), presence of toxic chemicals (e.g., pesticides or cyanotoxins), and whether the water is required to meet standards established by the USEPA for Primary and/or Secondary Maximum Contaminant Levels. How drinking water can enhance or exceed nutritional needs will be presented through comparison of nutritional requirements for livestock and the corresponding data and variability for specific chemical parameters in ground and surface waters. For example, the macronutrient sulfate and micronutrient iron can either negatively affect either livestock health or the taste of meat and milk. Sulfate and iron concentrations vary widely in drinking water due to local geology, as this controls which minerals are available to be dissolved into water. Another issue for livestock nutrition is its interplay with changing chemical water quality, as can be illustrated by total dissolved solids (TDS). Total dissolved solids is the composite measure of all dissolved minerals and organics in water; it is an indicator of overall water quality that is readily measured. Guidance for livestock is that TDS should be at or below 1000 mg/L, with an upper limit of 2500 mg/L, and although higher levels can be tolerated for drinking, about 3000 mg/L can cause diarrhea. Drought conditions increase TDS, both because there is insufficient water to dilute natural TDS and due to water evaporation. Total dissolved solids levels in the range of 3000 mg/L have occurred in the last few years and can negatively impact livestock health. Maintaining healthy livestock can be achieved through knowledge of which chemical parameters affect nutritional status, the natural occurrence of chemicals, plus regional and seasonal variability of water quality.

Key Words: water quality, nutrition, drinking water standards, minerals, livestock

0432 U.S. dairy water footprint in context.
Y. Wang*[1], A. D. Henderson[2], and O. Jolliet[3], *[1]Innovation Center for U.S. Dairy, Rosemont, IL, [2]University of Texas, Houston, [3]University of Michigan, Ann Arbor.*

Dairy production in the United States at the national scale is a distributed production system that entails great geographic diversity with respect to inputs and outputs. Milk therefore represents an interesting case study to develop and test spatialized life cycle approaches for both inventory and impact assessment. The study is to be used by the U.S. dairy industry to create a baseline of water footprint, helping that industry and its constituent milk producers to identify areas to target for improvement, explore the changes in impact associated with new management scenarios, and document those improvements. The result showed that water stress is 146 L in competition per 1 kg milk consumed, and 121 L in competition per 1 kg milk at farm gate (water consumption is 225 L per 1 kg milk consumed and 181 L of water consumed per 1 kg milk at farm gate).

Key Words: water footprint, spatialization, milk

0433 Rethinking the dairy supply chain: Innovative opportunities for creating value, efficiency, and sustainability.
R. T. Sirolli*, *Cargill Dairy Enterprise Group, Windsor, CO.*

In recent years, Consumer Packaged Goods (CPG) firms utilizing large volumes of dairy ingredients have ventured into new partnership models directly with dairy farms to address unmet needs relating to environmental sustainability, reducing market volatility, security of milk supply, improving the connectivity of consumers to dairy farms, and to create opportunities to en-

hance the value of the overall dairy supply chain. In the spring of 2012, the first model of this kind was implemented between a large dairy farm in Northwestern Kansas and a leading dairy CPG firm. To supply the desired products to the partnering CPG firm, the milk produced is initially processed directly on the farm. Three products are produced from the process, including heavy cream, condensed skim milk, and water. By creating a direct-supply model between the dairy farm and CPG firm, multiple opportunities are created to reduce environmental impact and improve water conservation. By removing water through a condensing process of whole milk, transportation required to move cream and condensed skim milk is reduced by > 75%. Approximately sixty thousand gallons of milk are produced per day, and of that, approximately forty thousand gallons of water are reclaimed for use on the farm. Western Kansas is an arid environment where water conservation is a critical component of the long-term sustainability of dairy production in the region. Water that is reclaimed is reused initially for watering cows or cleaning before eventually being irrigated on crops grown for feed. Water availability is one of the leading factors limiting dairy growth in the Western United States. Direct-supply models with on-farm milk condensing are growing in interest as a means of improving long-term sustainability of dairy production in arid environments, improving efficiency of the dairy supply chain, and creating opportunities for enhancing value for dairy farmers, CPG firms, and consumers.

Key Words: sustainability, water, dairy, milk

0434 Water usage at cattle feedlots and the potential for water conservation. K. D. Casey*[1], J. M. Sweeten[1], and R. Hagevoort[2], [1]*Texas A&M AgriLife Research, Amarillo,* [2]*New Mexico State University, Clovis.*

Water is increasingly valuable due to limited supply with declining aquifers and prolonged droughts, and higher water costs through infrastructure and energy costs. Environmental sustainability is an increasingly important issue for the general public, and the water use efficiency of industries is particularly topical during the current drought conditions. Water is an essential part of any beef feedlot or dairy operation. At beef cattle feedyards, fresh water is needed for cattle drinking, feed preparation, dust control, trough cleaning, system spillage, and staff amenities. While little potential exists to reduce genuine cattle water consumption, potential exists to reduce fresh water used to prevent troughs from freezing in winter and to control dust under dry conditions. Under summer conditions in the Texas High Plains, water use for dust control at feedyards has been measured at 8% of total fresh water use. Capture, treatment, and reuse of water from overflow waterers has been shown to be cost effective when compared with pumping extra fresh water. At dairies, fresh water is needed to water cows, cool cows and milk, flush alleyways, wash udders in wash pens, clean milking equipment, and increase feed moisture content. Similar to water intake requirements for cows, dairy operation water use can vary greatly depending on management practices, location, and the recycling of water on the dairy. Close attention to minimizing water wastage and a focus on reusing process water where possible can yield significant reductions in overall water use. On an open corral dairy and a freestall dairy on the Texas High Plains, monitoring on the overall facility water balance over 2 to 3 yr has shown that 30 to 40% of total fresh water usage is beneficially reused for irrigation.

Key Words: beef, water intake, reuse

NONRUMINANT NUTRITION: NUTRIENT REQUIREMENTS OF MONOGASTRICS AND AMINO ACID DIGESTIBILITY OF FEEDSTUFFS

0435 Determination of additivity of apparent and standard ileal digestibility of amino acids in different ingredients for mixed diets fed to growing pigs. P. Xue*, D. Ragland, and L. Adeola, *Purdue University, West Lafayette, IN.*

An experiment was conducted in growing pigs to investigate the additivity of apparent (AID) or standardized (SID) ileal digestibility of CP and AA in mixed diets based on multiple protein sources. Additivity refers to values calculated (predicted) from determined AID or SID of individual ingredients vs. measured values in mixed diets. Using the measured AID or SID for CP and AA in corn, soybean meal (SBM), corn distillers' dried grains with solubles (DDGS), or canola meal (CM), the AID or SID for 4 mixed diets based on corn-SBM (CS, 65% corn and 22% SBM), corn-SBM-DDGS (CSD, 57% corn, 17% SBM, and 11% DDGS), corn-SBM-CM (CSCM, 58% corn, 13% SBM, and 13% CM), or corn-SBM-DDGS-CM (CSDCM, 55% corn, 10% SBM, 10% DDGS, and 10% CM) were predicted and compared with measured AID or SID, respectively. *t* test was applied to test the difference between predicted and measured values. Eighteen pigs (initial BW = 61.3 ± 5.5 kg) were surgically fitted with T-cannula and assigned to a duplicated 9 × 4 incomplete Latin square design with 9 diets and 4 periods. The experimental diets consisted of 4 semipurified diets to determine the AID and SID in the 4 ingredients, 4 mixed diets, and a N-free diet. Chromic oxide was added as an indigestible marker. Pigs were fed 1 of the diets during each 7-d period, and the ileal digesta were collected on d 6 and 7, from 0800 to 1800. The results showed the predicted SID were consistent with determined values, except for Leu, Thr, Asp, Cys, Pro, and Ser, in CS diet; Met and Cys in CSD diet. The determined AID for total AA and 5 individual AA (Arg, His, Trp, Gly, and Pro) in CS diet were greater ($P < 0.05$) than predicted. For CSD diet, the determined AID were greater ($P < 0.05$) than predicted for CP, total AA, and all AA except for Arg, Leu, and Pro. In CSCM diet, the determined AID were greater ($P < 0.05$) than predicted for 3 AA (Arg, Cys, and Gly). When compared with determined values, predicted AID in CSDCM diet were lower ($P < 0.05$) for total AA and 4 AA (Arg, Met, Cys, and Pro). In conclusion, the results indicate that SID of AA are more consistent than AID for predicting ileal digestibility of AA in mixed diets containing multiple protein sources.

Key Words: additivity, amino acid, ileal digestibility

0436 Effects of dietary threonine:lysine ratio and sanitary conditions on performance and plasma urea nitrogen of weaned pigs fed antibiotic-free diets. B. Jayaraman*[1], J. K. Htoo[2], and C. M. Nyachoti[1], *[1]University of Manitoba, Winnipeg, Canada, [2]Evonik Industries AG, Hanau-Wolfgang, Germany*.

A growth trial was conducted to determine the optimum standardized ileal digestible (SID) Thr:Lys ratio for weaned piglets reared in clean or unclean sanitary conditions and fed antibiotic-free diets. Mixed-sex pigs (Duroc × [Yorkshire × Landrace]; average initial BW of 7.0 ± 0.5 kg) weaned at 21 ± 1 d were randomly assigned to 10 dietary treatments in a 2 × 5 factorial arrangement in a 42-d study giving 6 replicates (3 pigs per pen) per treatment. The main factors were sanitary conditions (clean, CL; unclean, UCL) and 5 dietary SID Thr:Lys ratios (55, 59, 63, 67, and 71%) in a completely randomized design. Diets were corn-wheat-soybean meal based with a constant SID Lys of 1.18% that was set to be seconding limiting AA. Pigs had ad libitum access to feed and water. For the first 21 d, CL group (90 piglets) were kept in a room that was disinfected before arrival of piglets and was cleaned weekly. The UCL group (90 piglets) followed immediately for the next 21 d in the same room. The UCL room was not disinfected and left uncleaned after CL group and manure from swine herd was added (5 kg per pen) to the pens on d 0 and d 7 of the experiment. Pigs and pen feed disappearance were recorded weekly to determine ADG, ADFI, and G:F. Blood samples were collected on d 0 and d 14 via jugular venipuncture for determination of plasma urea nitrogen (PUN). There were no significant interactions ($P > 0.05$) between sanitary conditions and dietary levels on any response criteria. Unclean conditions reduced ($P < 0.05$) ADG and ADFI throughout the experimental period, and tended to reduce ($P < 0.10$) G:F. The overall ADG was 494 vs. 404 g and ADFI was 736 vs. 579 g, for CL and UCL, respectively. Unclean group had significantly higher ($P < 0.05$) PUN (4.12 vs. 2.96) on d 14 compared with CL group. Increasing dietary SID Thr:Lys ratio had no effect on ADG and ADFI throughout the study; however, there was a linear trend ($P < 0.10$) in G:F showing that SID Thr:Lys of 71% improved G:F. The highest ADG was achieved at SID Thr:Lys of 71% for CL and 67% for UCL pigs, respectively. In conclusion, unclean conditions reduced ADG and ADFI in piglets, and increasing levels of SID Thr:Lys to 71% could improve G:F after weaning.

Key Words: threonine, sanitation, piglets

0437 Estimated lysine requirement of 25 to 50 kg growing gilts. J. K. Mathai* and H. H. Stein, *University of Illinois at Urbana-Champaign, Urbana.*

An experiment was conducted to determine the standardized ileal digestible (SID) Lys requirement of gilts (G-Performer × Fertilis 25) from 25 to 50 kg BW. Seventy gilts (G-Performer × Fertilis 25; initial BW: 24.54 ± 3.28 kg) were used in a growth

assay with 2 pigs per pen and 7 pens per treatment. Diets were formulated using corn and soybean meal as the sole sources of AA. Under the assumption that Lys is the first limiting AA in corn-soybean meal diets, soybean meal concentration was increased at the expense of corn to increase SID Lys in the diets. Five treatments with calculated SID Lys levels of 0.80, 0.93, 1.06, 1.19, and 1.32% were formulated using values from NRC (2012). Accuracy of diet formulations were confirmed by analyzing diets for total Lys. Daily feed allocations were recorded and individual pig weights were recorded at the beginning and at the conclusion of the experiment, 33 d later. Results indicated that ADG increased ($P < 0.05$) quadratically and G:F increased linearly ($P < 0.05$) as SID Lys increased from 0.80 to 1.32% (Table 0437). Broken-line and curvilinear-plateau regression analyses were used to estimate the requirement for SID Lys. Results indicated that 1.08% SID Lys was needed to maximize ADG and 1.10% SID Lys was needed to maximize G:F. Thus, results of this experiment indicate that the SID Lys requirement for 25- to 50-kg growing gilts is slightly greater than the recent estimate of 0.98% reported by NRC (2012). Under the conditions of this experiment, the requirement for SID Lys for 25 to 50 kg gilts is approximately 1.09%.

Key Words: amino acids, lysine requirement, pigs

Table 0437. Performance of pigs fed increasing levels of standardized ileal digestible Lys

	Standardized ileal digestible lysine, %					Contrasts (P-value)[1]	
	0.80	0.93	1.06	1.19	1.32	Linear	Quadratic
ADG, g	782	809	825	846	794	NS	0.03
ADFI, g	1758	1826	1738	1775	1658	NS	NS
G:F, g	432	444	462	465	467	< 0.01	NS

[1] NS indicates $P > 0.10$.

0438 Homocysteineinemia, growth performance, and immune responses in suckling and weanling piglets.

I. Audet, C. L. Girard, M. Lessard, L. Lo Verso, and J. J. Matte*, *Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada.*

Homocysteine, an intermediary sulfur AA, is recognized as a powerful pro-oxidant with deleterious effects on physiological and immune functions. In piglets, there is an acute 10-fold increase of plasma concentrations of homocysteine (PHcy) during the first 2 wk of life. This project aimed to create wide ranges of PHcy by varying folates and vitamin B_{12} (B_{12}) supplies to sows and piglets. Growth, immune response, and PHcy were studied until 56 d of age. Third-parity sows were randomly assigned to a 2 × 2 split-plot design with 2 dietary treatments (S) during gestation and lactation, S^- (1 mg/kg of folates and 20 μg/kg of B_{12}, $n = 15$) or S^+ (S^- × 10, $n = 16$), and 2 treatments to piglets (P) within each half-litter, i.m. injections (150 μg) of B_{12} (P^+) at d 1 and 21 (weaning), or sham-injections of saline (P^-). Within each litter of 12 piglets, 3 P^+ and 3 P^- were studied for growth, and the others for immunological responses. During lactation, the decrease of PHcy after i.m. B_{12} was more pronounced in S^- than S^+ piglets (S × P, $P < 0.02$), values were 32% lower in S^+P^+ (16.7 ± 0.7 μM) than S^-P^- piglets (24.7 ± 0.7 μ*M*) at 21 d of age. At 56 d of age, PHcy were lower ($P < 0.01$) for P^+ (15.7 ± 0.5 μ*M*) than P^- piglets (18.7 ± 0.5 μ*M*). No treatment effect was observed on growth except for a lower postweaning G:F in S^+P^- piglets than in others (S × P, $P = 0.03$). Positive correlations were observed between PHcy and growth ($r > 0.29$, $P < 0.02$). Antibody responses to ovalbumin were not affected by treatments. Proliferation of lymphocytes in response to the mitogen concanavalin A tended to be lower in culture media with sera from S^- piglets than S^+ ($P < 0.08$) and P^- piglets than P^+ ($P < 0.10$), and this response was more marked ($P = 0.04$) with high PHcy (> 21 μ*M*) as compared with medium (17 to 21 μ*M*) or low (< 17 μ*M*). In conclusion, vitamin supplementations to sows and piglets induced large variations of PHcy in piglets. Although apparently not harmful for growth performance, the detrimental effects of S^- and P^- treatments or high PHcy on some indicators of cell mediated immunity suggest that these young animals are immunologically more fragile.

Key Words: homocysteine, growth and immunity, piglets

439 Leucine supplementation of a restricted protein diet improves lean growth in neonatal pigs.

D. A. Columbus*[1], J. Steinhoff-Wagner[1], A. Suryawan[2], M. Kao[3], A. Hernandez-Garcia[1], C. Boutry[1], H. V. Nguyen[2], M. L. Fiorotto[1], and T. A. Davis[2], *[1]Children's Nutrition Research Center, Baylor College of Medicine, Houston, TX, [2]USDA/ARS–Children's Nutrition Research Center, Baylor College of Medicine, Houston, TX, [3]Neonatology, Baylor College of Medicine, Houston, TX.*

Early weaning of neonatal pigs frequently results in a reduction in food intake due to stress, environmental changes, and a shift from liquid to solid diet. In humans, many low birth weight infants also experience growth failure due to feeding intolerance, resulting in reduced nutrient intake. The branched-chain AA, leucine, has been shown to have anabolic effects on skeletal muscle. The objective of the study was to determine if prolonged enteral leucine supplementation improves lean growth in neonatal pigs fed a restricted protein diet. Five-day-old pigs ($N = 46$; 1.8 ± 0.3 kg initial BW) were fed by gastric catheter either a normal protein (NP; 22.5% protein, 2.4% leucine) or restricted protein (RP; 11.2% protein, 1.2% leucine) milk replacement diet or RP supplemented with leucine to the same level as in the NP diet (RPL). Pigs were fed 40 mL/kg BW per meal every 4 h for 21 d. Body composition was determined by dual-energy X-ray absorptiometry on d 0 and 20. Data were analyzed using the PROC MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). Feeding the NP diet resulted in greater total body weight (5.2 vs. 4.5 ± 0.20

kg) after 21 d and change in lean body mass (3.0 vs. 2.5 ± 0.17 kg) compared with RP-fed pigs ($P < 0.05$). Mass of the longissimus dorsi muscle (68 vs. 53 ± 4.2 g), heart (29 vs. 24 ± 1.2 g), and kidney (27 vs. 20 ± 2.1 g) were also greater in the NP- than RP-fed pigs ($P < 0.05$). Body weight (4.8 kg), lean body mass change (2.6 kg), and mass of the longissimus dorsi (61 g), heart (27 g), and kidney (23 g) in pigs fed the RPL diet were intermediate to the RP- and NP-fed pigs. Prolonged leucine supplementation of a restricted protein diet has the potential to improve overall growth in neonatal pigs and infants with restricted protein intake through an increase in lean tissue growth. *This project was supported by NIH HD072891 and USDA NIFA 2013–67015–20438.*

Key Words: protein, neonatal pig, body composition, lean growth, leucine

---

0440 Optimal sulfur amino acid to lysine ratio for weaned pigs fed antibiotic-free diets and raised under clean and unclean conditions.

R. K. Kahindi*[1], M. C. Nyachoti[1], and J. K. Htoo[2], [1]*University of Manitoba, Winnipeg, Canada,* [2]*Evonik Industries AG, Hanau-Wolfgang, Germany.*

Unsanitary production conditions can stimulate an immune response leading to increased sulfur amino acids (SAA) maintenance needs and consequently the SAA to Lys ratio, especially under antibiotic-free feeding regimen. Two 14-d experiments were conducted to determine the optimum SAA:Lys ratio in piglets when reared under clean or unclean condition and fed antibiotic-free diets. For each experiment, 90 mixed-sex pigs (Duroc × [Yorkshire × Landrace]; initial average BW of 7.3 ± 0.6 kg) weaned at 21 ± 1 d with 6 replicates of 3 pigs per pen were used. The basal diet was corn-wheat-soybean meal-based (1.18% SID Lys; 51% SID SAA:Lys). Diets 2 to 5 were the basal supplemented with 4 graded levels of DL-Met (55, 60, 64, and 68% SID SAA:Lys). Piglets were allowed free access to feed and water. In Exp. 1, piglets were raised in a clean room that was previously disinfected and washed weekly, whereas in Exp. 2, piglets were introduced into a room previously occupied by other pigs and was not disinfected. In addition, manure slurry from a sow herd was spread (5 kg per pen) on d 0 and 7 of the study and the room was not cleaned throughout the study. Blood was collected on d 0 and 14 for measurement of plasma urea nitrogen (PUN). On d 14, one pig per pen was slaughtered to collect jejunal tissue for measurement of villus height (VH), crypt depth (CD), and VH:CD. In both experiments, quadratic broken-line model was used to estimate optimum SAA:Lys ratio. The highest average daily gain was at SAA:Lys ratio of 60% (279 g) in Exp. 1 and 64% (305 g) in Exp. 2. Increasing SAA:Lys ratio linearly and quadratically increased ($P < 0.05$) VH and VH:CD in Exp. 1 and 2. In Exp. 2, increasing SAA:Lys ratio linearly reduced ($P < 0.05$) by 18% average daily feed intake and linearly and quadratically decreased PUN. Based on performance parameters, the optimum SAA:Lys ratio was 62 and 61% for piglets raised under clean and unclean conditions, respectively. However, VH and VH:CD estimates were 60 and 64% SAA:Lys ratio under clean and unclean conditions, respectively. Hence, SAA:Lys ratio for gut health was higher under unclean conditions.

Key Words: pigs, sanitation, sulfur amino acids

0441 Energy concentration and amino acid digestibility in two sources of canola meal fed to growing pigs.

N. W. Jaworski*, Y. Liu, and H. H. Stein, *University of Illinois at Urbana-Champaign, Urbana.*

Two experiments were conducted to determine DE and ME and standardized ileal digestibility (SID) of CP and AA by growing pigs in a novel canola meal (CM-HP) produced from high protein canola seeds and to compare these values with DE, ME, and SID values determined in conventional canola meal (CM-CV) and soybean meal (SBM). In Exp. 1, 32 growing barrows (initial BW: 47.25 ± 6.23 kg) were individually housed in metabolism cages and randomly assigned to 4 treatments in a randomized complete block design with 8 replicates per treatment. The 4 diets included a corn-based basal diet and 3 diets formulated by mixing corn and each source of canola meal or SBM. Fecal and urine samples were collected for 5 d following a 5-d adaptation period. The DE and ME in CM-HP, CM-CV, and SBM were calculated using the difference procedure. Concentrations of DE and ME in CM-HP and CM-CV were less ($P < 0.05$) than in corn and SBM (DE: 3419 and 3104 vs. 4012 and 4305 kcal/kg DM, respectively; ME: 2842 and 2720 vs. 3854 and 3894 kcal/kg DM, respectively). No differences in concentrations of DE and ME were observed between CM-HP and CM-CV. In Exp. 2, 8 growing barrows (initial BW: 46.4 ± 5.6 kg) had a T-cannula installed in the distal ileum and randomly allotted to a replicated 4 × 4 Latin square design, with 4 diets and four 7-d periods in each square. Three diets that contained CM-HP, CM-CV, or SBM as the sole source of CP and AA were formulated, and a N-free diet was also used. Ileal digesta were collected on d 6 and 7 of each period. The SID of CP and most AA in CM-HP and CM-CV were less ($P < 0.05$) than in SBM. The SID of CP in CM-HP was greater ($P < 0.05$) than in CM-CV. However, no differences were observed in SID of any AA between CM-HP and CM-CV. The concentration of standardized ileal digestible CP and almost all AA was greater ($P < 0.05$) in SBM than in CM-HP and CM-CV, and CM-HP contained more ($P < 0.05$) standardized ileal digestible CP and AA than CM-CV. In conclusion, increased concentration of CP in canola meal does not compromise the DE and ME and the AID or SID of AA. The novel CM-HP supplies more digestible AA than CM-CV.

Key Words: amino acid digestibility, canola meal, energy concentration

0442 Amino acid digestibility in processed soybean products and rapeseed products fed to weanling pigs. D. M. D. L. Navarro*[1], Y. Liu[1], T. S. Bruun[2], and H. H. Stein[1], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]Danish Pig Research Centre, Copenhagen, Denmark.*

An experiment was conducted to determine the standardized ileal digestibility (SID) of CP and AA in 4 sources of processed soybean meal, in conventional soybean meal (SBM-CV), in rapeseed expellers (RSE), and in a fermented co-product mixture (FCM) that contained rapeseed meal, wheat, soy molasses, and potato peel. The 4 processed soybean products included 2 sources of enzyme-treated soybean meal (ESBM-1 and ESBM-2), extruded soybean meal (SBM-EX), and soy protein concentrate (SPC). A N-free diet and 7 cornstarch-based diets that contained each of the 7 protein sources as the sole source of CP and AA were prepared. Twenty-seven ileal-cannulated weanling barrows (initial BW: 9.29 ± 0.58 kg) were allotted to three 9 × 5 Youden squares with 9 pigs and 5 periods in each square. In each square, 7 pigs were each fed 1 of the 7 AA-containing diets and 2 pigs were fed the N-free diet. Results indicated that the SID of CP was greater ($P < 0.05$) in ESBM-1 than in SPC, RSE, and FCM. The SID of Arg, His, Ile, Leu, Met, and Phe were greater ($P < 0.05$) in ESBM-1 than in SPC, and the SID of Lys was greater ($P < 0.05$) in SBM-CV than in ESBM-2. The SID of Thr, Trp, Val and total indispensable AA were not different among the soybean products. The SID of most AA in RSE and the SID of all AA in FCM were less ($P < 0.05$) than in all soybean products, but the SID of all AA in RSE was greater ($P < 0.05$) than in FCM. Results of this experiment indicate that, although processing of soybean meal results in increased concentration of CP, processing may also reduce the digestibility of some AA, which is likely due to heat damage during processing. There are, however, differences among processed soy products, with some products having greater SID of AA than others. Results also indicate that fermentation of a mixture of rapeseed meal, wheat, and relatively low quality co-products does not result in SID values that are similar to those of unfermented rapeseed expellers or soybean products.

Key Words: amino acid digestibility, soybean products, rapeseed products

0443 Standardized ileal crude protein and amino acid digestibility of eight wheat genotypes fed to growing pigs. P. Rosenfelder*[1], H. K. Spindler[1], K. E. B. Knudsen[2], H. Jørgensen[2], N. Sauer[1,3], J. K. Htoo[4], M. Eklund[1], and R. Mosenthin[1], *[1]University of Hohenheim, Institute of Animal Nutrition, Stuttgart, Germany, [2]Aarhus University, Department of Animal Science, Tjele, Denmark, [3]Landwirtschaftliche Untersuchungs- und Forschungsanstalt Speyer, Speyer, Germany, [4]Evonik Industries AG, Hanau-Wolfgang, Germany.*

The objective of this study was to determine in growing pigs the standardized ileal digestibility (SID) of CP and AA of 8 currently available wheat genotypes grown in Southern Germany under standardized field test conditions. The assay diets were formulated to contain 1 of the 8 wheat genotypes each, with wheat as the sole dietary source of CP and AA. All diets were supplemented with 0.7% titanium oxide as an indigestible marker. Nine ileal cannulated barrows (32 ± 2 kg BW) were fed 8 diets in 8 periods of 6 d each at a daily intake level of 40 g/kg of their average BW, corresponding to about 3 times the animals' energy requirement for maintenance (106 kcal of ME/kg of $BW^{0.75}$). The SID of the 8 wheat genotypes was calculated using literature data for correction of basal ileal endogenous losses of CP and AA. Data were analyzed using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) with genotype and pig as fixed effects, and periods and pigs as random effects. Effects of chemical composition of the wheat genotypes on SID of CP and AA in the wheat genotypes were analyzed by linear regression analyses. Among proximate nutrients, only small differences in DM, crude ash, and ether extract content were observed between the 8 different wheat genotypes. On as-fed basis, concentrations of CP and starch ranged from 10.9 to 13.3 and 61.5 to 64.4% in the 8 wheat genotypes, respectively. The greatest concentrations of NDF and ADF were 11.6 and 3.3% (as-fed), respectively, whereas ADL concentration did not exceed 0.7% (as-fed) in the 8 wheat genotypes. Among the 8 wheat genotypes, SID of CP, Lys, Met, Thr, and Trp ranged from 83 to 87% ($P = 0.010$), 69 to 74 ($P = 0.037$), 84 to 88 ($P = 0.010$), 78 to 82 ($P = 0.053$), and 80 to 85% ($P = 0.005$), respectively. Fiber fractions and CP contents in the 8 wheat genotypes had minor effects on SID of CP, Lys, Met, Thr, and Trp. Moreover, SID of CP, Lys, Met, Thr, and Trp of this study were up to 5, 15, 6, 8, and 8% lower when compared with current feed tables. Due to the observed variations in SID of CP and AA between wheat genotypes in the present study, differences in SID between different batches of wheat should be taken into account for pig diet formulations.

Key Words: digestibility, pig, wheat

0444 Standardized ileal amino acid digestibility in eight genotypes of rye fed to growing pigs.
E. J. P. Strang*[1], M. Eklund[1], P. Rosenfelder[1], H. K. Spindler[1], N. Sauer[1,2], J. K. Htoo[3], and R. Mosenthin[1], *[1]University of Hohenheim, Institute of Animal Nutrition, Stuttgart, Germany, [2]Landwirtschaftliche Untersuchungs- und Forschungsanstalt Speyer, Speyer, Germany, [3]Evonik Industries AG, Hanau-Wolfgang, Germany.*

A study was conducted to determine in growing pigs the standardized ileal digestibility (SID) of CP and AA in 8 currently available genotypes of rye. The rye genotypes were grown under the same standardized field conditions at the University of Hohenheim, Germany. The experiment was conducted with 8 barrows with an initial BW of 24 ± 2 kg, and fitted with a simple T-cannula at the distal ileum. The pigs were randomly allotted to an 8 × 8 Latin square design. Diets were based on 1 of the 8 rye genotypes each, with rye as the sole source of CP and AA. An N-free diet was fed to determine basal ileal endogenous losses of CP and AA in an additional period at the conclusion of the experiment. Diets were supplemented with titanium dioxide as digestible marker and fed at a daily intake level of 40 g/kg of pigs' average BW corresponding to about 3 times the pigs' energy requirement for maintenance (106 kcal of ME/kg of $BW^{0.75}$). Each experimental period consisted of 4 d for adaptation to the diets and 2 d for ileal digesta collection. Ileal digesta samples were collected consecutively for a total of 24 h. Data were analyzed by the Mixed Procedure of SAS (SAS Inst. Inc., Cary, NC) with genotype and pig as fixed effects, and pigs and periods as random effects. The CP and nonstarch polysaccharides (NSP) concentrations (as-fed) in the 8 rye genotypes ranged from 9.5 to 11.2%, and 10.7 to 12.9%, respectively. The greatest concentrations of NDF, ADF, and ADL were 15.1, 3.0, and 0.9% (as-fed) in the 8 rye genotypes. Among the 8 rye genotypes, SID of CP, Lys, Met, Thr, and Trp ranged from 70 to 74, 60 to 65, 74 to 78, 62 to 66, and 63 to 67%, respectively. The SID of CP and AA did not differ between the 8 rye genotypes, except for SID of Cys ($P = 0.044$). The SID of CP and AA were not affected by NSP and NDF content. Overall, SID of CP, Lys, Met, Thr, and Trp in rye derived from the present study were up to 13, 14, 7, 12, and 13%-units lower than the values reported in current feed tables. Using these SID values will aid for accurate AA balancing when these new rye genotypes are used in pig diet formulations.

Key Words: amino acid digestibility, growing pigs, rye

0445 Digestible phosphorus requirement of twenty-kilogram pigs—A cooperative study.
O. Adeola*[1], M. J. Azain[2], S. D. Carter[3], T. D. Crenshaw[4], M. J. Estienne[5], B. J. Kerr[6], M. D. Lindemann[7], C. V. Maxwell[8], P. S. Miller[9], M. C. Shannon[10], E. van Heugten[11], and NCCC-042 and S-1061[12], *[1]Purdue University, West Lafayette, IN, [2]University of Georgia, Athens, [3]Oklahoma State University, Stillwater, [4]University of Wisconsin, Madison, [5]Virginia Tech Tidewater AREC, Suffolk, [6]USDA-ARS, Ames, IA, [7]University of Kentucky, Lexington, [8]Department of Animal Science, University of Arkansas Division of Agriculture, Fayetteville, [9]University of Nebraska, Lincoln, [10]University of Missouri-Columbia, Columbia, [11]North Carolina State University, Raleigh, [12]Swine Nutrition Committee and Nutritional Systems for Swine to Increase Reproductive Efficiency Committee, West Lafayette, IN.*

A 28-d cooperative study involving 10 experiment stations was conducted to determine the standardized total-tract digestible (STTD) P requirement of 20-kg pigs using broken-line regression analysis. Six concentrations of STTD P were fed to 1032 pigs with an average initial BW of 19 kg in 240 pens (120 each of barrows and gilts). Monocalcium phosphate was added to a corn-soybean meal-based diet at the expense of cornstarch to establish the 6 concentrations of STTD P, ranging from 1.54 to 5.15 g/kg of diet, in increments of 0.62 g/kg. Limestone was added to maintain a constant Ca:total P at 1.5:1.0 among all diets. Average daily gain, ADFI, and G:F increased ($P < 0.05$) with increasing STTD P concentration for d 0 to 14, 14 to 28, and 0 to 28. From d 0 to 28, ADG and G:F increased ($P < 0.01$) from 639 to 809 g and 492 to 561 g/kg, respectively, as STTD P increased from 1.54 to 5.15 g/kg of diet. Barrows gained and ate more ($P < 0.05$) than gilts during d 14 to 28 and d 0 to 28. There was no interaction between gender and STTD P concentration for any of the growth performance response criteria. Metacarpal bone ash, Ca, and P increased ($P < 0.01$) from 45.6 to 52.6%, 17.6 to 19.9%, and 8.0 to 9.6%, respectively, with increasing STTD P concentration. Furthermore, Ca and P in metacarpal ash, as well as metacarpal and femur mineral density and content increased ($P < 0.01$) with increasing STTD P concentration. The STTD P requirement determined by broken-line regression using ADG as a response variable was estimated to be 4.21, 3.45, and 3.87 g/kg of diet for pigs from d 0 to 14 (19 to 28 kg BW), d 14 to 28 (28 to 40 kg BW), and d 0 to 28 (19 to 40 kg BW), respectively. Using G:F, the corresponding estimates of STTD P requirement were 4.34, 3.71, and 4.06 g/kg of diet. The STTD P requirement (g/kg of diet) using mineralization response for metacarpus and femur ranged from 3.50 for P in metacarpal ash to 4.28 for femur mineral density. Using an average of the estimates derived from ADG and G:F,

the mean STTD P requirement of pigs from 20 to 40 kg was determined to be 3.97 g/kg of diet.

Key Words: phosphorus, pigs, standardized total tract digestible, requirement

---

0446 The flow of inositol phosphate esters and phytate phosphorus in the proximal and distal parts of the digestive tract of broilers receiving diets adequate in available phosphorus and supplemented with high levels of phytase. L. A. Beeson*[1], C. L. Walk[2], and O. Olukosi[1], *[1]SRUC, Ayr, UK, [2]AB Vista Feed Ingredients, Marlborough, UK.*

The aim of this study was to characterize the flow of inositol phosphate (iP) esters and disappearance of phytate phosphorus (PP) in the gizzard and ileum of broilers receiving diets adequate in available phosphorus (aP) and supplemented with high levels of phytase. One-hundred-and-sixty-eight Ross 308 broilers at 1 d of age were allocated to 3 treatments (0, 1500, and 3000 FTU/kg phytase) in a randomized complete block design, where the pen was the experimental unit (6 birds per pen). Feed and water were provided ad libitum, and digesta from the gizzard and ileum were collected on d 21 and analysed for iPs and PP relative to TiO_2, the indigestible marker used. In the gizzard, iP6 and iP5 levels were lower ($P < 0.01$) and inositol higher ($P < 0.01$) in the diet supplemented with 1500 or 3000 FTU/kg phytase compared with the control. In the ileum, supplementation with 1500 or 3000 FTU/kg reduced levels of iP6 (3115, 3552, nmol, for 1500, 3000 FTU/kg respectively, $P < 0.01$) and increased that of iP4 and inositol (3115, 3552, nmol for 1500, 3000 FTU/kg, respectively, $P < 0.05$) compared with broilers fed the control diet (482 iP6, 1650 inositol), except for iP5 which was greater ($P < 0.01$) in control and with 1500 FTU/kg phytase compared with 3000 FTU/kg. There were no phytase effects on IP3 flow. In the gizzard, PP disappearance was greater ($P < 0.01$) in diets supplemented with 1500 or 3000 FTU/kg compared with control diet. No differences were seen in ileal PP disappearance between the control and diet supplemented with 1500 FTU/kg, or between supplementation of 1500 and 3000 FTU/kg; however, PP disappearance was greater in ($P < 0.01$) diets with 3000 FTU/kg than control. Total tract PP disappearance was greater ($P < 0.05$) in diets supplemented with 1500 or 3000 FTU/kg (74.5, 85.5%, respectively) than in the control diet (60.3%). The results show that the phytase rapidly hydrolysed iP6 and iP5 in the gizzard, leading to an accumulation of inositol, and the hydrolysis continued in the distal gut. It is concluded that the phytase was effective in rapidly hydrolysing phytate, releasing free inositol even in the gizzard and that higher phytase doses may lead to further phytate phosphorus hydrolysis in the ileum.

Key Words: phytase, inositol phosphate esters, phytate phosphorus

NONRUMINANT NUTRITION: NUTRIENT DIGESTIBILITY OF INGREDIENTS FOR MONOGASTRIC DIETS

0447 Digestible, metabolizable, and net energy in diets containing 0, 15, or 30% wheat bran fed to growing pigs. N. W. Jaworski*[1], D. Liu[2], D. Li[3], and H. H. Stein[1], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]State Key Lab of Animal Nutrition, China Agricultural University, Beijing, [3]Ministry of Agriculture Feed Industry Centre, Beijing, China.*

An experiment was conducted to determine the effects of including 0, 15, or 30% wheat bran in a corn-soybean meal based diet fed to growing pigs. Eighteen barrows (initial BW: 54.4 ± 4.3 kg) were individually housed in metabolism cages and randomly allotted to 1 of 3 dietary treatments in a completely randomized design. The experiment had 3 periods and 6 replicate pigs per diet. The control diet contained corn, soybean meal, and no wheat bran, and 2 additional diets were formulated by mixing 15 or 30% wheat bran with 85 or 70% of the control diet, respectively. Each period lasted 15 d. During the initial 7 d, pigs were adapted to their experimental diets and housed in metabolism crates in an environmentally controlled room and fed 573 kcal/kg $BW^{0.6}$ per d. On d 8, metabolism crates with the pigs were moved into open-circuit respiration chambers for measurement of O_2 consumption and CO_2 and CH_4 production. The feeding level was the same as in the adaptation period and feces and urine were also collected during this period. On d 13 and 14, pigs were fed 225 kcal/kg $BW^{0.6}$ per day, and pigs were then fasted for 24 h to obtain fasting heat production. The apparent total tract digestibility of DM, GE, crude fiber, ADF, and NDF linearly decreased ($P < 0.01$) as wheat bran inclusion increased in the diets. The DE (3454, 3257, and 3161 kcal/kg), ME (3400, 3209, and 3091 kcal/kg), and NE (1808, 1575, and 1458 kcal/kg) of diets linearly decreased ($P < 0.01$) as wheat bran inclusion increased. The daily O_2 consumption and CO_2 and CH_4 production by pigs fed increasing concentrations of wheat bran linearly decreased ($P < 0.01$). However, there was no effect of wheat bran on daily heat production per kg $BW^{0.6}$. In conclusion, increasing inclusion of wheat bran decreased DE, ME, and NE in diets, but did not change daily heat production if expressed as kg $BW^{0.6}$.

Key Words: dietary fiber, energy concentration, heat production

0448 Effects of feeding barley on growth performance and diet nutrient digestibility of weaned pigs. Z. Nasir*[1], M. G. Young[2], M. L. Swift[3], E. Beltranena[4], and R. T. Zijlstra[1], *[1]University of Alberta, Edmonton, Canada, [2]Gowans Feed Consulting, Wainwright, AB, Canada, [3]Alberta Agriculture and Rural Development, Lethbridge, Canada, [4]Alberta Agriculture and Rural Development, Edmonton, Canada.*

Cereal grains vary considerably in price and quality. Barley is usually priced 10 to 20% lower than wheat in Western Canada. Wheat contains more NE than barley and is preferred during the energy-dependent phase of growth. We investigated if feeding of low quality barley (LB) will reduce growth performance and diet apparent total tract digestibility (ATTD) in weaned pigs compared with high quality barley (HB) or hard red spring wheat. Diets contained 20% soybean meal and 62% cereal grain varying in NE (Mcal/kg) content (2.33, 2.23, and 2.44 for HB, LB, and wheat, respectively). Grain constituents used to predict the NE value were predicted by near-infrared reflectance spectroscopy. Starting 1 wk after weaning at 28 d of age, 280 weaned pigs (initial BW 8.7 ± 0.9 kg) were fed diets for 3 wk (d 1 to 21). Five pelleted diets were formulated as (Mcal NE/kg using canola oil; g standardized ileal digestible (SID) Lys/Mcal NE using synthetic AA): (A) wheat (2.39, 4.47); (B) HB (2.39, 4.46); (C) LB (2.33, 4.57); (D) LB, corrected for NE (2.39, 4.45); and (E) LB, low NE (2.25, 4.68). Feed intake and BW were measured weekly to calculate pen ADFI, ADG, and G:F. Feces were collected to calculate diet ATTD of DM, GE, and CP and diet DE and NE value. Compared with Diet A and B, pigs fed Diet D had greater ($P < 0.05$) ADFI (542, 596 vs. 652 g/d), ADG (365, 403 vs. 443 g/d), and G:F (0.646, 0.662 vs. 0.681); while differences were not observed among diets C, D, and E. Pigs fed Diet A had ADFI and ADG lower ($P < 0.05$) than pigs fed the other 4 diets. The ATTD of CP, GE, and DM of Diet E (77.0, 77.3, 76.9%) was greater ($P < 0.05$) than of Diet B (72.4, 74.3, 74.0%) and C (74.9, 75.3, 74.7%), and similar to Diet D (75.9, 76.4, 75.8%), respectively. Pigs fed Diet A had ATTD of GE greater ($P < 0.05$) than pigs fed other 4 diets. The DE value (Mcal/kg) of diet D (3.62) and E (3.55) were greater ($P < 0.05$) than of diet B (3.46) and lower than of diet A (3.71). In conclusion, feeding LB instead of HB and wheat did not reduce growth performance. Feeding barley instead of wheat is economical and achieved greater growth performance even though diet energy digestibility was lower.

Key Words: barley, pig, digestibility

0449 Nutrient profile and in-vitro digestibility of tubers in swine. U. P. Tiwari*, A. K. Singh, H. M. Zaleski, and R. Jha, *University of Hawaii at Manoa, Honolulu.*

To assure the sustainability of swine production in areas where traditional feed ingredients cannot be grown or fed to animals, it is important to study and develop alternative feeding systems. Tubers are grown widely in the tropics and are generally rich in starch, and thus have potential as an alternative energy source. Their use, however, is limited by limited information on nutritional value and digestibility. Five tuber samples grown in Hawaii [purple sweet potato (PSP), Okinawan sweet potato (OSP), *Dioscorea alata* yam (yam), taro, and cassava] were analyzed for their nutritional profile. In vitro digestibility of samples was determined using a 3-step enzymatic assay. On a DM basis, gross energy ranged from 3332 Kcal/kg (taro) to 4272 (yam), sweet potatoes and cassava were in between (PSP = 4137, OSP = 4157, and cassava = 4196 Kcal/kg). The CP content ranged from 3.4% (cassava) to 13.6 (taro), ether extract from 2.8% (PSP) to 14.5 (cassava), ADF from 5.7% (PSP) to 10.4 (taro), NDF from 8.0% (PSP) to 11.5 (taro), ash from 2.0% (PSP) to 3.8 (taro), and in vitro DM digestibility of PSP (87.4%), OSP (87.1%), and cassava (82.3%) was significantly higher ($P < 0.05$) than yam (30.0%), while taro was in between (66.0%). In conclusion, both sweet potato and cassava are rich in energy content with high in vitro DM digestibility and can be used as an alternative source of energy in swine diets, but protein needs to be supplemented as these tubers are low in protein.

Key Words: in vitro digestibility, tubers, swine

0450 Nutritional enhancement of dried distiller's grains with solubles via *Sporobolomyces roseus* fermentation. J. M. Wilson*, *Kansas State University, Manhattan.*

Whole stillage and thin stillage from the ethanol production process were evaluated as substrate sources for the production of β-carotenes by *Sporobolomyces Roseus* (ATCC28988). This product has the potential to be used as a novel feed ingredient for poultry, swine or cattle diets. β-carotenes have been supplemented in animal diets, typically from 150 to 300 mg/kg to improve animal health, enhance meat color and quality, and increase vitamin A levels in milk and meat. By supplementing a stillage fermentation with easily consumable carbon sources and protein sources the fermentation lag time will be reduced and the protein levels of the resultant product will be unaffected or increased. Microbial growth kinetics and stillage fermentations were performed in 500-mL baffled shake flasks and in a 5-L fermentation bioreactor. The HPLC method was used to analyze and quantify the β-carotenes. A 50-L bioreactor has been specifically designed to evaluate the scalability of the process and to perform subsequent feed production trails. Media optimization was conducted in shake flasks using supplemented glucose or glycerol and ammonium sulfate or urea. By supplementing the fermentation with additional protein sources which are easily consumed by the microbes, such as urea, the protein level of the resultant feed ingredient would be unaffected. Final β-carotene concentration was found to be highest for the whole stillage, with 10 g/L added glucose and 10 g/L N added through ammonium sulfate, at 272.57 ± 4.34 μg β-carotene/g biomass. Glycerol addition yielded no significant increase ($P > 0.05$) in β-carotene yield, while urea addition significantly decreased ($P > 0.05$) the final β-carotene concentrations. The resulting fermented product can be effectively blended with regular feed to generate a premium nutritionally enhanced feed product using either whole stillage as a dry feed ingredient or thin stillage as a liquid feed additive.

Key Words: β carotene, DDGS, feed, fermentation

0451 Performance of pigs fed diets containing canola meal produced from high protein or conventional varieties of canola seeds. Y. Liu*, T. Maison, and H. H. Stein, *University of Illinois at Urbana-Champaign, Urbana.*

Two experiments were conducted to determine effects of including high protein canola meal (CM-HP) or conventional canola meal (CM-CV) in diets fed to weanling pigs or growing-finishing pigs. In Exp. 1, 405 weanling pigs (10.07 ± 1.41 kg) were randomly allotted to 9 dietary treatments, with 9 replicate pens per treatment and 4 to 6 pigs per pen. Nine diets were prepared with the control diet being based on corn and soybean meal (SBM) and 8 diets were formulated by adding 10, 20, 30, or 40% of either CM-HP or CM-CV to the control diet. The experiment lasted 21 d. Increased inclusion rate of CM-CV increased (quadratic, $P < 0.05$) ADG of weanling pigs. Increased inclusion rate of CM-HP or CM-CV decreased (linear, $P < 0.05$) ADFI, but increased (linear, $P < 0.05$) G:F of weanling pigs. Weanling pigs fed CM-CV had greater ($P < 0.05$) ADG and G:F than weanling pigs fed CM-HP. In Exp. 2, 280 pigs (27.4 ± 2.92 kg) were randomly allotted to 7 dietary treatments. A 3-phase feeding program was used with grower diets fed from 27 to 57 kg, finisher-1 diets from 57 to 85 kg, and finisher-2 diets from 85 to 112 kg. The 7 treatments consisted of a corn-SBM diet (control) and 6 diets containing a low, medium, or high level of either CM-HP or CM-CV. Low, medium, and high levels of canola meal were defined as the levels needed to replace 33, 66, or 100% of SBM in the diets. Increased inclusion rate of CM-HP decreased (linear, $P < 0.05$) pig BW at the end of phase 2 and at the end of the experiment, decreased (linear, $P < 0.05$) G:F in Phase 2 and the overall period, and decreased (quadratic, $P < 0.05$) ADG in Phase 3. Increased inclusion rate of CM-CV increased (linear, $P < 0.05$) ADFI, but reduced (linear, $P < 0.05$) G:F in Phases 2 and 3 and for the overall period. Growing-finishing pigs fed CM-CV had greater ($P < 0.05$) ADG and ADFI than pigs fed CM-HP. In conclusion, inclusion of 20 to 30% CM-HP or CM-CV have no negative effects on growth performance

of weanling pigs and CM-CV and CM-HP may replace up to 66% of the SBM in diets for growing-finishing pigs.

Key Words: canola meal, high protein canola meal, pigs

0452 Physiochemical and nutritional composition of sorghum as potential food and feed for humans and poultry. M. Mabelebele*[1,2] and P. Iji[2], [1]*University of Limpopo, Polokwane, South Africa,* [2]*University of New England, Armidale, Australia.*

Sorghum is the fifth most important grain crop after wheat, rice, maize, and barley. Sorghum is cultivated for food and beverages for humans, and for feed and fodder for animals in America, Asia, Australia, and Africa. Physical characteristics, proximate composition, total phenols and antioxidant activity, mineral content, and AA profile of sorghum were studied. Forty-eight (± 2.5 kg) adult male broiler chickens were allocated to a complete randomized design with 4 sorghum diets to determine AA digestibility and metabolizable energy. Twelve birds per diet were starved for 24 h before receiving feed allowance of 50 g. Thousand-kernel weights ranged from 33 to 28 g, with brown visual colour and texture that is somewhat corneous to floury. The sorghum grains were higher ($P < 0.05$) in total phenolic and condensed tannins contents for NS5511 and PAN8625. The antioxidant activity of sorghum varieties PAN8816 and PAN8609 were higher ($P < 0.05$) than NS5511 and PAN8625. Crude protein content of PAN8609 (9.54%) and PAN8625 (9.53%) were higher ($P < 0.05$) than those of NS5511 (8.12%) and PAN8816 (8.45%). Starch (%) and GE (MJ/kg) contents differed among sorghum varieties. Mg (mg/kg) content was significantly higher ($P < 0.05$) for PAN8625 than that of NS5511. P and Zn (mg/kg) contents of PAN8609 were higher ($P < 0.05$) than those of PAN8625, NS5511, and PAN8816. Similarly, PAN8625 had higher ($P < 0.05$) P and Zn contents than those of NS5511 and PAN8816. Thr, Leu, Phe, Val, Pro, and Ala contents of varieties PAN8625 and PAN8609 were ($P < 0.05$) higher than those of NS5511 and PAN8816, which had similar ($P > 0.05$) contents. Sorghum NS5511 had low AA digestibility values for Arg, His, Phe, Thr, and Try. Apparent metabolizable energy corrected for nitrogen (AMEn) was the highest ($P < 0.05$) for PAN8816, followed by PAN8609 with lowest value for NS5511. True metabolizable energy corrected for nitrogen (TMEn) values were similar ($P > 0.05$) for PAN8816 and PAN8609, and low in NS5511.

Key Words: sorghum, total phenols, antioxidant activity, amino acid profile, minerals

0453 Comparative digestibility of energy and nutrients in feed ingredients fed to sows and growing pigs. J. E. Lowell*, Y. Liu, and H. H. Stein, *University of Illinois at Urbana-Champaign, Urbana.*

The objective of this experiment was to determine if there is a difference between growing pigs and gestating sows in DE and ME values and apparent total tract digestibility (ATTD) of energy and nutrients in diets and feed ingredients. Eleven feed ingredients were used. Three ingredients were cereal grains (corn, sorghum, and wheat), 4 were common protein sources (soybean meal, canola meal, distillers dried grains with solubles [DDGS], and low-fat DDGS), and 4 were high-fiber ingredients (corn germ meal, corn bran, wheat middlings, and soybean hulls). Eleven diets were formulated. Three diets were based on corn, wheat, or sorghum, and 8 diets were based on a combination of corn and each of the remaining 8 ingredients. A total of 88 gestating sows (parity 2 to 6) and 88 growing barrows (40.1 ± 4.69 kg BW) were randomly allotted to the 11 diets, with 8 replicate animals per diet. Fecal and urine samples were collected for 4 d following a 5-d adaptation period. The DE, ME, and ATTD of ADF, NDF, and CP in corn, wheat, and sorghum were calculated using the direct procedure, and the DE, ME, and ATTD of ADF, NDF, and CP in the other ingredients were calculated using the difference procedure. No differences were observed in DE and ME (as-fed and DM basis) or in the ATTD of GE, NDF, and CP between gestating sows and growing pigs for any of the ingredients. Gestating sows had less ($P < 0.05$) ATTD of ADF for soybean meal and greater ($P < 0.05$) ATTD of NDF for soybean hulls compared with growing pigs, but for the average of all ingredients, gestating sows had reduced ($P < 0.05$) ATTD of ADF compared with growing pigs. These results indicate that, under the conditions of this experiment, the ATTD of CP, NDF, and GE and values for DE and ME in growing pigs are not different from values obtained in gestating sows. However, the ATTD of ADF obtained in growing pigs is not always representative of the ATTD of ADF in gestating sows.

Key Words: digestibility, gestating sows, growing pigs

0454 Performance and nutrient digestibility of weaned rabbits fed cooked albizia seed meal (*Albizia* spp.) as replacement for full-fat soybean meal. A. R. Asafa* and F. P. Agbaye, *Lagos State Polytechnic, Ikorodu, Nigeria*.

Nine weaned rabbits, 6 wk of age, were housed singly and fed cooked albizia seed meal (CASM) in a completely randomized design (CRD) to evaluate the performance and digestibility. The rabbits were randomly allotted to 3 dietary treatment groups of 3 replicates each. The control diet, T_1 (maize, maize offal, groundnut cake full fat soybean, blood meal, palm kernel cake, wheat offal, bone meal, limestone, lysine, methionine, salt, and vitamin-mineral premix), had no CASM, while T_2 and T_3 contained 50% and 100% levels of CASM, respectively, as a replacement for full-fat soya meal (FFSM) on a crude protein (CP) basis. The proximate analysis, fiber fraction, and antinutrient content of cooked *Albizia* seeds were determined. Weekly body weight and feed intake were measured. At the end of wk 3, fecal samples were collected and analyzed to determine the level of digestibility. Data collected

were subjected to ANOVA, and significant means were separated using Duncan Multiple Range Test. Results showed that rabbits fed with the T_1 had the highest ($P < 0.05$) average weight gain of 81.11 g/rabbit, as against 63.90 and 51.11 g obtained for T_2 and T_3, respectively (Table 0454). The feed intake was best ($P < 0.05$) for rabbits on T_1, with value of 930 g/wk. Rabbits on T_2 had the best feed conversion efficiency (12.41). The high crude protein value 29.84 in CASM indicated that the seed could be used as a protein source in rabbit diet. However, the saponin content may serve as an antinutrient, inhibiting its digestibility and utilization. Feed intake, weight gain, as well as a digestibility coefficient were significantly affected above 50% inclusion of CASM in the diets. Cooked albizia seed could replace FFSM up to 50% on CP basis.

Key Words: performance characteristics, cooked albizia seed, digestibility, weaned rabbit

Table 0454. Weekly performance of weaned rabbits fed cooked albizia seed meal

Variable	T1	T2	T3
Feed intake, g	933[a]	767[b]	844[ab]
Weight gain, g	81.11[a]	63.9[ab]	51.11[b]
FCE[1]	13.14[ab]	12.41b	17.24[a]
Digestibility values, % Dry matter	61.93[b]	62.31[a]	62.29[a]
Ash content	86.91[b]	88.47[ab]	89.15[a]
Crude protein	73.88[b]	75.55a	76.00[a]
Crude lipid	87.35[a]	87.14a	84.02[b]
Calcium	81.64[a]	86.46[ab]	86.09[b]
Phosphorous	85.06[a]	81.29[ab]	76.48[b]

[1] FCE, feed conversion efficiency.

0455 Nutritional evaluation of raw *Anthonotha macrophylla* seed meal as a replacement for soybean meal in the diet of broiler chickens.

A. H. Akinmutimi*, *Michael Okpara University of Agriculture, Umudike, Umuahia, Nigeria.*

The objective of this study was to develop a high quality animal protein at reduced cost through the use of alternative feedstuffs (e.g., *Anthonotha macrophylla*). One-hundred-and-twenty-day-old Marshal broiler chicks were used to assess the quantitative replacement of soybean meal with raw *A. macrophylla* seed meal. Ten birds per treatment were replicated thrice in a completely randomized design. Diet 1 was soybean-based (control), while the test feedstuff (*A. macrophylla*) quantitatively replaced 5, 10, and 15% soybean in Diets 2, 3, and 4, respectively. Feed and water were given ad libitum for 56 d. The crude protein (27.74%) and gross energy values (4.69 Kcal/g) makes it a potential feedstuff. It contains antinutritional factors, namely: phytate (0.43%), tannin (0.06%), hydrogen cyanide (13.71 mg/kg), and nitrate (0.14%). For growth performance, there were significant differences ($P < 0.05$) among the treatment means for all the parameters measured, except initial weight. The final weight, weight gain/bird, and weight gain · $bird^{-1}$ · d^{-1} supported Diet 2. The feed conversion ratio also favored Diet 2 (2.93) among others (Diet 1 = 2.96, Diet 3 = 3.07, and Diet 4 = 4.14). For cut-parts, there were significant differences ($P < 0.05$) for all parameters measured, with Diet 2 comparing favourably with the control diet (Diet 1). All the organ weight parameters showed no significant difference ($P > 0.05$). The haematological parameters measured were within the normal range established for broiler chickens, except for monocytes in all the diets and lymphocytes and neutrophils for Diets 3 and 4, respectively. For serum chemistry, Diets 1, 2, and 3 fall within the normal range established for broiler chickens for albumin and globulin, while for alkaline phosphatase, all the diets fall within the normal range established for broiler chickens. Considering the economics of the diet, Diet 2 had the least cost/kg weight gain, highest revenue, and highest gross margin, making Diet 2 an economically viable diet. Diet 2 enhanced a high-quality animal protein production at reduced cost. This will lead to an increase in animal protein intake globally. It is therefore recommended.

Key Words: nutritional, evaluation, *Antonotha macrophylla*, soybean, chickens

0456 Effect of graded levels of defatted green microalgal inclusion into broiler diets on growth performance and digestibility.

S. K. Gatrell*, T. J. Derksen, E. V. O'Neil, and X. G. Lei, *Cornell University, Ithaca, NY.*

The objective of this experiment was to determine an optimal inclusion level of a defatted marine green microalgae (*Nannochloropsis oceanica*), a byproduct of biofuel production, in broiler diets. A total of 180 hatching Ross broiler chicks were divided into 5 groups ($n = 6$) fed a corn-soybean meal diet containing 0 (Control), 2, 4, 8, or 16% algal biomass (Cellana, Kailua-Kona, HI) for 6 wk. Body weights, feed intake, organ weights, and blood samples were collected at wk 3 and 6; and water intake was measured over the first 3 wk. Over the 6-wk period, ADG, ADFI and G:F were not affected by the algal inclusion up to 8%. However, the 16% inclusion reduced ADG ($P < 0.01$) and G:F ($P < 0.001$). Water intake was increased ($P < 0.001$) by 16 and 39% in chicks fed 8 and 16% microalgae diets, respectively. Relative heart weights were increased by feeding the 16% microalgae diet at both wk 3 ($P < 0.05$) and wk 6 ($P < 0.01$). However, relative liver, breast, gizzard, proventriculus, and intestinal weights or lengths were not affected by the dietary treatments. The same was also true for plasma uric acid, inorganic phosphorus, and protein concentrations at wk 3 or 6. Dry matter concentrations of total excreta collected from 2 birds per cage over a period of 3 d at wk 6 were reduced ($P < 0.05$) in the birds consuming the 8 and 16% microalgae diets, compared with the control. However, the excreta total dry matter or N retention was similar among the 5 experimental diets. In conclusion, dietary inclusion of this new defatted microalgal biomass up to 8% did not exert

any negative effects on growth performance or nutrient metabolism, except for the elevated water intake. *Supported in part by USDA/DOE Biomass R&D Initiative Grant.*

Key Words: green microalgae, broiler nutrition, biofuel

0457 Effects of duration of mixing diets with high inclusion of cereal grain co-products on growth performance and carcass measurements in finishing pigs. M. E. Morts*, J. D. Hancock, K. L. Kohake, and J. D. McAtee, *Kansas State University, Manhattan.*

A total of 200 finishing pigs (average initial BW of 68 kg) were used in a 62-d growth assay to determine the effects of mix time in corn-soybean meal-based diets with high inclusion of distillers dried grains with solubles (32% DDGS) and wheat middlings (32% midds). The pigs were sorted by gender and ancestry and assigned to pens (5 pigs/pen and 8 pens/treatment) in a completely randomized design. A Davis and Sons horizontal ribbon mixer (model DS30) was used to mix 1-t batches of the diets. All ingredients (corn, DDGS, midds, soybean meal, crystalline AA, limestone, salt, vitamin mix, mineral mix, and tylosin) were added with the mixer stopped. Mix times were 0, 15, 30, 60, and 420 s before discharge, transfer to a surge bin, and sacking into 22.6 kg bags for delivery to the swine farm. Diets were formulated to at least 120, 120, and 110% of requirements for essential AA, vitamins, and minerals for 75 to 100 and 100 to 135 kg pigs according to NRC (2012) nutrient requirements of swine. Feed and water were consumed on an ad libitum basis until the pigs were harvested (average BW of 125 kg) and processed at a commercial abattoir. As for results, there was a trend (quadratic effect, $P < 0.07$) for ADG to decrease as mix time was increased from 0 to 30 s and increase as mix time was further increased to 420 s. There was a trend (linear effect, $P < 0.06$) for G:F to increase as mix time was increased. Mix time did not affect ($P > 0.19$) ADFI, HCW, dressing percentage, or fat thickness at the last rib (BF). In conclusion, increasing mix time from 0 to 420 s in diets with high inclusion of DDGS and midds had inconsistent effects in growth performance, and no effect in carcass measurements.

Key Words: duration of mixing, distillers dried grains with solubles, pigs

Table 0457.

Item	0 s	15 s	30 s	60 s	420 s	SE	Linear	Quadratic
ADG, g	931	936	894	904	936	27	0.33	0.07
ADFI, kg	3.02	3.19	3.05	3.07	2.99	0.11	0.19	0.83
G:F, g/kg	308	293	293	294	313	7	0.06	0.12
HCW, kg	91.0	89.9	88.9	88.8	90.9	3.3	0.81	0.23
Dressing, %	72.2	72.2	72.5	71.9	72.1	0.6	0.56	0.58
BF, mm	21	21	21	20	20	1	0.29	0.76

NONRUMINANT NUTRITION: FUNCTIONAL AMINO ACIDS: NEW PARADIGM SHIFTS IN UNDERSTANDING ANIMAL PROTEIN NUTRITION

0458 Amino acid signaling for embryonic and fetal development. G. Wu*, F. Bazer, R. Burghardt, G. Johnson, M. C. Satterfield, and X. Wang, *Texas A&M University, College Station*.

Embryonic death losses in mammals are estimated to range from 20 to 50%, depending on species, with two-thirds of the losses occurring during the peri-implantation period of pregnancy. Additionally, intrauterine growth restriction (IUGR) is primarily responsible for the high rates (up to 15%) of neonatal mortality in livestock species. Among litter-bearing species, swine exhibit the most severe naturally-occurring embryonic loss and IUGR. Nutrient availability, limited uterine capacity, and placental insufficiency are major factors contributing to suboptimal reproduction in mammals. Emerging evidence also shows that concentrations of several AA (arginine, glutamine, and leucine) in the uterine lumen increase markedly during early pregnancy, and are particularly abundant in fetal allantoic fluid during early and mid-gestation. Besides serving as building blocks for proteins, these AA play signaling roles to regulate intracellular protein turnover, water and ion transport, apoptosis, immune responses, and antioxidative reactions in the conceptus (embryo or fetus and extraembryonic membranes). Specifically, arginine is the precursor for synthesis of nitric oxide and polyamines (putrescine, spermidine, and spermine) that are essential to DNA synthesis and cell proliferation. Interestingly, these synthetic pathways are regulated by physiological concentrations of glutamine and leucine to coordinate the cellular actions of arginine. In addition, glutamine and leucine increase expression and activity of glutamine:fructose-6-phosphate transaminase to stimulate formation of glucosamine-6-phosphate from glutamine and fructose-6-phosphate and, therefore, for active synthesis of amino sugars and glycoproteins by trophectoderm cells. Furthermore, arginine, glutamine, and leucine activate (1) the mechanistic target of rapamycin (MTOR) cell signaling through phosphorylation of the MTOR protein and its downstream target proteins (S6K1 and 4E-BP1), and (2) osteopontin-induced cell signaling (a major mechanism for regulation of cell adhesion and implantation) through binding αvβ3 and α5β1 integrin heterodimers and the subsequent phosphorylation of MAPK3/MAPK1 (Erk1/2) and MAPK14 (p38). The beneficial outcome is to promote conceptus growth and development. Arginine and osteopontin appear to activate sequentially PI3K, Akt1, and MTOR to amplify cell signal transduction and exert their physiological effects. Translating the basic research into feeding practices, that is, supplementing 0.4 or 0.8% arginine to a typical corn- and soybean meal-based diet (containing 0.7% arginine) for gilts between d 14 and 25 of gestation, increases embryonic survival and conceptus development. As profitability of the swine industry critically depends on reproductive efficiency of sows, our findings have important implications for increasing pork production to provide high-quality animal protein for human consumption.

Key Words: pig, nutrition and biochemistry

0459 Leucine: A potent nutrient signal for protein synthesis in neonates. T. A. Davis*[1], M. L. Fiorotto, A. Suryawan, and D. Columbus, *USDA/ARS-Children's Nutrition Research Center, Baylor College of Medicine, Houston, TX.*

Neonates are highly efficient at utilizing their dietary AA for skeletal muscle growth. In the neonatal pig, the sharp increase in muscle protein synthesis after eating is triggered by the rise in AA and insulin. Amino acids and insulin induce protein synthesis by activating independent signaling pathways that converge at mechanistic target of rapamycin complex 1 (mTORC1), leading to the activation of key regulators of translation. Leucine is the most effective single AA in triggering translation initiation factor activation. Although most information on leucine's action on mTORC1-dependent translation initiation has been generated from studies performed in cell culture, studies in the neonatal pig have identified components of the AA signaling pathway that regulate protein synthesis in vivo. Acute parenteral leucine administration at physiological levels increases muscle protein synthesis in neonatal pigs and this effect is due to the activation of mTORC1 and its downstream targets, including eukaryotic initiation factor 4E-binding protein 1 and ribosomal protein S6 kinase-1. Although acute administration of the other branched-chain AA, isoleucine and valine, are ineffective, the leucine metabolites, α-ketoisocaproic acid and β-hydroxy-β-methylbutyrate, stimulate muscle protein synthesis by activating mTORC1-dependent translation. The stimulation of protein synthesis by parenteral leucine can be sustained for prolonged periods, but is dependent on maintenance of the supply of other AA to support protein synthesis. Pulsatile administration of leucine during continuous orogastric feeding of a milk replacer enhances muscle protein synthesis by stimulating translation initiation. Enteral leucine supplementation of a low protein meal stimulates protein synthesis similar to a high protein meal, but this effect is diminished but not blocked with more prolonged supplementation. Further studies are needed to establish whether the anabolic effects of leucine can be sustained chronically to promote lean growth. *Supported by NIH AR444474, NIH HD072891, USDA NIFA 2013–67015–20438, and USDA/ARS 6250–51000–055.*

Key Words: amino acids, growth, swine, muscle, nutrition

0460 Tryptophan: Functions beyond protein synthesis. S. W. Kim* and Y. Shen, *North Carolina State University, Raleigh.*

Tryptophan is a limiting essential AA for the growth of pigs. In addition to its important role to support growth, Trp also has unique physiological functions when it is metabolized to other compounds such as serotonin, melatonin, and niacin in the body. Serotonin is a cerebral neurotransmitter, playing a major role in regulating physiological processes such as appetite, stress adaptation, activity, and aggressive behavior. Tryptophan crosses blood-brain barrier, and thus increasing Trp intake is shown to elevate serotonin synthesis in the brain of pigs. However, large neutral amino acids (LNAA) compete for a same type of transporter to cross the blood-brain barrier, and thus dietary ratio of LNAA to Trp can affect Trp availability for serotonin synthesis in the brain. In a typical production environment, pigs can be under social stress conditions as they go through regrouping when they are weaned and when they are moved from nursery to finisher pens. Pigs confront with new mates when they are regrouped in a same pen, causing social mixing stress such as fighting and other aggressive behaviors. Pigs with social stress are shown to undergo increased systemic oxidative stress which is negatively related to animal productivity. In our research, increasing Trp intake up to 10.8 g/d elevated serotonin concentration in hypothalamus, reduced salivary cortisol, and enhanced growth of pigs under social mixing stress. Reducing dietary LNAA content from 4.5 to 3.8% provided similar benefits of increased Trp intake when Trp to LNAA ratio was maintained at 0.157. This allowed reducing supplemental levels of Trp from 0.8 to 0.6%. In summary, in a typical pig production, pigs can be under social mixing stress, and increasing tryptophan intake seems to help to reduce stress and thus improve performance of pigs.

Key Words: pigs, serotonin, social stress, tryptophan

0461 New insights into sulfur amino acid function in gut health and disease. D. G. Burrin*, *USDA-ARS Children's Nutrition Research Center, Houston, TX.*

The gastrointestinal tract (GIT) is a metabolically significant site of sulfur amino acids (SAA) metabolism in the body. Aside from their role in protein synthesis, methionine and cysteine are involved in many biological functions and diseases. Methionine (MET) is an indispensable AA and is transmethylated to homocysteine via S-adenosylmethionine (SAM), the principal biological methyl donor in mammalian cells and a precursor for polyamine synthesis. We have examined the role of SAA metabolism in GIT health and disease. Our studies in young pigs showed that the whole-body methionine transmethylation and remethylation rates were higher during duodenal [^{13}C]-MET than intravenous [$^{2}H_3$]-MET infusion. Thus, transmethylation and transsulfuration in the GIT represented 27 and 23% of whole-body fluxes, respectively. Additional studies show how disruption of methionine cycle activity and dietary supplementation with methionine metabolites affects the susceptibility to colitis in mice. We found that mice fed vitamin B_{12} and B_6 deficient diets are protected against colitis, with reduced inflammation and tissue injury. We also found that B-vitamin deficiency suppressed inflammatory gene expression in association with altered MET cycle activity and indices of methylation status. We also showed that supplementation with the MET cycle metabolite, methylthioadenosine (MTA), prevented inflammation during colitis in mice. These results suggest that MTA also is protective against experimental colitis and reduced tissue injury and expression of multiple inflammatory genes. The presentation will discuss the evidence of SAA metabolism in GIT and consequences of MET cycle activity in health and disease.

Key Words: methionine, cysteine, gut

0462 Glutamate and glutamine: Nonessential or essential amino acid. M. Watford*, *Rutgers, New Brunswick, NJ.*

Rose defined an essential amino acid (EAA) as one that the body cannot make in sufficient amounts to maintain growth or N balance. Despite Rose's finding that glutamate added to diets of traditionally EAA improved the maximal rate of growth, glutamate and glutamine are not usually considered as essential. In part, this is due to the almost total metabolism of dietary glutamate and glutamine in the intestine, and the very high concentration, and turnover, of these 2 AA in the body. In human medicine, however, glutamine has been recognized as a conditionally EAA during hypercatabolic states, and while such conditions are not a concern in the domestic animal industry, the question arises, "is glutamine conditionally essential at other times"? We observed that plasma and skeletal muscle glutamine concentrations fall throughout lactation in both horses, pigs, and mice, and that this was accompanied by a loss of skeletal muscle. We proposed that this was due to the high demand for glutamine (and glutamate) both for milk production and as a fuel for the enlarged maternal intestine. Furthermore, the provision of supplemental glutamine to both suckling and weaned piglets has demonstrated improvements in growth and health, most probably related to improved intestinal status and immune function. The daily supplementation of suckling piglets is not feasible on an industrial scale, and we established that supplementing lactating sows with either glutamine, or a mixture of glutamine and glutamate, increased the glutamine and glutamate content of the milk and also prevented some of the loss of lean body mass in the sow. Furthermore, sows receiving the supplement had higher concentrations of lipids in both colostrum and mature milk, and similar increases were seen in milk somatic cell count. Thus, we propose that glutamate and glutamine should be considered essential both during lactation for the health of both the mother and the neonate.

Key Words: glutamine, glutamate, lactation

NONRUMINANT NUTRITION: FAT, FIBER, FERMENTATION, AND RESIDUAL FEED INTAKE

0463 Changing the dietary omega-6 to omega-3 fatty acid ratio impacts nursery pig performance more than increasing omega-3 intake alone.
L. Eastwood* and D. Beaulieu, *Prairie Swine Centre, Inc., Saskatoon, SK, Canada.*

The objective of this experiment was to determine if either increasing the intake of omega (ω)-3 fatty acids or the amount relative to ω-6 fatty acids (ω-6:ω-3 ratio) would impact nursery pig performance. A total of 300 newly weaned pigs (26 ± 2 d of age), blocked by gender, were housed in groups of 5/pen. Pens were assigned to 1 of 5 diets (n = 12 pens/diet) consisting of a control (Con; 10:1 ω-6:ω-3 ratio, 3.5% total fat, tallow based), 3 diets with 3.5% fat (plant based) and ω-6:ω-3 ratios of 10:1, 5:1, and 1:1 (3.5/10, 3.5/5, and 3.5/1 respectively), and a plant-based 10:1 ratio diet with 5% total fat (5/10). This design allowed us to examine the effects of increasing ω-3 intake at a constant ratio (10:1 ratio; 3.5 vs. 5% fat) and the effect of reducing the ω-6 to ω-3 ratio at a constant amount (3.5% fat; 10:1, 5:1, and 1:1 ratios). Pigs were weighed weekly for 4 wks. On d 0 and d 29, 6 pigs and 6 pigs/diet respectively, were slaughtered, allowing the calculation of whole body N, fat, and water deposition. The ADFI was higher for pigs consuming the 3.5/1 diet during d 21 to 28 (1.13 vs. 0.96 kg/d; P = 0.01) when compared with pigs fed all other diets. Increasing ω-3 amount (constant 10:1 ratio) did not affect ADFI or ADG (P > 0.10); but when the ω-6:ω-3 ratio decreased (constant total fat), ADFI was highest for pigs consuming the 3.5/1 diet relative to those consuming the 3.5/5 or 3.5/10 diets during d 21 to 28 postweaning (1.13 vs. 0.97 vs. 0.93 kg/d; P = 0.02). Pigs consuming the 3.5/5 diet had increased protein (82.5 vs. 71.1 vs. 74.2 g/d; P = 0.07) and water (342.1 vs. 301.0 vs. 313.0 g/d; P = 0.06) deposition rates relative to those consuming the 3.5/10 or 3.5/1 diets. Lipid deposition was unaffected by treatment (P > 0.10). Increasing the amount of dietary ω-3 fatty acids while keeping the ω-6:ω-3 ratio constant did not affect ADG, ADFI, or carcass composition; however, when total fat was held constant, a 5:1 ratio led to improved ADFI in older nursery pigs, as well as increased protein deposition without altering lipid deposition.

Key Words: swine, omega-3, performance

0464 The dietary omega-6 to omega-3 fatty acid ratio impacts the inflammatory response in nursery pigs more than increasing omega-3 intake.
L. Eastwood* and D. Beaulieu, *Prairie Swine Centre, Inc., Saskatoon, SK, Canada.*

The objective of this experiment was to determine if the intake of ω-3 fatty acids affects the inflammatory response of nursery pigs postweaning, and if this response depends on the ratio with ω-6 fatty acids. Individually housed, newly weaned pigs (26 ± 2 d of age; n = 100) were assigned to 1 of 5 diets and 1 of 2 inflammatory challenge groups arranged as a 5 × 2 factorial with repeated measures. Diets consisted of a control (Con; 10:1 ω-6:ω-3, 3.5% total fat, tallow based), 3 diets with 3.5% fat (plant based) and ω-6:ω-3 ratios of 10:1, 5:1, or 1:1 (3.5/10, 3.5/5, and 3.5/1 respectively), and a 10:1 ratio diet with 5% total fat (5/10). This allowed for the comparison of increasing ω-3 intake at a constant ratio (10:1 ratio; 3.5 vs. 5% fat) and decreasing ratio at a constant ω-3 intake (3.5% fat; 10:1, 5:1, and 1:1 ratios). Challenge groups consisted of a saline or lipopolysaccharide (LPS; 15 μg/kg BW *Escherichia coli* lipopolysaccharide) injection. Pigs were fed their assigned diets for 22 d before the 24-h inflammatory challenge on d 23. Rectal temperatures were measured hourly for the first 6 h, then at 12 and 24 h postinjection. Blood samples were collected at 0, 2, 6, and 12 h postinjection. The ADG and ADFI from d 0 to 22 or during the challenge period were unaffected by diet (P > 0.05). During the challenge, LPS pigs had lower (P < 0.01) ADFI (0.93 vs. 0.40 kg, saline vs. LPS) and ADG (+0.44 kg vs. -0.52 kg, saline vs. LPS). Rectal temperature, blood urea N, IL-1β, IL-6, and TNFα were unaffected by diet (P > 0.05), but were increased by LPS (P < 0.01). Serum IL-8 concentration was reduced with decreasing ω-6:ω-3 ratio (16.79 vs. 11.14 pg/mL, 10:1 vs. 1:1; P = 0.03) but was unaffected by dietary ω-3 amount at a constant ratio (P > 0.05). Pigs consuming the 3.5/1 diet had lower IL-8 responses relative to those consuming the 3.5/10 and 3.5/5 diets (diet × challenge P = 0.03). Additionally, the IL-8 response of pigs fed the 1:1 diet and challenged with LPS was similar to the saline injected pigs fed the 10:1, 5:1, or 1:1 diets (P > 0.05), indicating that reducing the dietary ω-6:ω-3 ratio impacts a piglets inflammatory response postweaning.

Key Words: swine, omega-3, inflammatory response

0465 Effect of fiber and fat on calculated values for standardized total tract digestibility of calcium in fish meal.
J. C. González-Vega*[1], C. L. Walk[2], and H. H. Stein[1], [1]*University of Illinois at Urbana-Champaign, Urbana,* [2]*AB Vista Feed Ingredients, Marlborough, UK.*

The objectives of the experiment were to determine the effect of fiber and fat on the standardized total tract digestibility (STTD) of Ca in fish meal and to evaluate the effect of type

of diet (cornstarch-based diet vs. corn-based diet) and digestibility procedure (direct procedure vs. difference procedure) on calculated values for STTD of Ca in fish meal. Seventy growing pigs (BW: 19.4 ± 1.0 kg) were randomly allotted to 7 diets with 10 pigs per treatment. Two diets were formulated to determine the effect of fiber on STTD of Ca in fish meal: (1) cornstarch-based diet + fish meal and (2) cornstarch-based diet + fish meal + Solka floc. Two additional diets were formulated to determine the effect of fat on STTD of Ca: (3) corn-based diet + fish meal + 1% fat and 4) corn-based diet + fish meal + 7% fat. To evaluate the effect of type of diet on the STTD of Ca in fish meal, diets 1 and 3 were compared. The STTD of Ca in fish meal was also determined using the difference procedure with a corn-soybean meal diet (0.33% Ca) and a corn-soybean meal-fish meal diet (0.89% Ca). A Ca-free diet was used to determine basal endogenous losses of Ca. Results indicated that fiber increased ($P < 0.001$) the STTD of Ca, but the STTD of Ca was not affected by inclusion of fat in the diet. The STTD of Ca (88.99%) in the corn-based diet was greater ($P < 0.05$) than in the cornstarch-based diet (45.79%). When comparing the direct and the difference procedure, the greatest ($P < 0.05$) values for the STTD of Ca in fish meal were obtained in pigs fed the corn-based diet using the direct method, followed by values calculated by difference procedure (77.66%; $P < 0.05$), and the least ($P < 0.05$) values were obtained in pigs fed the cornstarch-based diet using the direct method. In conclusion, fiber increased the STTD of Ca, but inclusion of fat did not affect the STTD of Ca. Values for the STTD of Ca were influenced by the type of diet and by the digestibility procedure used. These data indicate that values for the ATTD or the STTD of Ca obtained in synthetic diets may not always be representative for the ATTD and the STTD of Ca in practical corn-soybean meal diets.

Key Words: calcium digestibility, fish meal, pigs

0466 Response of pigs in ileal endogenous amino acid losses to different dietary fiber types determined using the regression method. S. A. Adedokun* and O. Adeola, *Purdue University, West Lafayette, IN.*

Dietary fiber, especially fiber with high water holding capacity, is theorized to increase ileal endogenous amino acid (EAA) losses in nonruminant animals. It is not known whether dietary fiber types have different effects on ileal EAA. Increase in EAA losses would decrease apparent ileal AA digestibility and increase N excretion into the environment. Information on basal ileal EAA losses in pigs will advance diet formulation on standardized ileal AA digestibility basis. The objective of this study was to evaluate the effect of 2 fiber sources, corn fiber or pectin, on ileal EAA losses in pigs. Total AA, crude protein, and crude fiber contents of corn fiber or pectin used in this study were 9.8, 10.8, and 10.0% or 1.1, 10.8, and 0.2%, respectively. For each fiber type, 3 semipurified diets were formulated to contain 3 levels of casein (40, 80, and 120 g/kg diet) and 100 g of fiber/kg diet. All fiber within a diet was supplied by either corn fiber or pectin. The experiment consisted of 3 periods of 7 d, each with ileal digesta collection on d 6 and 7. Within each period, there were 3 pigs on 3 levels of casein (40, 80, or 120 g/kg diet) in each of 3 blocks per fiber type; and each block served as the experimental unit. There were 18 cannulated pigs with average initial BW of 30, 31, and 30 kg for Periods 1, 2, and 3, respectively. Each pig received 3.5% of the starting BW of the smallest pig within each block in 2 equal portions at 0700 and 1800 h. Basal ileal EAA losses were determined from the ordinate intercept, at 0 AA intake, of the regression of ileal digesta AA concentration in mg/kg DMI against dietary AA intake in mg/kg DM. Corn fiber resulted in higher ($P < 0.05$) ileal endogenous His, Leu, and Tyr losses. Isoleucine, Phe, Thr, and Cys showed a tendency ($P < 0.1$) for higher endogenous loss in pigs fed diets containing corn fiber. In general, the effect of highly-fibrous but low-viscosity corn fiber on ileal endogenous N and AA losses is similar to that of low-fiber but highly-viscous pectin.

Key Words: corn fiber, endogenous AA, pectin

0467 Starch and fiber characteristics of barley influence site of energy digestion in ileal-cannulated grower pigs. J. M. Fouhse*[1], S. Moehn[1], J. Gao[1], T. Vasanthan[1], M. Izydorczyk[2], A. D. Beattie[3], and R. T. Zijlstra[1], *[1]University of Alberta, Edmonton, Canada, [2]Canadian Grain Commission, Winnipeg, MB, Canada, [3]University of Saskatchewan, Saskatoon, Canada.*

Chemical components of cereal grains such as amylose, β-glucan (BG), and total dietary fiber (TDF) may influence energy digestion in the gut. The objective was to determine the association between composition of barley and wheat and the site of energy digestion in pigs. Seven ileal-cannulated barrows were allotted to a 6 (periods) × 7 (diets) Youden square. Five cereal grain diets included (% amylose, β-glucan, and TDF): 3 hulless-barley cultivars: Diet 1, CDC Fibar (0, 10, 22); Diet 2, CDC Hilose (13, 7, 18); Diet 3, CDC McGwire (11, 5, 15); 1 hulled barley, Diet 4, Xena (12, 4, 17); and 1 hard red spring wheat, Diet 5, Utmost (12, 1, 14). Two reference diets, an N-free and a protein-energy mix, were included to calculate ingredient digestibility. Test diets included 80% cereal grain and were fed at 2.5 × maintenance. Feces and ileal digesta were sampled after a 5-d adaptation. The AID of GE, DM, and starch was lowest ($P < 0.05$) for Fibar (43, 42, 73%) and Hilose (48, 47, 69%) vs. McGwire (68, 67, 84%), Xena (65, 64, 92%), and Utmost (78, 80, 93%). In contrast, hindgut fermentation of GE, DM, and starch was greatest ($P < 0.05$) for Fibar (45, 46, 26%) and Hilose (48, 41, 30%) vs. McGwire (23, 23, 16%), Xena (17, 16, 8%), and Utmost (11, 14, 7%). Thus, Fibar and Hilose did not differ ($P > 0.05$) in ATTD of DM and GE from Utmost. McGwire had the greatest ($P < 0.05$) ATTD of DM and had a greater ($P < 0.05$) ATTD of GE

than Fibar, Hilose, and Xena but equal to that of Utmost ($P < 0.05$). Specifically, ATTD of DM was 90 vs. 87, 88, 81, and 88% and ATTD of GE was 91 vs. 88, 88, 83, and 89%, respectively, for McGwire vs. Fibar, Hilose, Xena, and Utmost. Starch ATTD did not differ among cereal grains ($P > 0.05$). Hulled barley, Xena, had an ATTD of GE and DM lower ($P < 0.05$) than all other cereal grains. Thus, the DE was lower ($P < 0.05$) in Xena than all other cereal grains, which did not vary ($P > 0.05$). In conclusion, a greater content of amylose, BG, and TDF in cereal grains decreased energy digestion in the small intestine and increased hindgut fermentation of energy, which may support maintaining pig gut health.

Key Words: grain, starch, fiber

0468 Effects of three types of dietary microalgal inclusions on n-3 and n-6 fatty acid profiles in egg yolks of laying hens. J. Kim, A. Magnuson, and X. Lei*, *Cornell University, Ithaca, NY.*

Two experiments were conducted to determine if including microalgal biomass into layer diets containing 0, 3, and 5% flaxseed oil (FO) affected fatty acid profiles in their egg yolk. In Experiment I, 90 Shaver-laying hens (20-wk old) were allotted into 9 groups ($n = 10$) and fed diets containing 3 levels of FO (0, 3, and 5%) and 3 levels of full-fat *Staurosira* spp. (SS) (0, 7.5, and 10%, Cellana, Kailua-Kona, HI) for 4 wk. In Experiment II, 50 Shaver-laying hens (28-wk old) were divided into 5 groups ($n = 10$) and fed control diet (without FO and MAB) or the diets containing 3% FO with SS at 7.5%, defatted *desmodesmus* spp. (DS) at 7.5%, or defatted *Nannochloropsis ocreanica* (NO) at 7.5 or 15% for 4 wk. Body weights, feed intakes, and egg quality (albumen, egg yolk, and egg shell weight) were measured weekly, and fatty acid contents of egg yolk were determined biweekly. In Experiment I, neither FO nor SS affected feed intakes, egg production, or egg quality. While body weights were decreased ($P < 0.05$) by 5% FO, the decrease was prevented by the inclusion of SS. At wk 2, the FO inclusion increased n-3 fatty acid ($P < 0.05$), and decreased n-6 fatty acid concentrations in the yolk. The SS inclusion affected ($P < 0.05$) yolk n-6 fatty acid concentrations. At wk 4, there were interactions ($P < 0.05$) between SS and FO on the yolk n-3 fatty acid concentrations or changes over time. The yolk concentrations of n-6 fatty acids were increased by FO, but decreased by SS. In Experiment II, egg production, egg component weights, body weights, and feed intakes were not affected by the 5 dietary treatments. While the combinations of 3% FO and 3 types of microalgal biomass elevated ($P < 0.05$) the yolk n-3 fatty acid contents, the 2 doses of NO (7.5 vs. 15%) showed no difference. In conclusion, inclusions of 3 types of microalgal biomass exerted moderate effects on n-3 and n-6 fatty acid profiles and concentrations in comparison with the much stronger effects of 3 or 5% FO. However, the microalgal biomass inclusion seemed to help offset the negative effects of 5% FO on the body weights of laying hens. *Supported in part by USDA/DOE Biomass R&D Initiative Grant.*

Key Words: Microalgal biomass, omega-3 fatty acid, laying hens

---

0469 Dose-dependent effect of a defatted green microalgal biomass on enriching omega-3 fatty acids in broiler chicken. S. K. Gatrell*, J. Kim, T. J. Derksen, E. V. O'Neil, and X. G. Lei, *Cornell University, Ithaca, NY.*

The objective of this experiment was to determine the feasibility of creating an omega-3 (n-3) enriched chicken product using defatted green microalgae (*Nannochloropsis oceanica*), a byproduct of the biofuel production research. A total of 180 hatching Ross broiler chicks were divided into 5 groups ($n = 6$) fed a corn-soybean meal diet containing 0 (control), 2, 4, 8, or 16% algal biomass (Cellana, Kailua-Kona, HI) for 6 wk. Plasma, breast muscle (pectoralis major) and liver were collected at wk 6. Plasma n-3 fatty acid concentrations showed dose-dependent increases with the microalgal inclusion levels, and the concentration in the birds fed the 16% microalgae diet was 15-fold higher ($P < 0.001$) than that of the control. Meanwhile, liver eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) were increased 8- to 22-fold ($P < 0.001$) and 2- to threefold ($P < 0.01$), respectively, by feeding the microalgal biomass compared with the control. Percentage of n-3 fatty acids, but not total fatty acid content, in the breast muscle was enhanced ($P < 0.0001$) by the microalgae inclusion in a dose-dependent fashion. Breast muscle EPA and DHA contents were elevated ($P < 0.0001$) by 38- and 60-fold, respectively, in the chicks fed the 8 and 16% microalgae diets compared with those fed the control diet. In conclusion, the defatted marine microalgal biomass tested in the present study was very effective in enriching n-3 fatty acids, in particular DHA and EPA, in broiler chicken tissues. Supported in part by USDA/DOE Biomass R&D Initiative Grant.

Key Words: biofuel, nutrition, health

0470 In vitro digestion and fermentation characteristics and in vivo digestibility of canola co-products in the pigs. T. A. Woyengo*[1], R. Jha[1,2], E. Beltranena[1], and R. T. Zijlstra[1], *[1]University of Alberta, Edmonton, Canada, [2]Univerisity of Hawaii at Manoa, Honolulu.*

Canola coproducts serve as source of dietary AA and energy to pigs. However, fermentation characteristics of solvent-extracted canola meal (CM) in the pig intestine are unknown. Thus, we determined in vitro degradation and fermentation characteristics of *Brassica juncea* CM (JCM) and *Brassica napus* CM (NCM) in comparison to soybean meal (SBM). Samples were first hydrolyzed using pepsin and pancreatin. Subsequently, residues were incubated in a buffer with fresh pig feces as inocula in a randomized complete block design providing 12 replicates

per feedstuff per run for 2 runs. Accumulated gas production was measured for 72 h and modeled to estimate kinetics of gas production. Concentration of VFA per unit weight of feedstuff was measured in fermented solutions. In previous studies, ileal and hindgut GE digestibility values for feedstuffs were obtained (by difference method) from ileal-cannulated barrows (~50 kg BW) fed cornstarch-based diets containing 50% feedstuffs for 5 d. On DM basis, SBM, JCM, and NCM contained 50.6, 44.0, and 38.1% CP; and 8.5, 22.3, and 30.6% NDF, respectively. The in vitro DM digestibility for SBM (82.3%) was greater ($P < 0.05$) than the in vitro DM digestibility for JCM (68.5%), which was greater ($P < 0.05$) than that of NCM (63.4%). Ileal GE digestibility was greatest ($P < 0.05$) for SBM followed by JCM and then NCM. Total gas production for SBM was greater ($P < 0.05$) than that of JCM, which was greater ($P < 0.05$) than that for NCM. Total VFA production was lower ($P < 0.05$) for SBM (0.73 mmol/g DM) than for NCM (1.05 mmol/g DM), which was lower ($P < 0.05$) than that of JCM (1.37 mmol/g DM). A similar trend was observed for hindgut GE digestibility (as percentage) for feedstuffs; 15, 21.4, and 24.4% for SBM, NCM, and JCM, respectively. In conclusion, in vitro fermentation characteristics of SBM, and canola meals simulated their digestion in the pig hindgut ($r^2 = 0.979$). The NCM or JCM can contribute more energy to the pig via hindgut fermentation than the SBM, whereas JCM can contribute more energy to the pig via hindgut fermentation than the NCM.

Key Words: canola meal, in vitro fermentation, pig

0471 In vitro pig cecal fermentation with different inoculum source with diets containing *Acrocomia aculeata*.

S. L. S. Cabral Filho*, L. S. Murata, C. A. Silva Júnior, H. dos Santos Sena, F. Lopes da Silva, F. Nishimoto Gomes da Costa, T. F. Braga, and J. F. Athayde Oliveira, *University of Brasilia, Brasilia, Brazil.*

The aim of this study was to determine the potential of different inoculum sources on in vitro gas production technique. Three different types of inoculum were used for fermentation in gas production analysis: fistulated bovine ruminal liquor grazing *Brachiaria brizantha* (RL); extract from slaughtered pig cecum raised in a conventional confined system (CS) and extract from slaughtered pig cecum raised in a free range system (CF), both collected directly from the cecum. The substratum used was 3 diets containing replacement of *Acrocomia aculeata* (AA) pulp being 100% (0% AA), 90% (10% AA), and 80% (20% AA) of a basal diet with soybean meals and corn grains to meet pig growth requirements, as well as *Braquiaria brizantha* grass. The accumulated volume of gas was measured at 0, 3, 6, 9, 12, 16, 24, 48, 72, and 96 h after incubation. The mathematical model used was France et al. (1993). A completely randomized design with factorial arrangement was used. All used inocula produced gases with the studied substrates (Table 0471). The pig cecum extract (CF) showed higher gas production ($P < 0.05$) with *Braquiaria brizantha*and 20%AA as substratum than CS. However, there was no statistical difference when compared with RL. The gas production was superior ($P < 0.05$) when basal diet (0%AA) was used with LR and CS inocula. There were no significant differences in gas production when 10% AA was used as a substrate. The pig cecum extract from slaughtered pigs raised in confined and free range systems produced gas as well as bovine ruminal liquor, and can be used for further gas production evaluation, mainly to study fiber usage in pork production. The pig cecum extract from pigs raised in free range (CF) pork production showed more important gas production potential ($P < 0.05$) than CS when the substrate had high fiber level, probably due to the increase of fiber intake in livestock breeding.

Key Words: gas production, fiber fermentation, alternative feed

Table 0471. Inocula gas production (mL) with distinct substrates after 96 h of incubation

Inocula	*Braquiaria brizantha*	0% AA	10% AA	20% AA
Bovine ruminal liquor	52.81[ab]†	112.14[a]	107.85	108.52[ab]
Pig cecum extract, standard	47.84[b]	98.47[a]	115.15	102.46[b]
Pig cecum extract, free range	60.14[a]	72.21[b]	83.54	110.4[a]
MSE	5.85	9.44	17.72	3.37
CV, %	10.92	10.02	17.34	3.14

† Means followed by different letters are significantly different by the Tukey Test 5%.

0472 Residual feed intake in pigs is associated with organ weight, nutrient digestibility, and intestinal nutrient transporter gene expression.

S. Vigors*[1], T. Sweeney[2], A. K. Kelly[1], C. J. O'Shea[1], D. N. Doyle[1], and J. V. O'Doherty[1], *[1]School of Agriculture and Food Science, University College Dublin, Dublin, Ireland, [2]College of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland.*

Increases in nutrient digestibility mediated by changes in intestinal nutrient transporter gene expression could possibly explain the differences in efficiency between animals differing in residual feed intake (RFI). The objective of this study was to examine the effect of divergent selection for RFI on organ weights, nutrient digestibility and intestinal nutrient transporter gene expression in pigs. Male pigs ($n = 75$; initial BW 22.4 kg were fed a standard finishing diet (8.3 g/kg lysine and 16.4 MJ/kg gross energy) for 43 d to evaluate feed intake and growth for the purpose of calculating RFI. Phenotypic RFI was calculated as the residuals from a regression model regressing DMI on ADG and midtest $BW^{0.75}$(MWT). Data was analysed using the GLM procedure of SAS (SAS Inst. Inc., Cary, NC). On d 43, 16 animals (average weight 85 kg sem 2.84 kg), designated as 8 high RFI (HRFI) and 8 low RFI (LRFI) were slaughtered and digesta from the ileum

and rectum were collected for the purpose of calculating the coefficient of apparent ileal (CAID) and total tract nutrient digestibility (CATTD). Tissue was collected from the jejunum, duodenum, and ileum for the purpose of examining intestinal nutrient transporter gene expression. As expected, LRFI pigs had lower ADFI (2.44kg vs. 1.87kg, sem 0.07) and improved feed conversion ratio (1.96 vs. 2.48) than HRFI pigs ($P < 0.001$) with no difference in ADG or MWT. When comparing weights of organs between RFI groups, HRFI pigs had increased weight of heart and visceral organs ($P < 0.05$) compared with the LRFI. There was a linear positive correlation between RFI and weight of large intestine ($r = 0.57$; $P < 0.05$). For the digestibility parameters measured, RFI was negatively correlated with CATTD of N ($r = -0.46$; $P < 0.05$) and GE ($r = -0.51$; $P < 0.05$). The RFI was negatively correlated with the intestinal glucose transporters SGLT1 ($r = -0.56$; $P < 0.05$) and GLUT2 ($r = -0.44$; $P = 0.09$). LRFI pigs had increased CAID of gross energy (GE) than HRFI pigs ($P < 0.05$). Similarly, LRFI pigs had improved CATTD of GE, while also having improved digestibility of N and dry matter (DM). LRFI pigs had higher gene expression of the fatty acid transporter FABP2 ($P < 0.01$) and glucose transporters SGLT1 ($P < 0.05$) and GLUT2. In conclusion differences in nutrient digestibility, intestinal nutrient transporter gene expression and differential organ weight are possibly some of the biological processes responsible for differences in feed efficiency in pigs.

Key Words: residual feed intake, nutrient transporter gene expression, pigs

---

0473 Effect of divergent selection for residual feed intake on cytokine gene expression in pigs following an ex vivo liposaccharide challenge.

S. Vigors*[1], J. V. O'Doherty[1], C. J. O'Shea[1], and T. Sweeney[2], [1]*School of Agriculture and Food Science, University of College Dublin, Dublin, Ireland,* [2]*College of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin 4, Ireland.*

Pathogenic microbes influence pig performance by stimulating an inflammatory immune response and disrupting metabolism. To date, little research has been undertaken to examine the effect of divergent selection for residual feed intake (RFI) on the immune system. The objective of this study was to examine the effect of divergent selection for RFI on colonic inflammatory cytokine gene expression following an ex vivo lipopolysaccharide (LPS) challenge. Male pigs ($n = 75$; initial BW 22.42kg [SD = 2.03]) were fed a standard finishing diet (12.5 g/kg lysine and 14.5 MJ/kg DE) for 43 d to evaluate feed intake and growth for the purpose of calculating RFI. Phenotypic RFI was calculated as the residuals from a regression model regressing DMI on ADG and midtest $BW^{0.75}$ (MWT). On d 43, 16 animals (average weight 85 kg, Std 2.84 kg), designated 8 high RFI (HRFI) and 8 low RFI (LRFI) were slaughtered. Colonic tissue was collected and stimulated for 3 h ex vivo with LPS. QPCR was performed to analyse the expression of *IL-1, IL-6 IL-8, IL-10, Il-17, TNF-α* and *IFN-γ*. As expected, LRFI pigs had lower ($P < 0.001$) ADFI (2.44kg vs. 1.87kg sem 0.04) and improved feed conversion ratio (1.96 vs. 2.48, sem 0.01) than HRFI pigs with no difference in ADG or MWT. Stimulation of the colonic tissue with LPS increased expression of *IL-8* ($P < 0.05$), *TNF-α* ($P < 0.0001$), *IL-10* ($P < 0.05$), *IL-1* ($P < 0.001$), *IFN-γ (P < 0.05)* and *IL-6* ($P < 0.001$) in both HRFI and LRFI pigs. There was an interaction between RFI and LPS challenge for the expression of *IL-8* ($P < 0.05$) and *IL-1* ($P < 0.01$) and *IFN-γ (P < 0.05)*. Following the LPS challenge there was an increase in the expression of *IL-1* ($P < 0.01$) and *IL-8* ($P < 0.05$) and *IFN-γ (P < 0.05)* in the HRFI pigs, with no change in the LRFI pigs. There was no difference between RFI groups for *IL-10* and *IL-17*. The upregulation of pro-inflammatory cytokines has an adverse effect on the gut mucosa and the reduced expression of the pro-inflammatory cytokines in this study could partly explain the increased efficiency in LRFI pigs.

Key Words: residual feed intake, cytokine, pigs

NONRUMINANT NUTRITION: FEED ADDITIVES, ENZYMES, AND DIETARY SUPPLEMENTS

0474 Effects of a blend of essential oil compounds, feed-grade antibiotics, and their combination on the growth performance of nursery pigs.
M. J. Azain*[1], R. Dove[1], C. W. Parks[2], and J. R. Bergstrom[2], [1]*University of Georgia, Athens,* [2]*DSM Nutritional Products, Inc., Parsippany, NJ.*

A total of 72 pigs (initial wt. of 6.2 kg) were utilized in a 35-d study to evaluate the effects of feeding a blend of essential oils (EO, Crina Piglet, DSM Nutritional Products, Parsippany, NJ), a feed-grade antibiotic (AB, Mecadox, Phibro, Teaneck, NJ), and their combination (EO + AB) on the growth performance of nursery pigs. Weaned pigs (3 wks of age) were placed into 24 pens containing 3 pigs per pen and allotted to 1 of 4 dietary treatments for a total of 6 replicate pens per treatment. Gender was balanced within pens in a weight block. Treatments were arranged as a 2 × 2 factorial arrangement to evaluate possible EO × AB interactions. Treatments consisted of (1) Control without EO or AB, (2) EO (200 mg/kg), (3) AB (50 mg/kg), and (4) OE + AB. All pigs were fed the same 3-phase nursery program with the exception of the added treatments, which replaced corn when added. Diet phases were 0 to 7 d, 7 to 21 d, and 21 to 35 d. Diets were formulated to meet or exceed all nutrient requirements based on NRC (2012). Overall, there were no EO × AB interactions ($P \leq 0.05$) for any parameters measured. The EO significantly improved G:F ($P \leq 0.05$) for the d 0 to 35 period as compared with pigs fed no EO, while AB significantly improved final body weight, ADG, and ADFI compared with pigs not fed AB ($P \leq 0.05$) during the d 0 to 35 period. In summary, it appears that dietary addition of both AB and EO can improve the growth performance of nursery pigs.

Key Words: essential oils, performance, pigs

Table 0474. Main effects of essential oils and antibiotics on nursery pig performance

Treatment	–	+	SEM	*P*-value	% Change
Essential oils					
BW, d 35	22.43	23.18	0.37	0.17	3.3
ADG, g (d 0–35)	464	485	10	0.17	4.5
ADFI, g (d 0–35)	659	661	14	NS	–
G:F (d 0–35)	0.703[a]	0.734[b]	0.007	0.006	4.4
Antibiotic					
BW, d 35	22.01[a]	23.59[b]	0.37	0.01	7.2
ADG, g (d 0–35)	452[a]	497[b]	11	0.01	10.0
ADFI, g (d 0–35)	637[a]	683[b]	15	0.05	7.2
G:F (d 0–35)	0.710	0.727	0.007	0.08	2.4

[a–b] Means within a row with different superscripts differ ($P < 0.05$).

0475 Impact of zinc and arginine dietary supplements on antioxidant capacity and oxidative status in weanling piglets under conditions of commercial production.
F. Guay and N. Bergeron*, *Universite Laval, Quebec, Quebec City, Canada.*

The effects of high levels of Zn and arginine (Arg) supplementation on the antioxidant capacity and oxidative status of weanling piglets raised under commercial conditions were examined. Weanling piglets aged 21 d were fed for 15 d a diet supplemented or not with 2500 mg kg^{-1} of Zn and 1% Arg. They were distributed among the 4 treatments in a randomized complete block design based on initial body weight, 6 pens per treatment, 13 animals per pen. Access to feed was ad libitum. Data were analyzed as a 2 × 2 factorial experiment using the SAS MIXED procedure (SAS Inst. Inc., Cary, NC), with Zn and Arg supplementation as the main independent variables. Blood sampling day was included as a third factor. Blood was collected from the same 2 piglets in each pen before the morning feeding on d 8 and 15. The Zn supplement increased average daily gain (ADG) from d 0 to 7(0.194 vs. 0.140 g d^{-1}), d 7 to 15 (0.368 vs. 0.280 g d^{-1}) and for the entire experimental period (0.289 vs. 0.217 g d^{-1}), average daily feed intake (ADFI) from d 0 to 7 (0.197 vs. 0.182 g d^{-1}), d 7 to 15 (0.454 vs. 0.358 g d^{-1}) and for the entire experimental period (0.338 vs. 0.279 g d^{-1}) and ADG:ADFI ratio from d 0 to 7(0.991 vs. 0.760), and for the entire experimental period (0.860 vs. 0.777; $P < 0.001$). Both supplements decreased the malondialdehyde concentration significantly (Zn:4.37 vs. 3.91, $P < 0.005$; Arg:4.38 vs. 3.89 μmol L^{-1}, $P < 0.002$). Total antioxidant capacity increased from d 8 to 15 (0.953 vs. 1.391 μmol equivalent Trolox L^{-1}), regardless of the dietary treatment ($P < 0.05$). The reduced glutathione concentration also was higher on d 15 than on Day 8 (3.37 vs. 2.22 μmol L^{-1}), regardless of the dietary treatment ($P < 0.001$). On d 8, the concentrations of total and oxidized glutathione were increased when Arg and Zn supplements were combined (Zn2500Arg1:5.42 and 1.20; Zn0Arg0: 4.19 and 1.04 μmol L^{-1}), but decreased in the presence of either supplement alone (Zn2500Arg0:2.57 and 0.41; Zn0Arg1:3.42 and 0.67 μmol L^{-1}; $P < 0.001$). Piglets fed Zn-supplemented diets had a lower haptoglobin serum concentration than those fed a nonsupplemented diet (509.5 vs. 1417.6 mg L^{-1}; $P < 0.001$). In conclusion, although a high level of Zn improved piglet growth performance, the results do not indicate any clear association between performance and oxidative status. Arginine supplementation had a limited effect on growth performance and oxidative status under these commercial conditions.

Key Words: piglets, zinc, arginine

0476 Effect of a 6-phytase derived from *Buttiauxella* spp. expressed in *Trichoderma reesei* on apparent total tract digestibility of Ca and P, bone ash, and growth performance in weaning piglets.

A. L. Wealleans[1], Y. Dersjant-Li*[1], R. M. Bold[1], and H. H. Stein[2], [1]*Danisco Animal Nutrition, DuPont Industrial Biosciences, Marlborough, UK,* [2]*University of Illinois at Urbana-Champaign, Urbana, IL*.

Two studies evaluated the effect of a 6-phytase derived from *Buttiauxella* spp. expressed in *Trichoderma reesei* (PHY) on apparent total tract digestibility (ATTD) of Ca and P, bone ash and growth performance in piglets. Five dietary treatments were tested, including a positive control (PC) based on corn-SBM-canola meal adequate in available P and Ca, a negative control (NC) with low available P and Ca and NC supplemented with PHY at 250, 500, and 1000 FTU/kg feed with low available P (-0.2%) and Ca (-0.17%). Experiment 1 used 232 male piglets (Initial BW = 9.62 ± 1.36 kg) with 10 replicates per treatment; 3 to 4 piglets/replicate. Experiment 2 used 160 piglets (Initial BW = 8.99 ± 0.16 kg) with 8 replicates/treatment; 4 piglets/replicate. Experimental diets were fed in mash form ad libitum in 2 phases for 6 wk in Exp. 1 and from 9 to 22 kg BW in Exp. 2. Fecal samples were collected from 1 pig/pen at the end of Exp. 1 and in the last 4 d of feeding in Exp. 2; samples were measured for ATTD using a TiO_2 marker. Femurs from both forelegs were collected for bone analysis. Linear and quadratic responses were determined using the Fit Model platform of JMP; trial was used as a random effect. In both experiments, NC reduced all growth and digestibility parameters compared with PC (Table 0476). PHY supplementation resulted in linear/quadratic improvement in BWG, G:F, digestible Ca and P, as well as bone ash. In conclusion, 1000 FTU/kg 6-phytase derived from *Buttiauxella* spp., expressed in *Trichoderma reesei,* can replace 0.2% available P in weaning piglet diets, based on BWG and bone ash data.

Key Words: phytase, swine, performance

0477 Effect of supplementation of nonstarch polysaccharide-degrading enzymes on nutrient digestibility of wheat and wheat millrun based diets in growing pigs.

Z. Nasir*[1], J. Broz[2], D. Pettersson[3], and R. T. Zijlstra[1], [1]*University of Alberta, Edmonton, Canada,* [2]*DSM Nutritional Products, Basel, Switzerland,* [3]*Novozymes, Bagsvaerd, Denmark*.

Nutrient digestibility of wheat millrun (WMR) is limited by nonstarch polysaccharides (NSP) such as arabinoxylans. Supplementation of NSP-degrading enzymes may increase nutrient digestibility of WMR. Effects of supplementation of 2 endo-xylanases, fed with or without 2 arabinofuranosidases, on nutrient digestibility of a wheat and WMR-based diet were evaluated in a 6 × 6 Latin square. Six ileal-cannulated barrows were fed 5 test diets and 1 N-free diet in six 9-d periods. Five test diets contained 56.2% wheat, 40% WMR, and added enzymes as follows: (1) control (Diet C), without enzyme; (2) 10 mg enzyme protein (EP)/kg of xylanase Ronozyme WX (Diet X1); (3) 10 mg EP/kg of xylanase GH11 (Diet X2); (4) 10 mg EP/kg of xylanase Ronozyme WX + 5 mg EP/kg of arabinofuranosidase GH43 + 5 mg EP/kg of arabinofuranosidase GH51 (Diet X1A); and (5) 10 mg EP/kg of xylanase GH11 + 5 mg EP/kg of arabinofuranosidase GH43 + 5 mg EP/kg of arabinofuranosidase GH51 (Diet X2A). Feces and ileal digesta were collected sequentially for 2 d. Data were analyzed using MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). Wheat and WMR contained 12.2 and 21.2% total NSP, respectively. Insoluble NSP were greater than soluble NSP, respectively, in wheat (10.8 vs. 1.4%), WMR (18.8 vs. 2.4%), and diets (14.6 vs. 5.1%). Digesta viscosity (resistance to flow) was greatest for Diet C. Compared with Diet C (377 Pa·s), digesta viscosity was reduced by 15.1% ($P < 0.05$) for Diet X2A (320 Pa·s), while viscosity was not affected for Diets X1 (362 Pa·s), X2 (354 Pa·s), and X1A (348 Pa·s). Apparent total tract digestibility (ATTD) of GE and CP were greater ($P < 0.05$) for Diets X2 and X2A than for Diet C. Specifically, ATTD of GE was 79.7, 80.3, 81.0, 80.3, and 81.3% and ATTD of CP was 81.9, 82.1, 83.3, 83.1, and 83.7%, respectively, for Diets C, X1, X2, X1A, and X2A. Diets X1A and X2A increased ($P < 0.05$) apparent ileal digestibility (AID) of NSP compared with Diets C, X1, and X2. Compared with control, Diets X1A and X2A

Table 0476. Effect of phytase supplementation on growth parameters, Ca and P digestibility, and bone ash percentage[1]

			Phytase dose, FTU					
	PC	NC	250	500	1,000	SEM	Linear	Quadratic
Body weight gain, g/d	566.8	377.1	466.2	484.3	536.3	11.84	< 0.0001	0.110
Feed intake, g/d	942.6	774.1	896.0	910.9	954.3	18.19	< 0.001	0.116
G:F	0.61	0.49	0.53	0.54	0.57	0.01	0.002	0.504
Phosphorous ATTD, %	28.52	6.08	23.04	43.32	47.89	1.09	0.023	0.372
Calcium ATTD, %	54.51	38.00	40.99	67.04	56.21	2.23	< 0.0001	< 0.001
Bone ash, %	46.45	36.82	41.06	42.45	43.67	2.15	< 0.0001	< 0.0001

[1]Assessment of linear and quadratic responses excluded positive control treatments.

increased ($P < 0.05$) AID of insoluble and total NSP, insoluble and total arabinose, insoluble and total xylose by 52, 42, 86, 80, 85, and 84%, respectively. In conclusion, combined application of xylanase and arabinofuranosidase was more effective than single application of xylanase to increase the nutritional value of diets based on wheat and WMR.

Key Words: wheat co-product, xylanase, arabinofuranosidases

0478 Efficacy of novel 6-phytase derived from *Buttiauxella* spp. expressed in *Trichoderma reesei* on ileal and total tract nutrient digestibility in growing pigs fed a corn-soy based diet. D. E. Velayudhan*[1], J. M. Heo[1], Y. Dersjant-Li[2], A. Owusu-Asiedu[2], and C. M. Nyachoti[1], *[1]University of Manitoba, Winnipeg, Canada, [2]Danisco Animal Nutrition, DuPont Industrial Biosciences, Marlborough, UK.*

The current study evaluated the effect of different levels of a 6-phytase derived from *Buttiauxella* spp. expressed in *Trichoderma reesei* on ileal and total tract nutrient digestibility in growing pigs. Twelve ileal cannulated pigs (initial BW = 25 kg) were randomly assigned to 1 of 6 treatments in a 6 × 6 Latin square design to give 12 observations per treatment. The experimental diets consisted of corn soybean meal based control diet (NC), NC supplemented with 4 levels of phytase (i.e., 250, 500, 1000, and 2000 FTU/kg) and a low-protein diet (5% casein) used to quantify endogenous AA losses. All diets contained titanium dioxide as indigestible marker. Pigs were given their daily feed allowance at a rate of 4.5% of BW determined at the beginning of each experimental period. Each period lasted for 9 d, with 5 d of adaptation to the assigned experimental diet followed by 2 d fecal and 2 d ileal digesta collections. Data were analyzed using the mixed model procedures of SAS (SAS Inst. Inc., Cary, NC). The final model had treatment as the main effect since pen and period effects were nonsignificant. Increasing levels of 6-phytase supplementation linearly increased apparent ileal digestibility (AID) of DM, CP and GE ($P < 0.01$). Compared with NC, AID of Ca and P respectively increased ($P < 0.05$) by 5.9, 11.7, 9.0, and 12.3% and 12.7, 46.6, 49.1, and 77.4% with 250, 500, 1000, and 2000 FTU/kg of phytase. Mean AID of dispensable and indispensable AA improved ($P < 0.05$) by 2.5, 2.0, and 1.0% and 2.0, 1.3, and 1.2%, respectively, for diets containing 500, 1000, and 2000 FTU/kg of phytase. Mean standard ileal digestibility (SID) of dispensable and non dispensable AA improved ($P < 0.05$) by 1.7, 1.2, and 2.8% and 1.0, 0.2, and 3.4% respectively, for diets with 500, 1000, and 2000 FTU/kg of phytase. Apparent total tract digestibility (ATTD) of DM, CP, and GE responded linearly ($P < 0.01$) to increasing levels of phytase. The ATTD of Ca and P respectively increased ($P < 0.05$) by 18.2, 30.4, 24.5, and 33.8% and 46.8, 98.4, 99.7, and 124.3% for diets supplemented with 250, 500, 1000, and 2000 FTU/kg of the 6-phytase. In conclusion, supplementation with a 6-phytase from *Buttiauxella* spp. expressed in *Trichoderma reesei* significantly enhanced the AID and ATTP of Ca, P, and other nutrients in pigs, in dose-dependent manner.

Key Words: amino acid, calcium, phosphorus, phytase, ileal digestibility, pig

---

0479 Nutrient digestibility of growing pigs fed phytase- and xylanase-supplemented wheat-based diets with low, medium, or high lysine level. T. A. Woyengo*[1], A. Owusu-Asiedu[2], and R. T. Zijlstra[1], *[1]University of Alberta, Edmonton, Canada, [2]DuPont Industrial Biosciences–Danisco Animal Nutrition, Marlborough, Wiltshire, UK.*

An experiment was conducted to determine the effect of adding xylanase to phytase-supplemented wheat-based diets containing low, medium, or high Lys on apparent ileal digestibility (AID) and apparent total tract digestibility (ATTD) of nutrients in growing pigs. Six ileal-cannulated barrows (initial BW = 39.1 ± 1.6 kg) were fed 6 diets in a 6 × 6 Latin square design. The 6 diets were a phytase-supplemented (500 FTU/kg) wheat-soybean meal-based basal diet with a standardized ileal digestible Lys content of 0.81% (low), 0.91% (medium), or 1.01% (high) and xylanase at 0 or 2000 XU/kg in a 3 × 2 factorial arrangement. The diets were similar in NE (1.79 Mcal/kg) and CP (25%); and the dietary AA levels were based on ideal AA ratio. The diets only differed in wheat and crystalline AA; the dietary level of AA was increased by increasing the dietary level of crystalline AA at the expense of wheat. All 6 diets contained 0.5% Cr_2O_3 as an indigestible marker. Dietary Lys level and xylanase interacted ($P < 0.05$) for AID of energy and all AA except Lys and Trp such that xylanase supplementation increased ($P < 0.05$) the AID of energy by 11%, and of the AA on average by 9% when the basal diet was low in Lys, but not when the basal diet was medium or high in Lys. Also, dietary Lys level and xylanase tended to interact ($P = 0.054$) on AID of Lys such that xylanase supplementation increased the AID of Lys only when the basal diet was low in Lys. Xylanase supplementation increased ($P < 0.05$) AID of Trp from 77.6 to 79.3%, and ATTD of energy from 79.1 to 80.2% regardless of dietary Lys level. In summary, an addition of xylanase to phytase-supplemented wheat-based basal diet for growing pigs can increase the AID and ATTD of energy but also AID of AA for diets limiting in Lys. In conclusion, the results from the present study indicate that diets could be formulated with reduced AA levels to optimize the benefits of xylanase supplementation to increase nutrient and energy digestibility in growing pigs.

Key Words: lysine, pig, xylanase

0480 The effects of β-mannanase (Hemicell HT) supplementation to nursery pig diets on nutrient digestibility and retention. C. Vonderohe*[1], A. M. Jones[1], B. T. Richert[1], J. E. Ferrel[2], P. D. Matzat[2], and J. S. Radcliffe[1], *[1]Purdue University, West Lafayette, IN, [2]Elanco Animal Health, Greenfield, IN.*

Three groups of 18 barrows with an initial BW of 10 ± 2.95 kg were blocked by BW and randomly assigned to diets containing 0, 32, or 48 kU/kg of β-mannanase (Hemicell HT, ChemGen Corp., Gaithersburg, MD) to investigate energy and N digestibility and retention. Pigs were individually housed in pens (0.35 m^2) and provided ad libitum access to feed and water for 7d. Following this 7d adaptation period, 12 pigs (4 pigs/diet in each group, 12 pigs/diet in total) were selected and moved to metabolic pens (0.84 m^2) where they remained for the final 7 d of the experiment. In the metabolic pens, feed was supplied at 9% of metabolic BW ($BW^{0.75}$) split evenly in 2 daily feedings and water was supplied ad libitum. A total collection of feces and urine was conducted for the final 4 d in the metabolism pens for subsequent determination of nutrient digestibility and retention. There was no effect of β-mannanase supplementation on growth ($P = 0.23$), feed efficiency ($P = 0.84$), or feed intake ($P = 0.27$) in either the adjustment period (d 0 to 7) or the collection period (d 7 to 14). Supplementing nursery pig diets with β-mannanase resulted in increased digestible ($P < 0.001$) and metabolizable ($P < 0.001$) energy and improved DM digestibility ($P < 0.001$) and N retention ($P < 0.02$). These responses to β-mannanase were greatest when β-mannanase was supplemented at 32 kU/kg. Feeding β-mannanase at 48 kU/kg resulted in DE, ME, and DM digestibility and N retention values that tended ($P < 0.10$) to be greater than control fed pigs, but were not significantly different from pigs fed 32 kU/kg β-mannanase. The results of this experiment indicate that β-mannanase supplementation improves energy digestibility and retention and DM digestibility and N retention in nursery pigs.

Key Words: pig, digestibility, β-mannanase

Table 0480.

β-mannanase, kU/kg:	0	32	48	MSE	*P*-value
DE, kcal/kg	$3300^{a,x}$	$3462^{b,y}$	$3385^{a,b,y}$	96.14	< 0.001
ME, kcal/kg	$3249^{a,x}$	$3429^{b,y}$	$3351^{a,b,y}$	94.96	< 0.001
N digestibility, %	91.2	91.4	91.8	0.88	0.18
N retention, %	72.2^{x}	77.2^{y}	$74.9^{x,y}$	4.49	0.02
DM digestibility, %	$83.5^{a,x}$	$87.2^{b,z}$	$85.6^{b,y}$	2.40	< 0.001

[a,b] Values in a row are different at α = 0.05.
[x,y,z] Values in a row are different at α = 0.10.

0481 Nucleotide supplementation in the diet of farrowing sows and its effect on milk quality, litter weight gain, and mortality. L. A. Vitagliano*[1], M. A. Bonato[2], R. L. D. C. Barbalho[2], G. D. Santos[2], and L. F. Araújo[1], *[1]Universidade de São Paulo, Pirassununga, Brazil, [2]ICC Brazil, São Paulo, Brazil.*

It is not yet understood whether increased nucleotides in sow milk are a response to a requirement of piglets or are part of the composition of milk, as it naturally occurs during lactation. However, exogenous nucleotide supplementation is able to further increase these levels. The objective of this study was to evaluate effects of nucleotide supplementation in farrowing sows diets on performance, RNA concentration in milk, and piglet litter performance. The nucleotides were derived from a yeast source containing hydrolyzed RNA (free nucleotides/nucleosides). The trial was conducted with 80 sows (Agroceres PIC) distributed in a completely randomized design (by parity order, avg. 3.7/treatment), with 4 treatments (0, 4, 8, and 12kg/MT of yeast or 0, 0.24, 0.48 and 0.72kg/MT of free nucleotides/nucleosides) and 20 replications of 1 sow in each. The sows were fed experimental diets starting 3 d before farrowing, until weaning of piglets at 21 d of age. The number of piglets per sow (10.48 ± 0.26) and piglet weight (1.70 ± 0.04kg) was equalized at birth. The sow parameters were weight after farrowing (WF, kg), weight after weaning (WW, kg), weight loss (WL, %), and feed intake (FI,kg). The number of weaned piglets (NWP), piglet weight at weaning (PWW,kg), litter weight at weaning (LWW, kg), litter weight gain (LWG, kg), mortality (MORT, %), and milk production (MP, kg; 1kg of piglet weight = 4 kg of milk) were measured. Samples of colostrum and milk (11, 20 d of lactation) were collected for laboratory analysis of RNA (mg/mL milk). The data were analyzed using the GLM (SAS Inst. Inc., Cary, NC), and means were compared by Tukey's test ($P = 0.10$). Nucleotide supplementation in the diet of farrowing sows resulted in no difference ($P > 0.10$) in WF, WW, WL, or FI. The piglets from sows fed diets supplemented with nucleotides had improved ($P < 0.10$) NWP, LWW, LWG, MORT, and MP compared with unsupplemented diets. There were no differences ($P > 0.10$) between treatments in PWW. In general, the 8 kg/MT and 12 kg/MT levels showed best piglet performance results (6 and 4.5% higher LWG than control group) and lower MORT (41.7 and 53.5% lower than control group). Nucleotide supplementation gave no significant response ($P > 0.10$) in total RNA in colostrums, but the amount of RNA present in milk at 11 and 20 d of lactation significantly increased ($P < 0.10$). This study demonstrated that supplementation of nucleotides to farrowing sows had a positive carryover effect on milk quality which, consequently, increased the litter weight gain and the number of weaned piglets (+3.5%).

Key Words: piglet, performance, RNA

0482 Evaluation of the efficacy of *Bacillus licheniformis* or sodium butyrate in front of a *Salmonella* Typhimurium oral challenge in piglets. E. Barba-Vidal*[1], L. Castillejos[1], V. F. Buttow Roll[2], J. J. Mallo[3], and S. Martín-Orúe[1], *[1]Animal Nutrition and Welfare Service, Department of Animal and Food Sciences Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Department of Animal Science, Faculty of Agronomy Eliseu Maciel, Federal University of Pelotas, Pelotas, Brazil, [3]Norel S.A., Madrid, Spain.*

The objective of the study was to evaluate the efficacy of *Bacillus licheniformis* (PROPORC, NOREL S.A.) or sodium butyrate (GUSTOR BP70, NOREL S.A.) in weanling pigs orally challenged with *Salmonella* Typhimurium. Seventy-two piglets (28 d old, 8.21 ± 0.79 kg) were divided into 24 pens allocated to 3 experimental diets: (1) CTR, base diet without additives; (2) PRO, base diet supplemented with 1 kg/t of PROPORC (equivalent to 10^9 CFU/kg of feed of *Bacillus licheniformis*); and (3) BUT, base diet supplemented with 3kg/t of GUSTOR BP70 (containing 70% sodium butyrate protected with vegetable fat). The base diet was multicereal (corn, wheat, and barley) with selected protein sources (soybean meal 44, fishmeal, and bovine sweet whey), without antibiotics and met NRC 2012 requirements. Consumption and weight gain of the animals were monitored during the trial (16 d). After a week of adaptation, the animals were orally inoculated with *Salmonella* Typhimurium (1×10^8 CFU). Parameters evaluated after the oral challenge were fecal consistency, rectal temperature (24 and 72 h postinoculation, PI) and fecal shedding of *Salmonella* (d 0, 1, and 7 PI). Moreover, on d 4 and 8 PI, 1 animal in each pen was euthanized to evaluate the serological inflammatory response (TNFα and Pig-Map), the microscopic ileal morphology, and the presence of *Salmonella* in the colon. No significant differences between treatments were seen on performance, fecal consistency, rectal temperature, or inflammatory markers ($P > 0.05$). However, a trend to reduction was observed in *Salmonella* prevalence in feces on d 7 PI (100, 75, and 75, $P = 0.074$) and significant reduction in colon on d 8 PI (88, 50, and 63, $P = 0.043$), for CTR, PRO, and BUT, respectively. Besides, on d 4 PI crypt depth showed a tendency to increase with the 2 supplemented diets (203, 239, and 251 203 μm, SEM ± 15.9, $P = 0.107$), for CTR, PRO, and BUT, respectively. The results obtained demonstrate that the administration of *Bacillus licheniformis* (10^9 CFU/kg) or sodium butyrate (3kg/mT) could improve intestinal morphology and reduce the colonization and fecal shedding of *Salmonella*Typhimurium in piglets.

Key Words: *Salmonella*, probiotic, sodium butyrate

0483 Effects of dietary supplementation of direct fed microbial on growth performance, nutrient digestibility, blood profiles, fecal microflora, and noxious gas emission in nursery pigs. J. H. Cho*[1], E. Kiarie[2], S. Indrakumar[2], and I. H. Kim[1], *[1]Department of Animal Science, Dankook University, Cheonan, South Korea, [2]DuPont Industrial Bioscience–Danisco Animal Nutrition, Waukesha, WI.*

A total of 128 weanling pigs [(Yorkshire × Landrace) × Duroc] with an average BW of 6.75 ± 0.59 were used in a 42-d experiment to investigate the efficacy of *Bacillus* spp. direct-fed microbial (DFM) on growth performance, indices of gut health and nutrient utilization in piglets. Pigs were allotted to experimental diets based on BW in a completely randomized block design. There were 2 dietary treatments: NC, basal diet (corn-soybean meal based diet); DFM, NC + DFM (1.5×10^5 cfu/g of feed). The DFM product was based on 1 strain of *B. subtilis* and 2 strains of *B. amyloliquefaciens* specifically selected and optimized for high enzyme production (Danisco Animal Nutrition, Marlborough, Wiltshire, UK). The diets were fed during the experiment in 2 phases: d 0 to 14, and 15 to 42. All diets, in pelleted form, were formulated to meet or exceed the nutrient requirements (NRC, 1998) for weanling pigs. Feed intake and BW were monitored weekly. We used 0.20% chromium oxide as indigestible marker and fecal samples were collected via rectal massage. Incidences of diarrhea were monitored in phase using a fecal scoring system (1 hard to 5 watery). At the end of each phase, 2 pigs/pen were bled for serum and fresh fecal samples were collected. At the end of the experiment, 1 pig/pen was killed to obtain small intestinal tissues for histomorphology and large intestinal digesta for select microbial counts. In the overall (d 0 to 42), pigs fed DFM had better G:F (0.694 vs. 0.680, $P = 0.04$) and tended to have a higher ADG (425 vs. 417 g/d, $P = 0.08$) compared with the NC fed pigs. Pigs fed DFM showed lower incidences of diarrhea ($P = 0.01$) than NC fed pigs on d 4. Duodenum and jejunum villi length of pigs fed DFM diets were longer ($P < 0.01$) than for pigs fed NC diet. Cecal digesta *Lactobacillus* counts tended to be higher ($P = 0.06$) in pigs fed DFM compared with the NC pigs; however, *Lactobacillu*s and *Escherichia coli* counts in the colon digesta were unaffected by the dietary treatments. Pigs fed DFM tended ($P < 0.09$) to have higher apparent total tract digestibility of crude protein and lower fecal ammonia release coinciding with low blood urea N concentration than the NC fed pigs. In conclusion, DFM supplementation improved growth performance and efficiency in nursery pigs linked to improved nutrients utilization and indices of gut health and function.

Key Words: weanling pigs, growth performance, gut health

0484 Tributyrin, a source of butyric acid, modulates the intestinal health of weaning pigs.

B. Tugnoli, M. Bertocchi, A. Piva, G. Sarli, and E. Grilli*, *DIMEVET University of Bologna, Ozzano Emilia BO, Italy.*

Aim of this study was to evaluate the intestinal architecture and expression of inflammatory and tight junction markers in piglets fed with tributyrin as dietary source of butyric acid. Twenty-one weaned pigs (n = 7), received a basal diet (control) or the diet supplemented with tributyrin or its encapsulated form at 1750 mg/kg (TB and m-TB, respectively), both providing 960 mg/kg of butyric acid equivalents. After 21 d, pigs were euthanized to collect duodenum, jejunum, ileum, and colon samples for histo-morphology, and cytokines and tight junction markers m-RNA analysis. Data were analyzed with 1-way ANOVA. Compared with control, m-TB induced deeper crypts in the duodenum (P = 0.09) and significantly reduced villi:crypts in the ileum (P = 0.04); goblet cells tended to be reduced by TB in duodenal villi (2.4-fold, P = 0.09), by both TB and m-TB in ileal villi (1.8- to 2.2-fold, respectively; P = 0.06), and by m-TB in colonic crypts (P = 0.08). Compared with control, TB tended to have higher TNF-α expression in the duodenum and ileum (P = 0.06 and P = 0.10), and higher IFN-γ level in the jejunum (P = 0.04), whereas in the colon m-TB downregulated IFN-γ and IL-1β level (2.2-fold and 1.7-fold; P = 0.06). Jejunal claudin-1 mRNA was reduced in m-TB compared with control (2.4-fold; P = 0.05). Similarly, in the colon claudin-1 mRNA was numerically lower in m-TB (2.1-fold) than in control group. Ileal occludin mRNA was reduced in both groups receiving tributyrin compared with control (1.6–2.2-fold for TB and m-TB; $P < 0.01$). In the colon occludin mRNA was downregulated in m-TB compared with control (1.4-fold; $P < 0.05$). The supplementation of tributyrin in the diet reduced the mucous-secreting goblet cells in a tract specific manner, tributyrin affecting the upper intestine while the microencapsulated form acting in the lower gut. The differential expression of cytokines in the upper and lower intestine by TB and m-TB, would suggest a differential modulation of cellular turnover and epithelial differentiation that would reflect differences in the anatomy and functionality of the gut segments. Nevertheless, the reduced expression of proinflammatory cytokines observed in the colon of m-TB indicate a reduced inflammation by butyric acid released via microencapsulated tributyrin. This beneficial effect mediated by m-TB would be substantiated by the parallel reduction of tight junction proteins gene expression in the hindgut probably indicating, by a mechanism of negative feed-back, a relatively higher abundance of these proteins and a tighter intestinal epithelium.

Key Words: tributyrin, microencapsulation, weaning piglet

0485 Effects of salmonella inhibitors on growth performance, relative organ weight, meat quality, salmonella populations, fecal gas emission, and blood profiles in broilers.

A. Hosseindoust*, H. L. Li, and I. H. Kim, *Department of Animal Science, Dankook University, Cheonan, South Korea*.

A total of 768 male and female ROSS308 broiler chicks [1 d old, BW = 37 ± 0.08 g] were used in this 5-wk trial (6 treatments with 8 replications/treatment and 16 chicks/pen) to evaluate the effect of salmonella inhibitors on growth performance, relative organ weight, meat quality, salmonella populations, fecal gas emission and blood profiles in broilers. A corn-soybean meal-based diet was formulated as a control diet and dietary treatments were as follows: (i) NC, basal diet (without antibiotics and *Bacillus subtilis*); (ii) PC, NC + 0.1% antibiotics (virginiamycin); (iii) A, NC + 0.1% *B. subtilis* 1.0×10^{10} cfu/kg; (iv) B, NC + 0.1% *B. subtilis* RX7 1.0×10^{10} cfu/kg; (v) C, NC + 0.1% *B. subtilis* B2A 1.0×10^{10} cfu/kg; (vi) D, NC + 0.1% *B. subtilis* RX7 1.0×10^{9} cfu/kg. Broilers were weighed and feed intake were recorded on d 14 and 35 for calculating BW gain (BWG), feed intake (FI), and feed conversion ratio (FCR). At d 35, 2 birds were randomly selected from each replication (16 broilers/treatment) and slaughtered by cervical dislocation for meat quality. During d 1 to 14, BWG was higher (393, 390 vs. 375 g; $P < 0.05$) in B and C treatments than NC treatment; moreover, NC treatment got higher (1.52 vs. 1.45; $P < 0.05$) FCR than B treatment. During d 15 to 35, NC treatment group had higher FCR (1.81 vs. 1.72; $P < 0.05$) than C treatment fed broilers. Overall, chickens fed with C diet had higher (1648 vs. 1569 g; $P < 0.05$) BWG and lower (1.65 vs. 1.74; $P < 0.05$) FCR than those fed with NC diet. No significant difference ($P > 0.05$) was observed in meat quality, relative organ weight, gas emission and blood profiles among treatments. However, the salmonella populations of chickens fed with NC diet was higher (2.94 vs. 2.50, 2.47, 2.51, 2.51 $\log_{10}$ cfu/g; $P < 0.05$) compared with those fed with PC, B, C, and D diets in large intestine, moreover, the salmonella populations of NC treatment was higher (2.81 vs. 2.56, 2.48, 2.48, 2.55, 2.47 $\log_{10}$cfu/g; $P < 0.05$) compared with other 5 treatments in small intestine. In conclusion, salmonella inhibitors partially improved BWG, FCR, while decreasing salmonella populations in intestine without any adverse effect on meat quality, relative organ weight, gas emission, and blood profiles in broilers.

Key Words: blood profiles, broilers, growth performance, meat quality, salmonella inhibitors, salmonella populations

PHYSIOLOGY AND ENDOCRINOLOGY: PREGNANCY, PLACENTATION, AND REPRODUCTIVE HEALTH IN RUMINANTS

0486 Bioinformatics analysis of mammary gland and liver transcriptome in response to an intramammary *Escherichia coli* lipopolysaccharide challenge in early-lactation dairy cattle.

A. Minuti*[1], D. E. Graugnard[2], E. Trevisi[1], and J. J. Loor[2], [1]*Università Cattolica del Sacro Cuore, Piacenza, Italy,* [2]*Universty of Illinois, Urbana, IL.*

During mastitis, pathogens are detected by the receptors on the epithelial cells of the mammary tissue and an acute phase response activates the immune system to eliminate the pathogens. The liver is a central organ during inflammation and synthesizes the necessary components for immediate defense at the site of tissue damage. The objective of this study was to determine gene expression patterns in mammary and liver tissue in response to an intramammary *E. coli* lipopolysaccharide (LPS) challenge in early lactating dairy cattle. Fourteen Holstein cows were used. At ~7 d in milk, 7 cows served as controls (CTR) and 7 cows (LPS) received an intramammary *E. coli* LPS challenge (200 μg in sterile saline). For transcript profiling the mammary and liver tissue were sampled by biopsy 2 h after the challenge. A bovine oligonucleotide (70-mers) microarray with > 13,000 annotated sequences was used for profiling. Data were analyzed using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) and a threshold of 1.5-fold change and a *P* value of 0.05 were considered to define differentially expressed genes (DEG). Bioinformatics analyses was conducted using the dynamic impact approach (DIA) and ingenuity pathway analysis (IPA; Ingenuity Systems, Inc.). In mammary tissue, a total of 189 DEG (20 downregulated, 169 upregulated) were observed in LPS vs. CTR cows. The most-impacted and activated KEGG pathways highlighted by the DIA analysis were NOD-like receptor signaling, RIG-I-like receptor signaling, apoptosis, cytosolic DNA-sensing, and chemokine signaling. The IPA analysis underscored the presence of 13 transcription regulators (2 downregulated, 11 upregulated) of which 4 upregulated (NF-kB, MYC, STAT3, and HIF1A) are key components of inflammatory response processes and are involved in cell apoptosis. In liver tissue, a total of 107 DEG (42 downregulated, 65 upregulated) were observed due to LPS. The DIA analysis highlighted the inhibition of Fatty acid elongation in mitochondria and activation of p53 signaling pathway. From IPA analysis, the most important upregulated transcription regulators (ZFP36, CEBPD, MYC, and CREM) are involved in the immune and inflammatory responses and are necessary to maintaining homeostasis of the organism during infection. Results suggest that within 2 h from intramammary LPS challenge the liver responds to stimuli and alters its transcriptome as a way to maintain homeostasis.

Key Words: system biology, mammary, liver, lipopolysaccharide

0487 The role of pH and progesterone on bovine uterine protein secretion in response to maternal recognition, interferon-tau.

J. A. Spencer*[1], K. J. Austin[2], K. G. Carnahan[1], and A. Ahmadzadeh[1], [1]*University of Idaho, Moscow,* [2]*Department of Animal Science, University of Wyoming, Laramie.*

Low uterine pH, associated with high dietary protein and blood urea, reduces fertility in dairy cows. The objective of this in vitro study was to determine the direct effects of a low pH on bovine endometrial (BEND) cells expression of Mx1 and ISG-15 in response to embryonic maternal recognition, interferon-tau (IFNτ), in the presence or absence of progesterone (P_4). In 2 experiments, using BEND cells as a model, the effects of a low pH environment was examined to determine the production of 2 IFNτ stimulated proteins, ISG-15 and Mx1. Bovine endometrial cells were grown to 80% confluency and further incubated for additional 24 h in culture media containing no P_4 (0 M; Exp. 1) or P_4 (10^{-7} M, Exp. 2). To reduce the pH, in both experiments, cells (90% confluent) were treated with dimethyldioxirane (DMD), at final concentrations of 0, 10, 15, and 20 m*M* (pH of 7.35, 7.17, 6.9, and 6.76, respectively) and subsequently, challenged with 0 or 10,000 antiviral units of rIFNτ. Cells were incubated for an additional 24 h. Once harvested, BEND cells were lysed and supernatants were analyzed and quantified for Mx1 and ISG-15, using SDS-PAGE and Western Immunoblotting protocols. Based on optical density, at 0 mM DMD, regardless of P_4 treatment, IFNτ increased ($P < 0.01$) Mx1 and ISG-15 in both experiments. In Exp. 1 (P_4 free environment), there was effect of DMD ($P < 0.01$) and DMD by IFNτ interaction ($P < 0.01$) on both Mx1 and ISG-15. The 15 and 20 m*M* DMD reduced ($P < 0.01$) IFNτ- induced Mx1 expression, whereas only 20 m*M* DMD reduced ($P < 0.01$) ISG-15 expression in response to IFNτ. In Exp. 2, in presence of P_4, there was a significant effect of DMD and IFNτ by DMD interaction ($P < 0.01$) on Mx1 expression. However, there was no effect of DMD or DMD by IFNτ interaction on protein expression of ISG-15 ($P = 0.2$ and 0.4) in a P_4 environment. These results show that in absence of P_4 and low pH, IFNτ-stimulated proteins secretion are abrogated; however, P_4 overcame pH-induced decreased of ISG-15 but not Mx1. Progesterone may regulate the secretion of IFNτ- stimulated proteins in an acidic uterine environment.

Key Words: acidic pH, progesterone, interferon, bovine endometrial cells

0488 Hepatic steroid inactivating enzymes, hepatic portal blood flow, and corpus luteum blood perfusion in lactating dairy cattle. C. G. Hart*, B. E. Voelz, K. E. Brockus, and C. O. Lemley, *Mississippi State University, Mississippi State.*

In ruminants, a decrease in pregnancy rates may be due to decreased concentrations of progesterone (P4). It is important to note that both production from the corpus luteum and/or hepatic steroid inactivation impacts peripheral concentrations of P4. Cattle with an elevated dry matter intake have increased blood flow to the digestive tract and liver. This in turn leads to an increased delivery rate of steroids to the liver, and thus increased metabolism of these substrates. Excessive hepatic steroid inactivation contributes to decreased peripheral concentrations, which can alter reproductive performance. The objective of this study was to examine the activity of hepatic steroid inactivating enzymes in pregnant vs. nonpregnant lactating Holstein cows. Cows were synchronized using the Ovsynch plus CIDR (controlled internal drug release device) protocol and bred via artificial insemination on d 0. At d 10 post-AI, hepatic portal blood flow was measured via transabdominal Doppler ultrasonography. Images of corpus luteum blood perfusion were collected using the power flow program of the Doppler ultrasound. Blood perfusion was analyzed by examining pixel density using ImageJ software. Liver biopsies were collected and frozen for later determination of cytochrome P450 1A (CYP1A), 2C (CYP2C), 3A (CYP3A), and uridine diphosphate-glucuronosyltransferase (UGT) activities via luminogenic substrates. Aldo-keto reductase 1C (AKR1C) activity was measured using the specific substrate 1-acenaphthenol. Pregnancy was determined at d 33 of gestation and treatment groups were retrospectively assigned as pregnant or nonpregnant. Data were analyzed using the mixed procedure of SAS (SAS Inst. Inc., Cary, NC). CYP1A, CYP2C, CYP3A, and AKR1C activity did not differ ($P > 0.10$) between pregnant and nonpregnant cows. Activity of UGT per kg of BW was increased ($P < 0.05$) in pregnant (60.1 ± 3.4 RLU·min^{-1}·kg^{-1}) vs. nonpregnant (50.6 ± 3.4 RLU·min^{-1}·kg^{-1}) cows. Blood perfusion of the corpus luteum did not differ ($P > 0.30$) between pregnant and nonpregnant cows. Absolute hepatic portal blood flow was increased ($P < 0.05$) in pregnant (997 ± 78 L/h) vs. nonpregnant cows (748 ± 78 L/h). Portal blood flow per kg of BW was increased ($P < 0.05$) in pregnant (1.65 ± 0.13 L/h/kg) vs. nonpregnant cows (1.27 ± 0.13 L/h/kg). The current study highlights the relevance of further investigation into steroid secretion and inactivation and their impact on the maintenance of pregnancy in dairy cattle.

Key Words: blood flow, cattle, steroid

0489 Effects of supplementing Holstein heifers with dietary melatonin during late gestation on growth and cardiovascular measurements of offspring. K. E. Brockus*, C. G. Hart, S. H. Ward, and C. O. Lemley, *Mississippi State University, Mississippi State.*

The objective was to examine the effects of supplementing dams with dietary melatonin during late gestation on offspring cardiovascular and growth measurements. On d 190 of gestation, heifers ($n = 20$) were blocked by BW and then randomly assigned to 1 of 2 dietary treatments: (1) 20 mg of dietary melatonin d^{-1} (MEL) or (2) no melatonin supplementation (CON). Dietary treatments were terminated on d 262 of gestation. At birth, calves were separated from their dams and given 3.8 L of colostrum. Calves were fed 5.7 L of whole milk daily and offered 0.9 kg/d of starter grain. Starter was increased by 0.9 kg/d when orts were 0 kg. Calf ($n = 18$) measurements of growth, blood pressure, and cortisol were collected on wk 0, 1, 2, 3, and 4 of age. Calf hepatic portal blood flow, determined by transabdominal Doppler ultrasonography, and concentrations of IGF-1 were determined on wk 0 and 4 of age. Dependent variables were analyzed using repeated-measures ANOVA of the mixed procedure of SAS (SAS Inst. Inc., Cary, NC) with the model statement containing treatment, age, and their respective interaction. Calf BW, abdominal girth, hip height, and wither height increased ($P < 0.05$) with age. An age by treatment interaction ($P < 0.01$) was observed for calf heart girth, which was decreased at wk 2 in calves from MEL treated heifers compared with calves from control treated heifers. Pulse pressure (41 ± 2 mm Hg), mean arterial pressure (90 ± 2 mm Hg), absolute hepatic portal blood flow (3137 ± 326 mL/min), and blood flow relative to body weight (74 ± 8 mL/[min × kg]) were not different ($P > 0.05$) between treatments. A main effect of calf age ($P < 0.05$) was observed for concentrations of IGF-1, which was decreased at wk 4 (9.0 ± 0.4 ng/mL) compared with wk 0 (10.8 ± 0.9 ng/mL). An age by treatment interaction ($P < 0.05$) was observed for concentrations of cortisol, which was decreased at wk 2 in calves from MEL treated dams (1.2 ± 0.8 ng/mL) compared with calves from CON treated dams (5.8 ± 0.8 ng/mL). Early postnatal growth and hepatic portal blood flow were not different in offspring born to dams supplemented with dietary melatonin. However, the difference in offspring concentrations of cortisol following maternal melatonin supplementation needs further investigation.

Key Words: cortisol, hepatic portal blood flow, melatonin

0490 Uterine blood flow, calf, and placental weights from beef cows supplemented during late gestation. V. C. Kennedy*, B. R. Mordhorst, M. L. Bauer, K. C. Swanson, and K. A. Vonnahme, *North Dakota State University, Fargo.*

Maternal nutrition impacts uterine blood flow (BF), thus offspring development. This study's objective was to investigate the effects of supplementing dried distiller's grains with solubles (DDGS) during late gestation on uterine BF, calf and placental weights. Multiparous beef cows were randomly divided into a control group (CON; $n = 15$) consuming a diet containing 90% corn stover and 10% corn silage (DM basis) ad libitum and a treatment group (TRT; $n = 12$) consuming the same diet and DDGS (0.3% BW). Corn silage inclusion was increased to 30% as gestation progressed. Intake was monitored and controlled via Insentec roughage feeders. Ipsilateral and contralateral uterine BF and cross-sectional area (CSA) at the bifurcation of each uterine artery was measured by Doppler ultrasonography on d 180, 216, and 246 of pregnancy. At parturition calves and placentas were weighed. Data analysis utilized the mixed procedure in SAS (SAS Inst. Inc., Cary, NC). Contralateral uterine artery BF and CSA increased ($P < 0.01$) as gestation advanced. For ipsilateral uterine artery BF and CSA, there was a treatment by day of gestation interaction ($P < 0.05$). The CSA was similar ($P = 0.30$) on d 181, but was greater ($P \leq 0.02$) in TRT vs. CON cows on d 216 and 246 (0.94 vs. 0.71 ± 0.07 cm^2 and 1.14 vs. 0.76 ± 0.07 cm^2, respectively). Ipsilateral BF tended to be greater ($P = 0.06$) on d 181 in TRT cows compared with CON (11.4 vs. 8.2 ± 1.1 L/min), and was greater on d 216 and 246 (21.1 vs. 15.4 ± 1.8 and 32.6 vs. 19.6 ± 2.7 L/min, respectively). There was no treatment by day interaction ($P = 0.17$) for total uterine BF, but there was a main effect of treatment ($P = 0.02$) and day ($P < 0.01$). DDGS cows had increased uterine BF compared with CON (25.5 vs. 19.1 ± 1.8 L/min). Total uterine BF increased ($P < 0.01$) as gestation advanced (12.2, 22.2, 32.7 ± 2.2 L/min for d 181, 216, and 246). While there was no effect of treatment on gestation length ($P = 0.43$) or placental weights ($P \geq 0.22$), there was a tendency ($P = 0.06$) for calves born to TRT cows to be heavier (43.3 vs. 40.5 ± 1.0 kg). Supplementation with DDGS increased uterine BF which contrasts with our previous study; protein and caloric intake differences between these studies is currently under investigation.

Key Words: beef cow, pregnancy, uterine blood flow

0491 Possible markers of uterine and metabolic health in transition dairy cows. G. Esposito*[1,2], A. Chapwanya[2], E. C. Webb[2,3], and P. C. Irons[1,2], *[1]Department of Production Animal Studies, Faculty of Veterinary Sciences, University of Pretoria, Onderstepoort, South Africa, [2]Institute of Food, Nutrition and Well-being University of Pretoria, Pretoria, South Africa, [3]Department of Animal and Wildlife Sciences, Faculty of Natural and Agricultural Sciences, University of Pretoria, Pretoria, South Africa*.

In transition dairy cows negative energy balance (NEB) status commonly leads to perturbed fertility, reduced immune function and decreased milk yield. The objective of this study was to investigate the relationship between indicators of NEB, systemic inflammation postpartum, and genital diseases in transition dairy cows. Prepartum Holstein cows ($n = 10$), from 20 d before the predicted day of calving until 35 d in milk (DIM) were assigned to 2 treatments: NEB (80% net energy requirements) and control. Dry matter intake (DMI) was recorded daily and clinical evaluation was conducted once a week. From the day of calving, milk yield, somatic cells count (scc), lactose, fat, protein, and fat/protein ratio were recorded daily. From 7 till 35 DIM, weekly endometrial samples were collected for cytological evaluation, metagenomic characterization of the endometrial DNA and measurements of the expression of inflammatory genes. Ovarian activity was monitored every other day from 7 DIM. Blood samples were collected weekly and analyzed for NEFA, β-hydroxybutyrate (BHBA) and cholesterol. Correlationship between variables was evaluated using Spearman's rank correlation test. Moreover, a stepwise regression analyses was performed to explain variability of indicators of uterine and metabolic status. As expected, NEB cows showed higher DMI ($P < 0.1$), lower milk production ($P < 0.05$) and a higher fat:protein ratio ($P < 0.05$) until 35 DIM. In addition, NEFA and BHBA were higher in the NEB cows ($P < 0.05$), while cholesterol was lower ($P < 0.001$). Moreover, even if not strong, a negative correlation was observed between BHBA levels and increment in BCS (-0.37), and between NEFA and numbers of dominant follicles observed (-0.25). In addition, a negative correlation was observed between percentage of polymorphonuclear cells (PMS), from the endometrial samples, and serum cholesterol (-0.40) supporting our hypothesis that total cholesterol level could be one of the possible markers for uterine health evaluation. In addition, a positive correlation was observed between NEFA and PMS cells (-0.40). Furthermore, the stepwise regression analysis confirmed that serum BHBA and cholesterol levels were the ones that better explained the other variables (clinical evaluation, intake, reproduction). Data regarding the metagenomic characterization of the endometrial DNA and on the expression of inflammatory genes are still pending. The preliminary results confirmed the effects of NEB on biochemical parameters with potential as

predictors of metabolic and genital diseases. Further validation based on larger data sets is required.

Key Words: negative energy balance, transition cow, uterine involution

0492 Pregnancy-induced changes in metabolome and proteome in ovine uterine flushings. T. R. Hansen*, J. J. Romero, C. Broeckling, and J. E. Prenni, *Colorado State University, Fort Collins.*

The endometrium serves as a primitive placenta by secreting histotroph, which nourishes the developing conceptus (embryo proper and extraembryonic membranes). Modern mass spectroscopy (MS) approaches allow for global analysis of proteins and metabolites in bodily fluids. We hypothesized that global MS can identify metabolites and proteins that are induced by pregnancy in uterine flushings. To test this hypothesis, uteri were collected on d 12 of the estrous cycle (n = 5 ewes not exposed to ram) or d 12 (n = 4), 14 (n = 5), or 16 (n = 5) of pregnancy (confirmed by presence of conceptus) and flushed using physiological buffered saline. Pregnancy status and Day were main effects analyzed by GLM-SAS (SAS Inst. Inc., Cary, NC). Metabolites were extracted from uterine flushings using 80% methanol and profiled using UPLC-MS. The proteome was examined by digestion with trypsin, followed by analysis of peptides with LC-MS/MS. Metabolite profiling resulted in the detection of 8510 molecular features, of which 5 were confirmed to be upregulated (> threefold and $P < 0.05$) in response to pregnancy by d 14 to 16 and were not detected on d 12: acetylcarnitine, carnitine, ecdysteroids, N-acetyl dileucine, and valine. These metabolites function in fatty acid transport (carnitines), antiapoptotic mechanisms (ecdysteroids), and availability of nutrients (amino acids). Proteome analysis resulted in the detection of 783 proteins that were differentially regulated ($P < 0.05$) by d 14 to 16 of pregnancy, 7 of which are described herein: annexin A1, A2, and A5; calcium binding protein (S100A11); profilin 1, trophoblast kunitz domain protein 1 (TKDP), and interferon tau (IFNT). These proteins have unique functions in mediating endocytosis, exocytosis, calcium signaling, and inhibition of prostaglandins (annexins and associated S100A11); protecting against maternal proteases (TKDP); remodeling cytoskeleton (profilin 1); and altering uterine release of prostaglandin F2 α, as well as inducing interferon stimulated genes in the endometrium and the corpus luteum (IFNT). It is concluded that global MS approaches are poweful in delineating the metabolome and proteome in uterine flushings and identifying differential expression in response to the conceptus by d 14 to 16 of pregnancy. *USDA NIFA AFRI 2011–67015–20067.*

Key Words: pregnancy, uterus, conceptus, proteome, metabolome

0493 Syncytin expression in uterine endometrium and fetal membranes during early pregnancy in sheep. K. J. McLean*, L. P. Reynolds, A. Grazul-Bilska, J. Haring, and J. S. Caton, *North Dakota State University, Fargo.*

Endogenous retroviruses may be involved in formation of the placental interface between the endometrium and fetal membranes (FM). When this interface is not adequately formed, fetal loss or growth retardation may occur. Syncytin is an integrated retroviral envelope gene thought to be involved in cell-cell fusion and immunosuppression within the mammalian placenta; however, in sheep the exact function of syncytin is unknown. Ewes also possess ~20 copies of another endogenous retrovirus (enJSRV) which is closely related to the exogenous Jaagsiekte sheep retrovirus. Integration and expression of enJSRV strains, in the placenta, is breed specific. To examine syncytin and enJSRV expression at the maternal-fetal interface throughout early gestation, crossbred western whiteface (primarily Rambouillet, Targhee, and Columbia) ewes were naturally mated and gravid uteri were obtained on d 14, 16, 18, 20, 22, 24, 26, 28, and 30 (n = 6 to 8/d) after mating (day of mating = d 0). Nonpregnant, mid-luteal ewes (d 10; n = 8) were used as controls. Expression of syncytin and enJSRV-18 was determined with snap-frozen caruncular (maternal placental) tissue and FM (chorion on d16 and chorioallantois thereafter) using quantitative real-time RT-PCR. Statistical analyses used PROC GLM of SAS (SAS Inst. Inc., Cary, NC) with orthogonal contrasts. Fetal length increased threefold ($P < 0.001$) from d 20 (5.50 ± 0.97 mm) to d 30 (19.29 ± 0.52 mm) of gestation. Fetal membrane expression of syncytin decreased from d 16 thru d 20, was increased from d 22 until d 26, and decreased, again, to d 30 ($P = 0.002$). Both fetal growth patterns and FM expression of syncytin had significant linear ($P < 0.005$) and cubic ($P < 0.001$) orthogonal contrasts. Pregnant ewes had greater syncytin expression ($P = 0.002$) compared with nonpregnant ewes. Syncytin expression in caruncular tissues decreased from d 14 until d 20, then increased to d 24 and remained steady to d 30 of gestation ($P = 0.009$) resulting in quadratic ($P = 0.01$) and cubic ($P = 0.001$) orthogonal contrasts. Interestingly, neither FM nor caruncular tissues of western whiteface ewes expressed detectable levels of enJSRV-18. Therefore, syncytin but not enJSRV-18 is likely involved in the regulation of placental function and growth during pregnancy in western whiteface sheep. *Supported by USDA-NRI Grant 2007–01215 to LPR and ATGB.*

Key Words: early gestation, placenta, syncytin

0494 Effect of postpartum treatment with nonsteroidal anti-inflammatory drugs (NSAID) on reproductive performance and removal from the herd in dairy cattle through mid-lactation.

A. J. Carpenter*[1], C. M. Ylioja[1], C. F. Vargas Rodriguez[1], L. G. D. Mendonça[1], L. Mamedova[1], J. F. Coetzee[2], L. Hollis[1], R. Gehring[3], and B. Bradford[1], [1]*Department of Animal Sciences and Industry, Kansas State University, Manhattan,* [2]*Pharmacology Analytical Support Team, Iowa State University College of Veterinary Medicine, Ames,* [3]*Department of Clinical Sciences, Kansas State University, Manhattan.*

Many studies have evaluated the use of postpartum NSAID treatment in dairy cattle, but few have monitored long-term responses to such treatments. To address this limitation in the literature, 153 multiparous dairy cattle were blocked by breed, dystocia, and twin births, and assigned to 1 of 3 treatments within 12 to 36 h after parturition. Treatments were 1 placebo bolus on the first day after parturition and 3 consecutive daily drenches of sodium salicylate (125 $g \cdot cow^{-1} \cdot d^{-1}$) beginning on the first day after parturition (SS); 1 bolus of the NSAID meloxicam (675 mg/cow) and 3 drenches of an equal volume of water (M); and 1 placebo bolus and 3 drenches of water (CON). As previously reported, milk production was increased in the first 9 wk of lactation by either NSAID treatment in cows experiencing dystocia, but in cows that calved normally, milk yield increased only after treatment with M. The objective of this analysis was to determine if NSAID treatment influenced reproductive performance and risk of removal from the herd in approximately the first half of lactation (up to 160 d in milk, DIM). Removal rate from the herd and time to pregnancy were evaluated by Cox regression proportional hazard analysis, and incidence of disease was tested by Fisher's exact test. Treatment, breed, dystocia, twin births, and their interactions did not ($P > 0.1$) affect time to pregnancy or first service pregnancy per AI (21.9%). A total of 33 cows left the herd during the period investigated, and M cows were ($P = 0.02$) removed from the herd at a slower rate than CON (AHR = 0.33, 95% CI = 0.13, 0.84), with no effect observed for SS ($P = 0.28$, AHR = 0.66, 95% CI = 0.30, 1.42). Treatment did not affect the risk of leaving the herd due to mastitis, low milk production, injury, lameness, or death (all $P > 0.1$). However, M tended to decrease the risk of culling due to other diseases—including respiratory disease, displaced abomasum, and suspected metabolic disorders—compared with CON ($n = 7$ CON vs. 1 M; $P = 0.06$). Furthermore, 4 of the CON cows in this category were removed from the herd before 19 DIM, whereas the M cow was removed at 149 DIM. These results indicate that in addition to elevated milk production, postpartum administration of M may have beneficial effects on dairy cow longevity.

Key Words: inflammation, NSAID, cull rate, reproduction

0495 Biology and molecular signatures of elongating preimplantation conceptuses in dairy cows.

E. S. Ribeiro*[1], L. F. Greco[1], R. S. Bisinotto[1], F. S. Lima[2], W. W. Thatcher[1], and J. E. P. Santos[1], [1]*Department of Animal Sciences, University of Florida, Gainesville,* [2]*University of Florida, Gainesville.*

The objectives were to investigate changes in transcriptome of preimplantation conceptuses during the process of elongation and associated changes in the concentration of interferon-tau (IFN-τ) in utero. Lactating dairy cows ($n = 160$) had estrous cycles synchronized and were subjected to induced ovulation and timed artificial insemination (AI). The day of AI was considered study d 0. On d 15, uteri were flushed and IFN-τ concentration in fluid measured. Recovered conceptuses were classified based on morphology and length as ovoid (OV; 1 to 4 mm), tubular (TUB; 5 to 19 mm), and filamentous (FIL; 20 to 85 mm). A subsample of conceptuses from each group had mRNA extracted and subjected to transcriptome analysis using Affymetrix Gene Chip Bovine Array (8 OV, 17 TUB, and 17 FIL). The experimental design was considered a prospective cohort study with 3 independent groups. Continuous variables were analyzed by ANOVA using the GLIMMIX procedure of SAS (SAS Inst. Inc., Cary, NC) and fitting adequate data distribution. Microarray data were analyzed using Bioconductor software in R environment. Data were preprocessed using Gene Chip Robust Multi-Array function. Limma package was used to fit a linear model and adjust variances by empirical Bayes adjustment. Moderate *t* test was performed for all pairwise comparisons, and *P* values were adjusted for multiple testing using the Benjamini and Hochberg false discovery rate. Adjusted $P < 0.05$ and fold change > 1.5 characterized significant differences. Functional analyses were performed using Ingenuity Pathway Analysis. Concentration of IFN-τ in uterine flushing differed ($P < 0.05$) among all 3 groups and was lower for cows with OV conceptus, followed by those with TUB and then FIL conceptuses (13.7, 326.8, and 2544.7 ng/mL, respectively). Transcriptome analyses revealed the upregulation of 321 and downregulation of 345 transcripts in the transition from OV to TUB, and the upregulation of 249 and downregulation of 154 transcripts in the transition from TUB to FIL. A total of 1441 transcripts were differently expressed when OV and FIL conceptuses were compared. Differently expressed genes were associated significantly with cellular movement, cell-to-cell signaling and interaction, cellular assembly and organization, lipid metabolism, small molecule biochemistry, and molecular transport. In conclusion, differences in conceptus morphology and length were associated with distinct concentrations of IFN-τ in utero and remarkable changes in transcriptome of trophectoderm cells that elucidate important cellular events occurring during conceptus elongation.

Key Words: conceptus elongation, transcriptome, dairy cow

0496 Modulation of the immune system during postpartum uterine infection. C. G. Walker*[1], S. Meier[1], J. R. Roche[1], M. D. Mitchell[2], and C. Burke[1], [1]*DairyNZ, Auckland, New Zealand,* [2]*University of Queensland, Australia.*

Postpartum uterine infection is associated with lower fertility at both the time of infection and after the infection has resolved. The objective of this study was to characterize genome-wide DNA methylation and gene expression in the endometrium of dairy cows with subclinical endometritis. It was hypothesized that aberrant DNA methylation may be involved in the subfertility associated with postpartum uterine infection. Endometrial tissues were obtained at 29 d postpartum (n = 12) and Agilent 2-color microarrays were used to characterize transcription and DNA methylation profiles. Analyses revealed 1856 probes to be differentially expressed in animals with subclinical endometritis (SUI) compared with control cows ($P <$ 0.05, Storey Multiple testing correction). No significant associations among DNA methylation and gene expression were detected. Further analysis using GeneGo Metacore and Gene Set Enrichment Analysis identified several pathways and processes enriched in the comparison. Several pathways that are involved in the innate immune response were enriched in SUI cows. Consistent with activation of toll like receptors (TLR) by microorganisms present in the uterus, there was enrichment for the TLR signaling pathway including increased expression of the transcription factor NFKB1, the proinflammatory cytokines IL1A and IL1B, downstream chemokines, cytokines, and acute phase and antimicrobial proteins in the endometrium of SUI cows. Further, the chemokine signaling pathway was enriched in SUI cows, with increased expression of genes that attract cells of the innate immune system. Increased expression of IL-8 and CXCL6, chemotactic factors for recruitment of neutrophils along with the immune cell surface marker PTPRC in SUI cows is consistent with the greater number of polymorphonuclear cells present in the uterus of these cows. Several antimicrobial peptides (LAP, TAP, DEFB1, DEFB10, DEFB103B, DEFB7) and acute phase proteins including SAA3, LBP, and the complement gene CFB had greater expression in SUI cows. Gene expression profiles in cows with subclinical endometritis in this study indicate that the immune response is activated, potentially resulting in a local proinflammatory environment in the uterus. If this period of inflammation is prolonged it could result in tissue damage or failure to complete involution of the uterus that may create a suboptimal environment for future pregnancy.

Key Words: endometritis, gene expression

0497 Carryover effects of postpartum diseases on early conceptus development in dairy cows. E. S. Ribeiro*, L. F. Greco, G. C. Gomes, R. Cerri, W. W. Thatcher, and J. E. P. Santos, *Department of Animal Sciences, University of Florida, Gainesville.*

Postpartum diseases constitute one of the major problems affecting fertility in dairy cows. The objective was to investigate the carryover effects of postpartum clinical diseases on early embryo development. From calving to first artificial insemination (AI), prevalence of calving problems, metritis, mastitis, lameness, digestive, and respiratory problems were recorded for a group of 617 dairy cows. Cows had estrous cycles synchronized and were subjected to induced ovulation and timed AI. A total of 419 cows had their uterus flushed on d 6 after AI and the structures recovered were evaluated for fertilization and embryo quality. The remaining 198 cows had their uterus flushed on d 15 after AI and interferon-tau (IFN-τ) concentration in fluid was measured and the recovered conceptuses were evaluated for size and morphology. A subsample of conceptuses (n = 22) had mRNA extracted and subjected to transcriptome analysis using Affymetrix Gene Chip Bovine Array. The experimental design was considered a prospective cohort study with 2 independent groups (healthy vs. diseased). Continuous variables were analyzed by ANOVA and binary data by logistic regression using the GLIMMIX procedure of SAS (SAS Inst. Inc., Cary, NC) and fitting adequate data distribution. Microarray data were analyzed using Bioconductor software in R environment. Data were preprocessed using Gene Chip Robust Multi-Array function. Limma package was used to fit a linear model and adjust variances by empirical Bayes adjustment. Moderate t test was performed for all pairwise comparisons, and P values were adjusted for multiple testing using the Benjamini and Hochberg false discovery rate. Adjusted $P < 0.05$ and fold change > 1.5 characterized significant differences. Functional analyses were performed using Ingenuity Pathway Analysis. Cows that had at least 1 clinical disease from calving to first AI had reduced fertilization, smaller proportion of good quality embryos on d 6, smaller size of conceptus and smaller concentration of IFN-τ on d 15 compared with cows that did not have clinical diseases. Controlling for size of the conceptuses, transcriptome analysis resulted in 41 transcripts that were differently expressed. The gene with the greatest difference in expression was FAT/CD36, which is important for cell signaling during conceptus elongation. FAT/CD36 was downregulated in conceptus recovered from cows that had diseases compared with those recovered from cows that did not have disease. In conclusion, clinical diseases prior insemination were associated with reduced fertilization and compromised early embryo development.

Key Words: embryo, dairy cow, disease

PHYSIOLOGY AND ENDOCRINOLOGY: INTERRELATIONSHIPS BETWEEN ENVIRONMENTAL, METABOLIC, AND PHYSIOLOGICAL PROCESSES I

0498 Insulin sensitivity of the lipid metabolism of precalving dairy cows across a range of body condition scores. J. De Koster* and G. Opsomer, *Department of Reproduction, Obstetrics and Herd Health, Faculty of Veterinary Medicine, Ghent University, Ghent, Belgium.*

Insulin plays a central role during the transition period of dairy cows by influencing glucose, lipid, and protein metabolism. At the adipose tissue, insulin stimulates lipogenesis and inhibits lipolysis, thereby regulating the circulating NEFA concentration. Overconditioning is known to induce insulin resistance of the glucose metabolism in dairy cows. In the present study, we identified if factors related to adiposity (BCS, BFT, NEFA concentration during the dry period) influenced insulin sensitivity of the lipid metabolism in 8 healthy dairy cows at the end of pregnancy across a range of BCS (2.75 to 5). Hyperinsulinemic euglycemic clamp tests were performed consisting of 4 insulin infusions: 0.1, 0.5, 2, or 5 $mU \cdot kg^{-1} \cdot min^{-1}$. At regular time intervals during the infusions, blood glucose concentration was determined using a glucometer and the speed of a concomitant glucose infusion was adapted to keep blood glucose concentration constant. At the end of each infusion, a steady state (SS) was maintained for 30 min. During the SS, minor changes of the glucose infusion were necessary to maintain normal blood glucose level. During the SS, blood samples were taken at 10 min interval to determine SS insulin (SSIC) and NEFA (SSNEFA) concentrations. The SSIC was 8.77 ± 3.04; 52.38 ± 16.11; 339.04 ± 122.01; 1411.5 ± 500.08 μU/mL and the SSNEFA was 0.62 ± 0.20; 0.26 ± 0.08; 0.14 ± 0.09; 0.11 ± 0.08 mmol/L for the insulin infusions of 0.1, 0.5, 2, and 5 $mU \cdot kg^{-1} \cdot min^{-1}$, respectively. The SSNEFA is the resultant of both the inhibitory effect of insulin on lipolysis and the stimulatory effect of insulin on lipogenesis. To correct for different basal NEFA levels, the NEFA lowering effect of insulin was calculated as % compared with basal values. Dose response curves were created using PROC NLIN in SAS (SAS Inst. Inc., Cary, NC) to determine maximal effect and insulin dose needed to elicit half-maximal effect (logED50). Maximal effect and logED50 were, respectively, 0.90 ± 0.07% and 1.24 ± 0.29 μU/mL. Effects on both parameters were analyzed using PROC MIXED in SAS, with parity as random factor and BCS, BFT, and NEFA concentration during the dry period as independent variables. Maximal effect of insulin was negatively influenced by NEFA concentrations during the dry period ($\beta = -0.3065$; $P < 0.05$) while the effect of BFT and BCS was not significant. None of the independent variables had a significant influence on logED50. It can be concluded that elevated NEFA concentrations during the dry period decrease the maximal effect of insulin on lipolysis and lipogenesis.

Key Words: insulin sensitivity, lipid metabolism, dairy cow

499 Effect of ractopamine hydrochloride and zilpaterol hydrochloride on the electrocardiogram and blood lactate in finishing steers. D. A. Frese*[1], C. Reinhardt[1], S. J. Bartle[1], D. N. Rethorst[1], B. S. Bawa[1], J. D. Thomason[1], G. H. Loneragan[2], and D. Thomson[1], *[1]Kansas State University, Manhattan, [2]Texas Tech University, Lubbock.*

Thirty Angus steers (506 ± 5.5 kg) were used to examine the effect of ractopamine hydrochloride and zilpaterol hydrochloride on the cardiac physiology and blood lactate concentration of finishing beef steers. Cattle were randomly assigned to 1 of 3 treatment groups: control (CON), ractopamine hydrochloride (300 $mg \cdot animal^{-1} \cdot d^{-1}$; RAC), and zilpaterol hydrochloride (8.3 mg/kg DM basis; ZIL). Cattle were allowed to acclimate to pens and Calan Gate feeders for 43 d before trial initiation. Steers were housed in outdoor dirt-floor pens with ad libitum access to feed and water. Holter electrocardiograph (ECG) monitors were placed on cattle on d -2, 6, 13, and 24 of the trial and recorded continuously for 72, 24, 24, and 96 h, respectively; d 0 was the first day of β agonist feeding. Blood samples were obtained via jugular venipuncture for complete blood count, serum chemistry, and blood lactate (BL) analysis at the time of ECG monitor application. Electrocardiogram recordings were evaluated for mean heart rate (MHR) in beats per minute (bpm), ventricular (VPB), and supraventricular arrhythmia events per day (SVPB). Cattle fed ZIL (77.6 bpm ± 1.19) and RAC (78.4 bpm ± 1.18) had greater MHR than CON (74.2 bpm ± 1.27). No differences were observed in VPB, or SVPB in the CON, RAC, or ZIL treated cattle. No differences were found among treatments in arrythmia rate when classified as single beat, paired beat, or > 2 beats per event. Single beat events represented 84% of VPB and 90% of SVPB events. No differences were observed in BL among CON (3.1 mmol/L), RAC (2.9 mmol/L), and ZIL (2.8 mmol/L). Creatinine kinase (CK) increased ($P < 0.03$) in ZIL cattle (220.3 U/L), compared with CON (111.9 U/L) and RAC cattle (120.2 U/L) at d 13. On d 24 CK was increased in ZIL (226.9 U/L), than CON (132.5 U/L) and RAC (135.4 U/L). In conclusion, RAC and ZIL increased MHR in feedlot cattle, but had no effect on arrythmia rate, arrythmia classification, or blood lactate. Also, ZIL increased CK compared with CON and RAC on d 13 and 24.

Key Words: β agonist, electrocardiogram, blood lactate, cattle

0500 Expansion and evaluation of a dynamic, mechanistic model of nutritional and reproductive processes in dairy cattle. J. P. McNamara*[1] and S. L. Shields[2], [1]*Washington State University, Pullman,* [2]*Elanco Inc, Pasco, WA.*

The effects of nutrition and genetics on fertility are multiple, and although we do have a large knowledge base and good management practices, reproductive efficiency does not match the biological potential. In part, this is because we lack a full systems approach to managing the genetics and nutrition of cows to improve reproduction. Our objective was to expand the integration of nutritional and reproductive processes in a mechanistic, dynamic model of the dairy cow; suitable for evaluation of data, concepts, and hypotheses regarding underlying genetic, nutritional, and physiological control of reproduction. A model of metabolism (Molly, UC Davis); which describes nutrient metabolism, as well as tracking energy transactions; was integrated with a model of reproductive processes, which describes growth and decay of the follicles and corpus luteum, gonadotropin releasing hormone, follicle stimulating hormone, luteinizing hormone, progesterone, estrogen, oxytocin, and prostaglandin F2α over time. The models are integrated at specific points based on available literature data, for example: glucose and IGF-I affect rates of synthesis and release of follicle stimulating hormone, luteinizing hormone, and follicular growth according: follicular_growth = {follicular_rate_constant = hp_fsh_mod + [follicular_ rate_factor_IGF_1(0.001833) × (IGF_1– average_IGF_1)]}, where follicular_rate_constant is the rate of follicular growth, hp_fs_mod is a Hill function describing the effect of FSH on growth, and follicular_ rate_factor_IGF_1 which affects follicular growth. Degradation of estrogen and progesterone is a function of metabolic rate in visceral tissues of Molly (AtAdV), for example: progesterone degradation = 0.0005669 (deg_const_P4 = progesterone degradation factor (0.0005669) + [metab_rate_degradation_factor_P4 × (AtAdV–avg_ATADV)]. During pregnancy, cycling ceases and the model maintains progesterone concentrations and describes fetal growth. A modeling analysis that varied milk production from 25 to 55 kg/d DMI from 18.8 to 27.3 kg DMI, gave a range of metabolic rate from 1090 to 1426 M/d and a range of IGFI from 86.4 to 106.4 ng/L). Increasing IFGI increased follicular growth], while increasing metabolic rate increased the degradation of estrogen and progesterone. Because most reproductive systems have negative and positive effects on each other, it is the interaction of these systems which provided an interesting pattern of change in follicular growth and steroid degradation. This model should be of use in testing hypotheses about effects of genetic selection and nutritional management in dairy cattle.

Key Words: systems biology, reproduction, nutrition

0501 Metabolic, paracellular permeability, and immune gene expression in ruminal epithelium during the transition period in dairy cattle. A. Minuti*[1], S. Alqarni[2], P. Cardoso[2], E. Trevisi[1], and J. J. Loor[2], [1]*Università Cattolica del Sacro Cuore, Piacenza, Italy,* [2]*University of Illinois, Urbana-Champaign, Urbana.*

The study was aimed to investigate the mRNA expression linked to systems involved in the metabolic, epithelial integrity, and immune function in ruminal epithelial tissue during the transition period in dairy cattle. Seven multiparous Holstein cows with a ruminal fistula were dried off at −50 d relative to the expected calving and fed a controlled-energy diet (NEL = 1.24 Mcal/kg of DM) until calving, and then a common lactation diet. Ruminal epithelial tissue was biopsied at -14, 10, and 28 d in milk (DIM). Extracted mRNA was used for profiling of 23 genes via quantitative real-time RT-PCR. The expression of genes was normalized using geometric mean of 3 internal control genes (CMTM6, ERC1, and MRPL39). Data were analyzed as a repeated measures study using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). The epithelial integrity genes OCLN and TJP1 had a decrease ($P < 0.05$) of expression from -14 to 10 DIM. For genes involved in the immune function, TNF did not change significantly. In contrast, the expression of CD45 decreased ($P < 0.05$) from -14 to 10 DIM and the expression of TL2 and TLR4 decreased ($P < 0.01$) until 28 DIM compared with -14 DIM. The transporters SLC14A1, SLC16A1, and SLC16A3 increased expression during the transition period with highest ($P < 0.05$) values at 28 DIM. The ketogenic gene HMGCS2 had higher ($P < 0.05$) expression at 28 DIM vs. -14 and 14 DIM. Expression of PPARA, PPARD, and PPARG did not change during the transition period; while, the nuclear receptor RXRA decreased ($P < 0.01$)from -14 DIM to 28 DIM. Expression of the insulin receptor (INSR) was lower ($P < 0.05$) at 10 DIM vs. -14 and 28 DIM. Expression of TGFB1, involved in cell growth and proliferation, had the highest ($P < 0.05$)expression at 10 DIM; while, its receptor (TGFBR1) had higher ($P < 0.05$) expression at -14 DIM and subsequently decreased. Results suggest that along with other tissues the ruminal epithelium also experiences changes at the transcriptome level. These are likely important for a successful transition into lactation. The observed changes could be driven by both changes in feed composition and nutrient intake typical of this period, and to the metabolic and hormonal changes that take place in preparation to the time of calving and the onset of lactation.

Key Words: rumen, transition cow, transcriptomics

0502 Energy expenditure is lower in efficient compared with inefficient lactating dairy cattle.

K. DiGiacomo*[1], L. C. Marett[2], W. J. Wales[2], B. J. Hayes[3], F. R. Dunshea[1], and B. J. Leury[1], *[1]The University of Melbourne, Parkville, Australia, [2]The Department of Environment and Primary Industries, Victoria, Ellinbank, Australia, [3]The Department of Environment and Primary Industries, Bundoora, Australia.*

Measuring the energy expenditure (EE) of an animal, particularly while it is at pasture exhibiting natural behaviours, is of particular importance to improve management, breeding, and feeding practices. Recently, the estimation of EE based on heart rate (HR) has been explored. In cattle, this relationship appears to be more stable than in other nondomestic animals, likely due to the acclimation and low fear response of domestic, particularly dairy, cattle. Sixteen lactating, primiparous Holstein-Friesian cows previously classed as efficient (n = 8) or inefficient (n = 8) based on residual feed intake (RFI) were housed in open circuit respiration chambers for a period of 48 h. Animals were fed lucerne hay cubes ad libitum and recieved 6 kg DM crushed wheat grain (and minerals) at milking (total diet CP 18% and ME 10.5 MJ/kg DM). Real time measurements of methane, CO_2, and O_2 flux were obtained in the chamber and real time HR measurements obtained using a Polar Equine HR monitor fitted to the cows for the duration of the chamber measurement period. Production measures (e.g., intake, milk yield, and milk content), heart rates, and O_2 consumption were not different between the efficiency groups. Oxygen consumption per heart beat (HB), defined as O_2 pulse, was calculated for the first 24 h of the study. The O_2/HB over the entire 24 h there was a significant effect of efficiency group such that efficient cows consumed less (0.01029 g min^{-1} per HB, $P < 0.05$) O_2 per heartbeat than inefficient cows. The finding of a relationship between efficiency and O_2 pulse being present in lactating dairy cattle is novel. Taken together, the lower pulse O_2 in efficient animals without a variance in intake or production indicates that there are fundamental differences in maintenance energy consumption between inefficient and efficient groups. This finding supports the idea that a more efficient animal will deliver less O_2 per HB whilst maintaining a level of health and production similar to that of an inefficient animal.

Key Words: energy expenditure, efficiency, residual feed intake

0503 Supplementation of OmniGen-AF during the receiving period modulates the metabolic response to a lipopolysaccharide challenge in feedlot steers.

N. C. Burdick Sanchez*[1], J. O. Buntyn[2], J. A. Carroll[1], T. Wistuba[3], K. DeHaan[3], S. E. Sieren[4], S. J. Jones[4], and T. B. Schmidt[4], *[1]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [2]University of Nebraska, Department of Animal Science, Lincoln, [3]Prince AgriProducts Inc., Quincy, IL, [4]University of Nebraska, Lincoln.*

The use of probiotic feed supplements to enhance animal health and growth are of great interest to the beef industry. Studies have demonstrated that some probiotic supplements may affect metabolism, and therefore influence an animal's response to an immune challenge. This study was designed to determine the effect of supplementing feedlot steers with OmniGen-AF (Prince Agri Products Inc., Quincy, IL) during the receiving period on the metabolic response to a lipopolysaccharide (LPS) challenge. Steers (n = 18; 270 ± 5 kg BW) were obtained and transported to the University of Nebraska Agricultural Research and Development Center feedlot. Upon arrival steers were processed and separated into 2 treatment groups (n = 9/treatment): 1 group was fed a standard receiving diet (Control, Cont) and the other group was fed the same receiving diet supplemented with OmniGen-AF at 4 g/45.4 kg BW/d for 29 d (OmniGen-AF). On d 27, steers were fitted with indwelling jugular cannulas and placed in individual stalls. On d 28, steers were challenged i.v. with LPS (0.5 µg/kg BW at 0 h), and blood samples were collected at 30-min intervals from -2 to 8 h and at 24 h postchallenge. Serum was isolated and stored at −80°C until analyzed for glucose, NEFA, and blood urea nitrogen (BUN) concentrations. Data were analyzed using the Mixed procedure of SAS (SAS Inst. Inc., Cary, NC) specific for repeated measures. Glucose concentrations were affected by treatment (P = 0.009) and time ($P < 0.001$). Glucose was greater in OmniGen-AF steers compared with Cont steers (76.4 ± 1.1 mg/dL vs. 72.4 ± 1.0 mg/dL). For NEFA concentrations, there was a treatment ($P < 0.001$) and time ($P < 0.001$) effect. Specifically, Cont (0.210 ± 0.007 mmol/L) steers had greater NEFA concentrations than OmniGen-AF steers (0.101 ± 0.010 mmol/L). There was a tendency (P = 0.07) for a treatment × time interaction such that NEFA concentrations were greater ($P \leq 0.03$) in Cont steers than OmniGen-AF steers from 3 to 8 h after LPS challenge. For BUN, there was a treatment ($P < 0.001$) effect such that concentrations were greater in Cont steers (12.4 ± 0.1 mg/dL) than OmniGen-AF supplemented steers (11.5 ± 0.1 mg/dL) throughout the study, and were not affected by time (P = 0.28). These data suggest that OmniGen-AF supplementation modulates the metabolic response to a LPS challenge and provides an indication that supplementation of feedlot steers with OmniGen-AF may prevent the breakdown of other substrates (e.g., protein and fat) for energy during an immune challenge.

Key Words: cattle, metabolism, OmniGen-AF

0504 Supplementation of *Saccharomyces cerevisiae* modulates the metabolic response to a lipopolysaccharide challenge in feedlot steers.

T. B. Schmidt*[1], J. O. Buntyn[2], N. C. Burdick Sanchez[3], E. Chevaux[4], K. Barling[5], S. E. Sieren[1], S. J. Jones[1], and J. A. Carroll[3], *[1]University of Nebraska, Lincoln, [2]University of Nebraska, Department of Animal Science, Lincoln, NE, [3]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [4]Lallemand Animal Nutrition, Milwaukee, WI, [5]Lallemand Animal Nutrition, Iola, TX.*

Live yeast has the potential to serve as an alternative to the use of low-dose supplementation of antibiotics in cattle due to the ability to alter ruminant metabolism; which in turn may influence the immune response. Therefore, the objective of this study was to determine the metabolic response to a lipopolysaccharide (LPS) challenge in feedlot steers supplemented with *Saccharomyces cerevisiae CNCM I-1079* (SC). Steers (n = 18; 266 ± 4 kg BW) were processed and separated into 3 treatment groups (n = 6/treatment): (1) steers were fed a standard receiving diet and served as the control (Cont); (2) steers were fed the receiving diet supplemented with SC (Lallemand, Inc.) at 0.5 g·animal^{-1}·d^{-1} (SC-0.5); and (3) steers were fed the control diet supplemented with SC at 5.0 g·animal^{-1}·d^{-1} (SC-5.0) for 29 d. On d 27, steers were fitted with indwelling jugular cannulas and rectal temperature (RT) probes, and were placed in individual stalls. On d 28, steers were challenged i.v. with LPS (0.5 µg/kg BW at 0 h), and blood samples were collected at 30-min intervals from -2 to 8 h and at 24 h postchallenge. Serum was isolated and stored at −80°C until analyzed for glucose, NEFA, and blood urea nitrogen (BUN) concentrations. There was a treatment (P = 0.02) and time effect (P < 0.001) for glucose; SC-0.5 steers had greater glucose concentrations (77.8 ± 1.6 mg/dL) than Cont (71.5 ± 1.3 mg/dL) and SC-5.0 steers (71.6 ± 1.4 mg/dL). Glucose concentrations also increased (P < 0.001) over time in response to LPS challenge. Concentrations of NEFA were also affected by time (P < 0.001) but were not affected by treatment (P = 0.42). For all treatments, NEFA concentrations increased in response to LPS challenge. There was a treatment (P < 0.001) and a time (P < 0.001) effect for BUN concentrations; BUN concentrations were greater (P < 0.001) in SC-0.5 steers (14.5 ± 0.2 mg/dL) than Cont (12.8 ± 0.2 mg/dL) and SC-5.0 (12.8 ± 0.2 mg/dL) steers. For all 3 groups, BUN concentrations increased (P < 0.001) in response to LPS challenge. These data demonstrate that *S. cerevisiae* supplementation may alter the metabolic response to LPS challenge. Repartitioning of nutrients may help explain the variations in the acute phase response observed in cattle supplemented with *S. cerevisiae*. Data from this study suggest that *S. cerevisiae* products may be useful as alternatives to antibiotic use in feed to enhance cattle health.

Key Words: cattle, live yeast, metabolism

0505 Circulating amino acids and biomarkers of metabolism and inflammation during the peripartal period in cows with different liver functionality index.

Z. Zhou*[1], J. J. Loor[1], F. Piccioli-Capelli[2], G. E. Lobley[3], and E. Trevisi[2], *[1]University of Illinois, Urbana, IL, [2]Università Cattolica del Sacro Cuore, Piacenza, Italy, [3]Rowett Institute of Nutrition and Health, University of Aberdeen, Aberdeen, UK.*

Objectives were to profile AA and biomarkers of inflammation during the peripartal period. Eighteen multiparous cows were used from -21 through 56 d around parturition. Cows were monitored for health status, milk yield, and DM intake. Body weight and BCS were measured every week. Blood samples were obtained twice weekly or daily from -10 to 10 d. Cows were ranked retrospectively in tertiles according to the liver functionality index (LFI), which includes 3 liver biomarkers of hepatic function: albumin, cholesterol, and total bilirubin. The LFI measures the relevant changes in concentrations between 3 and 28 d, standardized with the optimal pattern of change for the 3 parameters obtained from healthy cows at the same stage of lactation. A high LFI (better liver function) is characterized by lower bilirubin and higher cholesterol and albumin, and the opposite is true for low LFI. Although DMI (16.8 kg/d) and BCS (2.45) did not differ (P > 0.05) due to LFI or the interaction, cows in the high (39.2 kg/d) and medium (34.8 kg/d) vs. low (30.8 kg/d) LFI had greater (P < 0.05) milk production. As expected, there was a significant interaction (P < 0.05) for the concentration of albumin, cholesterol, and bilirubin such that cows in low vs. high LFI had lower cholesterol and albumin but greater bilirubin namely after calving. There was no interaction or LFI effect (P > 0.05) for NEFA, hydroxybutyrate, and haptoglobin but concentrations increased (P < 0.05) after calving. The interaction (P = 0.06) effect observed for concentration of essential AA was due in part to greater values in high and medium LFI cows namely during d 7 through 14. A similar type of response resulted in a trend (P = 0.10) for an interaction in the concentration of branched-chain AA (BCAA). There was no LFI or interaction effect (P > 0.05) for concentration of Lys, which decreased (P < 0.05) markedly from -21 d to calving followed by a gradual increase to prepartal values by d 14. In contrast, concentration of Met decreased markedly between -21 d and calving but did not reach prepartal values until d 42. Results suggest some alterations in postpartal EAA and BCAA concentration such that cows with high vs. low LFI produce more milk and maintain greater concentrations of these AA.

Key Words: transition period, inflammation, immunometabolism

0506 Peripheral leukocytic responses to ultraviolet radiation in prepubertal rabbits fed a turmeric-supplemented diet. V. A. Togun*, *Ladoke Akintola University of Technology, Ogbomoso, Nigeria*.

This study investigated the antioxidant/antiinflammatory effect of turmeric (*Curcuma longa*) to enhance developmental resilience in stress induced, UV irradiated (*R*) rabbits indexed by peripheral leukocytic responses. This study was conducted for a total of 85 d in 3 phased periods: 40 d preirradiation, 5 d irradiation, and 40 d postirradiation in 72 acclimatized prepubertal, unsexed rabbits of average body weight range of 600 g, randomly assigned to 6 groups of 12 rabbits each and treated as follows: Group 1 served as control; they were fed unsupplemented diet and forage (*Tridax procumbens*) basal diet (BD) for the entire study periods without any treatment. Group 2 animals were fed BD supplemented with 2% crude pulverized turmeric (T) during Periods 1, 2, and 3, but were not irradiated. Group 3 animals were fed unsupplemented BD at Periods 1, 2, and 3 and irradiated. Group 4 rabbits were fed supplemented BD during Periods 1 and 2 only, and irradiated. Group 5 animals were fed supplemented BD at Periods 1, 2, and 3 and irradiated. Group 6 animals were fed BD in Periods 1 and 2, and irradiated at Period 2, following which supplemented BD was served in Period 3. Blood was collected on d 86 from 00.09 h. Feed and water were available ad libitum. The experimental design was completely randomized block design. Data were analysed by ANOVA with graphic post-hoc test of significance. Evident from Table 0506 with data for all the periods, UV irradiation significantly ($P < 0.05$) suppressed WBC and absolute lymphocytic count. Turmeric supplementation significantly ameliorated these UV effects ($P < 0.05$).

Key Words: turmeric, leukocytic-response, ultraviolet radiation, rabbits

Table 0506. Table of results[1]

S/N	GROUP *n*	WBC (10^3)	LYM, %	ABS
1	CONTROL	6.00 + 1.01†	69.12 + 6.0	3954 + 722.65
2	T + T + T	5.88 + 0.80^{ns}	77.72 + 4.60*,**	4651 + 830.72*,**
3	– + R +–	4.53 + 1.18*	71.93 + 3.34^{ns}	3183 + 662.50*
4	T + TR +–	6.85 + 1.09**,^{ns}	68.87 + 6.27^{ns}	4526 + 667.66*
5	T + TR + T	9.98 + 1.74*,**	69.64 + 5.32^{ns}	5524 + 1269.08*,**
6	– + R + T	5.78 + 0.91**,^{ns}	70.64 + 5.96^{ns}	4080 + 750.69^{ns}

n, number of animals = 12; †mean + SEM; T, turmeric; R, UV irradiation; LYM, lymphocyte; ABS, absolute lymphocyte count, WBC, white blood cell count.

$P < 0.05$ vs. control.

**$P < 0.05$ vs. UV irradiation; not significant (ns) vs. control.

0507 Regulation of adipogenesis and key adipogenic gene expression by retinoic acid in 3T3–L1 preadipocytes. S. Ji*[1], M. Du[2], and R. A. Hill[1], *[1]University of Idaho, Moscow, [2]Washington State University, Pullman.*

Adipogenesis plays an important role in metabolic homeostasis and nutrient pathways, and is crucial for regulating body fat reserves and body weight of mammals. The transcriptional control of adipogenesis requires a sequential series of gene expression events and activation of a number of key signaling pathways. Retinoic acid is considered as a potent inhibitor of adipogenesis for decades, and understanding the mechanism of retinoic acid regulation of adipogenesis is useful for helping to control body fat and to manipulate meat quality in the beef industry. To investigate the function of retinoic acid in regulation of adipogenesis, adipocyte differentiation and key adipogenic gene expression were studied in 3T3-L1 preadipocytes. Lipid accumulation was measured by Oil Red O staining, and expression of key adipogenic genes was quantified using quantitative real-time PCR. Adipogenic responses to different concentrations of retinoic acid were determined on d 2, 4, 6, 8, and 10 after stimulation of adipogenesis with the traditional hormonal cocktail (dexamethasone, isobutyl-1-methylxanthine and insulin) in the absence or presence of retinoic acid. In response to high concentrations (10^{-6}, 10^{-7} M) of retinoic acid, lipid accumulation and the expression of PPARγ, C/EBPα, FABP4, and SCD-1 were inhibited through d 8, but on d 10, lipid accumulation and the expression levels of these genes rebounded to levels comparable with the control. Interestingly, the greatest effects of retinoic acid treatments were on expression of FABP4. However, expression of SREBP-1c was not affected. The lowest retinoic acid concentration (10^{-10}M) did not affect adipocyte differentiation or expression of adipogenic genes. These results indicate that retinoic acid inhibited adipogenesis via suppressing adipogenic specific genes, especially FABP4. Our data indicate that a deeper understanding of the roles of retinoic acid in regulating adipogenesis will be informed by further study of adipogenic specific gene promoter activity.

Key Words: adipogenesis, transcription factors, retinoic acid

0508 Cholesterol metabolism, transport, and hepatic regulation during negative energy balance in early and mid-lactation in dairy cows.

J. J. Gross*[1], E. C. Kessler[1], C. Albrecht[2], and R. M. Bruckmaier[1], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland, [2]Institute of Biochemistry and Molecular Medicine, University of Bern, Bern, Switzerland.*

The negative energy balance (NEB) in early lactation has considerable effects on the cholesterol metabolism of dairy cows. The objective of this study was to investigate the response of plasma and milk lipids, enzyme activities, and hepatic mRNA expression of transcripts encoding for factors involved in cholesterol metabolism to a NEB in early and mid-lactation. Fifty multiparous Holstein dairy cows (25 control [C], 25 feed-restricted [R]) were studied from wk 1 postpartum (pp) until wk 17 pp, with an almost 50% feed-restriction from wk 14 to 17 pp. Blood samples, liver biopsies, and milk samples were taken in wk 1, 14, and 17 pp. Blood and milk lipid concentrations [triglycerides (TG), cholesterol, lipoproteins] and enzyme activities [phospholipid transfer protein (PLTP), lecithin-cholesterol acyltransferase (LCAT)] related to cholesterol homeostasis were analyzed. Hepatic gene expression of 3-hydroxy-3-methylglutaryl-coenzyme A (HMGC) synthase 1 (HMGCS1) and HMGC reductase (HMGCR), sterol regulatory element-binding factor (SREBF)-2, microsomal triglyceride transfer protein (MTTP), ATP-binding cassette transporter (ABC) A1, and ABCG1 were measured. While values were lower for cows in wk 1 pp, plasma concentrations of TG, cholesterol, VLDL-cholesterol (VLDL-C) and LDL-C increased in R cows from wk 14 to 17 pp compared with C cows. Whereas in wk 1 pp, PLTP activity was increased and LCAT activity was lower, activities of PLTP and LCAT did not differ between wk 14 and 17 pp in C and R cows. Cholesterol concentration in milk did not change from wk 14 to 17 pp, whereas cholesterol mass in milk was decreased in wk 17 pp for R cows and tended to be lower in R cows compared with C cows. On the contrary, cholesterol concentration and mass in milk were higher in wk 1 pp. SREBF-2, HMGCS1, HMGCR, MTTP, ABCA1, and-G1 showed no changes during the experiment. In contrast, during the NEB at the onset of lactation the expression of HMGCS1, HMGCR, SREBF-2, and ABCA1 were increased. In conclusion, increased plasma concentrations of TG, cholesterol, VLDL-C, and LDL-C during the feed restriction period suggest that in later stages of lactation the liver is able to enhance the export of generated TG as VLDL. The diminished milk cholesterol mass might represent a measure to save cholesterol for the constitution of VLDL.

Key Words: cholesterol metabolism, lipoprotein, dairy cow

PHYSIOLOGY AND ENDOCRINOLOGY: INTERRELATIONSHIPS BETWEEN ENVIRONMENTAL, METABOLIC, AND PHYSIOLOGICAL PROCESSES II

0509 Effects of calcium salts of soybean oil on factors that influence pregnancy establishment in *Bos indicus* beef cows. B. I. Cappellozza*[1], R. F. Cooke[1], T. Guarnieri Filho[1,2], I. Bueno[2], D. W. Bohnert[1], R. L. A. Cerri[3], and J. L. M. Vasconcelos[4], *[1]Oregon State University–EOARC Burns, Burns, [2]Faculdade de Medicina Veterinária e Zootecnia, UNESP–Univ. Estadual Paulista, Botucatu, Brazil, [3]Faculty of Land and Food Systems–University of British Columbia, Vancouver, Canada, [4]UNESP–FMVZ, Botucatu, Brazil*.

This experiment compared fatty acid (FA) concentrations in plasma, reproductive tissues, as well as hormones, and expression of genes associated with pregnancy establishment in beef cows supplemented or not with Ca salts of soybean oil (CSSO) beginning after timed AI. Ninety nonlactating multiparous Nellore (*Bos indicus*) cows were inseminated on d 0 of the experiment, and divided into 18 groups of 5 cows/group. Groups were randomly assigned to receive (as-fed basis) 100 g of protein-mineral mix + 100 g of ground corn per cow/d, in addition to (1) 100 g/cow daily of CSSO ($n = 9$), or (2) 100 g/cow daily of kaolin (CON; rumen-inert indigestible substance; $n = 9$). Groups were maintained in a single *Brachiaria brizantha* pasture with ad libitum access to forage. However, groups were segregated daily and offered treatments individually during the experiment (d 0 to 18). Blood samples were collected and transrectal ultrasonography was performed to verify ovulation and corpus luteum (CL) volume immediately before AI (d 0), on d 7, and 1 d 8. On d 19, 36 cows (18 cows/treatment, 2 cows/group) diagnosed without the presence of a CL on d 0, but with a CL > 0.3 cm^3 in volume on d 7 and 18, were slaughtered for collection of conceptus, uterine luminal flushing, and tissue samples from the CL and endometrium. Data were analyzed using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) with group as experimental unit. Cows receiving CSSO had greater ($P \leq 0.08$) concentrations of linoleic and other ω-6 FA in plasma, endometrium, CL, and conceptus compared with CON. On d 7, CSSO-supplemented cows had greater plasma progesterone concentrations ($P = 0.02$) and CL volume ($P = 0.01$) compared with CON, whereas no treatment effects were detected ($P \geq 0.20$) for these parameters on d 18 (treatment × day interaction; $P < 0.01$). Cows receiving CSSO tended ($P = 0.09$) to have greater concentrations of IFNt in the uterine flushing media compared with CON. No treatment effects were detected ($P \geq 0.12$) for mRNA expression genes associated with pregnancy establishment in endometrial (cyclooxygenase-2 and oxytocin receptor), CL (steroidogenic enzymes), and conceptus (IFNt) samples. In summary, supplementing beef cows with 100 g of CSSO beginning after AI favored incorporation of ω-6 FA into their circulation, reproductive tissues, and conceptus, without impacting expression of genes associated with pregnancy establishment on d 19 of gestation.

Key Words: beef cows, calcium salts of soybean oil, pregnancy

0510 Metabolomics profiling of four biofluids from dairy cows fed different forages using gas chromatography–time of flight/mass spectrometry. H. Z. Sun*[1], B. Wang[1], D. M. Wang[1], J. K. Wang[1], L. L. Guan[2], and J. X. Liu[3], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada, [3]Zhejiang University, Hangzhou, China*.

The quality of forage can significantly impact milk production and quality. This study aims to investigate the effect of type of forage on metabolites in biofluids of dairy cow and their potential role in lactation. Sixteen multiparous Holstein dairy cows were blocked based on days in milk (164 ± 27.5 d, mean ± SD) and milk yield (29.4 ± 2.16 kg, mean ± SD), and were randomly assigned into 1 of 2 treatments. Isonitrogenous diets with a ratio of forage-to-concentrate at 45:55 contained similar concentrate mixtures and 15% corn silage, with 2 different forage sources (DM basis): 23% alfalfa hay and 7% Chinese wild rye hay (AH); and 30% corn stover (CS). After a 65-d feeding, 4 biofluids (rumen fluid, milk, serum, and urine) were collected from all cows to characterize the metabolites using a novel metabolomics method based on gas chromatography–time of flight/mass spectrometry). A total of 165, 195, 218, and 156 metabolites were identified in rumen fluid, milk, serum, and urine, respectively. Among them, 29 metabolites were mutual in all 4 biofluids. The chromatograms among 4 biofluids were obviously different, with a clear discrimination between diets CS and AH. Principal component analysis yielded the separated clusters of metabolite profiles between diets AH and CS. Partial least squares discriminant analysis also showed segregation in the metabolites from 4 biofluids between 2 diets. There were 56, 8, 31, 31 metabolites in 4 biofluids, respectively, that differed significantly between diets AH and CS (VIP > 1 and $P < 0.05$). These metabolites were mainly involved in AA metabolism and carbohydrate metabolism. Among 56 dissimilar metabolites in the rumen, 90% was lower for diet CS than for AH, while 74% of 31 dissimilar urinary metabolic wastes was higher in CS. The cumulative explanation rate (R^2Y) of orthogonal to partial least squares discriminant analysis was 0.899, 0.967, 0.899, and 0.982, respectively, suggesting that biofluid metabolomics combining metabolic profiles with multivariate analysis can be used to investigate the cow complex metabolic alteration in response to different type of forages with successful metabolites models.

Key Words: biofluids, metabolomics, dairy cow

0511 Separation of proteins from the milk fat globule membrane with minimal losses. W. Holzmüller*, *Technische Universität München, Freising, Germany.*

Components of the milk fat globule membrane (MFGM) are reported to have functional properties. However, determination of the specific properties of individual MFGM components is hardly possible, since the MFGM is a complex 3-layered structure consisting of phospholipids and proteins. Therefore, to assess the MFGM proteins' functionalities, first an isolation of the MFGM from the bulk milk proteins is required. Second, single MFGM proteins must be separated from the phospholipid phase. The aim of this project was to compare established and novel isolation methods in terms of the capacity to obtain MFGM proteins at high yield. First, the method of washing the cream for several times was used. After each washing step the cream sample was churned and the buttermilk obtained was analyzed regarding MFGM proteins using SDS-PAGE. The intensities of the different proteins (XO/XDH, BTN PAS6/7) were compared with a nonwashed sample. Beside the removal of caseins and whey proteins it was found that a significant loss of MFGM proteins up to 90% occurs, which has been neglected in previous studies. Particle size measurements showed that the fat globules increased during the washing process. This is due to coalescence of the fat globules and consequently results in a loss of MFGM material including membrane proteins. Second, filtration experiments with buttermilk were done. Because of an overlap in size between the casein micelles and the MFGM fragments a pre-treatment of the buttermilk was necessary to realize an isolation of the MFGM. In this study, a new approach based on the coagulation of casein micelles by adding rennet was developed. The supernatant (buttermilk-sweet whey) obtained was used for a subsequent diafiltration to remove the residual whey proteins. All permeates and retentates of each diafiltration step were again analyzed for the remaining MFGM proteins, caseins, and whey proteins by SDS-PAGE to evaluate the isolation procedure. However, significantly higher amounts (~70%) of the total MFGM proteins were recovered when the newly developed MFGM isolation method was used in comparison with the washing method. Concluding, both separation methods are applicable to realize MFGM isolates, but a simultaneous loss of MFGM proteins is hardly avoidable. As far as we oversee the literature, this fact was not sufficiently considered in previous studies. Finally, the results of this work show that different MFGM proteins are enriched in the particular isolates depending on their location in the MFGM and the applied extraction method.

Key Words: milk fat globule membrane proteins

0512 Serotonin (5-HT) receptor expression in bovine apocrine sweat gland epithelial cells isolated from cow skin. S. Hamzaoui[1], J. L. Collier[2], and R. J. Collier*[2], [1]*Universitat Autònoma de Barcelona, Bellaterra, Spain,* [2]*University of Arizona, Tucson.*

Apocrine sweat glands in bovine skin are involved in thermoregulation. Human, horse, and sheep sweat gland epithelial cells have been isolated and grown in vitro. However, isolation of bovine sweat gland epithelial cells (BSGEC) has never been reported. Recent studies have demonstrated that serotonin (5-HT) is an important local regulator of lactational homeostasis and involution in bovine, mouse, and human mammary epithelial cells. We hypothesized that, since the mammary gland is a modified sweat gland, that 5-HT receptors may also be present in BSGEC. The present study was conducted to identify a method to isolate bovine sweat glands and culture apocrine BSGEC in vitro and evaluate the expression of 5-HT receptors (1B, 2A, 2B, 4, and 7) in bovine skin, intact apocrine sweat glands and BSGEC. Collagenase digestion, neutral red staining and mechanical shearing were used to identify and isolate the apocrine glands from skin. The isolated material was transferred to complete media (keratinocyte serum-free media, K-SFM), bovine pituitary extract (BPE), and human recombinant epidermal growth factor (EGF) + 2.5% FBS in a T25 flask with media film then incubated at 37°C for 24 h. After sweat glands adhered to the bottom, an additional 2 mL of complete media was added, and the media was changed every 3 d. Isolated apocrine sweat glands and BSGEC were immunostained for cytokeratin and fibroblast specific protein, indicating fibroblast-free cultures. We also determined the mRNA expression of bovine 5-HT receptor subtypes in bovine whole skin, sweat glands, and BSGEC. The mRNAs for 5 receptor isoforms (5-HT 1B, 2A, 2B, 4, and 7) were identified by conventional PCR. We identified isoforms 5HT 1B, 2A, 2B, 4, and 7 in whole skin; 1B, 2B, and 7 in isolated sweat glands and BSGEC. We report a method for the isolation of bovine apocrine sweat glands and suggest that keratinocyte medium supplemented with 2.5% FBS is effective and suitable for the culture of BSGEC. The presence of 5-HT receptors in BSGEC indicates that the serotonergic system is involved in regulation of BSGEC function.

Key Words: apocrine gland, serotonin 5-HT receptors, dairy cow

0513 Responses to an insulin challenge in dairy cows classed as efficient or inefficient based on residual feed intake during mid-lactation and the dry period. K. DiGiacomo*[1], E. Norris[1], L. C. Marett[2], W. J. Wales[2], B. J. Hayes[3], F. R. Dunshea[1], and B. J. Leury[1], *[1]The University of Melbourne, Parkville, Australia, [2]The Department of Environment and Primary Industries, Victoria, Ellinbank, Australia, [3]The Department of Environment and Primary Industries, Bundoora, Australia*.

Cows selected for milk yield are insulin resistant and readily mobilize lipid energy stores during lactation. Upon exposure to a stressor, insulin secretion from the pancreas is inhibited by epinephrine and consequently adds to the hyperglycemic responses to stress. Insulin-induced hypoglycemia is an indirect means of stimulating the hypothalamic-pituitary-adrenal (HPA) axis to release adrenocorticotropic hormone (ACTH) and subsequently cortisol. This experiment was designed to explore the nutrient partitioning and stress hormone responses to an insulin challenge in mid-lactating and dry cows classed as efficient or inefficient based on residual feed intake (RFI). Sixteen multiparous Holstein-Friesian cows (589 ± 37 kg) were selected based on RFI extremes (8 inefficient and 8 efficient). On 2 occasions, during mid-lactation (122 ± 23 d in milk) and the dry period (~38 d dry), an i.v. insulin challenge was conducted. Animals were housed in metabolism stalls and fed lucerne hay cubes ad libitum and recieved 6 kg DM crushed wheat grain (and minerals) per day at milking (18% CP and 10.5 MJ ME/kg DM) and had food removed 12 h before the challenge. The day before the challenge cows were fitted with interdwelling jugular catheters. Insulin (0.12 U/kg) was infused via the catheter and blood samples collected at regular intervals pre- and postinfusion. Isolated plasma was analysed for cortisol, GH, IGF-1, NEFA, and glucose concentrations. Overall, responses to the insulin challenge were more pronounced during mid-lactation compared with the dry period. Basal plasma IGF-1 concentrations were greater in inefficient compared with efficient cows during mid-lactation (11.2 vs. 15.9 ng/mL respectively, $P = 0.006$) but not the dry period ($P = 0.78$). Peak plasma cortisol concentrations were not influenced by efficiency group during either measurement periods. Plasma cortisol and NEFA concentrations were greater, and glucose concentrations lower, in mid-lactation compared with the dry period. This experiment demonstrated a stress (cortisol) response to the insulin-induced hypoglycemia, although this response did not vary with efficiency. The diminished responses to insulin during the dry period are likely due to the varied metabolic states of the animals at these 2 varied stages of production. The greater basal IGF-1 concentrations in inefficient animals may in part explain their inefficiency as IGF-1 mimics the actions of insulin and reduces circulating glucose concentrations, reducing the concentration of glucose available for use in mammary tissues.

Key Words: stress responses, efficiency, insulin

0514 Interactions between metabolic load and dairy cow welfare-related parameters in herbage-based feeding systems. R. S. Zbinden[1], J. J. Gross*[1], M. Falk[2], H. A. van Dorland[1], A. Münger[2], F. Dohme-Meier[2], and R. M. Bruckmaier[1], *[1]Veterinary Physiology, Vetsuisse Faculty University of Bern, Bern, Switzerland, [2]Agroscope, Institute for Livestock Sciences ILS, Posieux, Switzerland.*

In Switzerland, herbage feeding with only little input of concentrates plays an important role in milk production. The objective here was to investigate the effects of a solely herbage based diet on production, metabolic, endocrine and welfare-related parameters of dairy cows. Twenty-five multiparous Holstein dairy cows were divided into 2 groups according to their previous lactation yield (4679 to 10,808 kg): a control (C, $n = 13$) and a treatment group (nC, $n = 12$) from wk 3 antepartum until wk 8 postpartum. Within C and nC, the median of the preceding lactation yields (7752 kg) was used to split cows into a high (CH, nCH) and low yielding (CL, nCL) subgroup. While CH/CL received fresh cut herbage plus additional concentrate according to their estiamted energy and nutrient requirements, no concentrate was fed to nCH/nCL throughout the experiment. Milk yield and DMI were recorded daily. Blood samples were weekly and analyzed for IGF-1, glucose, NEFA, BHBA, and welfare-related parameters haptoglobin (Hp), serum amyloid A (SAA), β-endorphin (BE), and alkaline phosphatase (AP). Saliva samples were taken biweekly and analyzed for cortisol. Data were analyzed using mixed models. Throughout the study, CH had a higher milk yield (35.9 kg/d) compared with the other subgroups (27.2 to 31.7 kg/d, $P < 0.05$). Plasma glucose (3.51 vs. 3.72 mmol/L) and IGF-1 (66.0 vs. 78.9 ng/mL) concentrations were lower in nCH/nCL compared with CH/CL cows ($P < 0.05$). Plasma NEFA and BHBA concentrations were higher in nCH (1.1 and 1.6 mmol/L) compared with the other subgroups (0.5 and 0.6 mmol/L, $P < 0.05$). Saliva cortisol (0.60 vs. 0.68 ng/mL), SAA (0.60 vs. 0.87 µg/mL), Hp (728 vs. 909 U/L), BE (30.0 vs. 32.1 pg/mL), and AP (48.5 vs. 45.9 mg/mL) were not different among C and nC. In conclusion, in herbage dominated feeding systems without supplementary concentrate especially high yielding dairy cows experience a higher metabolic load during early lactation leading in turn to a reduced lactational performance compared with cows of a similar potential fed according to their needs. Low yielding dairy cows can perform well without concentrate supplementation. Interestingly, the commonly accepted welfare-related parameters cortisol, Hp, SAA, BE, and AP did not indicate a reduced animal welfare induced by metabolic stress.

Key Words: welfare, metabolism, herbage feeding, dairy cow

0515 Effects of repeated short-term feed restrictions and lipopolysaccharide-induced systemic inflammation on metabolism and performance in dairy cows. J. J. Gross*[1], E. Kalaitzakis[2], O. Wellnitz[1,2], H. Bollwein[2], and R. M. Bruckmaier[1], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Bern, Switzerland, [2]Clinic of Reproductive Medicine, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland.*

A negative energy balance (NEB) may occur later in lactation when feed supply and/or quality are insufficient. We investigated if responses of metabolism, performance and immune system to energy deficiency differ between lactational stages. Fourteen multiparous Holstein dairy cows were grouped according to their previous lactation yield in 2 groups: a control (CON) group and a restricted (RES) group. The trial lasted from wk 3 antepartum until wk 12 postpartum (pp). Cows (CON and RES) were fed with grass ad libitum plus additional concentrate throughout the study, except the RES group, which received only grass during 1-wk feed-restrictions in wk 2, 5, 8, and 11 pp. At the end of the first restriction period, lipopolysaccharide (LPS) from *Escherichia coli* was infused intravenously (0.5 μg/kg BW) to mimic an inflammatory status interacting with a different metabolic status. Dry matter intake and milk yield were recorded daily. Blood was obtained weekly throughout the study, daily during the restriction periods in wk 2, 5, 8, and 11 pp, and every 0.5 h during the day of systemic LPS challenge. Blood samples were analyzed for glucose, NEFA, BHBA, and IGF-1 concentrations. Data were analyzed using a mixed model including group and wk as fixed effects. During restriction periods, RES had an elevated grass DMI (0.3 to 4.2 kg/d) compared with CON. In-between restriction periods, DMI did not differ between RES and CON. Milk yield was lower for RES in wk 2, 5, 8, and 11 pp (ca. 5 kg/d) compared with CON and recovered between restriction periods. On the day of LPS challenge, milk yield in RES dropped more distinct than in CON (9.5 vs. 11.3 kg/d). CON cows recovered faster in milk yield after the LPS challenge. During wk 2 pp, plasma concentrations of glucose, NEFA, BHBA were not different between RES and CON, while IGF-1 was lower in RES (41.1 vs. 82.6 ng/mL). During the restriction periods in wk 5, 8, and 11, NEFA and BHBA concentrations were elevated in RES (up to 0.67 mmol/L NEFA and 0.74 mmol/L BHBA), while glucose and IGF-1 concentration were lower in RES compared with CON (3.77 vs. 4.03 mmol/L glucose, 68.8 vs. 98.4 ng/mL IGF-1 in wk 8). In conclusion, the experiment showed the changing priority of the lactating mammary gland during different stages of lactation. Performance, metabolic and endocrine changes became less with progress of lactation. Further analyses are in progress.

Key Words: feed-restriction, metabolism, grass feeding, dairy cow

0516 Effects of heat stress on pancreatic insulin content and β-cell distribution in growing pigs. M. Sanz Fernandez*[1], J. S. Johnson[1], M. Abuajamieh[1], S. K. Stoakes[1], S. M. Lei[1], R. P. Rhoads[2], and L. H. Baumgard[1], *[1]Iowa State University, Ames, [2]Virginia Tech, Blacksburg.*

Heat stress (HS) induces postabsorptive metabolism changes, independent of inadequate nutrient intake. Despite marked hypophagia, HS inexplicably increases plasma insulin kinetics in a variety of animal models, and we have previously demonstrated that the HS pigs included in this study had increased plasma C-peptide (10%; $P < 0.05$), an indicator of insulin secretion. Whether higher plasma insulin is due to increased pancreatic insulin production or secretion is unknown. Seventeen crossbred gilts (57 ± 5 kg BW) were subjected to 1 of 2 environmental treatments: (1) constant HS conditions (32°C, 23% relative humidity) and ad libitum feeding ($n = 7$), or (2) pair-feeding in thermoneutral conditions (20°C, 36% relative humidity; PFTN; $n = 10$) to eliminate the confounding effects of dissimilar feed intake. After 8 d of environmental exposure, pigs were sacrificed and the pancreas was immediately collected. Insulin content was determined after acid-ethanol protein extraction from frozen samples using a commercially available ELISA kit. Fixed samples were sectioned and stained for insulin using an indirect immunoperoxidase immunohistochemical technique. Heat stress tended to decrease (32%; $P = 0.08$) insulin stained area compared with PFTN conditions. In agreement, pancreatic insulin protein content was numerically reduced (39%; $P = 0.18$) in HS pigs. There were no differences ($P > 0.10$) in the quantity of β-cell groups, determined as the number of insulin positive cells clusters. However, when classifying β-cell groups by size, HS decreased (66%; $P < 0.01$) the percentage of larger β-cell clusters (diameter > 100 μm), while increasing (4%; $P \leq 0.01$) the percentage of smaller clusters (diameter < 50 μm). In conclusion, the similar amount of β-cell groups between treatments, coupled with the decrease in pancreatic insulin content in the HS pigs, indicates that HS-induced changes on plasma insulin concentration might be due to increased pancreatic insulin secretion, rather than production.

Key Words: heat stress, pig, insulin, pancreas

0517 Effects of protein supplementation frequency on metabolic responses associated with reproduction of beef cows. M. M. Reis*[1], R. F. Cooke[1], B. I. Cappellozza[1], R. Marques[1], T. Guarnieri Filho[1,2], G. A. Perry[3], and D. W. Bohnert[1], *[1]Oregon State University–EOARC Burns, Burns, [2]Faculdade de Medicina Veterinária e Zootecnia, UNESP–Univ. Estadual Paulista, Botucatu, Brazil, [3]South Dakota State University, Brookings.*

This experiment evaluated if frequency of protein supplementation impacts physiological responses associated with reproduction in beef cows. Fourteen nonpregnant, nonlactating Angus cows were ranked by parity and BW, and allocated to 3 groups. Groups were assigned to a 3 × 3 Latin square design, containing periods of 21 d and the following treatments: (1) daily supplementation of soybean meal (7D), (2) soybean meal supplementation 3 times/wk (3D), and (3) soybean meal supplementation once/wk (1D). Within each period (d 0 to 21), cows were assigned to an estrus synchronization protocol; 100 μg of GnRH + controlled internal device release (CIDR) containing progesterone (P4) on d 1, 25 mg of $PGF_{2\alpha}$ on d 8, CIDR removal plus 100 μg of GnRH on d 11. Straw was offered for ad libitum consumption. Soybean meal was individually supplemented at 1 kg/cow daily. Moreover, 3D were supplemented on d 0, 2, 4, 7, 9, 11, 14, 16, and 18, whereas 1D were supplemented on d 4, 11, and 18 of each period. Blood samples were collected on d 11 and 18 from 0 to 72 h relative to supplement feeding, and analyzed for plasma urea N (PUN). Samples collected from 0 to 12 h were analyzed for plasma glucose, insulin, and P4 (d 18 only) concentrations. Uterine flush fluid was collected 28 h after supplementation for pH measurement. Data were analyzed with the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) and cow as experimental unit. A treatment × hour interaction ($P < 0.01$) was detected for PUN, which peaked ($P < 0.01$) for 1D and 3D at 28 h after supplement feeding, whereas the same response was not detected in 7D. Moreover, PUN concentration at 28 h was greater ($P < 0.01$) for 1D compared with 3D and 7D (42.7, 34.4, and 25.7 mg/dL, respectively), and also greater ($P < 0.01$) for 3D compared with 7D. No treatment effects were detected ($P \geq 0.65$) for plasma glucose and P4 concentrations, whereas mean plasma insulin concentrations were greater ($P \leq 0.02$) in 7D and 3D compared with 1D (4.61, 4.76, and 3.74 μIU/mL, respectively). Uterine flushing pH tended ($P \leq 0.10$) to be greater for 1D compared with 3D and 7D (6.204, 6.130, and 6.140, respectively). In conclusion, reducing frequency of protein supplementation to once/week impacted plasma insulin, PUN, and uterine flushing pH, which are known to modulate reproduction of beef cows.

Key Words: beef cows, protein, physiology, reproduction

0518 A vaccine-induced acute-phase reaction increases plasma leptin concentrations in beef cattle. R. Marques*[1], R. F. Cooke[1], B. I. Cappellozza[1], T. Guarnieri Filho[1,2], M. M. Reis[1], D. H. Keisler[3], and D. W. Bohnert[1], *[1]Oregon State University–EOARC Burns, Burns, [2]Faculdade de Medicina Veterinária e Zootecnia, UNESP–Univ. Estadual Paulista, Botucatu, Brazil, [3]University of Missouri-Division of Animal Sciences, Columbia.*

The objective of this experiment was to evaluate if a vaccine-induced acute-phase reaction also results in increased plasma leptin concentration, which would explain a potential DMI decrease in vaccinated beef cattle. Twelve yearling Angus × Hereford calves (9 steers and 4 heifers) were ranked by sex and BW, and allocated to 2 groups (6 calves per group, 4 steers and 2 heifers). Groups were assigned to a crossover design containing 2 periods of 14 d, and the following treatments on d 0 of each period: (1) vaccination against *Mannheimia haemolytica* (VAC; One Shot; Pfizer Inc., New York, NY), or (2) saline-injected control (CON). Calves were maintained in individual pens, offered grass hay for ad libitum consumption, in addition to 1.3 kg/d (DM basis) of a corn-based supplement. During Period 1, hay and concentrate intake were evaluated daily. During Period 2, blood samples were collected before (0 h) and at 2, 4, 6, 8, 12, 16, 24, 36, 48, 60, 72, 96, 120, 144, 168, 240, and 336 h after treatment administration. All samples were analyzed for plasma haptoglobin concentration. Samples collected from 0 to 36 h were also analyzed for plasma cortisol, whereas samples collected from 0 to 96 h were analyzed for serum NEFA and plasma leptin concentrations. Values obtained at 0 h served as covariates within each respective analysis. Treatment × day interactions were detected ($P = 0.05$) for hay and total DMI, given that these parameters were reduced ($P \leq 0.02$) in VAC compared with CON on d 0 and 1. Mean plasma cortisol was greater ($P \leq 0.01$) in VAC compared with CON (39.8 vs. 26.3 ng/mL, respectively; SEM = 2.4). Treatment × hour interactions were detected ($P < 0.01$) for all other blood variables. Serum NEFA concentration was greater ($P \leq 0.03$) in VAC compared with CON at 16, 24, 48, and 72 h. Plasma haptoglobin concentration was greater in VAC compared with CON at 8 h, and from 16 to 120 h. Plasma leptin concentration was greater ($P \leq 0.05$) in VAC compared with CON beginning at 6 h relative to treatment administration. In conclusion, plasma leptin concentration was increased during a vaccine-induced acute-phase reaction, and may explain the decrease in DMI observed herein in vaccinated cattle.

Key Words: acute-phase reaction, feed intake, leptin, vaccination

0519 A prepartum diet supplemented with rolled sunflower seed increased calf weight, the incidence of dystocia, and colostrum immunoglobulin content in Holstein cows. R. Salehi*[1], M. G. Colazo[2], M. Oba[1], and D. J. Ambrose[2], *[1]University of Alberta, Edmonton, Canada, [2]Alberta Agriculture and Rural Development, Edmonton, Canada.*

Supplementing dietary fats during late gestation period has certain advantages, but its effects on the incidence of dystocia, calf weight and colostrum quality are sparsely reported. Our objective was to investigate whether prepartum diets supplemented with sunflower or canola seed will affect calf birth-weight, calving-ease and colostrum immunoglobulin content. Pregnant Holstein cows, blocked by BCS, were assigned to 1-of-3 prepartum diets supplemented with canola (n = 43, CAN; high oleic acid), sunflower (n = 46, SUN; high linoleic acid), or control (no oilseed, n = 43; CON) from 35 d (d 35) before expected calving date until parturition (d 0). The concentrate portion of CAN- and SUN-diets contained 0.99 kg rolled oilseeds (DM basis), providing 0.27 kg/d oleic or 0.31 kg/d linoleic acid. Feed intake was recorded daily from d -35 to d 0, and BCS was evaluated on d -35 and d 0. After parturition, colostrum samples (n = 13 per treatment) were collected at first milking and stored at -20°C until evaluating total fat, protein, fatty acid profile and IgG. Calves (n = 132) were weighed at birth. Colostrum immunoglobulin content was estimated using a Brix refractometer. Cows fed CON had greater ($P < 0.05$) mean DMI (15.3 ± 0.6 kg/d) than those fed SUN (13.3 ± 0.5) and CAN (13.5 ± 0.5) during prepartum. The BCS on d -35 did not differ among treatments, but cows fed SUN (3.5 ± 0.0) and CAN (3.5 ± 0.0) had higher BCS on d 0 than CON (3.4 ± 0.0). The difference in BCS between d -35 and 0 was greater in SUN (0.22 ± 0.02) than in CON (0.12 ± 0.02) but not CAN (0.18 ± 0.02). Total fat content of colostrum (%) was higher in CON (5.8 ± 0.5) compared with CAN (4.5 ± 0.4) and SUN (3.8 ± 0.4), whereas, total protein (%) was significantly higher in SUN (15.0 ± 0.6) than in CON (12.1 ± 0.8) and CAN (12.5 ± 0.8) fed cows. Mean colostrum immunoglobulin (brix%) was significantly higher in SUN (24.1 ± 0.9) than in CON (20.4 ± 1.0) and CAN (20.0 ± 1.0). Cows given SUN during prepartum delivered heavier (kg) calves (44.3 ± 0.9) than those fed CON (41.2 ± 0.8) or CAN (42.9 ± 0.8). Moreover, cows fed SUN (35%) during prepartum had a tendency to have higher incidence of dystocia at parturition than those fed CON (17%, P = 0.07) or CAN (18%, P = 0.08). In summary, cows fed supplemental oilseeds during late gestation consumed less DM than those fed a no oilseed control diet, but had greater BCS at parturition. Calf birth weight and the incidence of dystocia were higher in cows fed SUN; colostrum IgG and total protein content were also higher in cows fed SUN.

Key Words: colostrum, immunoglobulin, oilseed

0520 Effect of altering the dietary ratio of n-6 to n-3 fatty acids on luteolytic mechanism in dairy cows. L. F. Greco*[1], J. T. Neves Neto[2], A. Pedrico[2], F. S. Lima[2], R. S. Bisinotto[1], N. Martinez[1], E. S. Ribeiro[1], W. W. Thatcher[1], C. R. Staples[1], and J. E. P. Santos[1], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]University of Florida, Gainesville.*

Objectives were to evaluate the impacts of altering the ratio of dietary n-6 to n-3 fatty acids (FA) on timing of luteolysis, uterine production of prostaglandin $F_{2\alpha}$, and endometrial fatty acid profile and gene expression in dairy cows. Diets were supplemented (1.43% DM) with a mixture of Ca salts of fish oil, safflower oil and palm oil to create different ratios of n-6 to n-3 FA; 4, 5, and 6 parts of n-6 to 1 of n-3 FA (R4; R5; R6). Cows were blocked by milk production from 6 to 10 d in milk (DIM) and then assigned randomly to 1 of the 3 dietary treatments. Cows had the estrous cycles synchronized starting at 40 DIM. An indwelling catheter was inserted in the tail vessel on d 15 of the estrous cycle and blood was sampled every 2 h from estrous cycle d 16 to 23. Progesterone and 13,14,dihydro-15-keto-$PGF_{2\alpha}$ metabolite (PGFM) were measured in plasma. Cows had the estrous cycle resynchronized and endometrial tissue was collected for biopsy on d 8 of the cycle. Gene expression and FA profile were measured. Data were analyzed using MIXED procedure of SAS (SAS Inst. Inc., Cary, NC). Treatment did not influence the length of the estrous cycle or concentrations of progesterone in plasma. Basal PGFM concentrations did not differ (P = 0.66) among treatments. The number of PGFM pulses decreased (P = 0.05) as the ratio n-6 to n-3 FA increase, and they averaged 5.6, 4.3, and 3.8 pulses, for cows fed R4, R5, and R6, respectively. The area under the curve of the largest PGFM pulse increased as the ratio n-6 to n-3 increased (P = 0.02) and were 764, 958, and 1953 pg/h per mL, for cows fed R4, R5, and R6, respectively. The concentrations of arachidonic acid increased (R4 = 8.09, R5 = 10.35, and R6 = 11.04% of the identified FA; P = 0.01) and of eicosapentaenoic acid decreased linearly (R4 = 2.29, R5 = 1.90, and R6 = 1.83% of the identified FA; P = 0.03) in the endometrium by altering the ratio of n-6 to n-3 from R4 to R6. Of the genes evaluated, expression of the oxytocin receptor, estrogen receptor and steroidogenic acute regulatory protein linearly increased as the diet change from R4 to R6. Altering dietary ratio of n-6 to n-3 FA of lactating dairy cows influenced the pattern of prostaglandin synthesis, the FA profile, and gene expression of the endometrium, but did not influence the length of the estrous cycle.

Key Words: dairy cow; fatty acid; luteolysis

PHYSIOLOGY AND ENDOCRINOLOGY: NOVEL APPROACHES TO IMPROVING REPRODUCTIVE SUCCESS IN DOMESTIC ANIMALS

0521 Ovarian and endocrine responses and efficacy associated with three ovulation synchronization strategies (Heatsynch, Doublesynch, and Estradoublesynch) in Murrah buffaloes.

R. Mirmahmoudi*[1] and B. S. Prakash[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Jiroft, Jiroft, Iran,* [2]*National Dairy Research Institute, Karnal, India*.

Experiments were conducted on 71 cycling and 37 anestrus buffalos to investigate; (a) the endocrine changes, timing of ovulation, and efficacy of Estradoublesynch ($PGF_{2\alpha}$ 0, GnRH 2, $PGF_{2\alpha}$ 9, Estradiol Benzoate; EB 10), Heatsynch (GnRH 0, $PGF_{2\alpha}$ 7, EB 8), and Doublesynch ($PGF_{2\alpha}$ 0, GnRH 2, $PGF_{2\alpha}$9, GnRH 11) protocols in cycling buffaloes, and (b) to compare the efficacy of Estradoublesynch, Heatsynch, and Doublesynch protocols for fertility improvement in cycling and anestrus buffaloes. Follicle size and ovulation rate were determined following all GnRH and EB treatments using transrectal ultrasonography at 2-h intervals. Plasma progesterone and total estrogen concentrations were determined in blood samples collected at daily intervals, beginning 2 d before onset of protocols until day of second ovulation detection. Plasma LH, total estrogen and progesterone concentrations were determined in blood samples collected at 30-min intervals post-GnRH and EB injections until detection of ovulation. The first ovulatory rates were significantly ($P < 0.05$) higher in Doublesynch (90%) and Estradoublesynch (83.3%) protocols than that in Heatsynch protocol (36.4%). The first LH Peak concentrations in Estradoublesynch (73.3 ± 9.2 ng/mL) and Doublesynch (99.8 ± 28.5 ng/mL) protocols were significantly ($P < 0.05$) higher than that of Heatsynch (55.3 ± 7.4 ng/mL) protocol. In both Estradoublesynch and Doublesynch protocols, the total estrogen concentration gradually increased from the day of GnRH administration coinciding with LH peak, and then gradually declined to the basal level until the time of ovulation detection. However, in Heatsynch protocol, the gradual increase in total estrogen concentration after GnRH was observed only in those buffaloes which responded to treatment with ovulation. In both Estradoublesynch and Heatsynch protocols, ovulatory follicles size increased from GnRH/EB injections until ovulation. The pregnancy rates after Estradoublesynch (62.2%) and Doublesynch (58.1%) protocols were significantly ($P < 0.05$) higher than that achieved after Heatsynch protocol (32.5%). Our observations demonstrated that the Estradoublesynch and Doublesynch protocols can be potentially used to obtained satisfactory pregnancy rates after TAI in both cycling and anestrus buffaloes.

Key Words: estradoublesynch, heatsynch, doublesynch

0522 Cholesterol-loaded cyclodextrin improves the post-thaw semen quality but not the fertility in Sahiwal bulls.

A. Sattar*[1], A. G. Tarin[1], N. Ahmad[1], K. Javed[2], M. Ahmad[1], A. Razzaq[1], K. Ahmad[3], and M. Younis[4], [1]*Department of Theriogenology, University of Veterinary and Animal Sciences, Lahore, Pakistan,* [2]*Department of Livestock Production, University of Veterinary and Animal Sciences, Lahore, Pakistan,* [3]*Livestock Experiment Station, Fazilpur, Rajanpur, Pakistan,* [4]*Semen Production Unit, Qadirabad, Sahiwal, Pakistan*.

Sahiwal cattle is the best dairy breed of Pakistan, whose pure-bred population is reduced to an extent where it can be declared as endangered. AI is a tested tool for genetic improvement and conservation. During cryopreservation, cholesterol is an important component in the regulation of membrane fluidity. The objective of the present study was to determine if addition of cholesterol in semen extender has a beneficial effect on its post-thaw semen quality and pregnancy rate in Sahiwal bulls. Experiment 1: Cholesterol was added to Tris-citric acid semen extender in the form of cholesterol-loaded cyclodextrin (CLC). Extended semen was incubated with CLC at room temperature for 15 min before the addition of egg yolk and glycerol. Five replicates of each bull ($n = 3$) were separately evaluated and further processed with at least 60% sperm motility. Semen samples were diluted at 37°C in extender containing either 1 mg (LOW), 2 mg (MEDIUM), 3 mg (HIGH) of CLC or without (CON) per mL containing 120 million spermatozoa. Post-thaw motility (PTM), live spermatozoa (LS), plasma membrane integrity (PMI), and normal apical ridge (NAR) were assessed using standard procedures. Mean PTM, LS, and NAR values were significantly ($P < 0.05$) higher in MEDIUM group (50.33 ± 1.50, 59.53 ± 2.32, and 65.13 ± 1.63%, respectively) as compared with CON and LOW groups, but did not differ ($P > 0.05$) with HIGH group. Mean PMI was significantly ($P < 0.05$) higher in MEDIUM group (60.73 ± 1.49%) as compared with CON, but did not differ ($P > 0.05$) with those of LOW and HIGH groups. Experiment 2: Semen doses from MEDIUM ($n = 94$) or CON ($n = 94$) were used for fertility trial ($n = 188$). Pregnancy rate was numerically higher (63%) in cows inseminated with semen of MEDIUM group as compared with CON (57%), but did not differ ($P > 0.05$). It is concluded that addition of cholesterol in MEDIUM concentration (2 mg CLC) to Sahiwal bull semen can improve post-thaw semen quality, but not fertility as compared with CON group.

Key Words: cholesterol-loaded cyclodextrin, Sahiwal bull, semen

0523 Effects of administration of prostaglandin $F_{2\alpha}$ at initiation of the 7-d CO-Synch + CIDR estrus synchronization protocol for replacement beef heifers. V. R. G. Mercadante*[1], L. E. Kozicki[2], F. M. Ciriaco[1], D. D. Henry[1], C. R. Dahlen[3], R. N. Funston[4], J. E. Larson[5], G. A. Perry[6], T. L. Steckler[7], and G. C. Lamb[1], *[1]University of Florida, Marianna, [2]Pontifical Catholic University (PUCPR), Curitiba, Brazil, [3]North Dakota State University, Fargo, ND, [4]University of Nebraska, North Platte, [5]Mississippi State University, Mississippi State, [6]South Dakota State University, Brookings, [7]University of Illinois, Simpson.*

We determined the effect of administration of $PGF_{2\alpha}$ at CIDR (controlled internal drug release device) insertion during the 7-d COSynch + CIDR ovulation synchronization protocol on subsequent pregnancy rates of replacement beef heifers. At 10 locations, heifers were synchronized with the 7-d CO-Synch + CIDR protocol (100 µg injection of GnRH at CIDR insertion [d -10] with 25 mg injection of $PGF_{2\alpha}$ at CIDR removal [d -3], followed by an injection of GnRH and fixed-time artificial insemination [TAI] 54 h later on d 0). Heifers were stratified by BCS before being assigned to 1 of 2 treatments: (1) CO-Synch + CIDR (n = 498); and (2) heifers received a 25 mg injection of PGF at CIDR insertion of the CO-Synch + CIDR protcol (PG-CO-Synch + CIDR; n = 501). Follicle dynamics and corpus luteum development were assessed on d -10 and -3, and pregnancy status determined on d 30 to 35. Blood was collected on d -20, -10, -3, and 0 to determine P4. Overall TAI pregnancy rates (54.0 ± 2.9% and 50.7 ± 2.9%, for CO-Synch + CIDR and PG-CO-Synch + CIDR, respectively) did not differ (P = 0.428) between treatments. A location effect (P < 0.001) existed with pregnancy rates being the greatest at the FL1 location (75.0 ± 8.1%) and the poorest at the MS1 location (28.6 ± 9.3%). Of the 521 heifers in which cyclic status was assessed 81% had attained puberty. No treatment × cyclic status interaction existed; however, pregnancy rates of heifers that had attained puberty (55.0 ± 2.5%) tended (P = 0.080) to be greater than those heifers that were prepubertal (44.2 ± 5.2%). A treatment × concentrations of P4 interaction existed where concentrations of P4 were greater (P < 0.001) for CO-Synch + CIDR (6.31 ± 0.40 ng/mL) than PG-CO-Synch + CIDR (4.63 ± 0.40 ng/mL) on d -3. Similarly, corpus luteum (CL) volume did not differ between treatments on d -10, but CL volume tended (P = 0.059) to be greater for CO-Synch + CIDR (2.24 ± 1.14 cm^3) than PG-CO-Synch + CIDR (1.47 ± 1.14 cm^3) on d -3. Diameter of the largest follicle on d -10 (10.7 ± 1.4 mm) and -3 (11.6 ± 1.4 mm) did not differ between treatments. We concluded that administration of $PGF_{2\alpha}$ at CIDR insertion of the CO-Synch + CIDR protocol failed to increase TAI pregnancy rates in replacement beef heifers, but decreased concentrations of P4 and tended to decrease CL volume at CIDR removal.

Key Words: ovulation synchronization, artificial insemination, beef heifer

0524 Modifications to Ovsynch improve fertility during resynchronization: Evaluation of presynchronization with GnRH 6 d before Ovsynch and addition of a second PGF treatment. P. D. Carvalho*[1], M. J. Fuenzalida[2], A. Ricci[2], M. Luchterhand[2], J. M. Mulcahy[2], R. V. Barletta[2], G. M. Baez[2], V. G. Santos[2], M. C. Amundson[2], J. N. Guenther[2], A. H. Sousa[2,3], M. C. Wiltbank[1], and P. M. Fricke[2], *[1]University of Wisconsin, Madison, [2]Department of Dairy Science, University of Wisconsin-Madison, Madison, [3]University of California Cooperative Extension, Tulare.*

Recent modifications to Ovsynch, such as presynchronization with GnRH and addition of a second PGF have, at times, appeared to improve synchronization and fertility to the timed AI protocol; however, combining these 2 methods may further optimize the hormonal environment. Lactating Holstein cows were randomly assigned to a 2x2 factorial design to compare main effects of presynchronization with GnRH (± GnRH) 6 d before beginning an Ovsynch protocol, and a second PGF injection (± PGF) administered 24 h after the first on P/AI. For first TAI, cows were presynchronized with 2 injections of PGF 14 d apart, and cows detected in estrus after the second PGF injection were inseminated and removed from the experiment. Nonpregnant cows were resynchronized using an Ovsynch protocol initiated 32 ± 3 d after AI. Blood samples collected from all cows at the first GnRH (G1), at the PGF, and at the last GnRH (G2) injections of the Ovsynch protocol were assayed for progesterone (P4) concentrations. At 32 d after TAI, pregnancies per AI (P/AI) was greatest for cows presynchronized with GnRH and receiving a second PGF injection, intermediate for cows receiving the second PGF injection only and for cows presynchronized with GnRH only, and least for controls [(39.6% (91/230), 35.6% (73/205), 31.8% (77/242), 30.3% (67/221), respectively; P = 0.18]. Interestingly, treatments affected P/AI only for resynchronized cows [41.0% (57/139), 32.8% (39/119), 27.9% (41/147), 24.6% (35/142), respectively; P = 0.02], but not for cows receiving first TAI [37.4% (34/91), 39.5% (34/86), 37.9% (36/95), 40.5% (32/79), respectively, P = 0.96]. Fewer (P < 0.01) cows presynchronized with GnRH had low (< 0.5 ng/mL) P4 at G1 compared with cows not presynchronized (12.8 vs. 24.8%), and P4 was greater (P = 0.05) at the PGF injection for cows presynchronized with GnRH (4.4 vs. 4.0 ng/mL). Surprisingly, differences in P4 at PGF were only detected for resynchronized cows (P = 0.09) and not for cows receiving first TAI (P = 0.23). Cows receiving the second PGF injection had less (P < 0.01) P4 at G2 compared with cows not receiving the second PGF injection (0.2 vs. 0.4 ng/mL). We conclude that presynchronization with GnRH 6 d before

beginning an Ovsynch protocol increased P4 at the PGF injection of an Ovsynch protocol, and a second PGF injection 24 h after the first decreased P4 at TAI resulting in more P/AI in resynchronized cows. Supported by Hatch project WIS01171.

Key Words: Ovsynch; resynchronization; fertility

0525 The effects of prenatal stress and postnatal temperament on age and body weight at first sperm, puberty, and sexual maturity in Brahman bulls. M. C. Roberts*[1], R. C. Vann[2], D. A. Neuendorff[1], B. P. Littlejohn[1], D. G. Riley[3], J. A. Carroll[4], T. H. Welsh, Jr.[5], and R. D. Randel[1], *[1]Texas A&M AgriLife Research, Overton, [2]MAFES–Brown Loam Experiment Station, Mississippi State University, Raymond, [3]Texas A&M AgriLife Research, College Station, [4]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [5]Texas A&M University Department of Animal Science, College Station.*

The objectives of this study were to determine if prenatal stress (PNS) or postnatal temperament affect age and BW at first sperm, puberty, and sexual maturity. Based on temperament, pregnant Brahman cows were assigned to a control (n = 44; C) or transport group (n = 45; transportation stress for 2 h on 60, 80, 100, 120, and 140 ± 5d of gestation; PNS). At weaning, bulls (n = 25 C and n = 18 PNS) were selected for this study. Temperament was assessed at weaning using temperament score [TS; (PS + EV)/2], pen score (PS; 1 = calm and 5 = excitable), and exit velocity (EV = m/s). These TS were then converted into temperament classes of calm (TS = < 1.78, n = 26), intermediate (TS = 1.7 to 2.90, n = 9) and temperamental (TS = > 2.90, n = 8). Bulls were measured every 2 wk from 10 mo of age for BW, scrotal circumference (SC), and right and left testis length. Electroejaculation was used to collect semen when SC reached 24 cm. Semen was analyzed for sperm motility and concentration using a hemacytometer. Sexual maturation was characterized by first sperm (the first visible sperm in the ejaculate), puberty (50 × 10^6 sperm in the ejaculate), and sexual maturity (500 × 10^6 sperm in the ejaculate). Paired testes volume (PTV) was calculated as PTV = [0.0396125 × (average testes length) × (SC) ^{2}]. Dependent variables were analyzed using repeated measures, mixed linear models. Fixed effects included temperament class, treatment, and interaction effects. Random animal effects were across repeated days. Age at first sperm, puberty and sexual maturity were similar between C and PNS bulls (P = 0.47, 0.73, 0.99, respectively). Times between first sperm and puberty (P = 0.32) and puberty to sexual maturity (P = 0.92) were not affected by PNS. Temperamental bulls had a greater (P = 0.009) time (69.25 ± 11.45 d) from puberty to sexual maturity than calm (28.47 ± 7.53 d) or intermediate bulls (38.19 ± 9.95 d). BW at first sperm was greater for PNS (382.16 ± 11.29 kg) than C bulls (353.19 ± 10.55 kg). Scrotal circumference at first sperm was greater (P = 0.03) in temperamental (26.8 ± 0.7 cm) than calm (25.5 ± 0.5 cm) or intermediate (25.1 ± 0.6 cm) bulls. There was a tendency for temperamental bulls to have a greater PTV at first sperm (P = 0.06) and sexual maturity (P = 0.07) than calm or intermediate bulls. While PNS influenced BW, SC, and PTV at first sperm, ages at puberty or sexual maturity were not affected by PNS. Temperamental bulls had retarded sexual development between puberty and sexual maturity.

Key Words: prenatal stress, temperament, bull sexual maturity

---

0526 Equine chorionic gonadotropin improves follicular dynamics, estrus expression, ovulation, and pregnancy rate in controlled internal drug release device based estrus synchronization protocol in Nili-Ravi buffalo. M. I. Naveed, A. Husnain, U. Riaz, M. Hassan, A. Sattar*, and N. Ahmad, *Department of Theriogenology, University of Veterinary and Animal Sciences, Lahore, Pakistan.*

Reproduction of buffalo is hampered due to poor ovarian reserves, vague estrus signs, anestrus, prolonged postpartum and calving intervals, and decreased fertility. Synchronization of estrus and ovulation including CIDR (controlled internal drug release device) based protocols are well established in cows and are gaining popularity in buffaloes. However, these need modifications based on physiology of estrous cycle in buffaloes. The present study tested the hypothesis that if the addition of equine chorionic gonadotropin (eCG) to a CIDR based synchronization protocol improves ovarian follicular dynamics, estrus behavior, ovulation and pregnancy rate in Nili-Ravi buffalo. Lactating multiparous Nili-Ravi buffaloes (n = 88) received CIDR (1.38 g progesterone Pfizer Co, USA) device for 7 d and prostaglandin F2α (Dalmazine, cloprostenol, Fatro, Italy) on d 6. These buffaloes were randomly assigned to receive either saline (without eCG, n = 45) or equine chorionic gonadotropin 1000 IU (Chronogest PMSG, Intervet, Holland) i.m. (eCG, n = 43) concurrent with prostaglandin F2α treatment of the CIDR protocol (d 6). Fixed time, 2 inseminations were performed at 48 and 60 h after CIDR removal (d 7). Pregnancy was diagnosed 35 to 40 d post-AI using transrectal ultrasonography. The mean size of dominant follicle just before ovulation did not differ in eCG treated buffaloes compared with or without eCG (14.8 ± 0.3 vs.14.5 ± 0.5; P > 0.05). Mean growth rate of the ovulatory follicle was higher in the eCG group compared with without eCG (1.8 mm ± 0.0 vs.1.4 mm ± 0.1; P < 0.05). Mean interval from CIDR removal to ovulation was shorter in eCG-treated buffaloes compared to no eCG (70.9 ± 2.0 h vs. 77.5 ± 2.3 h; P < 0.05). The estrus response and intensity was greater in the eCG group than the group without eCG (100 vs. 91%; P < 0.05), (3.2 ± 0.1vs. 2.4 ± 0.1; P < 0.05), respectively. Similarly, ovulation and pregnancy rates were higher in the eCG group than those without eCG (82.9% [34/41] vs. 69.4% [26/37]; P > 0.05), (53.4% [23/43] vs. 24.4% [11/45]; P < 0.05), respectively. Therefore,

we conclude that addition of eCG before P4 device removal improves ovulatory follicle growth rate, estrus behavior, and pregnancy rate in FTAI program in buffalo. These data have strong implications in hastening buffalo reproduction.

Key Words: equine chorionic gonadotropin, fertility, buffalo

0527 Effects of prenatal transportation stress on endogenous and exogenously-induced luteinizing hormone secretion in sexually mature Brahman bulls. B. P. Littlejohn*[1,2], M. C. Roberts[1,2], M. N. Bedenbaugh[1], A. W. Lewis[2], D. A. Neuendorff[2], D. G. Riley[1,3], J. A. Carroll[4], R. C. Vann[5], M. Amstalden[1], T. H. Welsh, Jr.[1,3], and R. D. Randel[2], *[1]Texas A&M University Department of Animal Science, College Station, [2]Texas A&M AgriLife Research, Overton, [3]Texas A&M AgriLife Research, College Station, [4]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [5]MAFES–Brown Loam Experiment Station, Mississippi State University, Raymond.*

The effect of prenatal transportation stress (PNS) on secretion of LH before and after GnRH stimulation in sexually mature Brahman bulls was studied in 12 control and 11 PNS bulls. Control bulls were derived from nontransported pregnant cows, and PNS bulls were derived from cows transported for a 2-h period at 60, 80, 100, 120, and 140 ± 5 d of gestation. Temperament of each bull was assessed at weaning by pen score (PS; 1 = calm and 5 = excitable), exit velocity (EV; m/sec) and temperament score [TS = (PS + EV)/2]. Bulls were electroejaculated every 2 wk beginning at a scrotal circumference of 24 cm through sexual maturity (i.e., 500,000,000 sperm/ejaculate). Within 7 to 21 d after reaching sexual maturity, bulls were fitted with jugular vein cannulas, and blood samples were collected at 15-min intervals for 6 h to determine the pattern of LH release. GnRH was then administered intravenously (10 ng/kg BW) and blood collection continued at 15-min intervals for an additional 8 h. Concentrations of LH in serum were determined by RIA. Amplitude of a detectable LH pulse, baseline concentration of LH, and area under the LH curve (AUC) were calculated for the 4-h period immediately preceding GnRH administration. Luteinizing hormone pulse incidence was evaluated using Pulse XP algorithm. The amplitude and height of the GnRH-induced LH release, AUC post-GnRH administration, and the duration of the GnRH-induced LH release were determined. Data were analyzed using a fixed effect model, with treatment and temperament classification included in the model. The occurrence of LH pulses during the pre-GnRH period was compared between treatment groups by chi-square analysis. More PNS bulls exhibited an LH pulse before GnRH injection (10 of 11; $P < 0.01$) than control bulls (3 of 12). No other characteristic associated with the release of LH during the pre-GnRH treatment evaluated in this study differed between groups ($P > 0.1$). All bulls responded similarly to exogenous GnRH, with the exception of the duration of the LH response which was greater ($P = 0.02$) in PNS bulls (268 ± 18 min) relative to control bulls (207 ± 16 min). Pattern of LH secretion before GnRH and duration of GnRH-induced LH release differed between PNS and control bulls. Stress during prenatal development may affect secretion of LH in sexually mature Brahman bulls.

Key Words: bulls, prenatal stress, luteinizing hormone

0528 Effects of artificial insemination and natural service breeding systems on calving characteristics and weaning weights of resultant progeny. P. L. Steichen[1], S. I. Klein[1], Q. Larson[1], K. M. Bischoff[2], V. R. G. Mercadante[3], G. C. Lamb[3], C. S. Schauer[4], B. W. Neville[5], and C. R. Dahlen*[1], *[1]North Dakota State University, Fargo, [2]University of Florida, NFREC, Marianna, [3]University of Florida, Marianna, [4]Hettinger Research Extension Center, Hettinger, ND, [5]North Dakota State University, Streeter.*

Angus crossbred females ($n = 1067$) were used to evaluate effects of 2 breeding systems on calving characteristics and weaning weight of progeny. In 2 yr, females were stratified by age and BCS, then assigned randomly to 1 of 2 breeding systems: (1) exposed to natural service bulls for duration of the breeding season (NS; $n = 541$), or (2) exposed to ovulation synchronization and a fixed-time AI (7-d CO-Synch + CIDR) on d 0, followed by exposure to natural service bulls for duration of the breeding season (TAI, $n = 535$). Bulls were introduced to all females on d 1 and both treatments were managed as a cohort in the same pastures. Calving date, calving ease (scale of 1 to 5; 1 = no assistance and 5 = caesarean), calf vigor (scale of 1 to 5; 1 = normal calf and 5 = stillbirth), and birth weights were recorded within 24 h of calf birth and weights were also collected from each calf at weaning. Binomial data were analyzed using Proc GLIMMIX of SAS (SAS Inst. Inc., Cary, NC), whereas continuous data were analyzed using Proc GLM. More ($P < 0.01$) TAI females (53.2%) gave birth in the first 21 d of the calving season compared with the NS treatment (41.3%). From d 22 to 42, more ($P < 0.01$) females in the NS treatment (32.3%) gave birth compared with females in the TAI treatment (21.6%). No differences ($P \geq 0.34$) existed between treatments in the proportion of females that calved after d 43 or failed to have a calf. Overall mean calving date for females in the TAI treatment (d 16.7 ± 0.05 d) was 7 d earlier ($P < 0.01$) than that of females in the NS treatment (d 23.6 ± 0.93). However, no differences ($P \geq 0.37$) were present between treatments in calving ease (1.13 ± 0.02) or calf vigor (1.13 ± 0.04). Calves from the TAI treatment (37.9 ± 0.32 kg) were lighter at birth compared with calves from the NS treatment (39.5 ± 0.35 kg). In contrast, calves from the TAI treatment (207.3 ± 1.51 kg) had greater ($P = 0.01$) weaning weights compared with calves from the NS treatment (202.4 ± 1.50 kg). Incorporation of TAI into beef cattle breeding systems resulted

in calves born earlier in the calving season and heavier calves at weaning compared with natural service breeding systems.

Key Words: artificial insemination, calving characteristics, natural service

0529 Impact of manipulation of progesterone concentrations during follicular development on ovulatory follicle growth and timed artificial insemination pregnancy rate in beef cows.

F. M. Abreu*[1], M. A. Coutinho da Silva[1], L. H. Cruppe[1], M. L. Mussard[1], B. R. Harstine[1], G. A. Bridges[2], T. W. Geary[3], and M. L. Day[1], *[1]The Ohio State University, Columbus, [2]University of Minnesota, Grand Rapids, [3]USDA ARS Fort Keogh, Miles City, MT.*

This experiment was conducted to investigate the role of decreased progesterone (P4) concentrations during follicular development on fertility in multiparous beef cows ($n = 228$; Angus × Simmental) from 3 locations ($n = 92$; $n = 63$; $n = 73$). Ovulation was presynchronized with the 5-d CO-Synch + CIDR (controlled internal drug release device) program with the day of the final GnRH designated as d −6. On d 0, all ovarian follicles were ablated. Cows were stratified by age and days postpartum within location, and assigned to receive either a previously used CIDR and two 25-mg PGF doses 8 h apart (low-P4; L; $n = 115$) or a new CIDR (high-P4; H; $n = 113$) on d 0. On d 5, CIDR were removed, two 25-mg PGF doses administered and estrus detection tail paint applied. Tail paint scoring (TPS; 1 = paint completely removed; 2 = paint partially removed; 3 = paint largely undisturbed and no evidence of mounting), timed-AI (TAI) and administration of 100 μg GnRH were performed on d 8. Blood samples for P4 analysis were collected on d 5. Ultrasonography was conducted on d 0, 5, and 8 to assess ovarian structures, and d 35 for pregnancy diagnosis. Cows without a CL on d 0 were removed from all analyses. Across locations, P4 concentrations on d 5 were greater ($P < 0.05$) in the H (4.91 ± 0.13 ng/mL) than L (0.99 ± 0.06 ng/mL); a treatment by location interaction ($P < 0.05$), predominantly due to elevated P4 concentrations in 1 location, was detected. Follicle diameter on d 5 was greater ($P < 0.05$) in the L (8.9 ± 0.2 mm) than H (7.4 ± 0.1 mm) treatment, but did not differ between treatments (12.0 ± 0.1 mm) at TAI. Hence, follicle growth from d 5 to 8 was greater ($P < 0.05$) in the H (1.5 ± 0.1 mm/d) than in the L (1.3 ± 0.1 mm/d) treatment. Distribution of TPS differed ($P < 0.05$) between treatments with a majority of cows in the H treatment with TPS 3 (57%) and a majority in the L treatment with TPS 1 (54%). Cows with TPS 1 or 2 had a greater ($P < 0.05$) PR than cows with a TPS 3. However, PR did not differ between the H (67.3%) and L (67.8%) treatments. In conclusion, decreased P4 resulted in an increased percentage of cows in estrus before TAI, but did not impact timed AI pregnancy rate in beef cows.

Key Words: progesterone, fertility, cows

0530 Reproductive performance of lactating dairy cows after resynchronization with ovsynch or a program aimed to maximize artificial insemination in estrus and fertility of timed artificial inseminations based on ovarian structures.

J. O. Giordano*[1], R. D. Watters[2], R. Wijma[1], and M. L. Stangaferro[1], *[1]Department of Animal Science, Cornell University, Ithaca, NY, [2]Quality Milk Production Services, Cornell University, Ithaca, NY.*

Our objective was to compare the reproductive performance of dairy cows after enrollment in a program that combined resynchronization with Ovsynch and AI in estrus based on activity (AIAct) vs. a program aimed to maximize AIAct and fertility of timed AI (TAI) services by assigning treatments according to the ovarian structures present at nonpregnancy diagnosis (NPD). One day after NPD by transrectal ultrasonography at 31 ± 3 d after AI, lactating cows were blocked by parity (primiparous vs. multiparous) and randomly assigned to: (1) Control (CON; $n = 469$): resynchronization with Ovsynch-56 (GnRH-7d-PGF-56h-GnRH-16h-TAI) at 32 ± 3 d after AI combined with AIAct or 2) Treatment (TRT; $n = 430$): cows with a corpus luteum (CL) ≥ 20 mm (TRT-CL) received a PGF injection and AIAct for 9 d. Cows with no CL or CL < 20 mm (TRT-NoCL) received a GnRH injection 2 d after enrollment. Cows in TRT-CL and TRT-NoCL not AIAct were enrolled in a 5d-Ovsynch+Progeterone protocol (GnRH + CIDR-5d-PGF + CIDRremoval-1d-PGF-32h-GnRH-16h-TAI) 9 and 7 d after the PGF or GnRH injection, respectively. The percentage of cows with a CL ≥ 20 mm at NPD was similar ($P = 0.79$) for CON (64.2%; 301/469) and TRT (63.3%; 272/430) whereas, it was greater ($P = 0.005$) for multiparous than primiparous cows (66.8 vs. 57.1%). Cows in CON (mean 9.5 d, median 10 d) were reinseminated at a faster rate ($P < 0.01$; HR 2.9 CI: 2.4 to 3.5) than cows in TRT (mean 13.2 d, median 17 d). Parity did not affect ($P = 0.76$) time to reinsemination. After enrollment, a greater ($P < 0.001$) percentage of cows received AIAct in TRT (29.8%) than CON (10.4%) whereas, a greater ($P < 0.001$) percentage of cows were AIAct in TRT-CL (38.6%) than TRT-NoCL (14.6%). Pregnancies per AI (P/AI) for cows AIAct were similar ($P = 0.65$) for CON (32.7%; 16/49) and TRT (28.8%; 36/125) and were not affected by parity ($P = 0.37$). Also, P/AI after TAI were similar ($P = 0.47$) for CON (27.9%; 113/405) and TRT (30.4%; 87/286) and were not affected by parity ($P = 0.55$). Pregnancy rate from 0 to 21 d after enrollment was similar ($P = 0.62$) for CON (28.4%; 129/454) and TRT (29.9%; 123/411). Thus, compared with a typical resynchronization program, a program aimed to maximize AIAct and fertility of TAI by assigning treatments according to ovarian structures; increased the percentage of cows AIAct and had similar pregnancy rate by 21 d after NPD, however, time to reinsemination was delayed which could be explained by the small percentage of cows inseminated on activity.

Key Words: resynchronization, estrous activity, dairy cow

PHYSIOLOGY AND ENDOCRINOLOGY: REPRODUCTIVE SUCCESS IN RUMINANTS: A COMPLEX INTERACTION BETWEEN ENDOCRINE, METABOLIC, AND ENVIRONMENTAL FACTORS

0531 Recent advances in the hypothalamic control of reproduction. I. Clarke*, *Monash University, Clayton, VIC 3800, Australia.*

Reproduction is driven by the GnRH cells of the brain, but the pulsatile secretion of GnRH into the hypophysial portal blood is controlled by kisspeptin cells. In the sheep, as in other species, the kisspeptin cells form 2 major populations in the brain, 1 in the arcuate nucleus and the other in the preoptic area. The former appear to mediate the negative feedback effects of sex steroids as well as being initiators of the *positive feedback* effect that elicits the GnRH surge to cause ovulation in the female. The latter facilitate the positive feedback effect. The arcuate nucleus population of kisspeptin cells also produce neurokinin B and dynorphin, leading to their designation as KNDY cells. Kisspeptin expression in the KNDY cells is reduced in the nonbreeding season, further reinforcing the fundamental role these cells play in control of reproduction. In addition, these KNDY cells appear to be involved in the response to altered bodyweight. This is achieved via the signalling of leptin to the KNDY cells either directly or indirectly—kisspeptin gene expression is lower in lean animals, but this can be reversed by administration of leptin. KNDY cells are interconnected to the cells of the arcuate nucleus that produce anorexigenic melanocortins and those that produce the orexigen, neuropeptide Y. This provides a bidirectional interface between metabolic circuits and reproductive circuits. Thus, melanocortins and neuropeptide Y may regulate reproduction independently or via control of kisspeptin cells, providing a way that metabolic function and reproduction are interlinked. Recent data provide strong evidence that KNDY cells are most likely to be the cells that drive the pulsatile secretion of GnRH. Thus, c-Fos labelling in KNDY cells is seen at the time of ram-induced LH secretion (proxy for GnRH pulses) in anestrous ewes. In addition, KNDY cells in brains of animals sampled within 30 min of an endogenous pulse of LH displayed increased c-Fos labelling, compared with cells from animals that were not experiencing an LH pulse at the time of brain collection. Most interestingly, the means by which KNDY cells cause GnRH secretion appears to be due to action on the GnRH terminals within the median eminence. Accordingly, direct application of kisspeptin to the median eminence in vitro causes GnRH secretion. This novel mechanism has forced a revision of the model for neuroendocrine control of reproduction.

Key Words: gonadotropin-releasing hormone

0532 Influence of stress on male reproductive physiology. T. H. Welsh, Jr.*[1], N. H. Ing[1], and R. D. Randel[2], *[1]Texas A&M University, Department of Animal Science, College Station, [2]Texas A&M AgriLife Research, Overton.*

Environmental, physiological, psychological, and managerial stressors have been implicated as causes of reproductive disorders and decreased fertility in animals and humans. Herd reproductive efficiency and the stud industry depend on the sperm producing capabilities and libido of bulls and stallions. With respect to male reproductive physiology, the steroidogenic and spermatogenic functions of the testis can be negatively impacted by stress-induced secretion of endogenous glucocorticosteroids (GC) as well as by treatment with exogenous GC agonists. The testes' gametogenic function, a primary component of male fertility, is dependent on appropriate transmission, receipt, and processing of specific endocrine signals. The deleterious effects of stress on reproductive performance are presumably signaled by GC activation of the glucocorticoid receptor (*NR3C1*). Questions related to molecular mechanisms whereby stress affects specific components of the hypothalamic-pituitary-testicular (HPT) axis of male rodents, primates, cattle, sheep, pigs, horses, and other species have been pursued by the use of in vitro and in vivo methods. This paper will provide a targeted overview of potential impacts of stressors on the endocrine aspects of the HPT axis, with particular focus on direct testicular effects. Specific data to be presented are derived from studies of the influences of endogenous and exogenous GC on androgen biosynthesis and gene expression in testes of bulls and stallions. Chronic administration of a synthetic GC has been reported to increase the incidence of abnormal spermatozoa by direct action or perhaps by disruption of the endocrine or genetic mechanisms that support sperm production in bulls and stallions. Acute elevation of the systemic concentration of GC by pharmacologic methods or by mimicry of physiologic stress have inhibited testicular steroidogenesis and transiently decreased the systemic concentration of testosterone. The inhibitory action of endogenous GC concentrations on testicular steroidogenesis under stressed and nonstressed conditions indicates that activity of the hypothalamic-pituitary-adrenal axis may be of critical importance in establishment or maintenance of a functional HPT axis during prenatal, prepubertal, and postpubertal life. Homeostatic regulation of reproductive processes involves a physiological integration of the adrenal and testicular axes. The biologic and economic importance of deleterious influences of stress on male reproductive processes dictate a thorough evaluation of adrenal–testicular interrelationships in domestic livestock species.

Key Words: stress, steroidogenesis, spermatogenesis

0533 Mechanisms linking infection and innate immunity in the female genital tract with infertility in dairy cattle. I. M. Sheldon*, *Swansea University, Singleton Park, Swansea, UK.*

One of the most common endemic diseases of dairy cattle is bacterial infection of the uterus after parturition. These infections damage the endometrium lining the uterus, reduce the production of milk, and cause infertility. Uterine disease is caused by *Escherichia coli, Trueperella pyogenes*, anaerobic bacteria, and viruses. These microbes posses a range of virulence factors that caused inflammation and damage in the endometrium. Innate immunity is an ancient system of defence against microbes, dependent on host cellular pattern recognition receptors such as toll-like receptors (TLR), which bind pathogen-associated molecular patterns. Epithelial and stromal cells are the first line of defence against microbes in the endometrium, and they express the most TLR. Activation of TLR signalling leads to the secretion of chemokines, cytokines, and prostaglandins, which attract and activate neutrophils and macrophages to clear the microbes. Microbial factors and host intracellular pathways regulate the scaling of the innate immune response, and the severity of postpartum uterine disease. Uterine disease also compromises ovarian function, with impacts on the corpus luteum, and on ovarian follicle development from primordial to antral follicles. Whilst healthy ovarian follicles are devoid of immune cells, granulosa cells express TLR and have roles in innate immunity. Pathogen-associated molecular patterns perturb granulosa cell endocrine function, stimulate the secretion of inflammatory mediators from granulosa cells, and lead to damage of oocytes. In conclusion, the fundamental mechanisms of innate immunity and inflammation in the female genital tract of dairy cattle are important for animal health and fertility. *Work in the Sheldon laboratory is funded by the Biotechnology and Biological Sciences Research Council (BBSRC) in the UK*.

Key Words: dairy cattle, uterus, parturition

0534 Influences of heat stress and uterine diseases on reproduction of dairy cows. J. E. P. Santos*[1], E. S. Ribeiro[1], E. Karakayan[2], K. N. Galvão[3], and F. S. Lima[4], *[1]Department of Animal Sciences, University of Florida, Gainesville, [2]University of Florida, Gainesville, [3]Department of Large Animal Clinical Sciences, University of Florida, Gainesville, [4]Cornell University, Ithaca, NY.*

Dairy cows undergo hyperthermia during the summer months in most of the world, which causes a dramatic reduction in establishment and maintenance of pregnancy. Hyperthermia has numerous effects on cellular metabolism and function that help explain reductions in fertility, including altered period of follicle dominance, reduced steroidogenic capacity of follicular and luteal cells, altered endometrial activity, and impaired oocyte quality. This multitude of effects results in reduced fertilization and influences subsequent embryo development, which impairs maintenance of pregnancy. Data are scarce on the associations between season and risk of uterine diseases in dairy cattle, but recent epidemiological studies indicate that incidence of retained placenta and metritis increases during the hot season. Therefore, it is suggested that hyperthermia during late gestation suppress the uterine defensive mechanisms, or elevated temperature and humidity during the hot months alters the environment that predisposes to increased pathogen challenge that induces disease. Unfortunately, data from studies at the University of Florida indicate that reducing hyperthermia by cooling cows during the entire dry period in the summer do not seem to alleviate the negative impacts of heat stress on metritis. It is well described that both retained placenta and metritis are important risk factors for clinical and cytological endometritis, and the multitude of diseases that affect the uterus of the cow also suppress fertility. Heat stress, but also endometrial inflammation, as observed in cows with cytological endometritis, compromises endometrial function, which can alter the secretory activity of the endometrium and lead to inability to establish and maintain pregnancy. Infection of the endometrium with *Trueperella pyogenes*, and likely also by other uterine pathogens, damages the superficial and glandular epithelium and increases the expression of inflammatory genes, and presence of inflammation seem to disrupt embryo development. Cows that develop uterine diseases, either metritis or cytological endometritis, have reduced fertilization, compromised early embryo development, impaired d 15 conceptus elongation, and increased risk of pregnancy loss. The d 15 conceptus of cows with metritis have marked changes in gene expression, and hyperthermia (in vivo or in vitro) dramatically alters mRNA expression of early embryos, and these changes might explain the differences in maintenance of pregnancy in cows that suffer from uterine diseases or heat stress. Collectively, heat stress directly and negatively impacts reproduction while also increasing the risk of uterine diseases that further depress the establishment and maintenance of pregnancy in dairy cows.

Key Words: heat stress, reproduction physiology, endometritis

0535 Cellular and molecular mechanisms of heat stress related to bovine ovarian function. Z. Roth*, *The Hebrew University of Jerusalem, Rehovot, Israel*

In light of the intensive genetic selection for high milk production and the onset of global warming, the reduced fertility of lactating cows during the summer is expected to worsen in coming years. While not entirely clear, the mechanism of fertility reduction appears to be multifactorial in nature, including altered follicular development, depressed follicular dominance, and impaired steroidogenesis and gonadotropin secretion. Heat-induced perturbations in the physiology of

the follicle-enclosed oocyte have also been documented, expressed by impaired cleavage rate and reduced developmental competence. Oocyte alterations include increased polyunsaturated fatty acids in the membrane, reactive oxygen species, ceramide formation, caspase activity, and induction of apoptosis via the sphingomyelin and/or mitochondrial pathways. New insight into the cellular and molecular alterations have revealed heat-induced perturbations in both nuclear and cytoplasmic maturation events—meiosis resumption, metaphase-II plate formation, cytoskeleton rearrangement and translocation of cortical granules. Alterations in mitochondrial distribution (i.e., a low proportion of category-I oocytes) and mitochondrial function (low membrane potential) have been recently reported for oocytes collected during the summer. These were associated with impaired expression of both nuclear (*SDHD* and *ATP5B*) and mitochondrial (*ND2*, *CYTB*, *COXII*) genes which are crucial in the mitochondrial respiratory chain. In addition, season-induced alteration in maternal-mRNA storage was documented, expressed by reduced transcript levels (*C-MOS*, *GDF9*, *POU5F1*, and *GAPDH*) in MII-stage oocytes and embryos, before (2-, 4-, and 8-cell stages) and after (8- to 16-cell stage) embryonic genome activation. These findings clarify the association between cellular and molecular modifications and reduced developmental competence during the hot season. This knowledge is essential for developing new approaches to coping with this unsolved problem.

Key Words: heat stress, bovine ovarian function

PHYSIOLOGY AND ENDOCRINOLOGY: ADVANCES IN ESTROUS SYNCHRONIZATION

0536 Detrimental effect of long term progestin-based protocol on oocyte quality and embryonic development in indigenous goats. C. Navanukraw*[1], A. Kraisoon[2], J. Thammasiri[2], V. Khanthusaeng[2], and S. Navanukraw[2], *[1]Khon Kaen University, Khon Kaen, Thailand, [2]Department of Animal Science, Khon Kaen University, Khon Kaen, Thailand.*

Long-term progesterone treatments for estrus synchronization have been associated with a lesser fertility in ruminants. This experiment was conducted to determine the effects of short-term (7 d) and long-term (14 d) progestin based and pregnant mare serum gonadotropin (PMSG) administration on number of follicles, oocyte quality, and embryonic development in goats. Nulliparous Thai-native goats (n = 36) were randomly assigned into short-term and long-term protocols. Goats in the short-term protocol were inserted with intravaginal sponges containing 60 mg medroxyprogesterone acetate (MAP; Synchrogest esponjas, Spain) for 7 d. Goats in the second group were inserted with the same synthetic progesterone for 14 d. Multiple follicular development was induced by intramuscularly injections of 300 IU PMSG (Synchrogest PMSG, Spain) in both groups on d 6 or d 13 (1 d before sponge withdrawal). Ovariectomy was performed at 24 h after sponge removal to evaluate number of follicles and collect oocyte for in vitro fertilization (IVF). Oocyte quality was determined by morphology of cumulus oocyte complex before in vitro maturation (IVM) as healthy or nonhealthy oocyte. After IVF, embryo was evaluated during the 8-d culture as numbers of cleaved oocyte, morula, and blastocyst embryo. Total numbers of follicles and oocytes were similar for both treatments. Plasma progesterone concentrations were not different during MAP insertion period ($P > 0.05$). However, goats that received the short-term protocol had greater number of follicles 4 to 6 mm, number of healthy oocytes, number of cleaved oocytes, and number of morula embryos than goats received the long term protocol ($P < 0.01$). These data highlight the detrimental effect of long term progestin-based protocol on oocyte quality and embryonic development in goats.

Key Words: synthetic progesterone, oocyte quality, indigenous goat

0537 Exogenous insulin effect on reproductive traits during a Heatsynch protocol in dairy cows. C. C. Brauner*[1], M. E. Lima[1], D. A. Velasco Acosta[1], L. F. Mielke[1], V. O. Freitas[1], E. G. Xavier[2], A. Schneider[1], F. B. Del Pino[1], V. R. Rabassa[1], and M. Nunes Corrêa[1], *[1]Universidade Federal de Pelotas, Pelotas, Brazil, [2]Granjas 4 Irmãos, Rio Grande, Brazil*.

The objective of this study was to evaluate the effects of exogenous insulin administration on reproductive traits in a Heatsynch protocol in dairy cows. Thirty-three multiparous Holstein cows, in a body condition score of 2.5 (on a 5-point scale) reared in a grazing system in Southern Brazil were submitted to a Heatsynch protocol at 84 ± 14 d in milk with an average of 28.33 ± 1.4 kg/d milk. The protocol consisted of one 25 µg of GnRH analogue i.m. injection, and insertion of an intravaginal device with 1.9 g of progesterone (CIDR, controlled internal drug release device) on d 0. Seven days later (d 7) the CIDR insert was removed and cows were given 25 mg PGF2α i.m., followed by 1 mg of estradiol cypionate i.m. (ECP) injection at d 8. At CIDR removal (d7) cows were randomly divided into 2 groups: The insulin group (n = 14) was given 0.25 IU/kg s.c. human insulin, and the control group (n = 19) was subjected to the same synchronization protocol, but without insulin injection. On the same day, blood samples were collected from the coccygeal and serum samples were analyzed for insulin concentrations. From d 8 to 10, cows that demonstrated estrus signs were then inseminated 12 h after detection. Follicular diameter evaluations were performed by transrectal ultrasonography on d 7, 9, and 10 of the protocol. The measurement of the increase in size of the dominant follicle was considered to be preovulatory follicular growth. Data were analyzed using the GLM procedures of NCSS (2005). There was no insulin concentration difference (P = 0.61) between groups at CIDR removal, which were respectively 25.8 ± 2.4 and 27.5 ± 2.4 ng/mL for control and insulin. Insulin administration did not affect (P = 0.85) pre-ovulatory follicular growth, being 5.16 ± 0.5 mm and 5.28 ± 0.6 mm, for the insulin and control groups, respectively. The interval from CIDR removal to AI was similar between groups (P = 0.81), being 59.6 ± 3.4 and 60.8 ± 3.4 h, respectively, for insulin and control groups. Also, no insulin concentrations difference (P = 0.81) were found in cows showing estrus signs or not, 26.32 ± 2.5 and 27.23 ± 2.9 ng/mL, respectively. In conclusion, exogenous insulin injection has no effect on reproductive traits in a Heatsynch protocol in dairy cows.

Key Words: artificial insemination, efficiency, reproduction

0538 Effects of administration of prostaglandin $F_{2\alpha}$ at initiation of the 7-d CO-Synch+CIDR estrus synchronization protocol for suckled beef cows.

V. R. G. Mercadante*[1], L. E. Kozicki[2], F. M. Ciriaco[1], D. D. Henry[1], C. R. Dahlen[3], J. E. Larson[4], B. E. Voelz[4], D. J. Patterson[5], G. A. Perry[6], T. L. Steckler[7], J. S. Stevenson[8], and G. C. Lamb[1], *[1]University of Florida, Marianna, [2]Pontifical Catholic University (PUCPR), Curitiba, Brazil, [3]North Dakota State University, Fargo, [4]Mississippi State University, Mississippi State, [5]University of Missouri, Columbia, [6]South Dakota State University, Brookings, [7]University of Illinois, Simpson, [8]Kansas State University, Manhattan.*

We determined the effect of administration of prostaglandin $F_{2\alpha}$ ($PGF_{2\alpha}$) at CIDR (controlled internal drug release device) insertion during the 7-d CO-Synch+CIDR estrus synchronization protocol on subsequent pregnancy rates of suckled beef cows. At 13 locations, cows were ovulation synchronized with the 7-d CO-Synch + CIDR protocol (100 μg injection of GnRH at CIDR insertion [d -10] with 25 mg injection of $PGF_{2\alpha}$ at CIDR removal [d -3], followed by an injection of GnRH and fixed-time AI [TAI] on d 0). Cows were stratified by days postpartum, BCS, and parity, and assigned to 1 of 2 treatments: CO-Synch + CIDR (n = 819) and PG-CO-Synch + CIDR (a 25-mg injection of $PGF_{2\alpha}$ was administered at CIDR insertion of the CO-Synch + CIDR protocol; n = 827). Follicle dynamics and corpus luteum development were assessed on d -10 and -3, and pregnancy status determined on d 30 to 35. Blood was collected on d -20, -10, -3, and 0 to determine progesterone (P4). Overall TAI pregnancy rates (53.5 ± 1.9% and 50.4 ± 1.9%, for CO-Synch + CIDR and PG-CO-Synch + CIDR, respectively) did not differ (P = 0.802) between treatments. A location effect (P < 0.001) existed with pregnancy rates being the greatest at the KS2 location (67.2 ± 6.1%) and the poorest at the KS4 location (15.3 ± 5.3%). Of the 1217 cows in which cyclic status was assessed, 55% were determined to be cyclic; however, incidence of pregnancy was not associated with cyclic status or the treatment × cyclic status interaction. Concentrations of P4 were greater (P < 0.001) for CO-Synch + CIDR (4.1 ± 0.3 ng/mL) than PG-CO-Synch+CIDR (3.4 ± 0.3 ng/mL) on d -3, whereas diameter of largest follicle on d -3 tended (P = 0.094) to be greater for PG-CO-Synch + CIDR (13.4 ± 0.3 mm) than CO-Synch + CIDR (12.6 ± 0.3 mm). We concluded that administration of $PGF_{2\alpha}$ at CIDR insertion of the CO-Synch + CIDR protocol failed to increase TAI pregnancy rates in suckled beef cows, but at CIDR removal, decreased concentrations of P4 and tended to increase dominant follicle diameter.

Key Words: ovulation synchronization, artificial insemination, beef cow

0539 Split-time artificial insemination: Delayed insemination of nonestrous beef heifers in timed artificial insemination following the 14-d CIDR-PG protocol.

J. M. Thomas*[1], M. R. Ellersieck[1], S. E. Poock[2], M. F. Smith[1], and D. J. Patterson[1], *[1]University of Missouri, Columbia, [2]University of Missouri, College of Veterinary Medicine, Columbia.*

An experiment was designed to test the hypothesis that pregnancy rates in beef heifers after fixed-time artificial insemination (FTAI) may be improved by delaying insemination of those heifers that have not expressed estrus before the standard FTAI time. Estrus was synchronized for 931 heifers across 3 locations using the 14-d CIDR-PG protocol (CIDR insert [controlled internal drug release, 1.38 gm progesterone] on d 0 with removal of CIDR on d 14; 25 mg $PGF_{2\alpha}$ 16 d after CIDR removal on d 30; and 100 μg GnRH on d 33, 66 h after $PGF_{2\alpha}$). Estrous detection aids (Estrotect) were applied at $PGF_{2\alpha}$ on d 30, and expression of estrus was recorded at GnRH on d 33. Treatments were balanced across locations, and heifers within each location were randomly assigned to 1 of 2 treatments based on reproductive tract score (RTS) and weight: (1) FTAI (concurrent with GnRH, 66 h after $PGF_{2\alpha}$) regardless of estrous expression prior or (2) FTAI for heifers having expressed estrus, and delayed AI (20 h after GnRH) for heifers failing to express estrus. A significant effect of treatment was found on AI pregnancy rate, with heifers assigned to treatment 2 achieving a higher AI pregnancy rate than heifers assigned to treatment 1 (54 vs. 46%, P = 0.012). The observed increase in AI pregnancy rate is attributed to the delayed AI of nonestrous heifers in Treatment 2, as AI pregnancy rates for nonestrous heifers were significantly greater for Treatment 2 (49 vs. 34%, P = 0.024), while AI pregnancy rates of estrous heifers did not differ by treatment **(**P = 0.244**)**. In summary, FTAI pregnancy rates in heifers can be improved through a strategy of split-time AI at the standard time of 66 h after $PGF_{2\alpha}$ for heifers that have expressed estrus and delayed insemination at 20 h after GnRH for heifers that have not expressed estrus before the standard AI time in the 14-d CIDR-PG protocol.

Key Words: artificial insemination, estrus synchronization, beef heifer

0540 Split-time artificial insemination: Delayed insemination of nonestrous beef cows in timed artificial insemination following the 7-d CO-Synch + CIDR protocol.

J. M. Thomas*[1], M. R. Ellersieck[1], S. E. Poock[2], M. F. Smith[1], and D. J. Patterson[1], *[1]University of Missouri, Columbia, [2]University of Missouri, College of Veterinary Medicine, Columbia.*

An experiment was designed to test the hypothesis that pregnancy rates in postpartum beef cows after fixed-time artificial insemination (FTAI) may be improved by delaying insemination of those cows that have not expressed estrus before the

standard FTAI time. Estrus was synchronized for 951 mature, suckled cows across 9 locations using the 7-d CO-Synch + CIDR (controlled internal drug release device) protocol (100 μg GnRH + CIDR [1.38 gm progesterone] on d 0; 25 mg $PGF_{2\alpha}$ at CIDR removal on d 7; and 100 μg GnRH on d 10, 66 h after CIDR removal). Estrus detection aids (Estrotect) were applied at $PGF_{2\alpha}$ and CIDR removal on d 7, and estrous expression was recorded at GnRH on d 10. Treatments were equally represented across locations, and cows within each location were assigned to 1 of 2 treatments based on age, days postpartum (DPP), and body condition score (BCS): (1) FTAI (concurrent with GnRH, 66 h after $PGF_{2\alpha}$) regardless of estrous expression before GnRH, or (2) FTAI for cows having expressed estrus, and delayed AI (20 h after GnRH) for cows failing to express estrus. In both treatments, cows that expressed estrus before FTAI achieved higher pregnancy rates than cows that did not ($P < 0.0001$). However, no significant effect of treatment was found on AI pregnancy rate ($P = 0.757$). In summary, mature suckled beef cows may be successfully artificially inseminated using a strategy of split-time AI at the standard time of 66 h after $PGF_{2\alpha}$ for cows that have expressed estrus, and delayed insemination at 20 h after GnRH for cows that have not expressed estrus before the standard AI time in the 7-d CO-Synch + CIDR protocol. However, such a strategy does not appear to offer a significant improvement in pregnancy rates compared with a standard FTAI approach.

Key Words: artificial insemination, estrus synchronization, beef cow

---

0541 Effect of double ovulation on corpus luteum blood perfusion, peripheral progesterone, and hepatic steroid inactivating enzymes in dairy cattle.

B. E. Voelz*, C. G. Hart, G. F. Cline, C. O. Lemley, and J. E. Larson, *Mississippi State University, Mississippi State.*

Double ovulation is more common in Holstein cows than other dairy breeds. The effects of double ovulation on the corpus luteum (CL) and subsequent peripheral progesterone and clearance have not been examined. Thus, the objective of this experiment was to determine if induction of an accessory CL, via hCG, alters blood perfusion of CL, peripheral concentrations of progesterone, or hepatic steroid inactivating enzymes. Lactating, nonpregnant Holstein cows ($n = 19$) were synchronized using Ovsynch. Seven days postovulation, 8 cows received an injection of hCG (1000 IU, i.m.) while 11 cows received no treatment. Size of CL were measured and photos of blood perfusion of CL were recorded (d 10 to d 18) via Doppler ultrasonography and a blood sample was collected daily. Picture images were analyzed visually by 2 consistent technicians, averaged, and categorized (0 to 9 with 0 = no perfusion and 9 = complete perfusion). Pictures were also assessed using ImageJ software for integrated density of pixels. On d 13 postovulation, a liver biopsy was performed and hepatic steroid inactivating enzymes were analyzed. The MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) was used with day as a repeated measure and cow as a random variable. LSMeans and pooled SEM are presented. Cows with 1 or 2 CL had similar ($P = 0.62$) peripheral concentrations of progesterone, 7.2 ± 0.7 and 7.7 ± 0.8 ng/mL, respectively. Compared with cows with 1 CL, cows with 2 CL had similar ($P > 0.80$) volume (7.3 ± 1.0 vs. 7.7 ± 1.2 cm^3) but greater ($P < 0.001$) total blood perfusion (3.8 ± 0.3 vs. 6.9 ± 0.3 visual score; 4403.7 ± 641.3 vs. 7781.8 ± 759.2 pixels). Both visual and pixel perfusion scores adjusted for CL volume (per cm^3 of luteal tissue) were greater ($P < 0.01$) in cows with 2 CL than 1 CL with a day × treatment interaction. Hepatic enzyme (cytochrome P450 1A, 3A, and 2C, aldo-keto reductase 1C, and uridine diphosphate-glucuronosyltransferase) activities were not different ($P > 0.23$) between treatment groups. Overall, the increased blood perfusion of CL in cows with 2 CL did not correspond to peripheral concentrations of progesterone or clearance as measured by hepatic enzyme activity, perhaps indicating that a double ovulation does not impact progesterone necessary to maintain pregnancy.

Key Words: blood perfusion, corpus luteum, progesterone

0542 A novel procedure using a gonadotropin-releasing hormone agonist to increase pregnancy rates in lactating dairy cattle.

A. Willmore*[1], C. Hammons[1], J. Peak[1], T. M. Nett[2], and T. L. Davis[1], [1]*University of Idaho, Moscow,* [2]*Colorado State University, Fort Collins.*

An earlier postovulatory increase in circulating progesterone (P4) concentration is associated with greater pregnancy success, likely through P4 alteration of the uterine environment conducive for embryo survival. We have shown that chronic administration of a gonadotropin-releasing hormone (GnRH) agonist (Deslorelin; 1 μg/kg BW^{-1} d^{-1}) beginning d 3 of the estrous cycle increases mean and basal secretion of luteinizing hormone, size of the corpus luteum (CL), and circulating P4 concentrations in beef heifers. The objectives of the present studies were to increase circulating P4 concentrations and pregnancy rates in lactating dairy cows with chronic administration of Deslorelin. Luteal volumes and P4 concentrations were analyzed using a mixed model procedure with repeated measures. Pregnancy rates were analyzed using a Chi Square Analysis. Data were considered different at $P < 0.05$. Deslorelin treatment for 12 d (d 3 to 15; d 0 = estrus) increased CL volumes in primiparous lactating dairy cows ($n = 4$) compared with untreated primiparous lactating dairy cows ($n = 6$). Circulating P4 concentrations were increased in cows treated with Deslorelin as compared with controls. In a small pilot pregnancy study, cows of various parity received Deslorelin treatment for 7 d (d 3 to 10) or 12 d (d 3 to 15) following estrous synchronization and timed AI (d = 0). Pregnancy rates were

50% greater in cows treated with Deslorelin 7 d (n = 10; P < 0.05) compared with controls (n = 10). No difference was observed in pregnancy rates for cows treated 12 d with Deslorelin (n = 10) compared with controls. In summary, chronic administration of Deslorelin altered luteal volume and increased circulating P4 concentrations in primiparous lactating cows only, albeit not during the early postovulatory critical period. Chronic administration of Deslorelin for 7 d increased pregnancy rates in cows although no differences in circulating P4 concentrations were observed. None of the animals in these experiments exhibited insufficient luteal function as defined by circulating P4 concentrations < 1 ng/mL; therefore, it is unlikely that the induced P4 concentrations by Deslorelin treatment resulted in increased pregnancy rates. These findings provide evidence that chronic administration of a GnRH agonist increases pregnancy rates in dairy cattle. The mechanism by which chronic administration of a GnRH agonist increases pregnancy rates is unknown, but could potentially be a direct effect of Deslorelin acting on the oviduct or uterine horn since GnRH receptors have been identified in bovine uterine tissue.

Key Words: dairy cow, gonadotropin-releasing hormone agonist, pregnancy rates

---

0543 Effect of an automated estrous detection system during a timed artificial insemination program on first postpartum artificial insemination.

T. A. Burnett*, A. M. L. Madureira, B. F. Silper, A. C. C. Fernandes, and R. L. A. Cerri, *Faculty of Land and Food Systems–University of British Columbia, Vancouver, Canada.*

The aim of this study was to compare 2 reproductive programs for first AI based on activity monitors and timed AI (TAI). Seven-hundred-and-seventy-four lactating Holstein cows from 2 commercial farms (Farm A, n = 322; Farm B, n = 452) were enrolled. Animals were presynchronized with 2 injections of PGF followed by an ovsynch protocol. Treatments were (1) TAI: all first inseminations performed by timed AI, and (2) ACT: first insemination based on estrous detection by activity monitors (Heatime, SCR Engineering, Israel) after the presynchronization, whereas the remaining noninseminated cows were enrolled onto the ovsynch protocol. All animals had their body condition score (BCS, scale 1 to 5), hock score (HS, scale 1 to 4), gait score (GS, scale1 to 4), and corpus luteum presence by ovarian ultrasonography recorded twice during presynchronization. Continuous data was analysed using ANOVA by PROC GLM whereas binomial data was analysed by logistic regression using PROC logistic of SAS (SAS Inst. Inc., Cary, NC). The ACT treatment had 52.3% of cows inseminated by estrous detection, whereas 90.3% of cows were bred by timed AI in the TAI treatment. Pregnancy per AI did not differ (P = 0.12), and was 30.0 and 34.5% for ACT and TAI, respectively. Overall, pregnancy per AI was similar in cows bred by estrous detection compared with the ovsynch protocol (29.5 vs. 31.8%; P = 0.38). Median days open was similar between treatments (P = 0.92). From all cows inseminated on estrus, only 30.9 and 36.3% were considered lame (GS > 2) and with a swollen hock (HS > 2), respectively. Fertility was affected by foot and leg conditions as animals that were classified as being lame, with a swollen hock, or both, had decreased pregnancy per AI compared with healthy animals (P < 0.01; 25.6 vs. 39.9%). The BCS did not affect the number of animals inseminated by estrous detection, but low BCS decreased pregnancy per AI (P < 0.01; 23.9 vs. 38.9%). The proportion of noncyclic cows during the presynchronization that were inseminated on estrus was 38.7% compared with 54.9% in cyclic animals (P = 0.05). In conclusion, pregnancy per AI did not differ between treatments; however, gait score, hock score, BCS and cyclic status highly impacted fertility and the number of animals detected in estrus. The use of activity monitors for automated estrous detection can be used strategically in a traditional reproductive program for first AI after calving.

Key Words: activity monitor, dairy cow, timed artificial insemination

---

0544 Effects of progesterone supplementation on reproductive responses in dairy cows subjected to timed artificial insemination programs: A meta-analysis.

R. S. Bisinotto*, N. Martinez, L. D. P. Sinedino, G. C. Gomes, L. F. Greco, W. W. Thatcher, and J. E. P. Santos, *Department of Animal Sciences, University of Florida, Gainesville.*

Objectives were to summarize the effects of progesterone supplementation during synchronization programs on pregnancy per AI (P/AI), and pregnancy loss in dairy cows through a meta-analysis. A systematic search for peer-reviewed manuscripts using Pubmed and ScienceDirect databases (Key Words: progesterone, dairy cow) yielded a total of 2384 results. Only controlled clinical trials were included (k = 16), in which lactating dairy cows were either assigned to receive a single intravaginal device containing progesterone or remained as untreated controls subjected to the same timed AI (TAI) protocol. Studies were classified on whether cows received the first AI postpartum or subsequent AI (first, 2+, mixed), if presynchronization was performed, and if cows were observed for estrus and allowed to be inseminated before TAI. A subset of studies with cows classified based on presence of CL at the initiation of the TAI protocol (k = 10) was used to assess the effects of progesterone supplementation according to CL status. First and second pregnancy diagnoses were performed on d 30 (27 to 150 d) and d 60 (41 to 150 d) after AI. Pregnancy loss was defined for cows that lost their pregnancies between d 30 and 60. Meta-analysis was conducted using the Metafor package for R. Study was considered random and moderator variables were included as fixed effects. Results were reported as adjusted relative risk (RR) and its 95% confidence interval. Pregnancy loss and P/AI were calculated from raw data.

Overall, progesterone supplementation increased ($P = 0.003$) P/AI on d 60 (RR = 1.19; 95%CI = 1.07–1.32; P/AI: 33.3 vs. 28.6%). Presynchronization of the estrous cycle and AI number did not impact the benefit from progesterone supplementation and accounted for 6.9 and 6.0% of the heterogeneity, respectively. Allowance for AI at detected estrus accounted for 47.4% of the heterogeneity and reduced ($P = 0.01$) the benefit from progesterone supplementation compared with TAI only (RR = 0.81; 95%CI = 0.68 to 0.95; P/AI supplemented vs. control: estrus-AI or TAI = 32.6 vs. 30.2%, TAI = 34.5 vs. 25.9%). Progesterone supplementation tended to reduce ($P = 0.09$) pregnancy loss (RR = 0.82; 95%CI = 0.66 to 1.02; pregnancy loss: 10.9 vs. 13.0%); all heterogeneity was explained by AI number as supplementation reduced pregnancy losses in cows receiving first postpartum AI (10.1 vs. 14.0%) but not subsequent AI (11.8 vs. 12.0%). Subgroup analyses depicted that the benefit of progesterone supplementation on P/AI at 60 d and pregnancy loss were not affected by CL status. In conclusion, progesterone supplementation improved fertility mainly in cows not detected in estrus during the TAI program.

Key Words: dairy cow, progesterone, meta-analysis

0545 Regimens of progesterone supplementation for lactating dairy cows according to the presence of corpora lutea at the initiation of the timed artificial insemination program. R. S. Bisinotto*, L. O. Castro, C. D. Narciso, N. Martinez, M. B. Pansani, L. D. P. Sinedino, P. E. Carneiro, N. S. van de Burgwal, H. M. Bosman, R. Daetz, W. W. Thatcher, and J. E. P. Santos, *Department of Animal Sciences, University of Florida, Gainesville.*

Objectives were to evaluate the effects of supplemental progesterone on fertility of dairy cows according to the presence of corpora lutea (CL) at the initiation of the Ovsynch-56 program (d-10 GnRH, d 3 $PGF_{2\alpha}$, h 16 GnRH, d 0 AI). Cows had their ovaries evaluated by ultrasonography (d 10) and those without CL were assigned randomly to receive 0 (NoCL; $n = 558$) or 2 intravaginal inserts containing progesterone (CIDR) from d 10 to d 3 (2CIDR; $n = 544$). Cows with CL on d 10 were matched by pen and used as positive controls (Diestrus; $n = 543$). The remaining cows bearing CL were assigned randomly to receive 0 (Control; $n = 388$) or 1 CIDR inserts (1CIDR; $n = 393$). Ovaries were scanned on d 3 for assessment of ovulation after the first GnRH and the presence of a newly formed CL. A subgroup of cows ($n = 365$) had their ovaries scanned on d 1 and d 1 for measurement of the ovulatory follicle and evaluation of the response to the second GnRH. Estrus was detected based on removal of tail chalk beginning on d -10. Pregnancy was evaluated 32 and 60 d after AI. Data were analyzed using the GLIMMIX procedure of SAS (SAS Inst. Inc., Cary, NC). A greater ($P < 0.01$) proportion of NoCL and 2CIDR cows had a new CL on d -3 compared with Diestrus (71.6, 68.7, 43.2%), whereas no difference was observed between Control and 1CIDR (51.2, 56.6%). Fewer ($P < 0.01$) NoCL and 2CIDR cows had CL on d -3 compared with Diestrus (71.6, 68.7, 88.0%) and no difference was observed between Control and 1CIDR (86.4, 87.6%). Progesterone supplementation reduced ($P = 0.05$) the proportion of cows without CL inseminated before timed AI for first postpartum AI (2CIDR = 10.9, NoCL = 17.7%), but not for subsequent AI (2CIDR = 19.0, NoCL = 17.5%) or cows with CL (1CIDR = 7.8, Control = 9.1%). Ovulation to the second GnRH was not affected by treatment and averaged 86.5%. The diameter of the ovulatory follicle tended to be reduced ($P = 0.07$) by progesterone supplementation in cows lacking CL (2CIDR = 17.0 ± 0.4, NoCL = 18.1 ± 0.4 mm), but not in those with CL (1CIDR = 17.5 ± 0.4, Control = 17.8 ± 0.4 mm). Pregnancy per AI was greater ($P \leq 0.08$) for 2CIDR compared with NoCL, and intermediate for Diestrus on d 32 (38.4, 32.7, 35.9%) and 60 (33.3, 28.3, 31.4%). This benefit was observed exclusively in cows not detected in estrus at AI. Progesterone supplementation reduced ($P = 0.05$) P/AI in 1CIDR compared with Control on d 32 (38.3, 45.7%) but not on d 60 after AI (33.4, 37.4%), which was associated with smaller ($P = 0.04$) pregnancy loss in the 1 CIDR group (4.0, 12.6%).

Key Words: anovulation, dairy cow, progesterone

0546 Effect of preovulatory concentration of estradiol and length of proestrus on pregnancy rate to timed-artificial insemination and embryo transfer in beef cows. L. H. Cruppe*[1], R. S. Cipriano[2], F. M. Abreu[1], M. L. Mussard[1], K. J. Wells[1], G. E. Fogle[1], B. R. Harstine[1], M. D. Utt[3], G. A. Bridges[4], and M. L. Day[1], *[1]The Ohio State University, Columbus, [2]UniSalesiano, Araçatuba, Brazil, [3]Select Sires Inc., Plain City, OH, [4]University of Minnesota, Grand Rapids.*

Postpartum beef cows ($n = 327$) were used to investigate the effect of preovulatory estradiol concentration (Pre-E2) and length of proestrus on timed-AI (TAI) and embryo transfer (ET) pregnancy rates. Ovulation was presynchronized with the 5-d CO-Synch + CIDR (controlled internal drug release device), follicle aspiration performed 6.5 d later (d −7 of experiment) and cows received 50 mg PGF2α on either d -3 (normal estradiol treatment; HiE), or on d -1.5 (deficient estradiol treatment; LoE). All cows received 100 μg GnRH on d 0, creating a proestrus of either 3 or 1.5 d. Ultrasonography was performed on d −7, 0, and 7 to confirm ovulation to pre-synchronization, ovulatory follicle diameter and corpus luteum (CL) formation after GnRH, respectively. Blood samples on d -3, -1.5 and 0 were used to determine Pre-E2. Blood samples on d -3, d 0, and d 7 were analyzed for progesterone to confirm presence of CL, its regression and formation of new CL, respectively. Cows in the HiE and LoE treatments were either TAI on d 0 or ET on d 7, resulting in 4 distinct combinations (HiE-AI, $n = 77$; HiE-ET, $n = 67$; LoE-AI, $n = 98$; LoE-ET,

$n = 85$) in a 2 × 2 factorial arrangement. Pregnancy diagnosis was performed on d 35. Ovulatory follicle diameter (11.9 ± 0.1 mm) and progesterone on d -3 (3.8 ± 0.1 ng/mL), d 0 (0.4 ± 0.0 ng/mL) and d 7 (2.6 ± 0.1 ng/mL) did not differ among treatments. As expected, Pre-E2 on d -3 was similar between HiE (4.5 ± 0.1 pg/mL) and LoE (4.5 ± 0.1 pg/mL). In contrast, Pre-E2 was greater ($P < 0.05$) in the HiE on d -1.5 and 0 (7.6 ± 0.2; 10.1 ± 0.3 pg/mL, respectively) compared with LoE (5.1 ± 0.2; 9.2 ± 0.2 pg/mL, respectively). Pregnancy rate was greater ($P < 0.05$) in the HiE treatment and AI group (HiE-AI, 68.8%; HiE-ET, 52.2%; LoE-AI, 46.9%; LoE-ET, 37.6%) compared with the LoE treatment and ET group, however no interaction treatment (HiE/LoE) and breeding technique (AI/ET) was detected for pregnancy rate. Reduced Pre-E2 was the primary outcome of shortened proestrus, which resulted in similar reductions in TAI (31.8%) and ET (28.0%) pregnancy rate; relative to that achieved in the Hi-E treatment. Based on the similarity of these responses, it is concluded that the primary impact of deficient Pre-E2 is to impair the ability of the uterus to sustain the embryo during early gestation.

Key Words: preovulatory estradiol, timed artificial insemination, embryo transfer

PRODUCTION, MANAGEMENT, AND THE ENVIRONMENT: INFLUENCE OF DIET AND MANAGEMENT PRACTICES ON ENVIRONMENTAL FOOTPRINT

0547 Effect of breed type and pasture type on methane emissions from weaned lambs offered fresh grasses. M. D. Fraser, H. R. Fleming, V. J. Theobald, and J. M. Moorby*, *Aberystwyth University, Aberystwyth, UK.*

To investigate the extent to which enteric methane emissions from growing lambs are explained by simple body weight and diet characteristics, a 2 × 2 Latin square changeover design experiment was performed using 2 sheep breed types and 2 fresh pasture types. Weaned lambs of 2 sheep breed types were used: Welsh Mountain (a small, hardy hill breed; mean LW = 27 ± 3.6 kg) and Mule × Texel (prime lamb; 35 ± 2.5 kg; n = 8 per breed). The lambs were zero-grazed on material cut from contrasting high (ryegrass) and low (permanent pasture) digestibility pastures and fed fresh. In each experimental period, ad libitum DMI was determined individually indoors following an adaptation period of 2 wk, and methane emissions were measured individually in open-circuit respiration chambers over a period of 3 d. Mean pasture composition, as fed, for ryegrass and permanent pasture respectively, was: DM, 21.9 and 21.9%; CP, 12.4 and 11.1% DM; NDF, 41.2 and 53.3% DM; GE, 17.3 and 17.1 MJ/kg DM. Although total daily methane emissions were lower for the Welsh Mountain lambs than for the Mule × Texel lambs (13 vs. 16 g/d respectively; SED = 1.0; $P < 0.05$) when offered fresh forage, the yield of methane per unit DMI was similar for the 2 breed types (16.4 vs. 17.7 g methane/kg DMI; SED = 0.79; NS). Total output of methane per day was higher when lambs were offered ryegrass compared with permanent pasture (16 vs. 13 g/d respectively; SED = 0.49; $P < 0.001$) which was likely driven by differences in DMI (986 vs. 732 g/d; SED = 22.4; $P < 0.001$). Methane emissions per unit DMI (16.4 vs. 17.7 g methane/kg DMI; SED = 0.37; $P < 0.01$) and proportion of GE intake excreted as methane (4.9 vs. 5.3%; SED = 0.11; $P < 0.01$) were both higher on the permanent pasture. No forage × breed type interactions were identified. The results indicate that forage type had a greater impact than breed type on methane emissions from growing weaned lambs. It can be concluded that, when calculating methane emissions for inventory purposes, it would be more important to know what feeds growing lambs are consuming than to know what breeds they are.

Key Words: lambs, grass, methane

0548 Effects of dietary nitrate supplementation on enteric methane and nitrous oxide emissions from beef cattle. C. J. Neumeier*[1], Q. Wang[1], A. R. Castillo[2], Y. Zhao[1], Y. Pan[1], and F. M. Mitloehner[1], *[1]University of California-Davis, Davis, [2]University of California Cooperative Extension, Merced.*

Feeding nitrate has been proposed as a means to reduce enteric greenhouse gas emissions from ruminants. Nitrate can compete with methanogens for hydrogen in the rumen and therefore reduce methane from eructation. However, increasing the nitrate concentration in the rumen could induce enteric nitrous oxide emissions, potentially nullifying the greenhouse gas reduction achieved from lowering methane emissions. The present study investigated the effects 2% nitrate (on DM basis) vs. an isonitrogenous concentration of urea supplemented to finishing steers on enteric methane and nitrous oxide emissions. Sixteen steers were allocated to nitrate and urea treatments in a randomized complete block design (n = 8). Eructated emissions were collected using head chambers for 12 h following the morning feeding. Methane was measured using the TEI 55C direct methane analyzer and nitrous oxide using the 46i nitrous oxide analyzer (both were Thermo Environmental Instruments, Franklin, MA). All data was analyzed using the Proc Mixed Model in SAS (SAS Inst. Inc., Cary, NC). The nitrate vs. urea treatment lowered methane production at measurement h 1 and 2 ($P < 0.01$), but did not lower overall methane production during the 12-h measurement period. The nitrate vs. urea treatment increased nitrous oxide production at h 1, 2, and 3 ($P < 0.05$) of measurement, and the overall 12-h measurement period ($P < 0.0001$). Nitrous oxide was detected in both treatments at each time point, with a sixfold increase in production in the nitrate (~600 mg/12 h) vs. urea treatment (~100 mg/12 h). Overall, combined greenhouse gas production expressed as carbon dioxide equivalents was similar between treatments. This study indicates that nitrate supplementation in finishing beef cattle is effective at reducing eructated methane in the time immediately following feeding, and might need to be supplemented at a higher concentration and/or more frequently to achieve more optimal methane reduction. Furthermore, this study suggests that cattle could be a source of the potent greenhouse gas nitrous oxide, which is further stimulated by nitrate supplementation. Additional research is necessary to evaluate more effective means of reducing methane with nitrate in finishing beef cattle and the production of nitrous oxide with and without supplementation of nitrate.

Key Words: greenhouse gas, hydrogen sink, ruminant

0549 Comparison of active flux and passive concentration measurements of methane emissions from cattle. P. Huhtanen*[1], E. H. Cabezas Garcia[1], S. R. Zimmerman[2], and P. R. Zimmerman[2], *[1]Swedish University of Agricultural Sciences, Umea, Sweden, [2]C-Lock Inc., Rapid City, SD*.

There are 2 new measurement techniques to measure emitted CH_4 and CO_2 from cattle in production systems, the passive concentration measurement method (PCM) and the active gas capture method (AGC). Both systems estimate cattle muzzle CH_4 and CO_2 emissions for short-term periods (3 to 15 min) while cattle visit a feeding station multiple times daily. The objective was to determine if the 2 techniques yielded comparable results under farm conditions. A GreenFeed (GF) system was used (C-Lock Inc., Rapid City, SD) that measures individual animal emissions over a feed trough. For AGC, an active airflow (2000 L/min) was induced around the animal's muzzle that attracted emissions into a air collection pipe where airflow and CH_4 and CO_2 concentrations were measured and the average flux was calculated for each visit. For PCM, a concentration sampling intake (at 1 l/min) was placed inside the feed trough, no active airflow was used, and the average CH_4 and CO_2concentrations for each visit were calculated. 32 Swedish Red dairy cows (BW 664 ± 72 kg, MY 30.2 ± 6.3 kg/d, and DMI 20.1 ± 2.8 kg/d) housed in a free-stall barn had an access to 2 separate GF units. The diets were fed ad libitum as TMR (60% forages, 40% concentrates on DM basis). The GF were configured for 10-d sampling periods using PCM and AGC repeated twice. The data was analyzed with linear mixed models using the MIXED procedure in SAS (SAS Inst. Inc., Cary, NC). Repeatability (R) was calculated as $R = \delta^2_{Animal}/(\delta^2_{Ánimal} + \delta^2_{Residual})$. The cows visited GF on average 2.85 ± 0.95 times per day. For CH_4, the between animal coefficient of variation (CV) was greater (11.0 vs. 17.6%) with PMC compared with AGC. Comparing CH_4 results for individual animals to determine if ranking was consistent between AGC and PCM, a weak correlation was found between CH_4 concentration with PCM and CH_4 flux with AGC:CH_4 Flux (g/d) = 363 ± 30.5 + 0.058 ± 0.0214 × CH_4 (ppm; R^2 = 0.13; RMSE = 52.1). For CH_4/CO_2 ratio, CV values were similar (6.4 and 6.6%) but averaged CH_4/CO_2 ratio was greater (P = 0.001) with PMC (0.107) compared with AGC (0.094). The repeatability for AGC and PCM were high (0.72 to 0.74). It is concluded that PCM methods are not sufficient for ranking animal's emissions on farms. Measuring concentration passively is not the same as measuring fluxes.

Key Words: methane, cattle, emissions

0550 Methane emission intensities by Holstein and Holstein × Jersey crossbreed lactating cows in two Brazilian grazing systems. A. Berndt, A. P. Lemes, L. A. Romero, T. C. Alves, A. M. Pedroso*, A. D. F. Pedroso, and P. P. A. Oliveira, *EMBRAPA, São Carlos, Brazil.*

The aim of this study was the evaluation of methane emissions from pure Holstein and half Jersey, half Holstein high-producing lactating cows grazing 2 different forages. The study was conducted at EMBRAPA's (Brazilian Agricultural Research Corporation) experimental station located in São Carlos city, in the Southeast region of Brazil. Treatments were a combination of 2 factors: 2 breeds (Holstein, HOL; and 1/2half Jersey half Holstein, JH) and 2 grazing systems (extensively grazed pastures with low stocking rate, ELS, or irrigated pastures under intensive management and high stocking rate, IHS). A total of 24 dairy cows were used (2 breeds × 2 grazing systems × 3 animals per paddock × 2 replicates), grouped according to age, stage of lactation, and level of milk production. Cows were kept on pasture and supplemented with minerals and concentrates in accordance with milk yield (1 kg of concentrate/3 kg of milk produced). The IHS pasture was rotationally managed and both IHS and ELS were managed under variable stocking rates ("put-and-take"). Forage production and animal performance variables were measured to determine environmental, technical, and economic assessments. Methane emission evaluation took place in May 2013 using the SF6 tracer technique. Each animal received 2 permeation tubes (average load of 1431.0 ± 76.2 mg of SF6 with an average emission rate of 1.74 ± 0.18 mg/d) 5 d before collection. Samples were collected every 24 h for 5 consecutive days. Gases were measured on a Shimadzu GC 2014. Data were analyzed using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) and averages were compared using Tukey's test with significant differences at $P < 0.05$. No interactions were observed between breed and grazing system. Crossbred JH presented lower ($P < 0.05$) methane emission intensity than pure Holstein (11.26 ± 1.11 vs. 14.62 ± 1.11 gCH_4/L milk) regardless of grazing system. Crossbreed JH cows emitted less ($P < 0.05$) methane per day than pure HOL (275.1 ± 20.8 vs. 337.2 ± 20.8 gCH_4/d) and produced the same amount of milk (25.11 ± 1.11 vs. 23.76 ± 1.11 L/d). Efficiency of milk production can be a mitigation strategy when less methane is emitted per liter of milk.

Key Words: dairy cows, emission intensity, methane emission

0551 Comparison between the sulfur hexafluoride tracer technique and the portable automated head chamber system for measurements of enteric methane fluxes in mid-lactation holstein cows.

A. B. D. Pereira*[1], C. D. Dorich[1], A. F. Brito[1], R. K. Varner[1], and R. Martineau[2], *[1]University of New Hampshire, Durham, [2]Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada.*

The objective of this study was to evaluate the concordance correlation coefficient (CCC) and coefficient of variation (CV) of enteric methane flux (Q_{CH4}) between the sulfur hexafluoride tracer technique (SF_6) and the portable automated head chamber system (The GreenFeed [GF]; C-Lock Inc., Rapid City, SD). Eleven multiparous and 4 primiparous lactating Holstein cows housed in a tie-stall barn and averaging 176 ± 34 d in milk (DIM), 42.9 ± 6.8 kg of milk yield and 681 ± 48 kg of BW were blocked by DIM, parity, and DMI (as % of BW) and, within each block, randomly assigned to 1 of 2 treatments: ad libitum intake (AI) or restricted intake (RI) (90% DMI) according to a crossover design. Each experimental period lasted 22 d with 14 d for treatments adaptation and 8 d for data and samples collection. Diets contained (DM basis): 40% corn silage, 12% grass-legume haylage, and 48% concentrate. Five-minute measurements were taken from all animals with intervals of 12 h between the 2 daily samplings using the GF. Sampling points were advanced 2 h from 1 d to the next to yield 14 gas samplings/cow over 7 d to account for diurnal variation in Q_{CH4}. For the SF_6 method, sampling was done twice a day before milking times with canisters placed in 5 different locations inside the barn for measuring background gas concentration. Animal performance data were analyzed using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC) while the comparison between methods was done using the CCC. Data inclusion criteria were a minimum of 5 measurements per animal per period and Q_{CH4} ranging from 150 to 800 g/d. There was a significant difference in DMI between treatments (23.7 vs. 22.3 kg/d for AI and RI, respectively) but no difference was found for milk yield and Q_{CH4} when using the GF system (471 vs. 458 g/d for AI and RI, respectively) or the SF_6 technique (406 vs. 409 g/d for AI and RI, respectively). Between animal Q_{CH4} CV averaged 14.5% (GF) and 36.5% (SF_6); within animal Q_{CH4} CV averaged 17.8% (GF) and 36.2% (SF_6). The CCC was 0.15 on 225 comparisons of 2 daily data points with error terms of 10% (central tendency), 17% (regression), and 73% (disturbance). Current results suggest that the SF_6 technique was twice more variable and yielded lower Q_{CH4} compared with the GF system. Poor concordance between these 2 methodologies warrants further investigations.

Key Words: methane, sulfur hexafluoride tracer technique, GreenFeed

0552 Nitrogen use efficiency and carbon footprint by beef cattle limit-fed co-product feedstuffs.

W. B. Smith*[1], K. P. Coffey[2], R. T. Rhein[1], E. B. Kegley[1], D. Philipp[1], J. D. Caldwell[3], and A. N. Young[1], *[1]Department of Animal Science, University of Arkansas Division of Agriculture, Fayetteville, [2]University of Arkansas, Fayetteville, AR, [3]Department of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO.*

In terms of energy density, the cost of importing hay is often not justified in years where adverse conditions limit local hay production. Coproduct feedstuffs could represent an alternative to feeding hay in these conditions. While the primary objective of our work was to determine if coproduct feedstuffs could be used to meet the energy demands for cows, also of interest was the N use efficiency of such a system, as well as the potential environmental impacts. Eight ruminally-fistulated cows (671 ± 32.0 kg BW) were stratified by BW and allocated randomly to 1 of 4 treatments in a 2-period study: (1) limit-fed soybean hulls (LSH), (2) limit-fed distillers' dried grains with solubles (LDG), (3) a limit-fed mixture of soybean hulls and distillers' dried grains with solubles (MIX), or (4) ad libitum mixed-grass hay (HAY; 10.6% CP, 71% NDF). Limit-fed diets were formulated to meet the ME requirements of an 11-mo postpartum mature beef cow. Diet amounts were increased over a 14-d period. Cows were then moved to indoor 3 × 4.3 m concrete pens fitted with rubber mats for a 14-d adaptation and 5-d total fecal collection period. Carbon footprint and emissions were predicted according to an IPCC (2006) model for cows housed on pasture. Excretion of total N, as well as percentage excreted in feces and urine, was not different ($P \geq 0.31$) among treatments. Concentration of ammonia-N in the urine was greater ($P = 0.02$), and concentration of urea-N tended to be greater ($P = 0.07$) from LDG than from other treatments. Both ammonia-N and urea-N, when expressed as a percentage of the total urinary N, were greater ($P \leq 0.04$) from LDG than other treatments. Predicted enteric CH_4, CH_4 from manure, direct loss of N_2O, as well as N_2O from volatilization and leaching were not different ($P \geq 0.12$) among treatments. Contribution of feedstuffs to total CO_2 load tended to be greatest ($P = 0.07$) from LDG and least from HAY, with MIX intermediate to LDG and LSH and LSH intermediate to MIX and HAY. However, total carbon footprint (kg CO_2 eq/d) was not different ($P = 0.55$) among treatments. Based on this information, coproduct feedstuffs may be used in lieu of hay to meet the energy requirements of cows without adverse effects on total N excretion or environmental impact.

Key Words: limit feeding, coproduct feedstuffs, carbon footprint

PRODUCTION, MANAGEMENT, AND THE ENVIRONMENT: **ANIMAL HEALTH: A RETROSPECTIVE LOOK**

0553 Antibiotic use in period 2005–2012 in dairy herds in the Netherlands, with outlook to some other countries. A. Kuipers*[1] and H. Wemmenhove[2], *[1]Expertise Centre for Farm Management and Knowledge Transfer, Wageningen UR, Wageningen, Netherlands, [2]Livestock Research, Wageningen UR, Lelystad, Netherlands.*

Use of antibiotics in animals has become part of the societal discussion. National goal was to reduce use by 50% in 2013 compared to 2009. A herd health and treatment plan have been introduced. From 2012 on 3/4 generation drugs (3/4GE) are only allowed in exceptional cases. To gain insight, antibiotic use and attitudes of farmers were examined on 94 farms during period 2005 through 2012. Number of Daily Dosages (NDD) indicates how many days per year an average cow in the herd is under treatment of antibiotics. NDD was on average 5.86 (SD 2.14). The NDD level was increasing in period 2005 through 2007, followed by a period of growing societal interest in animal antibiotic use resulting in a reduction in use in 2011 through 2012. On average, 68% of NDD was applied to the udder, dealing with mastitis (25%) and dry-cow therapy (43%). Drugs other than applied to udder health tended to decrease the most, while farmers were reluctant to lower use of dry-cow therapy tubes. Use of 3/4GE drugs minimized from 18% of NDD in period 2005 through 2010 to 1% in 2012. More use of penicillins and wide spectrum drugs took place. The drop in NDD use varied between three groups of farmers studied. The guided study groups reduced usage since 2007, the environmental group (not guided) had a significant drop in use in 2011 and the incidental group (not guided) in 2012. Reduction in use was modeled applying the Rogers diffusion of innovation theory. A logistic function fitted nicely to the adaptation process including the early adapters and late majority groups of farmers. Also farm and herd factors affecting antibiotics use were studied, practicing a step-wise regression procedure. Variation in total use and dry cow therapy were explained, respectively, for 39 and 46% by factors such as quota size, milk amount/cow, health status, cell count, and calving interval. A correlation of -0,55 between cell count and NDD was found. The "more successful and entrepreneurial " farmers, with a good relation to the veterinarian, tended to use somewhat more antibiotics than the other colleagues. They were also able to adapt more easily to the new conditions. The situation in some other countries is compared to the analysis above. Denmark, with a quite different focus on antibiotic use, is especially of interest in this respect.

Key Words: antibiotic use, dairy herds, farm factors

0554 Retrospective analysis of body energy content profiles of dairy cows with different production and metabolic diseases during the transition period. G. L. Smith*[1], M. G. Chagunda[1], C. J. Ashworth[2], and N. C. Friggens[3], *[1]Scottish Rural University College (SRUC), Edinburgh, UK, [2]The Roslin Institute, University of Edinburgh, UK, [3]Institut National de la Recherche Agronomique (INRA), Paris, France.*

Characteristics of body energy profiles for dairy cows with production and metabolic diseases during the transition period were studied. We used 542 cow-lactations from Holstein Friesians. Cows were from one of the four divergent production systems that were based on two feeding regimes (high forage and low forage) and two genetic lines (control and select). Control cows were of average UK genetic merit and select cows were of high genetic merit based on selection for fat and protein yield. Cows were milked three times daily, and stockmanship was similar across all systems. Live-weight of individual cows was recorded three times daily in lactation and weekly in the dry period. Body condition score (BCS) was recorded weekly using a 5-point scale. Health records were maintained throughout the study period. First, prevalence of disease within the first 4 wk after calving was determined as a proportion of cow lactations with disease relative to the total number of cow lactations per production system. Second, cow-lactations were categorized into disease-groups: retained placenta, metritis, metabolic, and healthy. The metabolic group comprised left displaced abomasum, ketosis, hypomagnesaemia, and hypocalcaemia. Body energy content in mega joules was calculated using the equation: EC = [(9.4 × body lipid weight) + (5.7 × body protein weight)] x 4.1868. Body lipid and protein weights were calculated using standard equations, which included live weight, BCS, and days pregnant. EC profiles covered the period between 6 wk pre-calving and 4 wk post-calving. Effects were determined using the GLM procedure of SAS. High genetic merit cows on a forage rich diet and average genetic merit cows fed a low forage diet had the highest prevalence of disease (30 and 25%, respectively). In the pre-calving period, healthy cows had an EC of 5878 ± 24 MJ which was significantly lower ($P < 0.01$) than those that had retained placenta (6384 ± 156 MJ) or metritis (6156 ± 46 MJ). Cows that developed metabolic diseases had significantly lower EC (5466 ± 216 MJ) than cows with retained placenta or metritis ($P < 0.01$). In the post- calving period, the metabolic disease group had significantly lower EC ($P < 0.001$) than all other disease groups. The study demonstrated that EC is an important lead indicator of production diseases in the transition period. Real-time tracking of EC could be used to rank individual cow risk of developing metabolic diseases.

Key Words: transition period, energy content, production disease

0555 Update on animal health concerns of recombinant bovine somatotropin (rbST): Meta-analysis of use in dairy cows. N. St. Pierre[1], G. A. Millikin[2], D. E. Bauman[3], R. J. Collier[*4], J. S. Hogan[5], J. K. Shearer[6], K. L. Smith[5], and W. W. Thatcher[7], *[1]The Ohio State University, Columbus, [2]Kansas State University, Manhattan, [3]Cornell University, Ithaca, NY, [4]The University of Arizona, Tucson, [5]The Ohio State University, Wooster, [6]Iowa State University, Ames, [7]Dep. of Animal Sciences, University of Florida, Gainesville.*

The commercial form of recombinant bovine somatotropin, sometribove zinc formulation (rbST-Zn), was approved by FDA as safe and has been successfully used by the U.S. dairy industry since 1994. However, a meta-analysis by an expert panel assembled at the request of Health Canada concluded that the commercial use of rbST would cause serious health and welfare problems. The present investigation utilized a series of meta-analyses to re-evaluate the efficiency and safety of rbST-Zn when used according to label. A total of 26 studies met the criteria: 1) published in peer-reviewed journals or reviewed by regulatory agencies, 2) used the rbST-Zn formulation (Posilac) available to U.S. producers, and 3) used according to label for dose (biweekly), treatment initiation (57–70 d postpartum), and administration method (subcutaneous injection). Meta-analysis results indicated that milk, fat, protein, and 3.5% fat-corrected milk yields were all increased ($P < 0.001$) by rbST-Zn (average of 4.00, 0.144, 0.137, and 4.04 kg/d, respectively), whereas milk concentrations of fat, protein, and lactose were unaltered ($P < 0.09$, 0.07, and 0.26, respectively). A 5.4% improvement in pregnancy proportion from rbST-Zn was detected for the first two breeding cycles after the voluntary wait period ($P < 0.01$). However, a 5.5% decrease ($P < 0.05$) in pregnancy proportion during the length of the trials was likely due to reduced estrous behavior. There was no effect of rbST-Zn on fetal loss, days open, services per conception, twinning, or cystic ovaries ($P < 0.65$, 0.96, 0.12, 0.68, and 0.43, respectively); on the odds of clinical mastitis or milk somatic cell count ($P < 0.12$ and 0.54, respectively); nor on rates of clinical lameness, lameness lesions, or traumatic lesions of the integumentary system (all $P < 0.99$). The rbST-Zn reduced body condition scores by 0.06 point (1 to 5 scale), a difference in body weight of about 3 kg ($P < 0.03$). No change to culling rate was associated with rbST-Zn ($P < 0.63$). Overall, the present meta-analysis demonstrates that rbST-Zn is effective and presents no unmanageable effects on health or welfare.

Key Words: bovine somatotropin, animal health, meta-analysis

0556 Trends in U.S. milk quality based on bulk-tank somatic cell counts. J. E. Lombard*, C. A. Kopral, and K. E. Bjork, *USDA:APHIS:VS: Center for Epidemiology and Animal Health, National Animal Health Monitoring System, Fort Collins, CO.*

The objective of this study was to evaluate changes in bulk-tank somatic cell counts (BTSCC) from 2000 to 2012. BTSCC data from four Federal Milk Marketing Orders (FMOs), representing about half of the milk marketed in the United States, were used to evaluate changes in BTSCCs. The four FMOs were: Mideast, Upper Midwest, Central and Southwest. Data were collected monthly and included herd identification, FMO, pounds of milk shipped, and official BTSCC. These data represent all milk shipped through the four FMOs, and conclusions apply only to this population of shipments. Because this study was a census, no estimates of sampling variability were calculated. A milk-weighted, 3-mo geometric mean BTSCC was calculated and summed for all herds in each FMO and for all herds. SAS software was used for all calculations. The Upper Midwest FMO accounted for approximately 45% of milk monitored on an annual basis. In 2012, 43.1 billion kg of milk from 309,343 shipments representing 28,274 producers were monitored. The milk-weighted mean BTSCC decreased from 296,000 cells/mL in 2000 to 194,000 cells/mL in 2012, while the producer-weighted mean BTSCC decreased from 320,000 to 230,000 cells/mL during the same period. The Mideast FMO had the lowest BTSCC for 11 of the 13 yr evaluated. Seasonal variations in BTSCC were consistent from 2000 to 2012, with the highest counts occurring in July through September. The U.S. BTSCC limit is 750,000 cells/mL; however, some countries that import dairy products from the United States have a limit of 400,000 cells/mL. From 2000 to 2012, the percentage of milk shipped from the four FMOs with BTSCCs of less than 400,000 cells/mL increased from 74.8 to 95.6%, while the percentage of shipments with counts less than 400,000 cells/mL increased from 65.0 to 87.4%. The percentage of producers from which all shipments counts were less than 400,000 cells/mL increased from 42.2 to 64.5%. BTSCCs in the United States have decreased approximately 35% since 2000. Many factors are likely responsible for these improvements in milk quality, e.g., producer motivation in the form of bonuses for providing quality milk, milk-quality regulations of countries that import U.S. dairy products, and an emphasis on improving milking procedures.

Key Words: BTSCC milk quality

0557 Somatic cell counts, mastitis infection prevalence, and mastitis pathogen distribution in compost bedded pack and sand freestall farms.

E. A. Eckelkamp*, J. L. Taraba, R. J. Harmon, K. A. Akers, and J. M. Bewley, *University of Kentucky, Lexington.*

The objective of this research was to describe the relationships among somatic cell counts (SCC), mastitis infection prevalence (MIP, percent of cows with SCS > 3.9), and mastitis pathogen distribution (MPD) in eight compost bedded pack (CB) and seven sand freestall (SF) farms in Kentucky from May 2013 to January 2014. The same observer evaluated cow hygiene scores (HYS, Cook and Reinemann, 2007) biweekly for 50 cows per herd. Throughout the study, producers collected aseptic milk samples from all quarters displaying clinical mastitis signs for bacteriological culturing. Test-day SCC and MIP were obtained from DHIA. The PROC MIXED of SAS (SAS Institute, Inc., Cary, NC) was used to assess fixed effects of barn type (BT), maximum ambient temperature (MT), and HYS on SCC and MIP. Stepwise backward elimination removed nonsignificant interactions ($P \geq 0.05$) with main effects remaining in the model regardless of significance. A χ^2 analysis was conducted using the FREQ procedure of SAS to determine MPD between BT. Maximum ambient temperature, BT, and MT × BT were significant predictors of MIP ($P < 0.05$). As MT increased, MIP increased more rapidly in CB than in SF ($P < 0.05$). Calculated MIP LSMeans(± SE) for CB and SF herds were 30.67 ± 3.02% and 25.33 ± 3.12%, respectively ($P < 0.05$). Hygiene score and BT × MT were significant predictors of SCC ($P < 0.05$). With increasing MT, herd SCC increased more rapidly in CB than in SF ($P < 0.05$). Somatic cell count LSMeans(± SE) for CB and SF were 255,700 ± 24,269 cells/mL and 223,520 ± 25,163 cells/mL, respectively ($P \geq 0.05$). Table 0557 summarizes MPD frequency by BT. Results of this study demonstrate potential challenges for managing mastitis in CBP.

Key Words: mastitis, sand freestall barn, compost bedded pack barn

Table 0557. Frequencies of pathogens isolated from clinical mastitis cases in compost bedded pack (CB) barns and sand freestall (SF) barns[1,2]

Pathogen isolated[1]	CB[2] (Total number of cases = 219) (Mean number of cows = 1208)	SF[2] (Total number of cases = 109) (Mean number of cows = 629)
Coagulase negative staphylococci	16 (7%)	4 (4%)
Environmental streptococci	32 (15%)	21 (19%)
Escherichia coli	63(29%)	19 (17%)
Gram-positive Bacillus species	4(2%)	1 (1%)
Staphylococcus aureus	7 (3%)	6 (6%)
Yeast species	5 (2%)	2 (2%)
Klebsiella species	4 (2%)	4 (4%)
Other gram-negative species	28 (13%)	14 (13%)
Other gram-positive species	6 (3%)	8 (7%)
No growth	32 (15%)	20 (18%)
Contaminated samples	20 (9%)	8 (7%)
Missing samples	2 (1%)	2 (2%)

[1] Number of pathogens isolated per species (percent of total samples per barn type).
[2] $\chi 2$ analysis indicated no significant differences for mastitis pathogen distribution between barn types ($P \geq 0.05$).

0558 Corn silage management practices on California dairies. J. M. Heguy*[1], D. Meyer[2], and N. Silva-del-Rio[3], *[1]UCCE Stanislaus and San Joaquin Counties, Modesto, CA, [2]Dep. of Animal Science, University of California–Davis, Davis, [3]VMTRC, University of California, Tulare, CA.*

The aim of this study was to describe current corn silage management practices on California¢s Central Valley dairies. In spring 2013, a forage management survey was mailed to dairy producers in California's San Joaquin Valley (n = 1100). Producers received an envelope containing an invitation letter, a double-sided two-page survey, and a pre-paid return envelope. Response rate was 14.5%. Median herd size was 1200 cows. Harvest date was decided solely by the dairy producer (53.3%) or by the producer with the assistance of the forage grower, the chopper, and/or the nutritionist (23.4%). When the dairy producer was not involved in setting a harvest date, the chopper (12.0%), the grower (7.3%), the nutritionist (0.7%), or the chopper and the grower (3.3%) were responsible for setting the harvest date. Most dairies (75.0%) estimated crop DM before harvest, mostly by visual analysis of the milk line. Only one dairy determined DM by shredding and drying plants before harvest. The number of choppers operating simultaneously was either one (35.9%), two (50.3%), three (11.1%), or four to five (2.7%). The most common chopper size was eight-row (67.3%), followed by six-row (17.7%), and 10-row (15.0%). One (68.8%), two (29.7%) or three (1.4%) tractors were used for packing the forage on the silage structure. Dairies (62%) weighed every load of fresh chopped corn delivered at the silage pit with a farm scale (58.9%), the custom harvester's mobile scale (23.2%), other certified scale (16.6%), or other methods (1.3%). Most dairies completed filling their largest silage structure in less than 3 d (48.5%) or in 4 to 7 d (30.9%). Thirty-two percent reported filling silage

structures with more than five different fields of harvested forage, comprised of one (36.8%) or two (40.6%) varieties. Dairies (68.8%) reported covering silage within 24 h, with all dairies covering silage structures within 72 h of completion. Daily covering of silage structures was reported from 19.6% of dairies. Dairies (51.0%) used a temporary cover during filling, with duration of filling ranging from 1 to 60 d on their largest corn silage structure. Dairies that did not use a temporary cover reported pile completion duration up to 15 d on their largest structure. Results from this survey study help us to identify critical control points for education and outreach activities to improve silage management practices at harvest, packing, and covering on California's Central Valley dairies.

Key Words: silage management, dairies, survey

PRODUCTION, MANAGEMENT, AND THE ENVIRONMENT: NUTRITION AND MANAGEMENT

0559 Zilpaterol hydrochloride repartitions chemical components of the empty body of Holstein steers.

T. J. McEvers*[1], N. D. May[1], L. A. J. Walter[1], J. P. Hutcheson[2], and T. E. Lawrence[1], *[1]West Texas A&M University, Canyon, TX, [2]Merck Animal Health, DeSoto, KS.*

A serial harvest from 254 to 534 d on feed (DOF) was conducted to quantify changes in growth and composition of calf-fed Holstein steers (n = 110, initial BW = 449.2 ± 19.9 kg). One-half were supplemented with the β-2 adrenergic agonist zilpaterol hydrochloride (ZH; 8.33 mg/kg 100% DM basis) with the remainder fed a control (CON) ration during the final 20 d followed by a 3 d withdrawal before harvest. Cattle were randomly allocated to dietary treatment and harvest endpoint (254, 282, 310, 338, 366, 394, 422, 450, 478, 506, and 534 DOF) in a 2 × 11 factorial randomized complete block experimental design conducted in the years 2012 and 2013. Cattle fed ZH had increased ($P \leq 0.03$) empty body weight (EBW; 17.8 kg), HCW (20.7 kg), dressed yield as a percentage of shrunk BW (DYSBW; 2.1%), dressed yield as a percentage of EBW (DYEBW; 1.3%), and empty body moisture (EBM; 1.3%) compared to CON steers regardless of DOF. Concurrently, cattle fed ZH had less ($P \leq 0.02$) digesta fill (6.1 kg) and empty body fat (EBF; 1.7%) compared to CON steers. Absolute weights of the empty body components including blood, hide, internal cavity components (ICC), and bone were not different ($P > 0.20$) for steers fed ZH or the CON diet. However, cattle fed ZH had increased ($P < 0.01$) carcass soft tissue (CST; 20.2 kg) compared to CON cattle. When comparing ZH and CON empty body components as a percentage of EBW, cattle fed ZH had less ($P \leq 0.02$) hide (0.3%), ICC (1.0%), and bone (0.5%). Furthermore, cattle fed ZH had more ($P < 0.01$) CST (1.7%) compared to CON steers with no difference ($P = 0.81$) in blood as a percentage of EBW. Comparing the chemical composition of the ICC, ZH steers had less ($P = 0.05$) protein (0.7%) with more ($P = 0.02$) ash (0.1%) compared to CON steers. Comparing the chemical composition of CST, cattle fed ZH had increased ($P = 0.02$) moisture (1.4%) with a concurrent reduction ($P < 0.01$) in fat content (2.0%) compared to CON cattle. This investigation proposes that the increase in dressed carcass yield observed in ZH supplemented cattle may best be explained by reductions in hide, fill, and ICC.

Key Words: beef, zilpaterol hydrochloride, composition

0560 Effect of organic grain supplementation on activity and rumination time of organic dairy cows.

L. S. Sjostrom*[1], B. J. Heins[2], M. I. Endres[3], R. D. Moon[4], and J. Paulson[5], *[1]University of Minnesota, West Central Research and Outreach Center, Morris, [2]University of Minnesota West Central Research and Outreach Center, Morris, [3]University of Minnesota, St. Paul, [4]University of Minnesota, St. Paul, [5]University of Minnesota, Hutchinson.*

Organic cows (n = 57) were used to evaluate activity and rumination time of cows fed three grain supplementation strategies during the grazing season. Cows were assigned to one of three replicate supplementation groups: 1) no corn grain supplementation (100% pasture, GRS, n = 19), 2) low corn grain (2.72 kg/head/day, LOW, n = 19), and 3) high corn grain (5.44 kg/head/day, HI, n = 19), and calved during two seasons at the University of Minnesota West Central Research and Outreach Center, Morris, from October to December 2012 and March to May 2013. Supplement (organic corn grain and minerals) was fed with a TMR of corn silage and alfalfa haylage, and at least 30% of diet DMI for LOW and HI cows consisted of organic pasture. Pasture and TMR intake were measured on a group basis, because cows were group fed. Activity and rumination time (daily and 2-h periods) were monitored electronically using HR-LD Tags (SCR Engineers Ltd., Netanya, Israel) for 125 d. Activity is reported in "activity units" from SCR DataFlow II software. The PROC HPMIXED of SAS was used for statistical analysis, and independent variables were season of calving (fall or spring), month of grazing (June to September), parity (1, 2, 3+), breed group, supplementation group and the interactions of month of grazing and supplementation group, breed group and supplementation group, and parity and supplementation group. Cow and replicate were random effects with repeated measures. The GRS (1138) cows had greater ($P < 0.05$) daily activity than HI (1001) cows but were similar to LOW (1019) cows. Daily activity was the greatest ($P < 0.05$) during July (1258) and least during September (819). Rumination was not different for the GRS (397 min/d), LOW (384), and HI (370) cows. Daily rumination was greater ($P < 0.05$) during September (402 min/d) compared to July (361). Daily activity increased rapidly from h 6:00 and 8:00 to h 16:00 and 18:00. From h 18:00 to 20:00, cows had a rapid decline in activity until h 6:00 the next day. All supplementation groups had the greatest rumination during h 2:00 and 4:00 and the least during h 10:00 and 12:00. In summary, GRS cows had greater activity but not greater daily rumination compared to LOW and HI supplemented cows. Monthly activity and rumination patterns of grazing organic cows may have been influenced by the weather and fly populations.

Key Words: activity, rumination, organic

0561 Effect of feeding kelp on growth and profitability of group-fed dairy calves in an organic production system. B. J. Heins*[1] and H. Chester-Jones[2], *[1]University of Minnesota West Central Research and Outreach Center, Morris, [2]University of Minnesota Southern Research and Outreach Center, Waseca.*

Heifer calves (n = 113) were used to evaluate the effect of feeding kelp on growth and economics of calves in an organic group management system. Calves were assigned to replicate feeding groups of 10 in super hutches by birth order during two seasons from September to December 2012 and March to May 2013 at the University of Minnesota West Central Research and Outreach Center, Morris. Calves in groups were the experimental unit. Breed groups of calves were: Holsteins (HO, n = 16) selected for high production; HO (n = 17) maintained at 1964 breed average level; crossbreds (n = 51) including combinations HO, Montbéliarde, and Swedish Red selected for high production; and crossbreds (n = 29) including combinations of HO, Jersey, Normande, and Swedish Red selected for robustness. Treatment groups were 1) control calf starter (CS; 18% CP as-fed; CON), 2) CS plus 56.7 g kelp/calf daily (Kelp2), and 3) CS plus 113.4 g kelp/calf daily (Kelp4). Calf groups were fed 1.5% DM solids of 13% total solids organic milk of birth weight once daily and then weaned at 60 d when the group consumption averaged 0.91 kg starter/calf daily. Body weight and hip height were recorded at birth, once/wk, at weaning, and at 90 d of age. Data were analyzed using PROC MIXED of SAS. Independent variables for analyses were the fixed effects of birth weight (co-variable), season of birth, breed group, treatment group, along with replicate as a random effect. Calf group ADG to weaning and weaning BW were 0.67, 82.9; 0.63, 79.4, and 0.61; 78.4 kg for CON, Kelp2, and Kelp4, respectively ($P < 0.10$). Hip heights at weaning were 93.8, 91.2, and 91.8 cm for CON, Kelp2, and Kelp4, respectively ($P < 0.05$). Daily gain to 90 d were 0.78, 0.74, and 0.68 kg for CON, Kelp2, and Kelp4 respectively, ($P < 0.05$). Total costs (grain, health, and organic milk) to 90 d of age for calf groups were $2,660.20 for CON, $2,711.39 for Kelp2, and $2,718.42 for Kelp4; however, the cost per kilogram of gain was significantly higher ($P < 0.05$) for the Kelp4 ($4.16) group compared to the CON ($3.69) group. In summary, calves fed a control calf starter had higher daily gains than calves fed high kelp calf starter rations. Feeding kelp in calf starter rations for organic dairy calves may not be economically justified.

Key Words: calf starters, organic production, kelp

0562 Reproductive performance of Barki ewes in Siwa Oasis as affected by including date seeds in the concentrate ration. E. B. Abdalla*, *Faculty of Agriculture, Ain Shams University, Cairo, Egypt.*

The present study investigated the effect of feeding date seeds on productive efficiency of Barki ewes in Siwa Oasis. Seventy-five adult Barki ewes (37.8 ± 0.63 kg) were divided into three equal groups: (G1) was kept as control (0.0% date seed), while the other two groups were fed on date seeds as a partial (50%, G2) or complete replacement (100%, G3) of the yellow corn in the concentrate diet. Animals were offered berseem *(Trifolium alexandrinum)* hay ad libitum and had access to fresh water twice a day. Estrus cyclicity and hormonal profiles during estrous cycle and pregnancy were determined. Reproductive parameters (number of services/conception, conception rate, lambing rate, average litter size, and mortality rate) were also recorded. Results indicated that date seeds contain estrogen-like compounds (β-sitosterol, stigmasterol and estradiol) with values of 0.01, 0.31, and 0.10 mg/kg, respectively. These levels did not affect estrus activity, since 90 and 80% of the ewes exhibited regular estrous cycle lengths with an overall mean of 17.3 ± 1.09 and 17.1 ± 0.86 d, respectively. Estradiol-17β (E_2) and progesterone (P_4) profiles either during estrous cycle or pregnancy were found to follow the normal pattern reported in the literature. Plasma (P_4) levels increased during pregnancy, especially during late pregnancy and decreased to the basal values during lactation, while plasma (E_2) levels were not significantly different among experimental groups. Date seeds, on the other hand, had improved all reproductive parameters studied as compared to the control group. Conception rate and lambing rate were found to be higher in both G2 (92 and 92%) and G3 (88 and 80%) as compared to the control group (76 and 72%), respectively. No abortions or stillbirths were found in the three groups. These results may confirm that date seeds have no estrogenic effects and could be used safely as a partial (50%) or complete replacer (100%) for the concentrate ration of ruminants, which in turn positively reflect on the Bedouins' income and animal health under desert conditions.

Key Words: date seeds, Barki ewes, estrus activity

0563 Impact of heifer development system on subsequent ADG and reproduction in two different breeding seasons. H. R. Nielson*[1], J. D. Harms[1], A. F. Summers[2], R. A. Vraspir[1], and R. N. Funston[1], *[1]University of Nebraska, West Central Research and Extension Center, North Platte, [2]University of Nebraska, Lincoln.*

The objective of this study was to determine the impact of heifer development system on subsequent growth and reproductive performance in two breeding seasons. In Exp. 1, over a 3-yr period, 196 May-born crossbred (5/8 Red Angus, 3/8 Continental) heifers were stratified by BW and randomly assigned to one of two post-weaning nutritional treatments (2 pastures·treatment^{-1}·yr^{-1}) beginning mid-January to mid-April. Heifers were offered ad libitum meadow hay (HAY) and 1.81 kg/d (29% CP, DM basis) supplement or allowed to graze meadow (MDW) and 0.45 kg/d supplement. Heifers were managed as a single herd before and following treatment. Heifers were synchronized with a single $PGF_{2\alpha}$ injection 5 d after

being placed with bulls for 45 d. Heifers on HAY treatment had greater ($P < 0.01$) ADG during the treatment period compared with MDW heifers (0.63 ± 0.01 kg/d vs. 0.33 ± 0.01 kg/d, respectively). However, heifers grazing meadow experienced a compensatory gain resulting in similar ($P \geq 0.12$) BW in June, July, and at pregnancy diagnosis. There was no difference ($P = 0.65$) in the proportion of heifers attaining puberty before the breeding season for HAY (62 ± 18%) and MDW (49 ± 18%) heifers. Pregnancy rates were similar ($P = 0.79$) between HAY vs. MDW treatments (69 ± 6% vs. 67 ± 6% respectively). In Exp. 2, 100 spring-born, crossbred (5/8 Red Angus, 3/8 Continental) heifers were, over 2 yr, stratified by BW and randomly assigned to HAY or MDW treatments. Similar to Exp. 1, HAY heifers had greater ($P < 0.01$) ADG during the treatment period than MDW heifers (0.80 ± 0.02 vs. 0.47 ± 0.02 kg/d). During the spring, HAY and MDW heifers had similar ($P = 0.14$) ADG, and BW was similar ($P \geq 0.17$) in May and September. Pubertal status before breeding was not affected by treatment ($P = 0.55$). Pregnancy rates were similar for HAY (88 ± 5%) and MDW (86 ± 5%, $P = 0.78$) heifers. Although ADG during the winter feeding period was greater for HAY heifers, BW was similar in the spring, summer, and at pregnancy diagnosis between treatments, suggesting a compensatory growth effect for MDW heifers. Similarly, there was no difference in pubertal status or pregnancy rate, indicating that a lower input winter management system is viable to maintain heifer pubertal status and pregnancy rates in two breeding seasons.

Key Words: beef heifers, development system, reproduction

0564 A comparison of serum metabolic profiles of dairy cows that maintained or lost body condition score 15 d before calving. M. R. Sheehy[*1,2], F. J. Mulligan[1], and A. G. Fahey[3], [1]*School of Veterinary Medicine, University College Dublin, Dublin, Ireland,* [2]*Devenish Nutrition Ltd, Belfast, Northern Ireland,* [3]*School of Agriculture and Food Science, University College Dublin, Ireland.*

Body condition score is an indirect measure of energy balance. Energy balance before calving may affect production and health in the following lactation. Energy restriction before calving has recently been advocated as a nutritional strategy that may result in BCS loss before calving. The objective of this study was to determine if loss of BCS 15 d before calving had an impact on the NEFA and calcium at wk -1 and wk 0 relative to calving and β-hydroxy butyrate (BHBA) and haptoglobin at wk 0 and wk +1 relative to calving from 93 Holstein-Friesian cows. On d -15 to d 0 relative to calving, BCS was assessed (1 = emaciated, 5 = obese). Cows were divided into two groups: those that did not lose BCS between d -15 and d 0 (MAINT, $n = 50$) and those that lost BCS from d -15 to d 0 (LOSS, $n = 43$). The fixed effects of BCS group, parity, wk and their interactions and a random effect of cow were analyzed for using PROC MIXED of SAS. Before calving LOSS cows tended to have higher NEFA concentrations than MAINT cows (0.88 ± 0.05 v 0.78 ± 0.04 mmol/L, $P = 0.10$) and a group by wk interaction was also found ($P < 0.01$), with an increase of 0.69 ± 0.09 mmol/L for LOSS and an increase of 0.59 ± 0.07 mmol/L for MAINT from wk -1 to 0. There was no difference in calcium concentrations between the LOSS and MAINT cows (2.21 ± 0.02 v 2.23 ± 0.02 mmol/L); however, a group by wk effect ($P < 0.01$) was found with a decrease from wk -1 to wk 0 of 0.32 ± 0.04 and 0.25 ± 0.03 mmol/L for LOSS and MAINT, respectively. After calving, LOSS cows were found to have higher concentrations of BHBA than MAINT cows (0.72 ± 0.04 v 0.57 ± 0.04 μmol/L, $P < 0.05$). A group by wk interaction ($P < 0.05$) was found for BHBA with an increase of 0.19 ± 0.07 μmol/L for LOSS and an increase of 0.02 ± 0.07 μmol/L for MAINT cows from wk 0 to 1. There was no difference found for haptoglobin between the LOSS and MAINT cows (115.41 ± 1.45 v. 114.71 ± 1.29 ng/mL, $P > 0.05$. In conclusion, LOSS cows tended to have significantly higher NEFA before calving and had a higher BHBA after calving with little effect on serum concentrations of calcium or haptoglobin.

Key Words: haptoglobin, NEFA, β-hydroxy butyrate

0565 Comparison of methods for isolation of miRNA from bovine milk whey. X. L. Jin[*1], H. Y. Liu[1], L. Liu[1], Z. H. Wei[1], and J. X. Liu[2], [1]*Institute of Dairy Science, Zhejiang University, Hangzhou, China,* [2]*Zhejiang University, Hangzhou, China.*

Milk miRNAs have great potential to utilize as noninvasive biomarkers for diagnosis or prognosis of diseases due to their high stability in the whey. More than 400 different miRNAs have been found in the mammalian milk. Some protocols have been established for isolation and quantification of miRNAs in whey, but the efficiency and effectiveness of these protocols are variable. The objective of the present study was to compare the methods for isolation of miRNAs from whey. Bovine milk samples were centrifuged and filtered to obtain the whey, 250 μL of which was lysed by Trizol LS. Total RNA was isolated from the whey RNA homogenate by two methods: 1) modified phenol based technique (alcohol precipitation with the addition of glycogen as carriers), and 2) column-based clean-up by miRNeasy Mini Kit. Yield and quality of total RNA isolated by these two methods were measured by NanoDrop ND-1000 spectrophotometer. Bioanalyzer 2100 instrument analysis using RNA6000 PicoKit was employed for precise detection of the RNA distribution-electropherogram of the microchip gel electrophoresis. The cycle thresholds of several endogenous miRNAs (bta-miR-141, bta-miR-148a, bta-miR-200c, and bta-miR-375) and a spike-in synthetic miRNA (cel-miR-39) were tested by RT-qPCR to compare their recovery efficiency between these two methods. Both methods could successfully isolate similar amount of small RNA (< 200nt)

from whey. Results of cycle thresholds of the endogenous miRNAs and spike-in cel-miR-39 indicated that the column-based cleanup method yielded approximately 10-fold miRNA than the alcohol precipitation. Nanodrop and bioanalyzer2100 based on RNA6000 PicoKit analysis could not reflect the real miRNA recovery efficiency of the whey. Whereas, spike-in control cel-miR-39 could be utilized as reliable and stable reference due to its perfect performance during the RT-qPCR. In summary, it is preferable to isolate miRNA from whey by combined phenol and column based approach.

Key Words: Isolation, miRNA, whey

PRODUCTION, MANAGEMENT, AND THE ENVIRONMENT: **ECONOMICS OF DIFFERENT MANAGEMENT PRACTICES**

0566 Effects of technology use in feedlot production systems on feedlot performance and carcass characteristics. *C. L. Maxwell[1], B. C. Bernhard[*1], C. F. O'Neill[1], B. K. Wilson[1], C. Hixon[1], C. Haviland[1], A. Grimes[1], M. S. Calvo-Lorenzo[1], D. L. VanOverbeke[1], G. G. Mafi[1], C. J. Richards[1], D. L. Step[1], B. P. Holland[2], and C. R. Krehbiel[1], [1]Oklahoma State University, Stillwater, [2]Merck Animal Health, DeSoto, KS.*

The objectives of this study were to examine the effects of conventional feedlot production systems with and without the use of a β-adrenergic agonist compared to a natural production program on feedlot performance and carcass characteristics. Natural crossbred beef steers (n = 336; initial BW = 379 ± 8 kg) were randomized to one of three treatments in a RCBD (14 steers/pen; 8 pens/treatment). Treatments consisted of a natural treatment (NAT), a conventional treatment (CONV), and a conventional treatment with a β-agonist (CONV-Z). The NAT cattle received no growth-promoting technologies. The CONV and CONV-Z cattle were implanted with 40 mg of estradiol and 200 mg of trenbolone acetate on d 0, and were fed 33 and 9 mg/kg of monensin and tylosin daily, respectively. The CONV-Z cattle were fed zilpaterol hydrochloride at 6.76 mg/kg (90% DM basis) for the last 20 DOF. There was no effect of treatment on DMI (P = 0.83); however, CONV-Z steers gained 3.8% faster (1.64 vs. 1.58 kg/d; P < 0.01) and were 5.3% more efficient (0.160 vs. 0.152; P < 0.01) than CONV steers, and CONV steers gained 32.8% faster (1.58 vs. 1.19 kg/d; P < 0.01) and were 26.7% more efficient (0.152 vs. 0.120; P < 0.01) than NAT steers. Hot-carcass weight was increased by 8 kg for CONV-Z steers compared to CONV steers (394 vs. 386 kg; P = 0.05) and 46 kg compared to NAT steers (394 vs. 348 kg; P < 0.01). Fat thickness was less for CONV-Z compared to CONV cattle (1.10 vs. 1.22 cm; P = 0.03), but not different from NAT (P > 0.05). Longissimus muscle area was increased by 3.6 cm^2 for CONV-Z steers compared to CONV steers (92.29 vs. 88.67 cm^2; P = 0.02) and 12.1 cm^2 for CONV-Z steers compared to NAT steers (92.29 vs. 80.16 cm^2; P < 0.01), resulting in a 17.9% unit reduction in USDA YG 3 for CONV-Z steers compared to NAT steers (30.70 vs. 48.61%; P < 0.05). There was no difference in marbling score for CONV steers compared to NAT steers (470 vs. 471; P = 0.99); however, CONV-Z steers had a lower marbling score compared to the other treatments (432; P < 0.01). The results of this experiment show that CONV-Z and CONV production results in a significant improvement in feedlot performance and USDA Yield Grade compared to NAT.

Key Words: conventional, beef cattle, natural

0567 The effects of technology use in feedlot production systems on the health status of finishing steers. B. C. Bernhard[*1], C. L. Maxwell[1], C. F. O'Neill[1], B. K. Wilson[1], C. G. Hixon[1], C. Haviland[1], A. Grimes[1], M. S. Calvo-Lorenzo[1], C. J. Richards[1], D. L. Step[1], B. P. Holland[2], and C. R. Krehbiel[1], *[1]Oklahoma State University, Stillwater, [2]Merck, Volga, SD.*

Crossbred steers (n = 336; initial BW = 379 ± 8 kg) were utilized in a RCBD (24 pens; 8 pens/treatment; 14 steers/pen) to determine the effects of technology use in feedlot production systems on animal health. Treatments consisted of an all-natural treatment (receiving no growth promoting technologies; NAT), a conventional treatment (implanted with 40 mg of estradiol and 200 mg of trenbolone acetate on d 0, and fed 33 and 9 mg/kg of monensin and tylosin daily, respectively; CONV), and a CONV treatment plus the addition of a β-adrenergic agonist (zilpaterol hydrochloride at 6.76 g/ton for the last 20 DOF with a 3–4 d withdrawal; CONV-Z). Steers were observed daily for signs of respiratory disease and lameness. Blood samples were collected from seven steers/pen every 28 d until d 112 and then every 10 d during the β-agonist feeding period to determine the hemogram. At harvest, livers were observed for abscesses, and lungs were palpated for abnormalities. Three steers died during the study, with necropsies indicating bloat (1-NAT; 1-CONV-Z before the zilpaterol feeding period; 1-CON-Z during the zilpaterol feeding period) as the cause of death, and no steers required treatment for respiratory disease. All blood analytes measured were within clinically normal concentrations throughout the experiment. Treatment had no effect on red blood cells, hematocrits, reticulocytes, or platelets (P > 0.34). There was a Treatment × Time interaction for total white blood cells (WBC; P < 0.01) with CONV and CONV-Z cattle having greater WBC counts than NAT cattle from d 28 (9.83 and 9.54 vs. 8.60 K/μL, respectively) through d 132 (10.83 and 11.25 vs. 9.83 K/μL, respectively; P < 0.03). There was a Treatment x Time interaction (P < 0.01) for neutrophils with CONV and CONV-Z cattle having greater neutrophil counts than NAT cattle from d 28 (2.57 and 2.47 vs. 1.99 K/μL, respectively) through d 132 (3.51 and 3.47 vs. 2.44 K/μL, respectively; P < 0.03). More monocytes were detected in the CONV and CONV-Z cattle compared to the NAT cattle (1.21 and 1.22 vs. 1.08 K/μL, respectively; P < 0.01). No differences in blood analytes were observed between CONV and CONV-Z during the zilpaterol feeding period (P > 0.25). There was no effect of treatment on liver abscesses (P = 0.74) or lung abnormalities (P > 0.09). Collectively, this experiment demonstrates that growth-promoting technologies did not affect overall health of finishing steers.

Key Words: β-adrenergic agonist, blood analytes, health status

0568 Survey of BQA cattle handling practices that occurred during processing feedlot cattle.

R. Woiwode* and T. Grandin, *Colorado State University, Fort Collins.*

The public is increasingly concerned with how animals in production agriculture are treated. The objective of this study was to ascertain feedlot performance in Beef Quality Assurance cattle handling categories. A survey was conducted to quantify prevalence of cattle handling practices that adhere to BQA guidelines. Data were collected at 28 feedlots ranging in size from 5000 to more than 100,000 head in Colorado, Kansas, and Nebraska. According to BQA guidelines, 100 cattle were observed during handling at every site except for two, where 90 and 78 head were observed due to lack of cattle. Data were collected on percentage of cattle moved with an electric prod, percentage that vocalized after capture in the squeeze chute before procedure, percentage of falls while exiting the squeeze chute, percentage stumbling while exiting, and percentage jumping and running on exit from the squeeze chute. Feedlots in this survey performed above BQA guidelines in the categories of electric prod use (5.5% vs. 10%); vocalization (1.4% vs. 5%), stumbles (6.7% vs. 10%), falls (0.8% vs. 2%), and cattle that jumped and ran from the squeeze chute (12.8% vs. 25%). The mean percentage of cattle moved with an electric prod was 5.5%, with a range of 0 to 45%; cattle that vocalized in the chute before procedure was a mean of 1.4% with a range of 0 to 5.1%. The mean percentage of cattle stumbling while exiting the squeeze chute was 6.7%, with a range of 0 to 28%; cattle falling was 0.5%, with a range of 0 to 2%. The mean percentage of cattle that jumped and ran out of the squeeze chute was 12.8%, with a range of 0.1 to 18%; cattle miscaught in the squeeze chute was 2%, with a range of 0 to 16.1%. Under BQA guidelines, there is zero tolerance for an improper catch that is not adjusted, and feedlots in this survey show some room for improvement, with a mean score of 2% vs. the BQA guideline of 0%. Of the improper catches, 60% were not adjusted. Round crowd pen handling systems were used at 25 yards, and three yards used Bud box handling systems. At one feedlot, a contract crew employee jerked out ear tags, resulting in some ear splits. Discussion with feedlot managers revealed increased awareness of the importance of moving small groups of cattle into the crowd pen and avoiding yelling.

Key Words: cattle handling, BQA guidelines, feedlots

0569 The effects of technology use in feedlot production systems on cattle behavior and mobility.

B. C. Bernhard*[1], C. L. Maxwell[1], C. F. O'Neill[1], B. K. Wilson[1], C. Haviland[1], A. Grimes[1], M. S. Calvo-Lorenzo[1], C. J. Richards[1], D. L. Step[1], B. P. Holland[2], C. R. Krehbiel[1], and C. G. Hixon[1], *[1]Oklahoma State University, Stillwater, [2]Merck, Volga, SD.*

Crossbred steers (n = 336; initial BW = 379 ± 8 kg) were utilized in a randomized complete block design (24 pens; 8 pens/treatment; 14 steers/pen) to determine the effects of technology use in feedlot production systems on animal behavior and mobility. Treatments consisted of an all-natural treatment (defined as cattle receiving no growth promoting technologies; NAT), a conventional treatment (implanted with 40 mg of estradiol and 200 mg of trenbolone acetate on d 0, and fed 33 and 9 mg/kg of monensin and tylosin daily, respectively; CONV), and a CONV treatment plus the addition of a β-adrenergic agonist (zilpaterol hydrochloride at 6.76 g/ton for the last 20 d on feed with a 3–4-d withdrawal; CONV-Z). Handling assistance, temperament, and exit scores at the chute and temperament in each home pen were collected every 28 d until d 112, and then every 10 d during the β-agonist feeding period. On the d of shipment, cattle mobility was scored before loading at the feedlot and while unloading at the abattoir. There was no effect of treatment on cattle requiring assistance to enter the squeeze chute (P = 0.35). There was a Treatment x Time interaction for chute temperament score (P = 0.03), with NAT cattle being more restless than CONV cattle at d 56 (2.24 vs. 1.98; P = 0.02) and CONV-Z cattle intermediary (2.14). Pen temperament was not affected by treatment (P = 0.14). Overall temperament score resulted in CONV-Z cattle being numerically calmer than NAT cattle (1.47 vs. 1.61; $P < 0.02$) and CONV cattle intermediary (1.57). Chute exit scores resulted in a Treatment x Time interaction ($P < 0.01$), with NAT cattle having a greater exit score than CONV and CONV-Z cattle (2.24 vs. 1.93 and 1.87; $P <$ 0.03) on d 132. There were no differences in exit velocity ($P >$ 0.37). Treatment displayed no effect on cattle mobility before loading or during unloading ($P \geq 0.14$), but numerically, cattle had a more difficult time moving at the abattoir than at the feedlot. The results of this experiment suggest that growth-promoting technologies have no negative effects on cattle mobility and could potentially improve cattle temperament at the end of the finishing period.

Key Words: behavior, β-adrenergic agonist, mobility

0570 Predicting dry matter intake by growing and finishing beef cattle: evaluation of current methods and equation development. U. Y. Anele*[1], E. M. Domby[2] and M. L. Galyean[3], [1]*Lethbridge Research Centre, Agriculture and Agri-Food Canada, AB,* [2]*Cargill Animal Nutrition, Amarillo, TX,* [3]*Texas Tech University, Lubbock.*

The NRC (1996) equation for predicting DMI by growing-finishing beef cattle, which is based on dietary NEm concentration and average $BW^{0.75}$, has been reported to over- and underpredict DMI depending on dietary and animal conditions. Our objectives were to: 1) develop more robust equations for predicting DMI from BW and dietary NEm concentration; and 2) evaluate the use of NE requirements and dietary NE concentrations to determine the DMI required (DMIR) by feedlot cattle. Two DMI prediction equations were developed from a literature data set that covered a wide range of dietary NEm concentrations, which represented treatment means from published experiments from 1980 to 2011. Predicted DMI from the two equations, which were based on NEm concentration and either the ending BW for a feeding period or the DMI per unit of average BW (End BW and DMI/BW, respectively), accounted for 61 and 58% of the variation in observed DMI, respectively, vs. 48% for the 1996 NRC equation. When validated with four independent data sets that included 7751 pen and individual observations of DMI by animals of varying BW and feeding periods of varying length, DMI predicted by the 1996 NRC equation, the End BW and DMI/BW equations, and the DMIR method accounted for 13.1 to 82.9% of the variation in observed DMI, with higher r^2 values for two feedlot pen data sets and lower values for pen and individual data sets that included animals on lower-energy, growing diets, as well as those in feedlot settings. The DMIR method yielded the greatest r^2 values and least prediction errors across the four data sets, but mean biases ($P < 0.01$) were evident for all the equations, ranging from as high as 1.01 kg for the DMIR method to -1.03 kg for the 1996 NRC equation. Negative linear bias was evident in virtually all cases, suggesting that prediction errors changed as DMI increased. Despite an expanded literature database for equation development, other than a trend for lower standard errors of prediction with the DMI/BW equation, the two new equations did not offer major advantages over the 1996 NRC equation when applied to the validation data sets. The DMIR method accounted for the greatest percentage of variation in observed DMI and had the least RMSE values in all data sets evaluated, indicating that this approach should be considered as a means of predicting DMI.

Key Words: beef cattle, dry matter intake prediction, feed intake

0571 Optimizing concurrently dairy farm profitability and environmental performance. D. Liang* and V. Cabrera, *University of Wisconsin, Madison.*

The objective of this analysis was to assess economic and environmental impacts of a dairy farm milk production using the Integrated Farm System Model (IFSM, version 4.0, University Park, PA). The IFSM was applied to integrate crop growth, feed storage, machinery usage, and herd management to simulate the highest possible milk production with the available on-farm resources and purchased feed. A representative Wisconsin dairy farm system was defined as a typical farm with 100 milking cows and 247 acres of cropland. Farm performance was then simulated using 25 yr of daily weather data (1986 to 2010). A sensitivity analysis was conducted by increasing the input target milk production starting at 9837 kg/cow per yr. The fat-protein-corrected milk production (FPCM) increased linearly as the target milk production was increased to 10,457 kg/cow per yr. Followed, the FPCM increased nonlinearly (at a decreasing rate) until the target milk production was increased to 10,980 kg/cow per yr. Thereafter, FPCM remained flat regardless of higher target milk production input. The per-kg FPCM net return ($/kg FPCM) showed a similar trend, increasing from $4.08 ± 2.32 to $6.20 ± 2.19, and then to $6.78 ± 2.18, respectively. Given the farm carbon footprint (kg CO_2eq/kg FPCM) as the result of dividing the net greenhouse gas emission (including methane, nitrous oxide, and carbon dioxide) by the FPCM, it decreased from 0.69 ± 0.04, to 0.67 ± 0.04, and then to 0.65 ± 0.04, respectively, as the FPCM and the net return increased. We concluded that increasing productivity using only farm available resources would elevate the net return and decrease carbon footprint at the same time. Further research is required to explore management strategies that determine increased productivity within farm-specific conditions.

Key Words: whole-farm simulation model, farm profit, greenhouse gas emission

Table 0571.

Input target milk production (kg/cow per yr)	Simulated actual milk production (kg/cow per yr)	Fat-protein-corrected milk production (FPCM; kg/cow per yr)	Net return per kg of FPCM (FPCM; $/kg FPCM)	Carbon footprint (kg CO2 eq/kg FPCM)
9834	9834 ± 0.00	9079 ± 0.00	4.80 ± 2.32	0.69 ± 0.04
10,457	10,455 ± 9.54	9652 ± 9.54	6.20 ± 2.19	0.67 ± 0.04
10,980	10,748 ± 96.82	9922 ± 89.54	6.78 ± 2.18	0.65 ± 0.04
11,457	10,746 ± 87.27	9921 ± 80.45	6.78 ± 2.15	0.65 ± 0.04

0572 Economics of transition cow management of dairy herds. G. M. Schuenemann[*1] and K. N. Galvão[2], *[1]Dep. of Veterinary Preventive Medicine, The Ohio State University, Columbus, [2]Dep. of Large Animal Clinical Sciences, University of Florida, Gainesville.*

It is common to observe large among-herd variation in culling risk within 60 DIM. The objective was to assess the effect of two culling risks within 60 DIM (6% vs. 12%) on the economic outcomes of dairy herds with the same reproductive performance using an individual cow-based model. For the simulation, two culling risks (6% vs. 12%) and two cow sale prices ($1.85 vs. $1.37 per kg) were compared using the same reproductive program and performance. Cows were enrolled in an Ovsynch (OVS) preceded by Presynch with two injections of PGF 14 d apart, and OVS for resynchronization of open cows at 32 d after AI. Also, cows undergo estrous detection (ED) and AI after first AI, and cows diagnosed open 32 d after AI are resynchronized using OVS. Cows were not inseminated after 365 DIM, and open cows were culled after 450 DIM. Culled cows were immediately replaced with primiparous cows. Herd was maintained at 1000 cows. Mortality was set at 6% and abortion at 11.3%. The dry period and VWP was 60 d. Conception rate to first service was set to 32% (decreased by 2.5% for every subsequent service), and ED was set to 60%. Accuracy of ED and compliance with each injection were set at 95%. Net daily value was calculated by subtracting the costs associated with replacement heifers ($1,600/heifer), feeding costs ($0.25/kg of lactating cow diet; $0.15/kg of dry cow diet), breeding costs ($0.15/cow/d for ED; $2.65/dose PGF; $2.4/dose GnRH; $0.25/injection administration), and other costs ($2.5/d) from the daily income with milk sales ($0.44/kg milk), cow sales ($1.85 or $1.37/kg live weight), and calf sales ($240/calf). Simulation was performed until steady state was reached (4000 d), then average daily values for the subsequent 1000 d were used to calculate profit ($/yr). According to the model (same herd size, synchronization program, reproductive performance, and feeding costs), the annual profit was $55,480 higher for herds with 6% compared to 12% culling risk within 60 DIM. When the cow sale price was $1.37/kg and replacement costs remain the same, the annual profit was $80,300 higher for herds with 6% compared to 12% culling risk within 60 DIM. Early removal of lactating cows from the milking herd affects the bottom line of dairy operations.

Key Words: culling risk, economics, dairy herds

0573 The impact of selected milking, feeding, and housing management systems on the profitability of Quebec dairy herds. H. A. Delgado[*1], R. I. Cue[2], A. Sewalem[3], R. Lacroix[4], D. Lefevre[4], E. Bouchard[5], D. Haine[5], and K. Wade[1], *[1]McGill University, Ste-Anne-de-Bellevue, QC, Canada, [2]McGill University, Dep. of Animal Science, Ste-Anne-de-Bellevue, QC, Canada, [3]Agriculture and Agri-food Canada AAFC, Guelph, ON, Canada, [4]Valacta, Ste-Anne-de-Bellevue, QC, Canada, [5]University of Montreal, Ste-Hyacinthe, QC, Canada.*

In Quebec, management of dairy herds is affected by various combinations of milking systems (milk line, milking parlor, or milking robot), housing systems (tie-stall or free-stall), and feeding systems (traditional feeding, automatic forage distribution, automatic concentrate distribution, computerized automatic concentrate distribution, automatic silage and concentrate distribution, and total mixed ration). The objective of this research was to determine if there were differences in the lifetime profitability of dairy cows, based on common Quebec management conditions, specifically with regard to their associated production and health costs. Grouping the three variables resulted in eight existing management combinations that contained data (e.g., milk line + tie-stall + total mixed ration). Health and production data for individual animals were provided by the Quebec Animal Health Files (DSA) and Quebec DHI (Valacta), respectively. Herds were required to have at least 12 calvings per year, resulting in a data set of 70 Holstein herds with both health and production data for the period 2000 though 2010, inclusive. Individual cumulative values by parity, as well as the last cumulative lifetime record, were computed for each animal. Four profitability measures were examined to account for different criteria, such as variable costs, opportunity costs, and discounted net present value, and mixed-model methodologies were used to test differences among those profitability measures for the different management combinations. Of the 70 herds, 58 used a milk line, seven used a milking parlor, and five used robotic milkers. There were significant differences among the management combinations for the four different profitability measures examined. Management groups associated with a milking parlor had the lowest estimated lifetime cumulative feed cost: $3,968 (± 73) vs. $4,297 (± 36) for milk lines and $4,057 (±86) for robotic milkers. They also had animals with an earlier age at first calving (1.1 mo earlier than those in groups with milk lines). Management groups with robotic milkers had the lowest lifetime cumulative health cost, explained in part by the lower average number of mastitis events per animal per parity: 0.12 (± 0.034) vs. 0.20 (± 0.028) for milking parlor groups and 0.23 (±0.020) for milk line groups. There were significant variations in profitability measures of milk-line groups that were attributable to feeding system. Variation in lifetime profitability of individual animals is, therefore, not

only explained by the obvious feed and health factors but also by the various management systems in which they occur.

Key Words: profitability, management, dairy cows

0574 Grazing alfalfa as an alternative to reduce production costs in intensive milk production systems.

F. A. Kuwahara[1], A. M. Pedroso[*2], G. B. Souza[3], and R. P. Ferreira[3], *[1]UNESP/FMVZ, Botucatu, Brazil, [2]EMBRAPA, São Carlos, Brazil, [3]EMBRAPA, Sao Carlos, Brazil.*

Intensively managed grass-based milk production systems in Brazil are highly dependent on concentrate supplementation of the milking cows to achieve high productivity levels. Depending on feed prices, the production costs can be very high, leading to low profitability. This study aimed to evaluate the use of grazing alfalfa (*Medicago sativa, sp*.) as an alternative to reduce concentrate inputs and reduce production costs. The trial was conducted at EMBRAPA's (Brazilian Agricultural Research Corporation) research station, located in Sao Carlos, SP, in the southeast region of Brazil. Thirty-six lactating dairy cows were used on a complete blocks design to evaluate the effect of allowing the cows to graze alfalfa for different periods on milk production, dry matter intake, and feed efficiency. Cows were allocated to four experimental treatments (A = control, no alfalfa grazing; B = access to alfalfa paddocks for 1 h; C = access to alfalfa paddocks for 2 h; D = access to alfalfa paddocks for 4 h) according to stage of lactation and milk production. All cows rotationally grazed tropical grass paddocks and were supplemented with different concentrate quantities (9.82, 9.32, 9.03, and 8.73 kg of DM daily for treatments A, B, C, and D, respectively) Cows on treatment A had no access to alfalfa, and cows on the other treatments had access to alfalfa paddocks for 1, 2 or 4 h immediately after the morning milking. Results are shown on Table 0574. Data were analyzed using PROC MIXED of SAS and averages were compared with Tukey test. Treatment differences were considered significant at $P < 0.05$. No effects were observed among treatments for any parameter analyzed. Based on the results, alfalfa grazing may be a good strategy to reduce production costs, depending on the prices of the concentrate supplements.

Key Words: milk production, grazing, alfalfa

Table 0574.

	Treatment A	Treatment B	Treatment C	Treatment D
DMI, kg/d	15.68	15.84	15.81	15.09
Milk, kg/d	23.86	23.28	23.41	24.21
FE, kg/kg	1.605	1.566	1.549	1.656

0575 Comparison of productivity and management practices on Dairy Herd Improvement Association (DHIA) and non-DHIA herds in the United States.

J. E. Lombard*, C. A. Kopral, M. A. Parke,r and C. A. Haley, *USDA:APHIS:VS: Center for Epidemiology and Animal Health, National Animal Health Monitoring System, Fort Collins, CO.*

The objective of this investigation was to compare productivity and management practices between DHIA and non-DHIA herds. Data for this comparison were collected as part of the National Animal Health Monitoring System¢s Dairy 2007 study, which surveyed 2194 randomly selected dairy herds in 17 top dairy states. The survey design was a stratified random sample, and all respondent data were statistically weighted to ensure that samples reflected the study population. Regression analyses were conducted and included multiple outcome variables of interest, herd size, region, and whether the operation participated in DHIA. *P*-values < 0.05 were considered significant. Almost half of herds in the study (46.0%) used DHIA for individual-animal recordkeeping. The average size for DHIA herds was 416 cows compared with 448 cows for non-DHIA herds. A higher percentage of herds in the east region (46.7%) were enrolled in DHIA compared with herds in the west region (37.3%). There were significant productivity differences between DHIA and non-DHIA herds. DHIA herds had a higher mean rolling herd average milk production than non-DHIA herds (9873 kg and 8521 kg, respectively) and a longer mean calving interval (13.6 and 13.0 mo, respectively). The percentage of DHIA herds that used bovine somatotropin was more than triple that of non-DHIA herds (23.8 and 7.8%, respectively). In addition, DHIA herds reported lower mortality rates for preweaned heifers than non-DHIA herds (8.3 and 9.5%, respectively). Best management practices, in general, were more widely adopted by DHIA herds than non-DHIA herds. A significantly higher percentage of DHIA herds were enrolled in quality assurance programs, used forage test results to balance rations, and fed a total mixed ration. Similarly, biosecurity practices were generally adopted by a significantly higher percentage of DHIA herds than non-DHIA herds. A lower percentage of DHIA herds than non-DHIA herds introduced new cattle to the operation during 2006 (36.9 and 40.9%, respectively). Brucellosis vaccinations were also administered on a higher percentage of DHIA herds than non -DHIA herds (51.7 and 33.0%, respectively). Common cow vaccinations (BVD, IBR, PI3, and BRSV) were administered on 87.9% of DHIA herds and 68.5% of non-DHIA herds. DHIA herds had higher milk production than non-DHIA herds, and a higher percentage of DHIA herds implemented best management practices compared with non-DHIA herds.

Key Words: DHIA, productivity, management, biosecurity

0576 Optimization of reproductive management programs using lift chart analysis and cost-sensitive evaluation of classification errors.
S. Shahinfar*[1], J. N. Guenther[1], D. Page[2], A. Samia- Kalantari[1], V. Cabrera[3], P. M. Fricke[1], and K. A. Weigel[3], *[1]Dep. of Dairy Science, University of Wisconsin–Madison, Madison, [2]Dep. of Biostatistics and Medical Informatics and Dep. of Computer Science, University of Wisconsin–Madison, Madison, [3]Unversity of Wisconsin–Madison, Madison.*

The common practice on most commercial dairy farms is to inseminate all cows that are eligible for breeding, while ignoring (or absorbing) the costs associated with semen and labor directed toward lowly fertile cows that are unlikely to conceive. Modern analytical methods, such as machine learning algorithms, can be applied to cow-specific explanatory variables for the purpose of computing the probabilities of success or failure associated with upcoming insemination events. Lift chart analysis can identify subsets of high fertility cows that are likely to conceive and are therefore appropriate targets for insemination (e.g., with conventional AI semen or expensive gender-enhanced semen), as well as subsets of low fertility cows that are unlikely to conceive and should therefore be passed over at that point in time. While such a strategy might be economically viable, the management, environmental, and financial conditions on one farm might differ widely from conditions on the next, and hence the reproductive management recommendations derived from such a tool may be suboptimal for specific farms. When coupled with cost-sensitive evaluation of misclassified and correctly classified insemination events, it can be potentially powerful tool for optimizing the reproductive management of individual farms. In the present study, lift chart analysis and cost-sensitive evaluation were applied to a data set consisting of 54,806 insemination events of primiparous Holstein cows (as experimental unit) on 26 Wisconsin farms, as well as a data set with 17,197 insemination events of primiparous Holstein cows on three Wisconsin farms, where the latter had more detailed information regarding health events of individual cows. In the first data set, the gains in profit associated with limiting inseminations to subsets of 79 to 97% of the most fertile eligible cows ranged from $0.44 to $2.18 per eligible cow, depending on days in milk at breeding and milk yield relative to contemporaries. In the second data set, the strategy of inseminating only a subset consisting of 59% of the most fertile cows conferred a gain in profit of $5.21 per eligible cow. These results suggest that, when used with a powerful classification algorithm, lift chart analysis and cost-sensitive evaluation of correctly classified and misclassified insemination events can enhance the performance and profitability of reproductive management programs on commercial dairy farms. Note: In machine learning methods, *P*-value is not a criteria of decision-making as it is in classic statistics.

Key Words: machine learning, reproductive management, cost-sensitive

0577 The cost of clinical mastitis in the first 30 d of lactation: an economic assessment tool.
E. Rollin*[1] and M. W. Overton[2], *[1]University Of Georgia College of Veterinary Medicine, Athens, [2]Elanco Animal Health– Dairy, Athens, GA*

Mastitis results in considerable economic losses for dairy producers and is most commonly diagnosed in early lactation. The objective of this study was to create a tool to estimate the predicted economic impact of clinical mastitis occurring during the first 30 d of lactation for a representative North American dairy. A deterministic partial budget model was created in spreadsheet software to estimate the projected direct and indirect costs per case of clinical mastitis occurring during the first 30 d of lactation in a typical dairy. The cost calculator was built by adapting published estimates from recent peer reviewed literature covering mastitis incidence, pathogen prevalence, recurrence risk, culling effects, reproductive effects, and milk production effects to estimate the value of projected future production, culling, death, and reproductive losses. Herd specific data including milk price, reproductive performance, lactational culling risk, diagnostic costs, treatment protocol costs, replacement costs, market cow prices, feed costs, labor costs, and veterinary costs are input to allow full customization of the projection model. The average case of clinical mastitis resulted in a net economic loss of $458, including $135 in direct costs and $323 in indirect costs. Direct costs included diagnostics ($3), therapeutics ($42), discarded milk ($20), veterinary service ($15), labor ($30), and death loss ($26). Indirect costs included future milk production loss ($135), future culling and replacement loss ($162), future reproductive loss ($21), and ongoing monitoring costs ($5). Accurate decision-making regarding mastitis control relies on understanding all of the economic impacts of clinical mastitis, especially the longer-term indirect costs that represent 71% of the total costs per case of mastitis. Future milk production loss represents 29% of total costs, and future culling and replacement loss represents 35% of the total costs of a case of clinical mastitis. In contrast to older estimates, these values represent the current dairy economic climate, including milk price ($0.48/kg), feed price ($0.286/kg DM), replacement costs ($2000), and use the latest estimates on the production and culling effects of clinical mastitis. This economic model is designed to be customizable for specific dairy producers and their herd characteristics to better aid them in developing mastitis control strategies.

Key Words: mastitis, economics, transition

PRODUCTION, MANAGEMENT, AND THE ENVIRONMENT: **EFFECTS OF TEMPERATURE ON PERFORMANCE**

0578 Urine metabolomics of heat-stressed dairy goats supplemented with soybean oil. A. Salama[*1,2], N. Nayan[3], A. Contreras-Jodar[1], S. Hamzaoui[1], and G. Caja[1], *[1]Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Barcelona, Spain, [2]Animal Production Research Institute, Dokki, Giza, Egypt, [3]Dep. of Animal Science, Faculty of Agriculture, University Putra Malaysia, Serdang.*

Biofluids assessment by ^{1}H nuclear magnetic resonance (NMR) spectroscopy would highlight the physiological mechanisms that may have occurred in goats when exposed to different management and environmental conditions. Our objective was to detect metabolomic changes in the urine of heat-stressed goats supplemented with soybean oil (SBO) for alleviating fat depression. Murciano-Granadina dairy goats (n = 8; 42.8 ± 1.3 kg BW) kept in metabolic cages were used in a replicated 4 × 4 Latin square design with 4 periods, 19 d each (14 d adaptation, 5 d for measurements). Goats were allocated to one of four treatments in a 2 × 2 factorial arrangement. Factors were no oil (C) or 4% SBO, and thermal neutral (TN; 15 to 20°C) or heat stress (HS; 12 h/d at 37°C and 12 h/d at 30°C) conditions, resulting in four treatments: TN-C, TN-SBO, HS-C, and HS-SBO. Urine samples were collected and analyzed with ^{1}H NMR spectroscopy for a qualitative metabolomic study. Principal component analysis (PCA) and partial least square–discriminant analysis (PLS-DA) were used to detect possible outliers and to identify possible metabolite markers of HS and SBO. The PLS-DA revealed that there were two separated clusters corresponding to TN (TN-C + TN-SBO) and HS (HS-C + HS-SBO) groups. Metabolites increased (P < 0.01) by HS were: hippurate, isoleucine, acetate, glutamate, glycine, and 3-hydroxybutyrate. On the other hand, L-phenylalanine and creatinine decreased (P < 0.01) by HS. Changes in those metabolites could be related to physiological responses to HS, including increased harmful gut microbiota activity (hippurate), increased catecholamine activity (conversion of L-phenylalanine to catecholamines), neurotransmitter inhibition (glycine), and decreased degradation of energy-related metabolites (acetate, isoleucine and glutamate). No significant regression model was found for the effects of SBO supplementation. We conclude that urine metabolomics could help in understanding the responses to heat stress and establishment of new alleviation strategies.

Key Words: heat stress, metabolomics, multivariate analysis

0579 Bovine core body and scrotal temperature measured using surgically implanted temperature-sensitive radio-transmitters, iButtons, and infrared thermography. A. Wallage[*1], J. B. Gaughan[1], A. Lisle[1], L. Beard[2], A. J. Cawdell-Smith[1], C. W. Collins[1], and S. Johnston[1], *[1]The University of Queensland, Gatton, Australia, [2]The University of Queensland, St Lucia, Australia.*

An ability to continuously and remotely monitor body (BT) and scrotal temperature (ST) without adverse or behavioral interference is fundamental to any study that investigates thermoregulation of the testis. Several methods for monitoring BT exist: loggers inserted into the rectum or vagina or placed in the ear close to the tympanic membrane, implantable radio-transmitters (RT), and rumen boluses. However, with all but RT and rumen boluses, data can only be collected for a few days. Previously, ST had only been measured via thermocouples for short durations (hours) or by manual scanning of microchips. This study compared the three most suitable technologies available for the coincident measurement of BT and ST: temperature sensitive RTs, data logging iButtons (IB), and infrared imaging (IRI). Bundles containing RT and IB were calibrated and surgically implanted in the abdominal muscle wall and scrotum of six bulls for between 29 and 49 d. IBs logged every 30 min, and RT pulse intervals were scanned every 15 min. Hourly IRI were taken of the body and scrotum of each bull for one 24 h period. Histology samples were obtained after castration at the conclusion of a series of heat-stress trials. IB were more reliable than the RT; all RT lost at least 11% of data, while 11 of the 12 IB had 100% data recovery. Pearson correlations between IB and RT were strong for both BT (r > 0.94, P < 0.001) and ST (r > 0.80, P < 0.001). Bland-Altman plots (limits of agreement) also showed stronger agreement with BT than ST, possibly due to the temperature gradient within the scrotum. The surgical procedure produced minor inflammation and hematoma in 2 animals immediately after the surgery. On castration, scar tissue was observed at all surgical sites but active spermatogenesis was evident in 10 of the 12 testicles. As all animals had been used in additional heat stress trials, it was impossible to determine the exact pathological effect of implant surgery. No significant correlation of IRI with either IB or RT existed, although sample size was small and, given that IRI measures surface temperature rather than BT, the usefulness of IRI is uncertain. IB provided a reliable, robust, and continuous BT and ST data set and can be successfully implanted in both the abdomen and scrotum of bovines.

Key Words: scrotal-temperature, iButton, radio-transmitter

0580 Rumen temperature of Brahman, Angus, and Charolais steers with and without access to shade. A. M. Lees*, J. B. Gaughan, M. L. Sullivan, J. C. Lees, and A. Lisle, *The University of Queensland, Gatton, Australia.*

Continuous measurement of body temperature (BT) is often difficult, and data collection is often restricted to short intervals. Remote assessment of BT through rumen boluses is a method of obtaining consistent BT over long periods of time without compromising animal comfort and potentially degrading carcass value. In this study, rumen temperature (T_{RUM}) of three cattle breeds, with and without access to shade, were assessed. Thirty-six steers (12 Angus, Charolais, and Brahman) with an initial BW of 318.5 ± 6.7 kg were used in a 180-d feedlot study with two treatments: un-shaded and shaded (3 m^2/animal; 90% solar block shade cloth). There were six steers (two/breed) per pen (162 m^2) and three pens/treatment. Ten-min T_{RUM} data were obtained over 130 d using rumen boluses. Individual T_{RUM} data were first converted to an hourly average, and then mean hourly T_{RUM} within breed x treatment were calculated. Rumen temperature was analyzed using a repeated measures model (PROC MIXED; SAS Inst. Inc. Cary, NC). The model analyzed the effect of breed ($P < 0.0001$), hour (h; $P < 0.0001$), breed x h ($P < 0.0001$), treatment x h ($P < 0.0001$), and breed x treatment x h ($P = 0.0036$). On average T_{RUM} of un-shaded Angus were greater ($P < 0.05$) than shaded and un-shaded Brahman's by 0.65 ± 0.05°C and 0.64 ± 0.05°C, respectively. Rumen temperature of shaded Angus were on average 0.46 ± 0.03°C ($P < 0.05$) lower than unshaded Angus between 1200 and 1600 h. Differences were observed between shaded and un-shaded Charolais between 1000 and 1700 h, with the shaded treatment on average 0.48 ± 0.02°C lower than unshaded. No h or treatment differences were detected between unshaded and shaded Brahman's, with a daily mean of 39.08 ± 0.08°C and 39.07 ± 0.08°C respectively, indicating that these animals may be utilizing breed specific behavioral and physiological mechanisms to regulate BT. These data suggest that providing feedlot cattle with shade during summer improves a non-heat-tolerant breed's ability to regulate BT. The relationship between rectal temperatures and T_{RUM} were also assessed ($r = 0.57$), with an average difference of 0.06 ± 0.06°C indicating that T_{RUM} is a robust measure of BT. Therefore, the assessment of an animal's thermal status can be undertaken through the remote assessment T_{RUM}.

Key Words: rumen temperature, body temperature, rectal temperature

0581 The effect of shade on vaginal temperature of cows housed outside under subtropical summer conditions. J. C. Lees*, J. B. Gaughan, A. M. Lees, and M. L. Sullivan, *The University of Queensland, Gatton, Australia.*

It is generally agreed that lactating dairy cows with access to shade have lower body temperatures than those without shade. The aim of this study was to determine the effect of shade on vaginal temperature (T_{VAG}) of cows housed outside in a sub-tropical environment. Holstein Friesian cows (n = 40) were paired based on milk yield and live-weight. Each pair was then allocated to either a shade (S) or a no shade (NS) treatment. Pairs were then randomly allocated to a T_{VAG} group (five pairs/group). Data were collected on one group per week, over 8 wk (two reps/group). A temperature logger was attached to a CIDR and inserted into the vagina for 5 d, logging every 10 min. Weather was monitored via an automated weather station (200 m from cows) and temperature humidity index [THI = 0.8 × ambient temperature + relative humidity x (ambient temperature – 14.3) + 46.3] was calculated using these data. Cows were milked twice daily at 0500 and 1500 h. Fans and sprinklers were used for 15 min before afternoon milking. Cows were placed within treatment from 0700 to 1445 h daily; fed a mixed ration twice daily, and turned out to improved pasture overnight. Averages for T_{VAG} and THI were obtained for each h over each 5-d period. Three data periods were examined: day (D), night (N), and evening (E); T_{VAG}_D and THI_D (0900 to 1500 h); T_{VAG}_N and THI_N (2200 to 0600 h); and T_{VAG}_E and THI_E (1700 to 2100 h). Pearsons correlations were performed on T_{VAG} against THI for each period. Overall, relationships were found between T_{VAG}_N and THI_N (r = -0.256; P = 0.041); T_{VAG}_D and THI_D (r = 0.34; P = 0.006); and T_{VAG}_D-N and THI_D-N (r = 0.61; $P < 0.000$) on the whole herd. Moderate correlations were determined for T_{VAG}_D-N and THI_D-N for S (r = 0.516; P = 0.003) and NS (r = 0.769; $P < 0.000$) cows. Shaded cows were better able to regulate T_{VAG} up to a THI of 76, after which T_{VAG} increased, whereas NS showed a positive, linear increase in T_{VAG} with increasing THI. It appears that S cows were better able to regulate body temperature than NS when THI_D-N was smaller than seven THI units. Above this point, the rate of increase in T_{VAG} against THI was greater in both treatments.

Key Words: vaginal temperature, shade, dairy cows

0582 Differences in panting score and shade usage between Brahman, Angus, and Charolais steers with and without access to shade during summer. J. B. Gaughan*, A. M. Lees, M. L. Sullivan, J. C. Lees, and N. B. Nquyen, *The University of Queensland, Gatton, Australia.*

The use of shade is largely a function of breed type and weather conditions. In this study the effect of breed on shade use and

subsequent respiratory response to heat load were evaluated. Thirty-six steers (12 each of Angus, Charolais, and Brahman; initial BW of 318.5 ± 6.7 kg) were used in an 81-d feedlot study with two treatments: no shade and shade (3 m^2/animal; 90% solar block shade cloth). There were six steers (two/breed) per pen (162 m^2) and three pens/treatment. Individual panting scores (PS) were obtained daily at 2-h intervals from 0600 to 1800 h. The PS system uses a seven-point score (0, 1, 2, 2.5, 3, 3.5, and 4) where PS0 indicates no thermal stress and PS4 indicates severe thermal stress (open mouth, tongue extended, rapid labored breathing). Individual PS were collated (breed and treatment), and mean panting scores (MPS) for each observation time (h) calculated. A MPS of 0.8 to 1.2 indicates high heat load, and if > 1.2 extreme heat load. Analysis of variance of MPS and shade usage was performed using repeated measures. The model analyzed the effect of breed, treatment, h, and all interactions. Angus used the shade in greater numbers ($P < 0.05$) at all times except 0600 h. For all breeds < 1% were under shade at 0600 h. For Angus maximum shade usage occurred at 1200 h (81.5%); for Charolais and Brahman maximum use occurred at 1400 h (39.4% and 24.6%, respectively). Mean PS was affected ($P < 0.05$) by treatment, treatment × h, breed, and breed × treatment. At 0600 h unshaded Angus had a greater ($P < 0.05$) MPS (1.06 ± 0.04) compared with unshaded Brahman (0.10 ± 0.02) and unshaded Charolais (0.90 ± 0.04). At 1400 h, when maximum MPS occurred, the values for unshaded (shaded in brackets) Angus, Charolais, and Brahman steers were 1.77 (1.52), 1.37 (1.31), and 0.78 (0.69), respectively. The percentage increase in MPS (0600 to 1400 h) of unshaded Brahmans was 87% ($P < 0.05$) (97% for shaded); for unshaded Angus the increase was 40% (47% for shaded), for Charolais it was 34% for unshaded and 41% for shaded. The MPS for shaded cattle suggests that the provision of shade allows cattle to improve thermoregulation. The greater percentage rise in MPS of Brahmans indicates that this breed does use increased respiratory dynamics in thermoregulation.

Key Words: panting, shade, cattle

0583 Correlation between mean panting score and temperature humidity index in lactating dairy cows in a sub-tropical summer. M. L. Sullivan*, J. B. Gaughan, N. Son, J. Lees, and A. M. Lees, *The University of Queensland, Gatton, Australia.*

Climate directly influences production and physiological responses of lactating dairy cows. Panting score (PS) can assist in determining the level of heat stress within a herd, but there is little research in this area for dairy cows. Forty lactating Holstein-Friesian cows were used in a 103-d study investigating the influence of summer conditions on animal response to heat load. The cows were managed within a partial mixed ration system and were milked twice daily (0530 h, 1400 h). The cows were observed twice daily [1000 h (AM); 1400 h (PM)] by the same observer. Individual PS were obtained once at each observation. Panting score system uses a seven-point score (0, 1, 2, 2.5, 3, 3.5, and 4), with PS0 = no thermal stress and PS4 = severe thermal stress (open mouth, tongue extended, rapid labored breathing). Individual PS were collated and converted into mean PS (MPS) for 40 cows at AM and PM. A MPS of 0.8 to 1.2 = high heat load, MPS > 1.2 = extreme heat load. In both instances milk production and reproduction are adversely affected. Ambient temperature (T_A) and relative humidity (RH) were obtained at 10-min intervals from an automated on-site weather station. THI was calculated from these data (THI = 0.8 × T_A) + [(RH/100) × (T_A - 14.4)] + 46.4). Mean PS were analyzed using repeated measures model. Correlations between MPS and THI at time of observation (0 h; AM/PM) and for 2- and 1-h lags were determined using Pearson correlation analysis. The MPS of cows (0 h) at PM (1.3 ± 0.05; extreme heat load) was greater ($P < 0.01$) than AM (1.1 ± 0.05; high heat load). Overall, MPS and THI were moderately correlated ($P < 0.001$) for 0-, 1-, and 2-h lags for AM and PM. For AM the best correlation between MPS and THI was $r^2 = 0.50$ for 1-h lag. For PM the best correlation between MPS and THI was $r^2 = 0.69$ for no lag (0 h). Elevated PS during AM may be an attempt to reduce heat load while there is a positive temperature gradient between the cow and the environment.

Key Words: panting, heat stress, temperature humidity index

0584 Correlation between milk production, days in milk, and temperature humidity index in lactating dairy cows in a sub-tropical summer. M. L. Sullivan*, J. B. Gaughan, N. Son, J. Lees, and A. M. Lees, *The University of Queensland, Gatton, Australia.*

Heat load is a significant factor that contributes to reductions in milk production in sub-tropical dairy cows. Forty lactating Holstein-Friesian cows were used in a 103-d study investigating the influence of summer conditions on animal responses. The cows were managed within a partial mixed ration system (70% total mixed ration and 30% pasture) and were milked twice daily at 0530 h and 1400 h. Individual milk production (MP) was recorded at each milking. Ambient temperature (T_A) and relative humidity (RH), were obtained at 10-min intervals from an automated on-site weather station, and temperature humidity index (THI) was calculated based on these data: (THI = 0.8 x T_A) + [(RH/100) x (T_A - 14.4)] + 46.4. Individual MP were collated and converted into mean MP for the 40 cows. Correlations between MP and mean THI for -1, -2, and -3-d lags were examined using Pearson correlation analysis. The mean MP over the duration of the study was 23.3 kg/cow.d^{-1} (range 18.9 to 28.3 kg/cow.d^{-1}), and DIM was < 50 d at the commencement of the study. The mean monthly THI for the duration of the study progressively increased: December, 71.0 ± 0.07 (range 51.5 to 84.7); January, 73.2 ± 0.07 (range 60.2 to 86.4); February, 74.1 ± 0.09 (range 59.7 to 87.1). Milk production was negatively correlated with THI ($P < 0.01$) for

1-, 2-, and 3-d lags. The correlation between MP for the 1-, 2-, and 3-d lags and THI on d 0 were -0.57, -0.55, and -0.53. Fluctuations in MP during summer are generally attributed to changes in THI, and this is supported by the current study. However, there was a negative correlation (r = -0.72, P < 0.001) between MP and DIM. During the study, increasing heat load corresponded with increasing DIM. Reductions in MP due to increasing DIM need to be accounted for so as not to confound the reductions in MP due to heat load. This study suggests that there is a strong negative correlation between the THI, MP, and DIM and that the effects are cumulative.

Key Words: heat stress, milk production, temperature humidity index

---

0585 Effects of metabolizable energy intake on tympanic temperature and ADG of steers finished in southern Chile during wintertime. R. A. Arias[*1], T. Brown-Brandl[2], and T. L. Mader[3], *[1]Universidad Católica de Temuco, Núcleo de Investigación en Producción Alimentaria, Temuco, Chile, [2]ARS-USDA, Clay Center, NE, [3]Mader Consulting, LLC, Gretna, NE.*

A total of 24 Angus x Hereford steers (BW = 479.8 ± 4.48) were used to assess the effect of ME intake (MEI) on ADG and tympanic temperature (TT) during the wintertime in southern Chile. The study was conducted at the experimental field of the UC Temuco and included a period of 21 d for adaptation to diet and facilities. Steers were randomly allocated in four pens (six/pen) equipped with a Calan Feeding System. Steers were sorted by BW, assigned to block (lighter or heavier), and then allocated into one of two treatments: T1 = 1.85x or T2 = 2.72 x MEI for maintenance. All steers were fed 1x/day with the same diet; treatments were applied by controlling DMI. Subsequently, five animals/treatment received a device to collect TT; those were retrieved 10 d later. Climatic data were obtained from a weather station located 5 km southeast from the research site. All data were analyzed under a complete randomized block experimental design (α = 0.05), and each steer was considered an experimental and observational unit. The steers fed with higher MEI showed higher TT than those fed with lesser MEI (P < 0.0001) through all days. In addition, both groups followed the same TT pattern throughout the TT collection period. This could be explained by changes in precipitations (PP) and wind speed (WS). The highest TT was observed in those days without PP and low WS. On the other hand, the lowest TT was observed when WS and PP were higher. Thus, in adult animals it appears that WS has an important role in the thermal balance during the wintertime. Similarly, steers fed with less MEI showed lesser TT when compared with those fed high MEI (P < 0.0001) through every hour of the day, even when both groups had theoretically enough energy to cover maintenance requirements. Following the same trend, observed ADG was higher (P = 0.0004) for those steers fed the high MEI compared with those fed the less MEI (0.54 vs. 0.17 ± 0.06 kg/d, respectively). This represents a performance of 3.18 times better for T2; however, MEI was only 1.47 times higher in this treatment. In conclusion, based on the data collected so far, it can be said that MEI has a direct effect on the TT and ADG of steers finished during the winter period in an open feedlot. In addition, both variables are directly affected by climatic conditions.

Key Words: tympanic temperature, thermal comfort, climate

0586 Conductive cooling as an alternative to cool down dairy cows. X. A. Ortiz[*1], J. F. Smith[1], F. Rojano[1], C. Y. Choi[2], J. Bruer[3], T. Steele[3], N. Schuring[4], J. D. Allen[5], and R. J. Collier[6], *[1]University of Arizona, Tucson, [2]University of Wisconsin-Madison, Madison, [3]Conco Technology Inc., Phoenix, AZ, [4]GEA Farm Technologies, Naperville, IL, [5]Northwest Missouri State, Maryville, [6]The University of Arizona, Tucson.*

The typical cooling system utilized to reduce heat stress in dairy operations requires high energy and/or water usage. With the steady increase in electricity costs and reduction of water availability and increase in water usage regulations, passive cooling systems need to be investigated as ways to cool cows and reduce the utilization of water and electricity. An experiment was designed to investigate the use of heat exchangers buried 25 cm below the surface as components in a conductive system for cooling cows. Six cows were housed in environmentally controlled rooms with tie-stall beds that were equipped with a heat exchanger and filled with 25 cm of either sand or dried manure. Beds were connected to supply and return lines and individually controlled. Two beds (one per each kind of bedding material) constituted a control group (water OFF), and the other four (two sand and two dried manure) used water at 7°C passing through the heat exchangers (water ON). The experiment was divided in two periods of 40 d, and each period involved three repetitions of three different climates (hot dry, thermo neutral, and hot humid). Sand bedding remained cooler than dried manure bedding in all environments and at all levels of cooling (water ON or OFF). Bed temperatures were lower and heat flux higher during the Sand ON bed treatment. We also detected a reduction in the core body temperatures (CBT), the respiration rates (RR), rectal temperatures, and skin temperatures of those cows heat-stressed during the Sand ON treatment. Dry matter intake and milk yield numerically increased during the Sand ON bed treatment for all climates. No major changes were observed in the lying time of cows or the composition of the milk produced. We concluded that use of heat exchangers is a viable alternative to systems that employ fans, misters, and the evaporative cooling methods to mitigate the effects of heat stress in dairy cows. Sand was a better bedding material to use in combination with heat exchangers. Additional research is needed to investigate alternative ways to increase the ex-

change of heat through conduction. Future studies should investigate the benefits of placing the heat exchanger closer to the skin surface and further reducing the water temperature through mechanical cooling.

Key Words: conductive cooling, heat stress and dairy cow

0587 Comparison of winter feeding systems for the evaluation of beef cow performance, reproductive efficiency, and system costs. D. Jose[*1], G. B. Penner[1], J. J. McKinnon[1], K. Larson[2], and B. Lardner[1,2], *[1]University of Saskatchewan, Saskatoon, Canada, [2]Western Beef Development Centre, Humboldt, SK, Canada.*

Extensive winter grazing has been proven as a successful strategy to reduce production and labor costs in a cow-calf operation without much adverse effects on animal health and performance. Two experiments were conducted during the winter of 2012–13, to evaluate three winter feeding systems: 1) field grazing standing whole plant corn (SC; TD*N* = 59.5%, CP = 7.8%), 2) field grazing swathed barley hay (SB; TD*N* = 66.2%, CP = 8.5%), and 3) barley hay bales fed in drylot pens (DL; TD*N* = 60.1%, CP = 12.7%). The specific objectives were to compare beef cow performance, reproductive efficiency, and system costs in experiment 1 (EXP 1), and ruminal pH parameters in experiment 2 (EXP 2). In EXP 1, dry pregnant Angus cows (n = 60, body weight (BW) = 651.2 ± 7 kg), stratified by body weight and days pregnant, were randomly allocated to one of three replicated (n = 2) winter grazing treatments for 77 d. Cow BW, body condition score (BCS), and rib and rump fats were measured at the start and end of the trial. Increases in rump fat were greater (P = 0.002) for SC cows compared to DL cows (1.90 mm vs. 0.55 mm, respectively). Calves born to cows on SC were heavier (P < 0.001) at birth compared to calves from SB cows (42 vs. 40 kg respectively). In EXP 2, nine cannulated beef heifers were cycled through the three winter systems concurrently within EXP 1 in a replicated 3 × 3 Latin square design for 63 d to evaluate effect of forage type on rumen pH. Results from EXP 2 indicated that SB heifers had the lowest (P < 0.003) mean, minimum, and maximum rumen pH and greatest duration and area under pH < 5.8 (P < 0.001) compared to heifers on SC and DL winter systems. Economic analysis revealed that total costs were greatest for the DL ($2.29/head/d) compared to SC ($1.78/head/d) and SB ($1.65/head/d) systems. Results suggest that both SC and SB systems are cost-effective alternatives to DL system and do not negatively affect cow body weight or reproductive performance in winter.

Key Words: winter grazing, corn grazing, swath grazing, reproductive performance

0588 Effect of two winter housing systems on production, body weight, somatic cell count, BCS, and dry matter intake of organic dairy cows. L. S. Sjostrom[*1], B. J. Heins[1], M. I. Endres[2], R. D. Moon[2], and U. S. Sorge[3], *[1]University of Minnesota, West Central Research and Outreach Center, Morris, [2]University of Minnesota, St. Paul, [3]University of Minnesota, Dep. of Veterinary Population Medicine, St. Paul.*

Organic cows (n = 83) were used to evaluate the effect of two winter housing systems (December 2012 to May 2013) on production, SCC, body weight, BCS, and DMI. Cows were assigned to one of two treatments (two replicates per group): 1) outdoor (straw pack, n = 42) or 2) indoor (compost-bedded pack barn, n = 41). There were 21 cows per replicate for the outdoor housing and 21 and 20 cows per replicate for the indoor housing. Cows calved during two seasons (March to May 2012 and September to December 2012) at the University of Minnesota West Central Research and Outreach Center, Morris, MN, organic dairy. Organic wheat straw was used as bedding for the two outdoor bedded packs, which were 12 m wide by 27 m long, and maintained by farm management to keep cows dry and absorb manure throughout the winter. The open-front compost-bedded pack barn (two pens in the barn) was bedded with organic-approved sawdust, and the bedding material was stirred twice per day with a small chisel plow. Cows were fed a TMR that included organic corn silage, alfalfa silage, corn, expelled soybean meal, vitamins, and minerals. Milk, fat, and protein production and SCC were recorded from monthly DHIA testing. Body weight and BCS were recorded bi-weekly as cows exited the milking parlor. The PROC MIXED of SAS was used for statistical analysis, and independent variables were fixed effects of season of calving (fall or spring), parity (1, 2, 3+), breed group, housing system, with replicate and cow nested within the interaction of housing system and season as a random effect. Energy-corrected milk and SCC was not different for the outdoor (15.5 kg/d, 206,000 mL) and indoor (16.1 kg/d, 357,000 mL) housing systems, respectively. In addition, outdoor and indoor housing systems were not different for body weight (523 vs. 538 kg) and BCS (3.15 vs. 3.08), respectively. Daily DMI was 17.8 kg/d for indoor cows and 17.6 kg/d for the outdoor cows (P = 0.47). Total bedding costs during the winter was $8,275 for the outdoor system and $9,248 for the indoor system. In summary, cows housed outdoors on straw-bedded packs did not differ from cows housed in an indoor compost-bedded pack barn for production and SCC, as well as body weight, BCS, or DMI.

Key Words: organic, outwintering, compost barn

RUMINANT NUTRITION I

0589 Feedlot performance and diet digestibility of feed efficiency-ranked beef steers fed corn or roughage-based diets and finished with corn or byproduct-based diets. J. R. Russell*[1], N. O. Minton[2], W. J. Sexten[2], M. S. Kerley[2], and S. L. Hansen[1], *[1]Iowa State University, Ames, [2]University of Missouri, Columbia.*

The objective was to determine effects of growing phase (GP) diet and feed efficiency (FE) ranking, as well as finishing phase (FP) diet, on beef steer diet digestibility and FP growth. At University of Missouri, 193 steers were fed whole-shell corn (GPC) or roughage-based (GPR) diets using GrowSafe individual feed intake system for 70 d and FE was determined. At Iowa State University, the 12 greatest (HFE) and 12 least (LFE) feed efficient steers from each GP diet (n = 48; 509 ± 7 kg) were blocked by GP diet and FE ranking into GrowSafe-equipped pens of six. Steers were fed 10 g titanium dioxide (TiO_2) daily in diets similar to GP diets for 14 d, followed by 2 d fecal collection to determine GP diet DM digestibility (GPdig). Steers were then transitioned to FP corn (FPC) or byproduct-based diets (FPB), receiving FP diets for 14 d before again being fed TiO_2 daily for 14 d followed by 2 d fecal collection to determine FP diet DM digestibility (FPdig). Data were analyzed using PROC MIXED of SAS. There was a tendency for greater (P = 0.07) GPdig in HFE versus LFE steers, and FPdig was greater (P < 0.05) for steers fed FPC versus FPB diets. There was no relationship between FPdig and finishing phase G:F. There was a positive correlation between G:F in GP and FP (R = 0.29; P < 0.05). A positive correlation between GPdig and FPdig (R = 0.31; P < 0.05) was driven by a strong positive correlation between GPdig and FPdig (R = 0.71, P < 0.05) in cattle grown and finished on corn diets. Compared to LFE, HFE steers had greater finishing phase G:F (P < 0.05) and tended to have greater FP final BW and ADG (P = 0.07), while DMI did not differ due to FE rank (P > 0.1). No differences in ADG, G:F, or DMI (P > 0.1) during FP were noted due to GP or FP diet effects. In this study, G:F during FP was positively related to growing phase FE ranking, and FP performance was greater in steers ranked as highly FE during GP. Differences in GPdig may help explain growing phase FE ranking. The strong correlation for diet digestibility in steers grown and finished on corn diets supports the assertion that cattle FE testing should likely be conducted using the diet most similar to the environment of interest.

Key Words: cattle, digestibility, feed efficiency

0590 Effects of processing of treated corn stover and distillers grains on intake and digestibility of feedlot diets. J. L. Harding*, M. L. Jolly, J. C. MacDonald, and G. E. Erickson, *University of Nebraska-Lincoln, Lincoln.*

Four ruminally fistulated steers were utilized in a 4 × 6 Latin rectangle design to evaluate the effects of replacing dry-rolled corn (DRC) with a pelleted feed containing treated corn stover and distillers grains (DGS). The control (CON) treatment contained 50.3% DRC, 40% DGS, 5% stalks, and 1.7% limestone. The first treatment (TRT 1) consisted of 27% DRC, 40% DGS, 25% treated stover pellet, and 5% stalks. The second treatment (TRT 2) contained 25.9% DRC, 40% DGS, 10% treated stover pellet, 10% DGS, 5% solubles, 5% stalks, and 1.1% limestone. Treatment 3 (TRT 3) contained 27% DRC, 40% DGS, 25% treated corn stover and distillers pellet, and 5% stalks. The diet for TRT 2 was formulated to be of similar energy value as the treated stover and distillers pellet in TRT 3. Pellets used in TRT 1 contained corn stover that had been processed differently compared to the pellets fed in TRT 3. All treatments contained 3% supplement. Data were analyzed using the PROC MIXED of SAS. There were no ($P \geq 0.15$) differences observed among the CON, TRT 1, TRT 2, or TRT 3 for DM (10.10, 7.45, 8.49, and 8.52 kg/d, respectively), OM (8.07 ± 2.15 kg/d), or NDF (2.71 ± 0.65 kg/d) intakes. Correspondingly, no differences ($P \geq 0.50$) were observed between the CON, TRT 1, TRT 2, or TRT 3 for DM (75.41 ± 5.21%), OM (78.59, 78.81, 77.40, and 79.98%, respectively), or NDF (62.35, 72.63, 68.35, and 68.11%, respectively) digestibilities. Proportions (mMol/100 mMol) of acetate (54.75 ± 0.72), propionate (26.71 ± 1.10), and butyrate (12.05 ± 0.72) were not different between the four treatments (P > 0.50). There was a difference (P < 0.05) in maximum ruminal pH recorded with the treatments having a maximum pH of 6.30 (CON), 6.66 (TRT 1), 6.29 (TRT 2), and 5.96 (TRT 3). There was a tendency (P = 0.09) for differences in average ruminal pH, with treatment differences following the same trend as seen in maximum pH. Differences in maximum pH were attributed to varying pH of the two pellet types. It was concluded that the DRC could be replaced with a pelleted stover and distillers in the finishing diet without altering total tract digestion.

Key Words: cattle, pellet, treated stover

0591 Effects of dietary glycerin inclusion at 0, 5, 10, and 15% of dry matter on energy metabolism and nutrient balance in finishing beef steers. *K. E. Hales*, A. P. Foote, T. Brown-Brandl, and H. C. Freetly, USDA-ARS-MARC, Clay Center, NE.*

Expansion of the biodiesel industry has increased the glycerin (GLY) supply. Glycerin is an energy-dense feed that

can be used in ruminant species; however, the energy value of GLY is not known. Therefore, the effects of GLY inclusion at 0, 5, 10, and 15% in dry-rolled corn (DRC)-based diets were evaluated in eight steers (BW = 503 kg) using a replicated Latin square design. Data were analyzed with the fixed effects of dietary treatment and period and random effects of square and steer within square were included in the model. Contrast statements were used to separate linear and quadratic effects of GLY inclusion. Diets were based on DRC and GLY replaced DRC at 0 (GLY-0), 5 (GLY-5), 10 (GLY-10), and 15% (GLY-15) of dietary dry matter. Dry matter intake decreased linearly ($P = 0.02$) as GLY increased in the diet. As a proportion of GE intake, fecal energy loss tended to decrease linearly ($P < 0.07$), and DE also tended to decrease linearly ($P = 0.07$) as dietary level of GLY increased. Urinary energy loss was not different ($P > 0.31$) as a proportion of GE as GLY increased in the diet. Methane energy loss as a proportion of GE intake tended to respond quadratically ($P = 0.10$) decreasing from 0 to 10% GLY inclusion and increasing thereafter. As a proportion of GE intake, heat production increased linearly ($P = 0.02$) as GLY increased in the diet Additionally, as a proportion of GE intake, retained energy (RE) tended to respond quadratically ($P = 0.07$) increasing from 0% to 10% GLY inclusion and decreasing thereafter. Total dry matter digestibility tended ($P < 0.01$) to respond quadratically. As a proportion of N intake, urinary and fecal N excretion increased linearly ($P < 0.04$) as GLY increased in the diet. Furthermore, g of N retained and N retained as a proportion of N intake both decreased linearly ($P < 0.02$) as GLY increased in the diet. Overall, RE tended to decrease as GLY increased in the diet in conjunction with a decrease in N retention. The increase in N excretion as GLY increased in the diet could indicate an increase in microbial N excretion caused by a shift from ruminal fermentation to post gastric fermentation. *USDA is an equal opportunity provider and employer.*

Key Words: cattle, energy metabolism, glycerin

0592 Intake and digestibility of diets without forage in Nellore and Angus young bulls. *M. M. Ladeira[*1], J. R. R. Carvalho[1], M. L. Chizzotti[2], D. R. Casagrande[1], P. D. Teixeira[1], M. C. L. Alves[1], R. A. Gomes[1], and L. A. Silveira[1], [1]Universidade Federal de Lavras, Lavras, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Brazil.*

The objective was to evaluate intake and digestibility of nutrients in Nellore and Angus young bulls fed a corn silage/concentrate diet and a whole shell corn (WSC) diet without the use of forage. Thirty-six animals with average body weight of 381.2 ± 11.87 kg were used in a completely randomized design using a 2 × 2 factorial arrangement (two breeds and two diets). The corn silage/concentrate diet contained 30% silage and 70% of concentrate based on corn and soybean meal. The WSC diet had 85% whole shell corn and 15% of a pellet based on soybean meal and minerals. Both diets had 12.5% of crude protein and 2.88 Mcal/kg of ME. The animals were allocated in individual pens and fed during 81 d of experiment. However, the digestibility trial started at Day 65 with total collection of feces and orts for five consecutive days. Intake was measured daily. Data were analyzed using PROC GLM of SAS 9.3. Angus animals had greater nutrient intake (kg/d) due to their greater body weight, compared to Nellore (Table 0592). However, there weren't differences on dry matter (DM) and neutral detergent fiber (NDF) intake, when data were analyzed on live weight percentage. WSC diets decreased DMI on both breeds studied. Breeds affected digestibility of non-fiber carbohydrates (NFC) only when WSC diet was used, being greater in Angus animals. WSC diet had greater digestibility of NDF, less digestibility of NFC and a tendency to increase DM digestibility. In conclusion, Angus young bulls have more capacity to digest NFC than Nellore. *Funded by Fapemig, CNPq, CAPES and INCT-CA.*

Key Words: breeds, corn, feedlot

Table 0592. Intake and digestibility of diets without forage (WSC) and with 30% corn silage (30:70) in Nellore and Angus young bulls

	Nellore		Angus			*P*-value		
Item	30:70[1]	WSC[2]	30:70	WSC	SEM	Breed	Diet	B*D
DMI (kg/d)	14.1	7.5	16.2	9.6	0.71	< 0.01	< 0.01	0.97
DMI (%LW)	3.0	1.8	3.0	1.8	0.15	0.92	< 0.01	0.92
NDFI (kg/d)	4.7	1.7	5.2	2.2	0.20	0.02	< 0.01	0.93
NDFI (%LW)	1.0	0.4	1.0	0.4	0.04	0.83	< 0.01	0.67
NFCI (kg/d)	6.7	4.0	7.8	5.3	0.38	< 0.01	< 0.01	0.93
DMDig (%)	78.6	80.7	78.0	83.7	1.91	0.58	0.07	0.39
NDFDig (%)	68.8	78.5	64.0	81.7	2.35	0.73	< 0.01	0.12
NFCDig (%)	98.6 a	88.9 c	99.1 a	94.4 b	1.21	0.02	< 0.01	0.04
CPDig (%)	78.3	78.9	77.1	80.3	1.77	0.96	0.27	0.45

0593 A survey of dry-rolled corn particle size and fecal starch in U.S. feedlots. E. Schwandt*, *Kansas State University, Manhattan, KS.*

Optimizing grain processing practices in cattle feeding operations is critical to maximize feed efficiency. A survey was conducted to evaluate dry-rolled corn (DRC) processing practices on particle size distribution and fecal starch in finishing cattle. Twenty-four feedlots across South Dakota, Minnesota, Iowa, Nebraska, Kansas, and Colorado participated in the study. Samples of dry-rolled corn, freshly voided feces, and the finishing diet were collected from each feedlot. Particle size distribution of dry-rolled corn samples was determined at the Kansas State University Feed Technology Innovation Center (Manhattan, KS) using a Tyler Ro-Tap Sieve Shaker. The average geometric mean particle size across all operations was 4.6 ± 0.87 mm with a range of 3.2 to 6.8 mm. Fecal starch content averaged 18.2 ± 6.84%; by-product inclusion level averaged 27.0 ± 14.26%; roughage inclusion level averaged 8.3 ± 1.82%; NDF levels averaged 18.7 ± 4.02% on a dry matter basis. Fecal starch values indicate the amount of undigested starch in the feces, which may be influenced by corn particle size. There may be an opportunity to increase the degree of grain processing in some feedlot operations to improve total tract starch utilization.

Key Words: feedlot, grain processing, fecal starch

0594 Effects of feeding zilpaterol hydrochloride on feedlot performance and carcass characteristics of Nellore bulls and steers. A. L. Brichi[1], C. F. Costa[1], A. Perdigao[1], M. A. Factori[1], I. C. Pereira[1], D. D. Estevam[1], R. S. Goulart[2], C. L. Martins[1], D. D. Millen[*3,4], and M. D. Arrigoni[1], *[1]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [2]MSD Saúde Animal, Sao Paulo, Brazil, [3]Supported by São Paulo State Foundation (FAPESP), [4]São Paulo State University (UNESP), Dracena, Brazil.*

This study, conducted at the São Paulo State University feedlot, Botucatu Campus, Brazil, was designed to determine the effects of feeding zilpaterol hydrochloride (ZH) on feedlot performance and carcass traits of Nellore steers and yearling bulls. The experiment was designed as a completely randomized block with a 2x2 factorial arrangement of treatments. Thirty-six 22-mo-old Nellore steers and 36 22-mo-old Nellore yearling bulls (483.9 ± 26.0 kg) were allocated in 24 pens and fed one of two finishing diets containing either 0.0 mg or 7.50 mg of ZH per kilogram of diet DM, replicated six times (three animals/pen), for 20-d before slaughter with a 3-d withdrawal. The finishing diet contained: 70.0% high moisture corn grain, 15.0% sugarcane bagasse, 5.5% peanut meal, 4.0% cottonseed hulls, 3.0% supplement, 1.0% Coast cross hay, 0.8% urea, and 0.7% limestone (DM basis). Cattle were fed ad libitum twice daily for 112 d, and feed offerings and refusals were weighed daily. Cattle were weighed 20 d before slaughter and at the end of the study. A significant ($P < 0.01$) ZH main effect was observed, in which cattle fed ZH had greater final BW (518.6 vs. 510.3 kg) and ADG (1.73 vs. 1.31 kg), improved F:G ratio (5.55 vs. 7.55), heavier HCW (292.7 vs. 280.0 kg), and increased dressing percentage (56.6 vs. 55.1%). In addition, a significant ZH x sex interaction was observed ($P = 0.04$) for DMI, expressed in kg, in which steers not fed ZH had greater DMI than steers fed ZH (9.88 vs. 9.00 kg). However, yearling bulls not fed ZH presented similar DMI when compared to yearling bulls fed ZH (9.61 vs. 9.47 kg). Likewise, a significant ZH x sex interaction was observed ($P = 0.03$) for DMI, expressed as % of BW, in which steers not fed ZH had greater DMI than steers fed ZH (2.00 vs. 1.81%). However, yearling bulls not fed ZH presented similar DMI when compared to yearling bulls fed ZH (1.91 vs. 1.87%). Thus, feeding ZH improves the feedlot performance, as well as carcass traits of Nellore cattle regardless of sex.

Key Words: intake, sex, Zebu

0595 Effects of Next Enhance concentrations in finishing diets on performance and carcass characteristics of yearling feedlot cattle. *C. J. Bittner*[*1], G. E. Erickson[1], K. H. Jenkins[2], M. K. Luebbe[2], G. I. Zanton[3], and M. A. Andersen[3], [1]University of Nebraska-Lincoln, Lincoln, [2]University of Nebraska, Scottsbluff, NE, [3]Novus International, Inc., St. Charles, MO.*

A feedlot study evaluated the effects of Next Enhance 300 (NEXT) essential oil concentration in finishing diets on yearling steer performance and carcass characteristics. Crossbred yearling steers ($n = 288$; BW = 446 ± 23 kg) were utilized in a randomized block design experiment. Cattle were separated into three weight blocks (light, medium, and heavy), stratified by BW, and assigned randomly within strata to 36 pens. Pens were assigned randomly to one of four treatments with nine replications per treatment and eight steers per pen. Treatments consisted of feeding NEXT at concentrations of 0, 16.5, 33.1, and 49.6 mg/kg of diet DM. Light, medium, and heavy blocks consisted of 3, 4, and 2 replications, respectively. Monensin and tylosin were provided in all treatments at 360 and 90 mg/steer daily, respectively. Steers were fed a common basal diet consisting of 54% dry-rolled corn, 25% wet distillers grains plus solubles, 15% corn silage, and 6% supplement (DM basis). Steers in the medium and heavy blocks were fed for 98 d, while steers in the light block were fed for 118 d. Animal performance and carcass characteristics were

analyzed using the PROC MIXED of SAS with pen as the experimental unit. Increasing NEXT concentration in the diet had no effect on DMI, ADG, or G:F ($P > 0.59$; linear or quadratic). Hot carcass weight, fat thickness, and calculated yield grade were not affected ($P > 0.21$; linear or quadratic) by NEXT concentration. As NEXT concentration increased, LM area tended ($P = 0.06$) to decrease quadratically. Greatest LM area were observed when steers were fed 0 or 49.6 mg/kg NEXT, while feeding 33.1 mg/kg NEXT produced the smallest LM area. These data suggest that feeding increasing concentrations of NEXT had little impact on feedlot performance of large yearlings.

Key Words: beef cattle, essential oil, feedlot performance

0596 Effects of plane of nutrition during late gestation and weaning age on transcriptome profiles of Longissimus muscle in Simmental x Angus offspring. S. Moisa*, L. M. Shoup, D. W. Shike, and J. J. Loor, *University of Illinois, Urbana, IL.*

The aim of this study was to evaluate potential carryover effects of maternal diet during late gestation and effects of weaning age on the transcriptome profiles of Longissimus muscle of Angus x Simmental offspring. Pregnant cows blocked by breed were utilized in a 2 × 2 factorial design. Three months before the projected parturition date, cows were assigned to diets (low or medium plane of nutrition). Low plane of nutrition was achieved by grazing endophyte-infected tall fescue/red clover pastures with no supplement, while medium plane of nutrition was achieved by grazing endophyte-infected tall fescue/red clover pastures supplemented with 2.3 kg of dried distiller's grains with solubles and soyhulls. Steer calves were randomly assigned to early or normal weaning treatments within each gestational diet ($n = 20$). At 80 d postpartum, early-wean offspring (EW) were weaned, and received a high-energy finishing diet. At 186 d postpartum, normal-wean offspring (NW) were weaned and joined EW steers at the feedlot where they received the same diet. Longissimus muscle (LM) biopsies were harvested on 81, 187, and 354 d of age. A 45,220 bovine microarray (Agilent) was used for transcript profiling ($n = 5$ steers/group). Functional analysis was performed by means of the Dynamic Impact Approach (DIA). ANOVA statistical analysis (FDR < 0.05 and $P < 0.05$) revealed 8400 differentially expressed genes (DEG) due to time alone and 856 DEG due to treatment alone. Treatment × time affected 33 genes and no DEG were detected for time × treatment × diet. Within the 8400 DEG, the functional analysis revealed that nitrogen metabolism and drug metabolism were the canonical pathways with the highest impact, specially comparing 81 to 354 d of age ($P < 0.05$). For the 856 DEG due to treatment, fatty acid biosynthesis, pyruvate metabolism and insulin signaling pathways were the most–impacted when comparing EW to NW at different time points. Within the 33 DEG due to treatment × time fatty acid biosynthesis was the only impacted canonical pathway ($P < 0.05$). Moreover, initial analysis based on expression pattern (i.e., up- or downregulation) of the 33 DEG indicated most were activated. Results indicated a minor response of the offspring transcriptome to level of maternal plane of nutrition at least when applied during the last 90 d of pregnancy. Post-natal nutritional management, however, led to marked differences in transcriptomics particularly between the growing (81 to 187 d) and finishing phases (187 to 354 d).

Key Words: nutrigenomics, bioinformatics, nutrition

0597 Post-natal nutritional management alters transcription regulator gene networks in Longissimus muscle of Angus x Simmental offspring. S. Moisa*, L. M. Shoup, D. W. Shike and J. J. Loor, *University of Illinois, Urbana, IL*

The aim of this study was to evaluate potential carryover effects of the maternal diet during late gestation and also effects of weaning age on the transcription regulator (TR) gene networks in Longissimus muscle. Angus x Simmental beef cows blocked by breed were utilized in a 2 × 2 factorial design. Three months before the projected parturition date, cows were assigned to treatments (low or medium plane of nutrition). Low plane of nutrition was achieved by grazing endophyte-infected tall fescue/red clover pastures with no supplement, while medium plane of nutrition was achieved by grazing endophyte-infected tall fescue/red clover pastures supplemented with 2.3 kg of dried distiller's grains with solubles and soyhulls. Steer calves were randomly assigned to early- or normal-weaning groups ($n = 20$). At 80 d of age, early-wean offspring were weaned and received a high-energy finishing diet. At 186 d of age, normal-wean offspring were weaned and joined early-wean steers at the feedlot where they received the same diet. Steers were group-fed and intake recorded using the GrowSafe system. Longissimus muscle (LM) biopsies were harvested at 81, 187, and 354 d of age. A 45,220 bovine microarray (Agilent) was used for transcript profiling ($n = 5$ steers/group). Differentially-expressed TR, ligand-dependent nuclear receptors, and their networks with differentially-expressed genes (DEG) were mined using Ingenuity Pathways Analysis (FDR < 0.05 and $P < 0.05$). The statistical model included treatment, maternal diet, time and its interactions, as fixed effects, and steer as random effect. Among the 8400 DEG ($P < 0.05$) affected by the overall effect of time IPA analysis revealed 625 TR and ligand-dependent nuclear receptors (NR). TP53 was the TR with the highest network of target genes. Considering only the DEG due to treatment ($P < 0.05$), among 856 DEG the IPA analysis revealed that 78 were classified as TR and NR. TP53 was also the TR with

the highest network of target genes. In the separate analysis of genes affected by time and treatment ($P < 0.05$) TP53, MYC, HTT, and ERS1 were the TR with highest networks of DEG in both analyses. Results suggest that different plane of nutrition during the last 90 d before calving did not markedly affect the expression of transcription regulators or ligand-dependent nuclear receptors in the offspring's skeletal muscle transcriptome. However, post-natal nutritional management seems to affect TR and NR by activating their expression at growthing stage (i.e., 81 to 187 d) especially when early-weaned.

Key Words: gene networks, nutrigenomics, bioinformatics

0598 Effect of ractopamine hydrochloride and dietary protein content on performance and carcass traits of Nellore bulls.

N. R. B. Cônsolo[1], F. Rodriguez[1], M. O. Frasseto[1], R. A. P. Maciel[2], V. Rizzi[3], and L. F. P. Silva[*1], [1]University of Sao Paulo, Pirassununga, Brazil, [2]University of Sao Paulo, [3]Ouro Fino, Cravinhos, Brazil.*

The objective of this research was to evaluate the effects of ractopamine hydrochloride (RH) and dietary crude protein (CP) on performance and carcass traits of Nellore young bulls. Forty-eight Nellore bulls were grouped by BW, and randomly assigned to treatments in a 2x2 factorial arrangement of treatments. The factors were two levels of dietary CP (100 and 120% of MP requirement), and two levels of RH (0 and 300 mg/animal/d). Treated animal received RH for the final 35d before slaughter. Dry matter intake was measured and adjusted daily. The animals were weighed at intervals of 21 d, at the beginning of supplementation, after 18 d of supplementation and before slaughter. Feed efficiency was calculated from ADG and DMI. On d 113 hot carcass weights were recorded at slaughter. After 24 h of chilling, longissimus muscle area (LMA), and fat thickness were measured at the left half-carcass. The statistical analyses were conducted using SAS, version 9.1.2 for Windows. There was no effect of RH supplementation on final BW ($P = 0.26$). However, animals supplemented with RH had 19% greater ADG than control animals (1.51 vs. 1.27 kg/d, $P = 0.03$), this effect was not dependent on the level of CP in the diet ($P = 0.43$). Increasing dietary CP content above requirements had no effect on final BW, ADG or G:F ratio ($P > 0.05$). For DM intake, the RH x CP interaction was significant ($P = 0.01$), where RH supplementation had no effect on DMI at CP100 ($P = 0.12$) yet it reduced DMI at CP120 (1.95 vs. 1.81% BW for RH0 and RH300, respectively; $P = 0.03$). Addition of RH to the diet considerably improved G:F ratio, independently of the CP concentration of the diet (0.15 vs. 0.13, $P = 0.02$). Treatments had no effect on HCW or dressing percentage of the carcass ($P > 0.10$). There was a tendency ($P = 0.07$) for RH supplementation to increase LMA, independently of dietary CP levels (83.2 vs. 87.9 cm^2). Ractopamine did not alter fat thickness ($P = 0.29$); however, increasing dietary CP above requirements (CP120) decreased fat thickness (5.1 vs. 4.3 mm for CP100 and CP120, respectively). In conclusion, ractopamine supplementation increased gain, improved feed efficiency, and increased LMA even in intact Nellore young bulls.

Key Words: β-agonist, cattle, muscle growth

0599 Effect of 300 or 400 mg daily of ractopamine hydrochloride on growth performance and carcass characteristics of finishing steers during the last 14, 28, or 42 d.

C. J. Bittner*[1], D. B. Burken[1], G. E. Erickson[1], and N. A. Pyatt[2], [1]*University of Nebraska-Lincoln, Lincoln,* [2]*Elanco Animal Health, Greenfield, IN.*

Crossbred yearling steers ($n = 576$; BW = 408 ± 29 kg) were utilized in a randomized block design ($n = 4$ BW blocks) with a 3 × 3 factorial treatment design to study the effects of ractopamine hydrochloride (RAC) dosage and duration on growth performance. Factors included RAC feeding duration (14, 28, or 42 d before harvest) and RAC dosage (0, 300, and 400 mg/hd/d). During the treatment phase, RAC dose was top-dressed daily using fine-ground corn as the carrier. There were no significant duration x dosage interactions ($P > 0.07$) for growth performance or carcass characteristics; however, simple effects will be presented. Live final BW was not different ($P > 0.44$) for steers fed 0, 300, or 400 mg RAC for 14 d. At 28 d, steers fed RAC at 400 mg were significantly ($P < 0.01$) heavier than steers receiving 0 mg. There was a tendency at 28 d for increased live final BW for steers fed RAC at 300 mg ($P = 0.07$) compared to 0 mg and steers fed 400 mg of RAC compared to 300 mg ($P = 0.07$). Live final BW was greater ($P < 0.01$) for steers fed RAC for 42 d at 300 and 400 mg compared to cattle receiving 0 mg; however, live final BW was similar ($P = 0.57$) between 300 and 400 mg of RAC. Between treatments, DMI was similar ($P = 0.27$). Hot carcass weight was similar ($P = 0.33$) between yearlings fed 0 and 300 mg of RAC for 14 d, but tended to be greater ($P = 0.07$) for steers fed 400 mg of RAC compared to 0 mg. Hot carcass weight was greater ($P < 0.01$) for steers fed 300 and 400 mg of RAC compared to cattle fed 0 mg for 28 d. Carcasses from yearlings fed RAC for 42 d at 300 and 400 mg were heavier ($P < 0.01$) than 0 mg fed steers. Feeding 300 mg of RAC for 28 or 42 d increased live final BW by 7 and 13 kg, while feeding RAC at 400 mg resulted in 14 and 11 kg increases relative to control steers. Feeding 300 mg of RAC for 28 or 42 d would suggest 4.9 and 7.5 kg improvements in HCW, while feeding 400 mg of RAC would suggest 8.7 and 9.3 kg heavier carcasses compared to steers fed no RAC.

Key Words: dose, duration, ractopamine

0600 Comparison of the total tract digestibility in feedlot cattle fed barley grain treated with lactic and citric acid. M. Nematpoor[*1], K. Rezayazdi[2], and M. Dehghan-Banadaky[1], *[1]University of Tehran, Karaj, Iran, [2]Dep. of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran.*

RUMINANT NUTRITION II

0601 Using a dynamic metabolic model to investigate differences in metabolic patterns among lactating animals. L. Oliveira[1], H. Kimball[2], J. P. McNamara[*2], and A. Fix[2], *[1]Sao Paulo State University, Brazil, [2]Washington State University, Pullman, WA.*

In dairy cattle, the metabolic flux in body tissues, primarily in visceral, muscle, and adipose tissues make up a large contribution to variations in efficiency among animals housed and fed alike. Metabolic processes are affected by genotype, phenotype, and intake; genotypic differences eventually result in variation in patterns of metabolism that have different metabolic efficiencies. In continued work with the objective of identifying the patterns of metabolic flux in the most efficient dairy cattle, an existing mechanistic metabolic model (Molly, UC Davis) was used to describe differences in energetic and nitrogen efficiency among cows fed and housed alike. Data were from 42 high producing cows fed an alfalfa/corn/SBM based TMR. Data on genetic merit and DMI were input into the model, and milk component output, changes in adipose tissue lipid metabolism; visceral and body protein and lipid, nitrogen were output. Each cow was simulated separately. There was a range in metabolic processes from 27% (maintenance costs) to 93% (MUN) (Table 0601). Tissue metabolism rates (lipogenesis, lipolysis) varied by 48 to 74%; indicating a wide range in potential to metabolize nutrients. The intricate range of patterns of nutrient metabolism underlay the 21% range in net energy efficiency (milk energy/ME intake). A systems approach and model can be used, eventually, to improve selection of cows to reduce the variation in energy efficiency. Integrating all the biological processes with data on genomics and transcriptomics using systems models will help reduce variation in energy efficiency.

Key Words: efficiency, systems biology, metabolic model

Table 0601.

Item	Min	Max	SD	% range
DMI	19.8	31.5	3.2	159%
MILK, kg/d	28.7	49.8	5.1	174%
Lipolysis, M/d	8.1	12	1.3	148%
Lipogenesis, M/d	5.4	9.4	0.87	174%
MES, Mc/d	17.8	30.1	3.07	169%
Maint, Mc/d	25.4	32.4	3.5	127%
HI Main, kg/d	7.4	11.0	1.16	148%
Prot Intake, kg/d	1.3	2.0	0.21	159%
Aa to Milk, M/d	7.8	13.5	1.4	174%
MUN, mg/dl	5.5	10.6	1.3	193%
MES/MEI, %	34.0	41.0	1.7	121%

0602 A dynamic, mechanistic model of metabolism in adipose tissue of lactating dairy cattle. J. P. McNamara[*1], K. Huber[2], and A. Kenez[2], *[1]Washington State University, Pullman, [2]University of Hannover, Germany.*

Research in dairy cattle biology has resulted in a large body of knowledge on nutrition and metabolism supporting and underlying milk production and efficiency. The adipose tissues are an essential part of the overall efficiency of dairy cattle. Therefore we constructed a dynamic, mechanistic model of control of metabolism in the adipose tissues of dairy cattle. The model describes the biochemical interconversion of glucose, acetate, glycerol, fatty acids, and triacylglycerols. Data from our own research and published references were used to set equation forms and parameter values. Metabolites are absorbed from blood, and fatty acids are activated to the Acyl CoEnzymeA counterparts. Fatty acids are partitioned to palmitic, stearic, oleic and linoleic acids. Enzymatically catalyzed reactions are explicitly described with parameters including maximal velocity and substrate sensitivity. Energetic stoichiometry is maintained by the balance of ATP utilizing and generating reactions. Changes in gene transcription or post-translational modification of enzyme activity control nutrient metabolism, including control by insulin and norepinephrine. The model behavior to availability of nutrients and insulin or norepinephrine is in agreement with published data. For example, triacylglycerol synthesis when glucose is low (1 mM) is 17.82 + 1.9 X ln (Fatty Acyl CoA); when glucose is high (5 mM) it is 44.96 + 5.67 ln (Fatty Acyl CoA). Triacylglycerol lipolysis is -13.28- 4.33 ln (Fatty Acyl CoA) when norepinephrine is low, and is- 22.14- 7.22 ln (Fatty Acyl CoA) when it is high (25% more than basal). This model can form a basis for more sophisticated integration of existing knowledge and future studies on metabolic efficiency of dairy cattle.

Key Words: adipose, metabolism, mechanistic model, lactation

0603 Total volatile fatty acid concentrations are unreliable estimates of treatment effects on in vivo ruminal fermentation. M. B. Hall[*1], T. D. Nennich[2], and P. H. Doane[3], *[1]U. S. Dairy Forage Research Center, USDA-ARS, Madison, WI, [2]Purdue University, West Lafayette, IN, [3]ADM Research, Decatur, IL.*

The sum of ruminal acetate, propionate, butyrate, and valerate concentrations ([VFA], m*M*) are used to assess impact of dietary treatments on pattern of carbohydrate fermentation, typically with intent to indirectly relate microbial products to nutrient supply to the cow. However, discrepancies in statistical results of treatment effects between [VFA] and VFA pool size (VFAmol) within one study suggested there were problems with this approach. We investigated relationships among [VFA], VFAmol, and rumen digesta liquid kg (LIQ) measured

2 h post-feeding using individual lactating cow data (175 observations) measured in seven separate feeding trials. Regression analyses were performed using mixed models with "trial" as a discrete random variable; dependent (Y) and independent (X) variables are in Table 0603. Correlations (*r*) are the mean of individual trial values. Across studies, [VFA] had a numerically smaller within-study coefficient of variation (13%) than did VFAmol (23%). Rumen liquid increased with VFAmol. Change in LIQ was likely a function of water flux in the rumen based on the osmotic gradient of rumen liquid and blood; VFAmol represents a large ruminal pool of solute. Rumen liquid and [VFA] were poorly correlated. Concentration of VFA increased with VFAmol. The ratio of [VFA]/VFAmol ranged from 9.0 to 24.1 and changed as a function of 1000/LIQ. The equation reflects the inherent relationship among the three variables, and that [VFA] at differing LIQ differ in their relationship to VFAmol. Mean within-trial LIQ was 73 kg (standard deviation = 11.2), with an average within-study range of 43 kg. Assumption of equivalent ruminal liquid volumes is incorrect. Occupying variable LIQ, [VFA] are not on the equivalent basis needed for comparison of treatments. Alternate approaches must be developed to appropriately use [VFA] to assess treatment effects.

Key Words: rumen, VFA, liquid

Table 0603. Relationships between rumen measures[1]

Y	X	Intercept (SE)	Slope (SE)	p-value of X	Average r
[VFA]	VFAmol	83.9 (5.1)	5.83 (0.38)	< 0.01	0.74
LIQ	VFAmol	32.8 (2.15)	3.68 (0.18)	< 0.01	0.83
[VFA]	LIQ	113 (10.9)	0.473 (0.124)	< 0.01	0.26

[1] Y = dependent variable, X = independent variable, SE = standard error, r = correlation coefficient, [VFA] = VFA concentration, mM, VFAmol = moles of VFA, LIQ = rumen liquid, kg.

0604 Effects of diets differing in starch, fiber, and fatty acid concentrations on milk production and energy partitioning.

J. P. Boerman*, S. E. Burczynski, M. J. VandeHaar, and A. L. Lock, *Michigan State University, East Lansing, MI.*

Effects of feeding diets similar in energy composition, yet differing in starch, fiber, and fatty acid (FA) concentrations, on yield of milk and milk components and energy partitioning were evaluated in a crossover design experiment. Holstein cows (*n* = 32; 102 ± 22 DIM) were randomly assigned to treatment sequence. Treatments were a high starch diet containing 34% corn grain (mixture of dry ground and high moisture corn; HS) or a high FA diet containing 2.5% palmitic acid-enriched FA supplement (HF). Diets contained corn silage, alfalfa silage, and wheat straw as forage sources and contained 34 or 18% starch, 3.2 or 6.3% FA, and 26 or 34% NDF for HS and HF, respectively. Treatment periods were 28 d with the final 5 d used for data and sample collection. The statistical model included the random effect of cow and fixed effects of treatment and period. DMI was 27.4 and 26.9 kg/d for HS and HF, respectively ($P = 0.11$). Compared with HF, HS increased milk yield (47.1 vs. 45.8 kg/d; $P = 0.02$), milk protein concentration (3.07 vs. 2.93%; $P < 0.01$), and milk protein yield (1.44 vs. 1.34 kg/d; $P < 0.01$), did not alter ECM ($P = 0.47$), but reduced milk fat concentration (3.58 vs. 3.95% kg/d; $P < 0.01$), milk fat yield (1.68 vs. 1.81 kg/d; $P < 0.01$), and milk to feed ratio (ECM/DMI, 1.73 vs. 1.78; $P = 0.03$). HS increased the yield of de novo synthesized (< 16-carbon) milk FA (58 g/d; $P < 0.01$) and reduced the yield of 16-carbon milk FA (179 g/d; $P < 0.01$). Yield of preformed (> 16-carbon) milk FA was not affected ($P = 0.80$). HS increased plasma concentration of insulin by 27% ($P < 0.01$) but decreased triglycerides by 10% ($P < 0.01$) and NEFA by 28% ($P < 0.01$). Compared with HF, HS increased BW gain by 14 kg/28 d ($P < 0.01$), change in BCS by 0.25 pt/28 d ($P < 0.01$), and fat thickness over the rump by 0.79 mm/28 d and between the 12th and 13th rib by 0.23 mm/28 d (both $P = 0.04$). Calculated body energy gain as a fraction of NE_L use was greater for HS (10 vs. 3%; $P < 0.01$), whereas milk energy as a fraction of NE_L use was decreased for HS (68 vs. 74%; $P < 0.01$). We conclude that the two diets resulted in similar NE_L intake but the HS diet partitioned more energy toward body gain, whereas the HF diet partitioned more energy toward milk. A high fiber and FA diet might diminish the incidence of over conditioning in mid-lactation cows.

Key Words: starch concentration, fatty acid concentration, energy partitioning

0605 Propionic acid decreased meal size and feed intake compared with glycerol when infused abomasally in cows in the postpartum period.

L. B. Gualdron-Duarte* and M. S. Allen, *Michigan State University, East Lansing, MI.*

Our objective was to evaluate effects of propionic acid (P) and glycerol (G) on dry matter intake (DMI) and feeding behavior for cows in the immediate postpartum period. We hypothesized that propionic acid will decrease DMI and meal size compared to glycerol because of differences in their hepatic metabolism. Isoenergetic infusions of P or G were administered abomasally to eight ruminally cannulated multiparous Holstein cows (4.8 ± 2.3 DIM) in a double crossover design with four, 2-d infusion periods. Treatment sequences (P-G-P-G or G-P-G-P) were assigned alternately to cows based on date of parturition. Treatments were propionic acid (99.5%, 1.00 M) and glycerol (99.7%, 0.92 M) infused at 483 mL/h, which provided 4.26 Mcal/d. Feeding behavior was recorded by a computerized data acquisition system. Data were averaged within period, and period means were analyzed by analysis of variance; the model included the random effect of cow, the fixed effects of period and treatment, and interactions between treatment and period and between treatment and cow. No difference was detected for the amount of each treatment infused (11.6 L/d). Propionic acid decreased DMI

16.7% compared with glycerol (12.5 vs. 15.0 kg/d, $P = 0.04$) by decreasing meal size (1.04 vs. 1.18 kg DM, $P < 0.05$). No interaction was observed between treatment and period indicating a sustained treatment effect over time. Propionic acid tended to increase the time between meals 35 min (114 vs. 79 min, $P = 0.11$) but did not affect meal frequency (12.3 meals per d; $P = 0.48$) compared with glycerol. Propionic acid decreased the hunger ratio (meal size to time since the previous meal) by 25% compared with glycerol (20.3 vs. 27.1 g/min, $P = 0.05$) as well as the satiety ratio (meal size to time until the next meal) by 27% compared with glycerol (24.6 vs. 33.6 g/min, $P < 0.02$). Consistent with our hypothesis, propionic acid decreased meal size and DMI compared with glycerol possibly because of differences in their metabolism in the liver.

Key Words: fresh cows, feed intake, hepatic metabolism

0606 Responses to starch infusion on milk synthesis in low yield lactating dairy cows. Y. Zou*, Z. Yang, Y. Guo, S. Li, and Z. J. Cao, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing.*

The effect of starch infusion on production and metabolic parameters was investigated in low yield lactating cows from 86 d in lactation. Six Holstein cows fitted with permanent ruminal cannulas were arranged into two complete 3 × 3 Latin squares, infused a starch solution containing 800 g starch for 16 d. The three treatments were: 1) ruminal and abomasal infusion with water (Control); 2) ruminal infusion with cornstarch solution and abomasal infusion with water (Rumen); 3) ruminal infusion with water and abomasal infusion with cornstarch solution (Abomasum). There was no significant difference ($P > 0.05$) among the three treatments with low yield lactating cows in dry matter intake, body condition and milk yield, and milk component concentrations. However, cows receiving starch through rumen performed better than through abomasum directly during the glucose tolerance test procedure with higher area under the curve (AUC; $P = 0.08$) and shorter half-time ($t^{1/2}$; $P = 0.11$) of plasma insulin, therefore, it increased glucose disposal, which stated a lipid anabolism other than mobilization after energy supplementation. In conclusion, extra starch infusion at concentration of 800 g/d did not ameliorate energy supplies to mammary gland and improve the lactating performance as we expected but resulted in a tendency of shifting metabolic event toward the pathway of subcutaneous adipose accumulation at low yield lactating cows.

Key Words: starch infusion, lactation performance, glucose tolerance test

0607 The effect of starch digestibility of two corn silage varieties on lactation performance in dairy cows. E. E. Klingensmith*, L. Harthan, and M. D. Hanigan*, Virginia Polytechnic Institute and State University, Blacksburg.*

The objective of this study was to investigate the effect of storage on two corn silage varieties with varying amounts of floury and vitreous endosperm. Floury endosperm is expected to have faster rates of ruminal starch digestion at harvest, resulting in increased overall starch digestibility. However it is unclear if these differences persist during storage. Two multiparous, ruminally cannulated dry cows were used to assess ruminal degradability of starch in ensiled corn silage derived from a floury and vitreous varieties of corn. Cows were fed lactating high cow TMR twice daily ad libitum. Ruminal degradability characteristics were determined as described by NRC (2001). Approximately 10 g of dried and ground corn silage stored for 54 and 80 d sealed in duplicate polyester bags and suspended in the rumen in a large nylon mesh bag for 2, 4, 8, 12, 24, and 36 h. Samples were placed in the rumen in reverse order at varying times and removed simultaneously at the end

Table 0606. Effects of starch infusion with 800 g/d on performance, production and glucose tolerance test in lactation dairy cows

Items	Treatment			Pooled SEM	Contrast	
	Control	Rumen	Abomasum		Infusion	Site
Dry matter intake, kg/d	18.58	17.96	17.67	0.30	0.26	0.70
Body weight, kg	584.5	590.5	600.7	8.35	0.55	0.63
Body condition score	2.71	2.75	2.79	0.06	0.64	0.79
Backfat thickness, mm	17.50	19.33	19.87	0.61	0.37	0.83
Milk yield, kg/d	21.05	21.02	21.07	0.28	0.99	0.93
Milk fat, %	3.43	3.42	3.35	0.03	0.43	0.25
Milk protein, %	2.88	2.91	2.88	0.02	0.71	0.56
Milk lactose, %	4.93	4.98	4.94	0.03	0.70	0.62
Insulin resistance						
Basal concentration, μIU/mL	18.4	16.5	18.7	1.88	0.83	0.79
Peak concentration, μIU/mL	30.3	27.7	41.4	1.36	0.91	0.62
Clearance rate, %/min	3.64	2.59	5.83	0.65	0.90	0.83
Area under the curve, μIU × min/mL	347.8	333.8	374.5	17.59	0.81	0.08
$t^{1/2}$, min	19.1	26.7	13.6	3.14	0.97	0.11

of the experiment. A 0-h sample was immersed in 39°C water for 20 min. Residues were submitted to Agri Analysis for fiber and starch content determination. Starch disappearance was calculated as the difference between the original starch mass and the mass remaining after ruminal fermentation and expressed as a percentage of the original starch mass. The two varieties of corn silage did not differ for soluble starch (24.10 vs. 26.41%; $P = 0.99$), degradation rate (0.35 vs. 0.24%/hr; $P = 0.79$), slowly digestible starch (67.65 vs. 68.22%; $P = 1.00$), and resistant starch (8.24 vs. 5.36%; $P = 0.70$) after 54 d storage. There were also no differences after 80 d of storage for rapidly digestible starch (19.06 vs. 36.71%; $P = 0.28$), degradation rate (0.23 vs. 0.24 $P = 1.00$%/h), slowly digestible starch (78.49 vs. 59.11%; $P = 0.11$), and resistant starch (2.45 vs. 4.18%; $P = 0.90$). Thus, any differences amount corn varieties did not persist by 54 d of storage. References: (1) National Research Council. 2001. Nutrient Requirements of Dairy Cattle. Natl. Acad. Sci., Washington, DC.

Key Words: starch digestibility, corn silage

0608 Effects of calcium oxide treated corn stover as a partial replacement for corn silage, Chinese wildrye or concentrate on milk yield and composition of dairy cows. H. T. Shi*, S. L. Li, Z. J. Cao, and Y. Q. Wu, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing.*

The utilization of corn stover was limited by its poor digestibility for ruminants. Studies showed that the nutritive value of corn stover can be improved by calcium oxide (CaO) treatment. The objective of this experiment was to determine the effect of replacing a portion of corn silage (CS), Chinese wildrye (CW), or concentrate (CT) in the diets with CaO-treated corn stover on milk yield and milk composition of dairy cows. Sixty-four Holstein cows in mid to late lactation were assigned to one of the four treatments in a randomized block design (16 cows/group): 1) control treatment (CON), diets included 15% Chinese wildrye, 25% corn silage, 10% alfalfa hay, and 50% concentrate; 2) replacing 15% Chinese wildrye with treated stover (RCW); 3) replacing 12.5% corn silage with treated stover (RCS); 4) replacing 7% concentrate with treated stover (RCT). Cows were offered the total mixed ration (TMR) thrice daily and the experiment was lasted for 90 d. The inclusion of treated stover in treatment diets as a substitute for CW, CS, and CT had no effects ($P > 0.05$) on lactose percentage, 4% fat-corrected milk yield, milk fat yield, and milk protein yield. Cows in RCW and RCT treatments had similar milk yield ($P > 0.05$) compared with that in CON treatment. Cows in CON treatment had higher ($P < 0.05$) milk protein percentage than that in other treatments. Cows in RCS treatment had higher ($P < 0.05$) milk yield and milk lactose yield than that in CON treatment. Milk fat percentage was decreased ($P > 0.05$) for the RCW treatment compared with the CON treatment. The CON treatment had higher ($P < 0.05$) total solids percentage and MUN concentration than other treatments. The RCS treatment had lower ($P < 0.05$) somatic cell count than other treatments. These results suggest that a portion of corn silage, Chinese wildrye, or concentrate can be replaced by CaO-treated corn stover without negative effects on 4% FCM, milk fat, milk protein, and milk lactose yields of dairy cows.

Key Words: dairy cow; performance; treated corn stover

0609 Effects of dried sugar beet pulp as a replacement for corn silage on performance of dairy cows. G. R. Ghorbani*, N. Naderi, A. Sadeghism, and I. Sadrearhami, *Isfahan University of Technology, Isfahan, Iran.*

This study investigated the effects of feeding dried beet pulp (BP) as a replacement for corn silage (CS) on performance of dairy cows. Four multiparous (126 ± 13 d in milk) and four primiparous (121 ± 11 d in milk) Holstein cows were used in a replicated 4 × 4 Latin square design with four 21-d periods. Dry matter intake was not affected by treatments. Nonetheless,

Table 0609. Effects of treatments on dry matter intake, milk, and digestibility

	Treatment[1] (CS:SBP)					*P*-value[2]		
Item	A (100:0)	B (50:50)	C (25:75)	D (0:100)	SEM	Trt	L	Q
DM intake, kg/d	22.58	22.60	23.09	22.43	0.23	0.772	0.978	0.477
Milk yield, kg/d	38.49	39.33	40.94	39.64	0.26	0.026	0.041	0.052
3.5% FCM[3]	37.71	38.45	38.88	35.86	0.46	0.142	0.232	0.058
FCM/DMI	1.67	1.71	1.69	1.61	0.02	0.468	0.349	0.209
Milk fat, %	3.46	3.47	3.27	3.00	0.05	0.021	0.004	0.204
Milk protein, %	3.03	3.10	3.11	3.12	0.02	0.203	0.062	0.392
Milk lactose, %	5.62	5.63	5.69	5.68	0.01	0.360	0.111	0.773
MUN, mg/dl	12.20	11.08	10.48	10.73	0.19	0.03	0.01	0.09
DM digestibility, %	69.25	62.93	72.59	69.23	1.29	0.100	0.418	0.574
OM digestibility, %	71.06	64.95	74.14	71.02	1.27	0.113	0.435	0.564

[1]Treatments were four different ratios of corn silage to beet pulp: 100:0 (A), 50:50 (B), 25:75 (C), or 0:100 (D).
[2]Trt: treatment effect, L: linear effect, Q: quadratic effect.
[3]3.5% fat-corrected milk.

as corn silage was replaced with dried beet pulp, milk yield increased in a curvilinear manner (Table 0609), which led to a trend ($P = 0.058$) for increasing 3.5% yield quadratically. Milk fat percentage linearly decreased ($P = 0.004$) as corn silage was replaced with dried sugar beet pulp. However, milk protein percentage tended ($P = 0.062$) to increase linearly as corn silage was replaced with dried beet pulp. As beet pulp was increasingly substituted for corn silage milk urea nitrogen (MUN) was decreased linearly ($P < 0.001$). Replacing corn silage with dried sugar beet pulp tended ($P = 0.100$) to have an effect on DM digestibility, which led to a trend ($P = 0.113$) for OM digestibility. The results of this experiment indicate that replacing of dried sugar beet pulp for 75% of corn silage can increase actual milk, 3.5% FCM and protein yields and decrease MUN.

Key Words: corn silage, dried sugar beet pulp, dairy cows

0610 Effect of feeding different types of sugars on rumen fermentation and productivity of lactating dairy cows. X. Gao* and M. Oba, *University of Alberta, Edmonton, Canada.*

The objective of this study was to investigate the effect of feeding different types of sugar (sucrose or lactose) on rumen fermentation and milk production of lactating dairy cows. Our hypothesis was that sucrose diets have lower rumen pH and milk fat yield compared with diets supplement with lactose. Twenty-eight multiparous lactating Holstein cows (141 ± 50 DIM; 614 ± 53 kg of BW) including eight ruminally cannulated cows were used in this study. Cows were assigned to four dietary treatments in a 4 × 4 Latin square design. Two high sugar diets contained 27% starch and 9% sugar with sucrose (SUC) or lactose (LAC) as a supplemental sugar. In addition, high starch diet (STA) contained 32% starch and 4% sugar, and control diet (CON) contained 27% starch and 4% sugar. All diets were formulated to contain 17% crude protein. There was no significant difference in DMI between two high sugar diets, but it was higher for SUC than CON (27.8 vs. 26.2 kg/d; $P < 0.01$). In addition, both high sugar diets had higher DMI than STA diet (27.8 and 26.9 vs. 25.5 kg/d; $P < 0.01$). There was no difference in minimum rumen pH, duration and area of rumen pH < 5.8 among treatments, though LAC diet tended to have lower mean rumen pH than STA diet (6.17 vs. 6.32; $P = 0.08$). Milk yield and milk composition were not different between two high sugar diets, but STA diet had lower fat yield compared to CON, SUC, and LAC diets (1.26 vs. 1.36, 1.32 and 1.33 kg/d; $P < 0.01$). Milk CP yield tended to be higher for SUC diet than STA diet (1.32 vs. 1.26 kg/d; $P = 0.08$), and both high sugar diets had higher CP concentration than CON (3.51 and 3.50 vs. 3.46%; $P = 0.04$). However, all STA, SUC and LAC diets had lower MUN concentration compared with CON (13.2, 12.9 and 13.3 vs. 14.5 mg/dL; $P < 0.01$), which was probably due to more carbohydrate fermentation in the rumen for high-starch or high-sugar diets compared with CON diet, providing more energy for microbes to capture NH_3–N. These results suggested that feeding different type of sugar (sucrose or lactose) to lactating cows might not affect rumen fermentation and animal performance.

Key Words: sucrose, lactose, milk fat content

0611 Effects of alfalfa and cereal straw as a forage source on nutrient digestibility, rumen microbial protein synthesis, and lactation performance in lactating dairy cows. B. Wang*[1], S. Y. Mao[2], H. J. Yang[3], Y. M. Wu[1], J. K. Wang[1], S. L. Li[4], Z. M. Shen[2], and J. X. Liu[5], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Nanjing Agricultural University, China, [3]China Agricultural University, Beijing, [4]State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, [5]Zhejiang University, Hangzhou, China.*

This study was conducted to investigate nutrient digestibility, rumen microbial protein (MCP) synthesis, and lactation performance when alfalfa was replaced with cereal straw in the diet of lactating cows. Forty-five multiparous Holstein dairy cows were individually fed, blocked based on days in milk (164 ± 24.8 d) and milk yield (29.7 ± 4.7 kg), and randomly assigned into one of three treatments. Three isonitrogenous diets with a forage-to-concentrate ratio at 45:55 contained similar concentrate composed by ground corn grain, wheat bran, soybean meal, and cottonseed meal and 15% corn silage, with three forage sources (DM basis): 23% alfalfa hay and 7% Chinese wild rye hay (AH); 30% corn stover (CS); and 30% rice straw (RS). The trial lasted for 14 wk. The rumen MCP was estimated using purine derivatives and creatinine in urine, and metabolizable protein was the sum of the intestinally absorbable MCP plus intestinally absorbable dietary protein estimated by modified three-step procedure. Apparent nutrients digestibilities were measured with acid-insoluble ash as internal marker. The data of animal performance are summarized in Table 0611. Cows fed AH had higher MCP yield ($P < 0.05$) and metabolizable protein ($P < 0.01$) than those fed RS and CS, which may be attributed to the higher content of soluble carbohydrates in AH. Total volatile fatty acids concentration in ruminal fluid collected by an oral stomach tube was higher in AH than in CS and RS. Apparent digestibilities of nutrients were higher in AH than in CS and RS ($P < 0.05$). In summary, when cereal straw was used to replace alfalfa as a main forage source for lactating cows, the shortage of easily fermented energy may reduce the rumen MCP synthesis, resulting in lower milk protein yield, and lower nutrient digestibility may restrict milk production.

Key Words: forage source, lactation performance, ruminal microbial protein

Table 0611. Dietary composition and lactation performance in dairy cows

Item	Treatment			SEM	*P*-value
	AH	CS	RS		
Composition, % of DM					
Crude protein	16.7	16.2	16.0		
Neutral detergent fiber	31.1	36.3	36.9		
Non-fibrous carbohydrate	40.6	36.0	34.6		
Dry matter intake, kg/d	18.0	18.2	18.0	0.18	0.64
Milk yield, kg/d	23.5[a]	19.4[b]	20.8[b]	0.52	< 0.01
Milk composition, %					
Protein	3.30[a]	3.20[ab]	3.10[b]	0.055	0.05
Fat	4.21	4.20	4.19	0.077	4.21
Lactose	4.89[a]	4.84[a]	4.70[b]	0.026	< 0.01
Total solid	13.7[a]	13.5[ab]	13.2[b]	0.15	0.13

[a,b]Values with different letters differ significantly ($P < 0.05$).

0612 Feeding lactating dairy cattle long hay separate from the TMR can maintain DMI during incidents of low rumen pH.

A. D. Kmicikewycz* and A. J. Heinrichs, *Penn State University, University Park.*

The objective of this study was to investigate effects of orchardgrass hay (H) quality and feeding method on rumen pH and feed preference in lactating dairy cows. Eight rumen-cannulated Holstein cows (104 ± 34 DIM, 601 ± 116 kg, and parity of 2.38 ± 1.69; mean ± SD) were used in a replicated 4 × 4 Latin Square. Each period encompassed 21 d divided into five phases: adaptation, d 1 to 14, ad libitum TMR; baseline, d 15 to 17, ad libitum TMR; restricted feeding, d 18, cows fed for 75% of baseline DMI; challenge, d 19, 4 kg (as-fed) fine ground wheat mixed into the digesta of each cow via rumen cannula before feeding; and recovery, d 20 to 21, ad libitum TMR. Cows were assigned to squares by parity and randomly assigned to treatments. Treatments were: corn silage (CS) with coarse H TMR (CC), CS and fine H TMR (CF; both hays chopped and included in TMR), CS TMR with 5.2% supplemental long coarse H (TMR+C), and CS TMR with 5.2% supplemental long fine H (TMR+F; both hays fed separate from TMR). Coarse H was 8.6% CP and 67.1% NDF, fine H was 14.4% CP and 56.2% NDF. Animals were housed individually, milked 2x/d, and fed 1x/d for 10% refusal rate. Data was analyzed using PROC MIXED of SAS. Rumen challenge decreased weighted average rumen pH from 5.72 to 5.51. Cows fed TMR+C had higher rumen pH compared to CC and TMR+F on d 19. During d 20, cows fed H had higher rumen pH than cows fed supplemental long H. Cows fed supplemental long H had greater DMI during baseline and challenge d compared to TMR H treatments. Minimal differences among diets were found for TMR particle size selection during challenge d; however, cows had a greater preference for fine long H during recovery d. Milk production averaged 38.3 kg/d and did not differ among treatments. Fat, protein, and lactose yields were also not different among treatments. Milk fatty acid profile was altered by treatment. The TMR+C and CF treatments increased production of conjugated linoleic acid (CLA) *cis*-9, *trans*-11 ($P = 0.02$). Results of this study indicate that feeding TMR plus supplemental long H can maintain DMI during incidents of and recovery from periods of low ruminal pH.

Key Words: subacute ruminal acidosis, ruminal pH, particle size

RUMINANT NUTRITION III

0613 Performance of and digestion in calves fed conventional, moderate, and aggressive milk replacer programs. T. M. Hill*, J. D. Quigley, H. G. Bateman, II, J. M. Aldrich, and R. L. Schlotterbeck, *Provimi North America, Brookville, OH.*

Calves fed large amounts of milk replacer (MR) gain more BW pre-weaning than calves fed less MR; however, post-weaning growth may be reduced. Limited research suggests that impaired nutrient digestion may depress growth post-weaning. We compared growth and post-weaning digestion in 3-d old male Holstein calves fed one of three MR programs. Programs were Conventional (C, 0.45 kg/d of powder containing 21% CP, 21% fat (DM basis), fed for 42 d), Moderate (M, 0.68 kg/d of powder containing 27% CP, 17% fat (DM basis), fed for 42 d), and Aggressive (A, up to 0.91 kg/d of powder containing 27% CP, 17% fat, fed for 49 d). All calves were fed a 20% CP (DM basis) textured starter and water ad libitum for 56 d. The trial used 96 calves (initial BW = 41.4 ± 1.86 kg) received 5 wk apart in two replicates of 48 calves. During d 51 to 55, fecal samples were collected from five calves per treatment randomly selected from calves in the first replicate. Selected nutrients and acid insoluble ash (used as an internal marker) were analyzed in starter and feces to estimate nutrient digestibility. Data were analyzed as a randomized complete block design with replicate as block. Repeated measures analysis was performed on overall (0 to 56 d) data. Means were separated with a protected LSD test. Pen was the experimental unit. Calves fed C had lower ($P < 0.05$) average daily BW gain (0.35, 0.51, and 0.55 kg/day, respectively, for C, M, and A; SEM = 0.018), gain/feed (0.35, 0.49, and 0.48; SEM = 0.016), and change in hip width (3.3, 4.1, and 4.1 cm; SEM = 0.20) compared to other calves. Calves fed A had greater ($P < 0.05$) change in body condition score and lower ($P < 0.05$) starter intake compared to other calves. Digestibility of OM was 79, 78, and 68% and NDF digestibility was 54, 51, and 26% for calves fed C, M, and A, respectively, and were lower ($P < 0.05$) in calves fed A. Results are similar to previous published results in calves and suggest that depressed post-weaning digestion may be related to reduced starter intake and impaired rumen development.

Key Words: calves, milk replacer, digestion

0614 Performance of and digestion in calves fed two levels of milk replacer and functional ingredients. T. M. Hill*, J. D. Quigley, H. G. Bateman, II, J. M. Aldrich, and R. L. Schlotterbeck, *Provimi North America, Brookville, OH.*

We compared growth and post-weaning digestion using 48 male Holstein calves (initial BW = 42.6 ± 1.50 kg; initial age = 2 to 3 d) fed to 56 d. Calves were fed diets in a 2 × 2 factorial arrangement of feeding rate (Low [L], 0.68 kg/d of milk replacer (MR) powder and High [H], up to 1.36 kg/d of MR powder) and inclusion of a functional ingredient (without [NT-] or with [NT+] NeoTec5 g, Provimi North America, Brookville, OH). The MR contained 27% CP and 17% fat (DM basis) and was fed to weaning at 49 d. The NT+ treatment was administered in MR before weaning and in calf starter (CS) from weaning to d 56. All calves were fed NT- CS before weaning. The CS were textured (pellets, oats, corn) and contained 20% CP (DM basis). Starter and water were available for ad libitum consumption throughout the study. During d 51 to 55, fecal samples were collected from five calves per treatment selected at random. Selected nutrients and acid insoluble ash (as an internal marker) were analyzed in CS and feces to estimate digestibility. Data were analyzed as a completely randomized design with a factorial arrangement of MR rate (L/H) and NeoTec5 g (NT+/NT-) using a repeated measures ANOVA. Pen was the experimental unit. There were no interactions of main effects. Average daily BW gain (ADG), change in body condition score (BCS), and average fecal score from d 0 to 56 were greater ($P < 0.05$) in calves fed H vs. L. Calf ADG, hip height change, and BCS change were greater ($P < 0.05$) in calves fed NT+ vs. NT-. Intake of CS during the digestion period tended ($P < 0.10$) to be lower in calves fed H vs. L. Digestibility of DM, OM, NDF, and ADF was reduced by 7, 7, 65, and 58%, respectively, in calves fed H compared to L ($P < 0.05$). Feeding NT+ increased digestibility of DM, OM, NDF, and ADF by 4, 4, 65, and 74%, respectively ($P < 0.05$) compared to NT-. Feeding high rates of MR reduced ADG by 12% during the last 2 wk of the trial (0.58 vs. 0.65 kg/d for H and L, respectively), which was likely due to reduced intake and digestion of CS as calves transitioned from MR to CS. Feeding NeoTec5 g improved ADG, hip width change, and digestion of nutrients.

Key Words: calves, milk replacer, digestion

0615 The effect of solid feed diet on the oral and cross-sucking behavior of pre-weaned dairy calves. J. K. Margerison* and C. Hansen, *Massey University, Palmerston North, New Zealand.*

In the dairy industry calves are most frequently artificially reared in groups, which create a greater opportunity for solid feed consumption and cross-sucking behavior. This study aimed to compare the effect of differing solid feed diets on the pre- and post- weaning feed intake, growth rate and oral behav-

ior of calves reared artificially in groups. This experiment was a randomized block design with the treatments diets allocated at random, in blocks. The research was completed at Massey University's dairy calf unit No. 4 and involved 108 Friesian and Jersey x Friesian dairy calves that were allocated to one of three treatment diets: lower forage (LF) alfalfa total mixed ration (TMR); a higher forage alfalfa (HF) TMR; and perennial ryegrass hay along with a pelleted starter (HPS). Calves were reared in 36 groups of three calves per group and monitored until 12 wk of age. The data was transformed and analyzed using PROC MIXED GLM in SAS using diet as a fixed effect and calf as a random effect in the model. Data was presented as means with standard errors for each observation according to diet treatment. Calves fed HPS had the greatest dry matter intake [LF: 0.80 (0.012), HF: 0.95 (0.012), HPS: 1.70 (0.011) kg/DM/d], live weight at 40 d of age [LF: 60.3 (1.41), HF: 63.8 (1.41), HPS: 67.1 (1.38) kg] compared with TMRs. These calves also spent the most time eating [LF: 129.1 (0.14), HF: 163.7 (0.14), HPS: 154.1 (0.14) mins/d], and spent the least amount of time engaged in non-nutritive pen sucking [LF: 13.4 (0.16), HF: 11.2 (0.17), HPS: 10.3 (0.16) mins/d]. It was concluded that, while cross-sucking was not entirely eliminated, providing perennial ryegrass hay along with a pelleted starter resulted in the least non-nutritive sucking behavior, along with the greatest feed intake and growth rates compared with low and high forage alfalfa based total mixed rations.

Key Words: calves, growth, feed intake, behaviour, sucking

0616 Development of a modified accelerated milk replacer feeding program through 8 wk of age.

B. M. Strayer*[1], D. Ziegler[2], D. Schimek[3], B. Ziegler[3], H. Chester-Jones[2], J. L. Anderson[1], K. F. Kalscheur[1], and D. Casper[1], *[1]South Dakota State University, Brookings, [2]University of Minnesota Southern Research and Outreach Center, Waseca, [3]Hubbard Feeds Inc., Mankato, MN.*

Our previous studies have demonstrated that a modified accelerated milk replacer (MR) having a 24:20 crude protein (CP):fat concentration fed at higher feeding rates (FR) resulted in improved growth performance and gain/feed, but not linearly. The current study was to evaluate pre- (d 1 to 42) and post-weaning (d 43 to 56) calf performance when modified accelerated MR was fed at higher FR compared to a MR having similar or higher CP and lower fat concentrations. One-hundred thirty (1 to 6 d old) fed Holstein heifer calves (40.1 ± 0.76 kg) were blocked by birth date and randomly assigned to one of five treatments. Treatments of MR fed at 14.7% solids were: 1) Control (C): all milk 24:20 MR fed at 0.26 kg at 2x/d from d 1 to 35; 2) C+: C MR fed at 0.32 kg 2x/d from d 1 to 35; 3) LF: CP and low fat (24:16) MR fed at 0.32 kg 2x/d from d 1 to 35; 4) LF+: LF MR fed at 0.32 kg 2x/d from d 1 to 7 and at 0.39 kg from d 8 to 35; and 5) HP+: High CP:LF MR (26:16) fed at the rates of LF+. All MR were fed 1x/d from d 36 to weaning at d 42 with water and 18% CP texturized calf starter (CS) offered free choice from d 1 through 56. Calves fed C+ had greater ($P < 0.05$) ADG (0.71, 0.75, 0.70, 0.72, and 0.72 kg/d for C, C+, LF, LF+, and HP+, respectively) from d 1 to 56 compared to calves fed LF, with other treatments being intermediate. Calves fed C+, LF, and HP+ were similar, but taller at the hips ($P < 0.05$) than calves fed C and LF+ (98.1, 99.6, 99.8, 98.5, and 99.8 cm). However, calves fed C+ had greater hip widths on d 56 (22.3, 22.6, 21.7, 21.8, and 22.3 cm) and on d 84 (26.2, 26.5, 26.0, 26.2, 26.4 cm) than calves fed LF with other treatments similar. This study demonstrates that feeding a modified accelerated MR (24:20) at a moderate FR improves ADG and frame measurements compared to calves fed MR having similar or different CP and fat concentrations. The development of a modified accelerated feeding program optimized the protein energy ratio for the potential of producing a dairy heifer with a frame that is taller and wider without having a weaning slump.

Key Words: milk replacer, protein concentration, fat concentration.

0617 Amino acid supplementation of calf milk replacers containing bovine plasma protein.

S. Y. Morrison*[1], K. A. Myers[1], A. E. Volland[1], P. Cardoso[1], J. M. Campbell[2], and J. K. Drackley[1], *[1]University of Illinois, Urbana, [2]APC, Inc., Ankeny, IA.*

Plasma protein (PP) is an effective alternative protein source for young calves, but utilization at higher amounts may be limited by Ile and Thr content. We determined the effects of PP and supplemental AA in milk replacers (MR) on calf growth and health. Male Holstein calves (n = 104) were blocked by BW and randomly assigned to 1 of 5 MR formulated to contain 22% CP, 20% fat, and 2.0% Lys. Treatments (trt) were: all milk protein (A); 5% PP plus Met to equal trt A (B); 5% PP plus Met, Ile, and Thr to equal A (C); 10% PP plus Met to equal A (D); or 10% PP plus Met, Ile, and Thr to equal A (E). Treatments (12.5% solids) were fed twice daily at 10% of BW for d 1 to 2, 12% of BW for d 3 to 7, and 14% of BW for d 8 to 35, adjusted weekly. No starter was fed. Calves were housed in individual hutches bedded with straw and offered water ad libitum. Health data were recorded daily and growth measured weekly. Serum obtained on d 28 before and 4 h after feeding was analyzed for total protein (TP), urea nitrogen, albumin, and globulin. Data were analyzed using the MIXED and GLIMMIX procedures of SAS. Initial BW (41.9 ± 4.38 kg) and serum TP (5.7 ± 0.09 g/dL) were similar among groups. Intakes of DM, CP, ME, and Lys did not differ ($P > 0.35$) among trts. Average daily gain tended ($P = 0.08$) to be decreased by 10% PP (D), but not when AA were supplemented (E). Gain:DMI ($P = 0.10$) and gain:Lys intake ($P = 0.08$) tended to be lower for trt D. The Logistic model revealed that during the first 21 d, scours occurrence

was higher in trt A than trt D and E (odds ratio [OR] = 1.35, P = 0.07 and 1.61, P = 0.01, respectively), and trt C tended to be higher than trt E (OR = 1.41, P = 0.08). The chance of antibiotic treatment was greater in trt A than trt B, C, and E (OR = 3.55, P < 0.0001; 3.39, P = 0.0002; 2.48, P = 0.001) and lower in trt B and C than trt D (OR = 0.31, P = 0.0003; 0.32, P = 0.0006). Serum albumin was highest (P = 0.02) for trt B, and urea nitrogen tended (P = 0.10) to be higher for trt A; TP and globulin did not differ (P > 0.11). Inclusion of PP in MR improved health of young calves; when AA were balanced, growth and efficiency were similar to all milk protein.

Key Words: amino acid, plasma protein, milk replacer

0618 The use of highly digestible corn grain in calf starters when calves are fed an accelerated milk replacer.

D. Casper[*1], S. Srivastava[2], M.Kkirk[3], S. Harris[4], K. Koone[4] and B. M. Strayer[1], *[1]South Dakota State University, Brookings, [2]South Dakota University, Hyderabad, India, [3]Masters Choice, Anna, IL, [4]Masters Choice, Anna, IL.*

New corn hybrids have been developed by Masters Choice (MC) seeds that vary in energy density and starch digestibility. These MC hybrids have lower starch densities due to an altered starch structure, which allows for greater ruminal and intestinal starch digestion. Altered starch structure of these new hybrids results in reduced feed manufacturing (i.e., grinding). Thirty (1- to 3-d old) Holstein heifer calves (40.6 ± 1.72 kg) were randomly assigned to one of two calf starters to evaluate growth performance of Holstein heifer calves through 8 wk of age. Treatments were: 1) Control (C) starter: containing 40% (DM basis) conventional ground shelled corn and 2) MC starter: containing (40% DM basis) MC corn. Experimental calf starters were formulated to contain 24% CP (DM basis) and were fed for ad libitum consumption as a pellet starting on d 1. The study was conducted from April 25 through August 1, 2013. Body weights and body measurements were collected weekly. All calves were fed a 28% (CP):18% fat accelerated milk replacer 2x/d at the rate of 0.68 kg/d up to 10 d, 1.02 kg/d from 11 to 35 d, and fed 1x/d at 0.51 kg/d from 35 to 42 d. Data were analyzed as a completely random design using the PROC MIXED of SAS Version 9.3. Initial body weights (40.6 and 40.7 kg for C and MC, respectively) were similar (P > 0.10), while final body weights (64.5 and 66.7 kg) were numerically greater for calves fed the MC starter. Body weight gains (23.9 and 26.0 kg) and average daily gains (0.68 and 0.74 kg/d) were similar but numerically greater for calves fed MC starter. No significant differences were detected (P > 0.10) in frame parameters as measured by change in body length (12.3 and 11.4 cm), heart girth (8.7 and 9.3 cm), hip height (6.8 and 6.6 cm), and wither height (13.1 and 12.3 cm). While no significance improvements in growth rates were detected in this study, which was conducted during the early summer, but the MC starter resulted in a numerical increase in body weight gains and average daily gains.

Key Words: corn hybrids, calf starter, starch

0619 Intensive milk feeding in calves affects growth performance, metabolic and endocrine traits, but not rumen development.

H. M. Hammon[*1], J. Maciej[1], J. Gruse[1], E. Wirthgen[2], R. Zitnan[3], M. Piechotta[4], and A. Hoeflich[1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]Ligandis GbR, Gülzow, Germany, [3]National Centre of Agriculture and Food Nitra, Kosice, Slovakia, [4]University of Veterinary Medicine, Hannover, Germany.*

Restricted milk feeding during the pre-weaning period is supposed to stimulate solid feed intake, but growth performance is insufficient in calves. The objective of the present study was to compare feed intake, growth performance, metabolic traits, and rumen development during the pre-weaning period in calves with different milk feeding levels. The hypothesis was tested that intensive milk feeding supports metabolic changes related to enhanced growth but does not impair solid feed intake and rumen development. Four d after birth, 28 Holstein × Charolais calves (male and female) were fed either 6 L milk replacer (MR; 125 g powder/L)/d for 8 wk (RES) or unlimited amounts of MR up to d 35 of life (AL) that was stepped down to 6 L/d afterward. Concentrates and hay were available ad libitum for both groups. Blood samples were taken weekly for determination of plasma concentrations of glucose, triglycerides, NEFA, BHBA, urea, insulin, IGF-I, and IGF binding proteins (IGFBP). Calves were slaughtered at d 60 ± 2 and rumen tissue samples were taken for measurements of papilla size. Data were analyzed by the MIXED Model of SAS with feeding, sex, time, and feeding × time interaction as fixed effects. MR intake increased (P < 0.001) in AL to 14.5 ± 0.4 L/d in wk 5 of life, but did not change in RES calves. Concentrate intake increased (P < 0.001) in both groups from wk 4 on, but did not differ between groups. Body weight and ADG were greater (P < 0.001) in AL than in RES calves. Plasma concentrations of triglycerides, glucose, insulin, and IGF-I were higher (P < 0.05) and concentrations of NEFA, urea, and IGFBP-2 and −4 were lower (P < 0.05) up to d 35 of life in AL than in RES calves. Plasma concentrations of BHBA tended to be higher (P < 0.1; mainly from d 21 to d 35 of life). Rumen empty weight and papillae length were not different, but papillae densities in atrium and ventral sac were greater (P < 0.05) in RES than in AL. Intensive milk feeding resulted in enhanced body growth and changes in metabolic and endocrine traits supporting anabolic metabolism in AL calves. Intensive milk feeding did not impair concentrate intake and slightly affected rumen papillae growth.

Key Words: calf, milk feeding, rumen development

0620 Fish oil supplementation on growth and health of pre-weaning dairy calves. R. Panivivat*[1], P. Sopannarat[1], and S. Sriwichai[2], [1]*Kasetsart University, Bangkok, Thailand,* [2]*Dairy Promotion and Organization of Thailand, Saraburi.*

The objective of this study was to study the effect of fish oil (energy source) for preweaning calves. Preweaning calves were more sensitive to environment and stress to sickness. Thirty-six male dairy calves fed with 0% (group 1), 2.5% (group 2), and 5% (group 3) of fish oil in milk replacer. All calves were assigned with randomized complete block design. The calves were placed into individual pen after birth randomly. Calves were fed with colostrum after birth until 3 d of age. Calves were fed calf starter and milk replacer from d 4 to d 42 of age. All calves fed with calf starter and water in different bucket set in the front of pen. Calves were fed 5 kg/h/d milk replacer 2x/day. All calves were weaned on d 42. Body weights were measured after birth and d 1, d 21, and d 42. Feed and milk replacer intake and fecal scores were measured daily after feeding in the morning. Blood samples were collected on d 1, d 21, and d 42 after morning feeding for 2 h for chemical analysis. Growth, health and neutrophils and lymphocytes (stress indices) were evaluated for 42 d. Average daily gain (131.6, 141.5, and 118.4 g/d for group 1, 2, and 3, respectively), feed intake, fecal score, and body cleanliness score of calves did not differ ($P > 0.05$) among treatments but feed intake was affected by week ($P < 0.0001$). Calf health was also affected by week ($P < 0.001$). Immunoglobulin G was higher on d 1 (40.1 mg/ml, $P < 0.05$). The ratio of neutrophils and lymphocytes (1.13, 0.46, and 0.26 for d 1, d 21, and d 42, respectively), glucose concentration (163.7, 115.1, and 104.1 mg/dl for d 1, d 21, and d 42, respectively) decreased when calf was older ($P < 0.001$). Growth and health performance of calves fed with three levels of fish oil did not differ ($P > 0.05$). At 3 wk of age, immunoglobulin G of calves was increased as calf fed 2.5% fish oil supplemented in milk replacer.

Key Words: fish oil, dairy calf, health

0621 The effects of corn silage inclusion in pre-weaned calf diets. S. I. Kehoe*[1], S. L. Retz[1], T. J. Pogreba[1], K. Dill-McFarland[2], and G. Suen[2], [1]*University of Wisconsin–River Falls, River Falls,* [2]*University of Wisconsin–Madison, Madison.*

The objective was to evaluate the effects of corn silage inclusion in starter feed provided to calves after birth through weaning. Thirty-six heifer calves and nine bull calves were reared at the U.S. Dairy Forage Research farm, where they were individually housed in hutches. All treatments were fed pasteurized milk with either all calf starter (C), 60% calf starter and 40% corn silage (CC), or all corn silage (CS). Feed intake and health scores were recorded daily. Every other week, calves were sampled for weight, withers and hip height, heart girth, serum protein, hematocrit, blood urea nitrogen, glucose, and β-hydroxybutyrate. Nine bull calves were sacrificed 1 wk post-weaning at 8 wk of age. Rumen and intestinal tissue were collected and preserved with formalin for later analysis. One intestinal tissue sample was taken at consistent lengths from the duodenum, jejunum, ileum, and colon; from each tissue sample, three blocks were cut and 24 tissue slides were stained from each block for measurement. Three rumen samples were taken from four areas within the rumen and 12 random papillae per sample were measured for length and width. Daily and biweekly measurements were analyzed using a repeated measures analysis of the PROC MIXED and intestinal and ruminal measurements were analyzed using the General Linear Model procedure of SAS 8.3 (2010). Initial growth measurements were used as covariates for growth analysis and significance was found at $P < 0.05$. Feed intake was not different between treatments; however, there was a treatment by week interaction ($P < 0.0001$). Least squares means of rumen papillae lengths were different (9.3, 7.5, and 3.9 ± 0.3 mm for treatments C, CC, and CS, respectively; $P < 0.05$). Jejunal villi lengths tended to be different (97.65, 105.61, and 89.57 ± 5.8 μm for treatments C, CC, and CS, respectively; $P = 0.12$), and crypt depths were different (46.10, 48.58, and 38.69 ± 2.8 μm for treatments C, CC, and CS, respectively; $P = 0.03$). Treatments did not differ for weight ($P < 0.15$), heart girth ($P < 0.4$), hip height ($P < 0.7$), withers height ($P < 0.15$), serum protein ($P < 0.8$), and hematocrit values ($P < 0.6$). This data indicates the inclusion of corn silage to starter feed does not affect growth and overall feed intake but may affect weekly feed consumption. Solely feeding corn silage as starter feed stunted the growth of the rumen papillae and reduced crypt depths indicating reduced absorption and efficiency. Future milk production will be monitored.

Key Words: calves, corn silage, calf starter feed

0622 Growth performance and health of dairy calves fed with *Schizochytrium* sp. R. Panivivat* and K. Taboonpong, *Kasetsart University, Bangkok, Thailand.*

Thirty-six dairy calves were studied on *Schizochytrium* sp. supplementation affecting on growth performance and health. Repeated measurement in completely randomized design was assigned. Treatment had three groups (12 calves per group). Group 1 was control (fresh milk added with lactobacillus). Group 2 was control plus 3 g/h/d of *Schizochytrium* sp. supplementation. Group 3 was control plus 6 g/h/d of *Schizochytrium* sp. supplementation. After birth, calf was placed in individual pen. Each calf fed colostrum immediately until 3 d of age. On d 4, all calves were fed ad libitum of calf starter and water separated bucket in the front of individual pen. Calves were also fed fresh milk 5 kg/h/d, 2 times a day from d 4 to 42 of age. Feed intake, fecal fluidity score and calves cleanliness score were recorded daily. Initial body weight, d 7, d 21, and final body weight were measured. On d 1, d 21, and d 42 fresh

blood analyzed for neutrophil:lymphocyte ratio (N:L ratio; stress indicator), serum immunoglobulin G (IgG), serum glucose, serum urea-nitrogen (SUN) were collected. Feed intake (778.8, 763.3, and 758.3 g for group 1, 2, and 3, respectively) and average daily gain (ADG 552.5, 552.1, and 557.1 g/d for group 1, 2, and 3, respectively) did not differ ($P > 0.05$). However, feed conversion ratio (FCR; 1.40 for group 3) had lower than others (1.49 and 1.83 for group 1and 2; $P = 0.060$). Serum IgG (37.7, 38.6, and 37.6 mg/ml for group 1, 2, and 3, respectively), serum glucose (159.1, 171.9, and 179.4 mg/dl for group 1, 2, and 3, respectively) and SUN (9.6, 10.17, and 9.6 mg/dl for group 1, 2, and 3, respectively) did not differ ($P > 0.05$). The percentage of white blood cells count and N:L ratio (0.2, 0.17, and 0.16 for group 1, 2, and 3, respectively) also did not differ ($P > 0.05$). However, on d 1, serum IgG and serum glucose were the highest in three groups. Overall blood N:L ratio decreased when calf was older ($P < 0.05$).

Key Words: *Schizochytrium* sp., dairy calf, health

0623 Growth performance, health, and immunocompetence of preweaning dairy calves fed with stevioside.

R. Panivivat[*1], C. Boonkaewwan[1], and S. Sriwichai[2], [1]*Kasetsart University, Bangkok, Thailand,* [2]*Dairy Promotion and Organization of Thailand, Saraburi.*

The objective of this study was to study the effect of stevioside (medical herbs) supplementation on growth and health of preweaning calves. The preweaning calves were more sensitive to sickness because of lower immunoglobulin and more stress after birth. Thirty-six dairy calves fed with 0, 150, and 300 mg/kg of stevioside supplemented in calf starter. All calves were assigned with randomized complete block design. The calves were placed into individual pen after birth randomly. Calves were fed colostrum after birth until 3 d of age. Calves were fed calf starter and milk from d 4 to d 42 of age. Calves were fed 5 kg/h/d milk, 2x/d. All calves were fed with calf starter and water in different bucket set in the front of pen. Growth, health, and stress indices were evaluated for 42 d. Average daily gain (367.8, 348.5, and 315.5 g/d for group 1, 2, and 3, respectively), feed intake, fecal score, and body cleanliness score of calves did not differ ($P > 0.05$) among treatments, but feed intake was affected by week ($P < 0.05$). Calf health was also affected by week ($P < 0.05$). Immunoglobulin G was greater ($P < 0.05$) when calf was older. The ratio of neutrophils and lymphocytes (stress indices), serum glucose, and butyrate concentration decreased ($P < 0.05$), while immunoglobulin G increased ($P < 0.05$) when calf was older. The concentration of α-1 acid glycoprotein (AGP) and TNF-α did not differ ($P > 0.05$) among treatments. Growth and health performance of calves fed with three levels of stevioside did not differ ($P > 0.05$). At 3 wk of age, immunoglobulin G of calves increased ($P < 0.05$) as 150 mg/kg stevioside was supplemented in calf starter.

Key Words: stevioside, dairy calf, health

0624 An evaluation of a calf-side betahydroxybutyrate test in dairy calves fed a high plane of nutrition and weaned at six versus 8 wk of age.

H. E. Brown[*1], E. C. Eckert[1], M. A. Steele[2], T. J. DeVries[1], and K. E. Leslie[1], [1]*University of Guelph, Guelph, ON, Canada,* [2]*Nutreco Canada Agresearch, Guelph, ON.*

Recent research suggests that circulating betahydroxybutyrate (BHBA) levels may be a meaningful indicator of grain intake and rumen development in pre-ruminant calves. As such, BHBA levels may be a surrogate measure of rumen function to assure minimal weaning stress during the transition from liquid to solid feed. The Precision Xtra test for BHBA in whole blood has been validated in lactating dairy cows. The objective of this study was to validate the Precision Xtra test against a gold standard laboratory method in calves at weaning, and to determine preliminary associations between circulating BHBA levels and amount of solid feed intake in dairy calves fed higher planes of nutrition and weaned at 6 vs. 8 wk of age. A total of 20 Holstein female calves were randomly assigned at birth to be weaned at 6 wk ($n = 10$) or 8 wk ($n = 10$). Milk replacer (mixed at 150 g/L) was offered at 1.2 kg/calf/d in two meals until a 1-wk step down, where meals were reduced by 50% 1 wk before weaning. Measurements included daily starter, chopped straw, and water intake, as well as weekly blood BHBA, until 70 d of life. Whole blood BHBA was determined by the Precision Xtra test at calf-side. In addition, serum was separated from a clotted sample, frozen, and stored until laboratory analysis was performed. Data were plotted, and Spearman correlation coefficients between the Precision Xtra and laboratory BHBA levels were determined. Using an arbitrary level of BHBA to indicate meaningful rumen function, the sensitivity and specificity of the Precision Xtra test were calculated. Finally, the correlation between BHBA levels and solid feed intake was determined. The correlation coefficient between Precision Xtra and laboratory BHBA was high ($r = 0.95$; $P < 0.05$). Using a cut-off level of ≥ 250 μmol/L BHBA on the laboratory test, the sensitivity and specificity of the Precision Xtra test were 91% and 93%, respectively. These test characteristics were even higher, when the assessment was restricted to calves weaned at 8 wk (100% and 94%, respectively). The correlation between BHBA results and solid feed intake was also high ($r = 0.90$; $P < 0.05$). These results indicate that the Precision Xtra whole blood BHBA test conducted at calf-side is a highly accurate test and shows some promise for use in the decision-making process of determining appropriate weaning age.

Key Words: calves, weaning, betahydroxybutyrate

RUMINANT NUTRITION: SYMPOSIUM: THE RUMEN MICROBIOME AND NUTRITIONAL HEALTH AND PRODUCTION

0625 [Withdrawn]

0626 The microbiome and health. *G. B. Penner*[*1], *E. Khafipour*[2], *J. C. Plaizier*[2], *and L. L. Guan*[3], *[1]University of Saskatchewan, Saskatoon, Canada, [2]Dep. of Animal Science, University of Manitoba, Winnipeg, Canada, [3]Dep. of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

The linkage among the microbial community and health outcomes in monogastric species has been well documented along with demonstrated evidence for species-dependent health consequences. While a symbiotic relationship between the microbial inhabitants and the ruminant host has been accepted from the perspective of feed digestion, the mechanisms for host-regulation of the microbial community is not well understood and the influence of individual microbial species on health outcomes has been poorly defined. Major challenges include understanding the structure of the digesta associated and epimural populations and how these populations change across the gastrointestinal tract. Current research efforts are examining the establishment of the microbiome in newborn calves to gain an improved understanding of the colonization process. It is currently accepted that the dominant phyla within the microbiome consist of firmicutes, bacteroidetes, and proteobacteria and that these remain relatively stable for most of a healthy cow's life. However, variations in the composition, proportion, and functional properties of the rumen and intestinal microbiomes exist among individuals. To help understand the relationship between the microbiome and animal health, ruminal acidosis induction protocols have developed and proven to be an excellent model. In fact, it has been demonstrated that changes in the microbial community structure, specifically and increase in *Escherichia coli*, can be related to the systemic immune response induced by ruminal acidosis. However, it is still not clear whether the translocation of antigens induced by ruminal acidosis occurs in the reticulo-rumen or more distally in the gastrointestinal tract. The latter is especially important given the large changes in epithelial barrier function and marked changes in the concentration of lipopolysaccharide across the gastrointestinal tract. An in depth understanding of both the microbiome and host gastrointestinal physiology is key to addressing this challenging area.

Key Words: gastrointestinal tract, health, microbiome

0627 Use of genomics and transcriptomics to identify strategies to lower ruminal methanogenesis. T. A. McAllister[*1], L. L. Guan[2], G. Henderson[3], G. Attwood[3], and P. H. Janssen[3], *[1]Agriculture and Agri-Food Canada, Lethbridge, AB, [2]University of Alberta, Edmonton, Canada, [3]AgResearch Limited, Grasslands Research Centre, Palmerston North, New Zealand.*

Globally, methane emissions account for 40 to 45% of greenhouse gas emissions (GHG) from ruminant livestock, with more than 90% of these emissions arising from enteric fermentation. Reduction of carbon dioxide to methane is critical for efficient ruminal fermentation, as it prevents the accumulation of reducing equivalents in the rumen. Methanogens exist in a symbiotic relationship with rumen protozoa, fungi and within biofilms associated with feed and the rumen wall. Genomics and transcriptomics are playing an increasingly important role in defining the ecology of ruminal methanogenesis and identifying avenues for its mitigation. Genomic approaches have provided information on changes in abundances as well as the species composition of the methanogen community among ruminants that vary naturally in their methane emissions, their feed efficiency and response to methane mitigators. Sequencing the genomes of rumen methanogens has provided insight into surface proteins that may prove useful in the development of vaccines and allowed assembly of biochemical pathways for use in chemogenomic approaches to lowering ruminal methane emissions. Metagenomics and metatranscriptomic analysis of entire rumen microbial communities are providing new perspectives on how methanogens interact with other members of this ecosystem and how these relationships may be altered to reduce methanogenesis. Identification of community members that produce anti-methanogen agents that either inhibit or kill methanogens could lead to the identification of new mitigation approaches. Discovery of lytic archaeophage that specifically lyse methanogens is one such example. Efforts in using genomic data to alter methanogenesis have been hampered by a lack of sequence information that is specific to the microbial community of the rumen. Programs such as the Hungate 1000 and the Global Rumen Census are increasing the breadth and depth of our understanding of global ruminal microbial communities, steps that are key to using these tools to further define the science of ruminal methanogenesis.

Key Words: ruminal methanogenesis, genomics, transcriptomics

0628 Increasing condensed corn distillers solubles alters the rumen microbiome of beef cattle.

J. C. McCann*[1], S. A. Alqarni[1], J. R. Segers[2], D. W. Shike[1], and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]University of Georgia, Tifton.*

Five ruminally fistulated steers were used in a 5 × 5 Latin square design to determine the effects of increasing dietary fat from corn distillers solubles (CDS) on the rumen microbiome. Treatments included a corn-based control (CON), and four levels of CDS (0, 10, 19, and 27%) in a coproduct-based (corn gluten feed and soybean hulls) diet. Fat concentrations were formulated to 3, 5, 7, and 9%, respectively, for diets containing CDS, and all steers were fed to ad libitum intake once daily. After 18 d of adaptation to the diet, ruminal samples were collected 3 h post-feeding and separated into solid and liquid fractions. Bacterial DNA was extracted from the solid fraction after physical homogenization. Real-time quantitative PCR was used to determine dietary effects on the relative abundance of culturable bacterial species. Orthogonal contrasts were used to compare diets formulated to similar fat concentrations (CON and 10% CDS), determine linear, quadratic, and cubic effects of CDS inclusion, and compare CON with all CDS treatments. Of the evaluated species, *Selenomonas ruminantium* was the most prevalent at 0.5 to 1.9% relative abundance. Moreover, *Selenomonas ruminantium* increased with greater CDS inclusion ($P < 0.001$). *Anaerovibrio lipolytica* was affected by treatment ($P < 0.001$); steers fed 0% CDS had eight-fold greater relative abundance than any other treatment. A quadratic effect was observed for *Butyrivibrio proteoclasticus,* with the greatest relative abundance at 0 and 27% CDS and the lowest at 19% CDS. *Butyrivibrio proteoclasticus* was also greater in steers fed 10% CDS compared with CON. *Eubacterium ruminantium* was not affected by treatment but was the second most abundant species evaluated (0.03 to 0.1%). *Fibrobacter succinogenes* was affected by treatment ($P = 0.005$) with a marked decrease for steers fed 19 and 27% CDS, yet relative abundance remained similar for steers fed CON and 10% CDS. *Prevotella bryantii* had a cubic response ($P = 0.005$) to CDS inclusion with the greatest relative abundance for steers fed 10% CDS, followed by the lowest abundance for steers fed 19% CDS. *Megasphaera elsdenii* was affected by treatment ($P < 0.001$); the lowest relative abundance was observed for steers fed CON compared with CDS diets ($P < 0.001$), and the greatest relative abundance was observed for steers fed 19% CDS. Results suggest the rumen microbiome is impacted by substantial changes in dietary CDS.

Key Words: microbiome, distillers solubles, dietary fat

0629 The microbiome composition of the hindgut is altered following weaning in dairy calves: impact of different weaning strategies.

S. C. Li*[1], M. A. Steele[2], P. Azevedo[1], M. Carson[2], J. C. Plaizier[1], H. Derakhshani[1], and E. Khafipour[1,3], *[1]Dep. of Animal Science, University of Manitoba, Winnipeg, Canada, [2]Nutreco Canada Agresearch, Guelph, ON, [3]Dep. of Medical Microbiology and Infectious Diseases, Winnipeg, MB, Canada.*

Composition of calf intestinal microbiota has immediate and long-term effects on health and productivity of the animal. Weaning stress may alter the colonization process due to dietary shifts and environmental factors. The objective of this study was to examine the effects of different weaning strategies on fecal microbiota of dairy calves. Twenty-four male and 20 female Holstein dairy calves were blocked according to gender and birth weight and randomly assigned into a step-down weaning (SW) or an abrupt weaning (AW) treatment at birth. Calves had free access to water and starter intake throughout the experiment and 9 L/d of milk until d 36 of life and weaned on d 49 of life. Calves in SW group were weaned gradually by reducing milk intake from 9 to 4.5 L/d from d 37 to d 48 while the AW calves were abruptly weaned on d 49 by reducing milk intake from 9 to 0 L/d. Fecal samples were collected on d 36 (pre-weaning) and on d 54 (post-weaning) of life. DNA was extracted and V4 region of 16S rRNA gene was amplified and subjected to paired-end Illumina sequencing. The output paired-end reads were merged using PANDASeq assembler and analyzed using QIIME. The resulted operational taxonomic units (OTUs) were aligned to Greengenes database. Alpha-diversity of bacterial community was calculated using different richness estimators. Differences in β-diversity of microbiota across treatments and time points were tested using PERMANOVA. Diversity of fecal microbiota was low before weaning but increased significantly post-wean indicating new species benefited from dietary change. However, different weaning strategies did not affect α and β-diversity measures. Before weaning, firmicutes (49.2%) and bacteroidetes (42.2%), proteobacteria (3.8%), tenericutes (1.7%), and actinobacteria (1.5%) were predominant phyla. Another 16 phyla were present at low abundance, each less than 1% of population. After weaning, the percentage of firmucutes and actinobacteria decreased to 42% and 0.4%, while proteobacteria, and tenericutes increased to 5.6% and 3.9%, respectively. Different weaning strategies did not affect fecal bacterial population at the phylum level. In total, 415 core OTUs, defined as OTUs shared amongst 50% or more of the calves, were different between pre- and post-wean. However, none of the core OTUs was affected by weaning strategies. Data showed fecal microbiota of dairy calves was undergoing a drastic change and became more diversified during the weaning process. However, weaning strategies had no substantial effect.

Key Words: calves, fecal microbiota, weaning

0630 Effects of different dry period managements on rumen microbiome composition. H. Khazanehei*[1], S. Li[1], J. C. Plaizier[1], and E. Khafipour[2], [1]*Dep. of Animal Science, University of Manitoba, Winnipeg, Canada,* [2]*Dep. of Medical Microbiology and Infectious Diseases, Winnipeg, MB, Canada.*

The effects of two different dry period managements on rumen bacterial population were examined during pre- and postpartum periods. Twenty-four Holstein dairy cows were paired according to their expected calving date and randomly assigned to one of the two treatments. Treatments included a 60-d dry period (60-d trt) with separate far-off and close-up diets and a 40-d dry period (40-d trt) during which only the close-up diet was fed. The far-off diet contained 1.28 Mcal/kg NE_l, 14.7% CP, and 50% NDF on a DM basis. The close-up diet contained 1.43 Mcal/kg NE_l, 14.6% CP, and 38% NDF. A common lactation diet was fed to all cows after calving, which contained 1.69 Mcal/kg, 17.6% CP, and 31% NDF. The forage portion of ration consisted of timothy hay, barley, and corn silage, and the concentration portion consisted of soybean, canola, barle, and wheat. Rumen fluid was sampled using stomach tube at wk -2, -1, +1, +2 and +7, relative to calving. DNA was extracted, normalized and used for amplification of the V4 region of bacterial 16S rRNA and subjected to Illumina sequencing. The QIIME pipeline was used for downstream data analyzing. After removing all chimeric reads, sequences were assigned to operational taxonomic units and aligned to Greengenes database. The α- and β-diversity of rumen microbiota were calculated using Chao1 and Unifrac distance matrices, respectively. PERMANOVA procedure was used to compare differences in bacterial communities between treatments and sampling time points. Partial least square discriminant analysis (PLS-DA) of SIMCA was performed to identify taxa associated with each treatment and time point. PERMANOVA analysis revealed significant differences in rumen bacterial composition between pre- and postpartum in the 60-d trt ($P < 0.01$); however, no difference was observed between pre- and postpartum in the 40-d trt ($P < 0.2$). At the genus level, *Bulleidia*, *Coprococcus* and *Ruminococcus* increased in 40-d trt compared with 60-d trt prepartum ($P < 0.05$). After calving, *Olsenella* increased and *Coprococcus*, *Bifidobacterium* and *Treponema* decreased ($P < 0.05$) in the 40-d trt compared with the 60-d trt. At the phylum level, no significant difference was observed between treatments prepartum ($P < 0.9$). However, after calving, spirochaetes and chloroflexi populations decreased ($P < 0.05$) while proteobacteria and firmicutes increased ($P < 0.05$) in 40-d trt compared with 60-d trt. Differences between treatments, at the phylum and genus levels during pre- and postpartum were likely due to longer consumption of close-up diet in the 40-d trt compared to the 60-trt.

Key Words: dairy cow, dry period management, rumen microbiome, illumina sequencing

RUMINANT NUTRITION IV

0631 Effect of sunflower seed or sunflower oil as diet supplement on milk production, milk composition, and milk fatty acid profile in lactating goats.
T. A. Morsy*[1], S. Kholif[1], O. Matloup[1], and A. Abu Elella[2], [1]*National Research Center, Cairo, Egypt,* [2]*Animal Production Research Institute, Agriculture Research Center, Cairo, Egypt.*

Seeds are natural source of fats and proteins in dairy animal feed, which contains unsaturated fatty acids. Some of these seeds, especially sunflower seed contain about 40% oil and the oils are protected in the seeds as long as has not been crushed. Given the importance of some of these seeds and oils to improve the performance of the animals and his reproductive activity and also increase the percentage of unsaturated fatty acids in milk specialty conjugated linolenic acid (CLA) which is of great importance to human health. Therefore, in this study we try to investigate the effect of a diet supplemented with sunflower seed or sunflower oil on milk production and composition and also milk fatty acids profile in dairy goats. Fifteen lactating Damascus goats were used in this experiment, starting by the first week of lactation stage through a 90-d period. Goats divided into three aged groups and assigned at random to receive one of three dietary treatments, five animals each, using complete randomized block design. The treatments were 1) control, 2) control +50 g/head/day sunflower seed, and 3) control +20 mL/head/day sunflower oil. Control ration consisted of concentrate feed mixture (CFM):bersem clover (50:50 dry matter bases). Milk was sampled every 2 wk during the experimental period for chemical analysis. Results indicated that experimental additives, especially sunflower oil had significantly increased ($P < 0.05$) milk yield, fat, and lactose contents compared with the control; however, urea nitrogen milk was decreased ($P > 0.05$) by treatments compared to the control. The experimental additives were increased ($P < 0.05$) unsaturated fatty acids in milk specially [C18:2 *trans*-10, *cis*-12] and conjugated linoleic acids (CLA). Moreover all additives increased ($P > 0.05$) C18:3N3 and C18:3N6 (omega 3 and omega6) compared with control. In conclusion, adding either whole sunflower seed or sunflower oil to lactating goats ration had beneficial effects on milk yield and milk composition and so enhance healthy fatty acids (CLA and omega 3) contents in milk, without detrimental effects on animal performance.

Key Words: lactating goats, sunflower, milk composition

0632 The relationship between human daily requirements of CLA, the potential enrichment of milk through cow's nutrition, and daily human consumption.
A. Siurana* and S. Calsamiglia, *Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain.*

Interest in functional foods has increased in recent years, being the enrichment of milk with conjugated linoleic acid (CLA) one of the targeted products. The objectives of this research were: a) to identify the source of human daily recommendations (literature search), b) to determine the effect of feeding strategies on CLA concentration in milk (meta-analysis), and c) to determine current average human intake of CLA and the expected improvement if milk and milk products were consumed in a CLA enriched form (literature search). The most commonly reported intake recommendations for human are 0.8 g/d (from 0.6 to 3.0 g/d). All recommendations have been extrapolated from animal models and the few human studies reported contradictory results. We selected published papers ($n = 69$) where dairy cows were fed different fats and the milk fat content and fatty acid (FA) profile were reported. Treatments were categorized by source (vegetable oils, fish oils or the combination) and method of processing (raw, processed or extruded seeds, and oils). Data were analyzed using meta-analysis techniques. The combination of fish and vegetable oils resulted in the greatest increase (0.61 vs. 1.34 g CLA/100 g FA; $P = 0.01$), but milk fat content decreased (3.61 vs. 3.12%; $P = 0.01$). Linseed increased CLA proportion (0.61 vs. 0.90 g CLA/100 g FA; $P = 0.01$) without affecting milk fat content. The best processing methods to enriched milk with CLA were extruded seeds (0.57 vs. 1.11 g CLA/100 g FA; $P = 0.01$) and oils (0.57 vs. 1.10 g CLA/100 g FA; $P = 0.01$), but extruded seeds decreased milk yield (30.4 vs. 28.9 kg/d; $P = 0.01$) and oils decreased milk fat content (3.61 vs. 3.31%; $P = 0.01$). Considering the changes in CLA and milk fat content, supplementation with fish oils together with vegetable oils would be the best strategy (118% increase). The estimated current average human consumption in Europe, the United States, and Canada is 0.21 g/d, ranging from 0.06 g/d in Portugal to 0.40 g/d in Germany, well below the requirements. If we assume an increase content of 118% in CLA in milk and milk products, average human consumption would increase from 0.21 to 0.46 g/day. Although there is sufficient data on feeding strategies to increase CLA content in milk, human requirements have not been well-established and, based on current recommendations, they are unattainable even if all milk and milk products were consumed as CLA enriched products.

Key Words: conjugated linoleic acid (CLA), dairy products, human requirements

0633 Tolerance study of rumen protected conjugated linoleic acid on dairy cows during the transition and early lactation period. Z. H. Wei*[1], J. S. Shen[1], J. X. Liu[2], Y. J. Zhang[3], and Y. Jiang[3], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Zhejiang University, Hangzhou, China, [3]BASF (China) Company Ltd., Shanghai, China.*

The objective of the current study was to investigate the effects of dietary addition of rumen protected conjugated linoleic acids (CLA) on lactation performance and blood biochemical and hematological parameters of dairy cows during transition and early lactation period, and to evaluate the acute toxicity when it was added with the 10-fold of the recommended level. Twenty-seven perinatal Holstein cows were selected based on their parity and milk production of previous lactation and assigned to one of three treatments according to a randomized complete block design: 1) basic diet added with no extra CLA (control), 2) 50 g/d of CLA per head (recommended level), and 3) 500 g/d of CLA per head (10-fold of the recommended level). The CLA used in this trial contained 12.0% of cis-9, trans-11 and 11.9% of trans-10, cis-12 CLA isomer. The experiment started 3 wk before expected calving day and finished at 8 wk after calving. Milk yield was recorded, and milk samples were collected to analyze milk composition weekly. The blood samples were collected on d 21 and 10 prepartum and d 1 and week 1, 2, 4, and 8 postpartum to analyze the blood biochemical and redox parameters. An aliquot of blood samples collected on d 21 prepartum and 8 wk postpartum were used for hematological analysis. Addition of CLA did not exert significant effects on dry matter intake, milk yield, content and yield of milk protein and lactose, and somatic cell count ($P > 0.10$). Compared with control and recommended dose group, CLA addition at 500 g/d significantly reduced content and yield of milk fat, milk urine nitrogen, and total solids content ($P < 0.01$). No significant differences were observed in hematological parameters including red blood cell count, hematocrit, hemoglobin, white blood cell count, and its differential count and percentage, platelet count among groups ($P > 0.10$). Addition of CLA significantly decreased plasma levels of non-esterified fatty acids ($P < 0.05$), which is beneficial for alleviating negative energy balance status of dairy cows. The CLA also tended to improve the total antioxidant capacity ($P = 0.09$). There were no significant differences in plasma glucose, total protein, albumin, globulin-to-albumin ratio, creatinine, alanine transaminase, aspartate aminotransferase, and alkaline phosphatase among the three groups ($P > 0.10$). These results indicated that there is no adverse effects of CLA addition on dairy cows' health even at a 10-fold of recommended dose.

Key Words: conjugated linoleic acids, dairy cows, tolerance

0634 Effect of different dietary fat supplements on milk odd and branched chain fatty acids in dairy cows. E. Baumann*, P. Y. Chouinard, Y. Lebeuf, and R. Gervais, *Université Laval, Québec, Canada.*

The odd and branched chain fatty acid (OBCFA) profile of milk has emerged as an interesting, noninvasive option for evaluating rumen function. These fatty acids (FA) are synthesized by different ruminal microbe populations, absorbed in the intestine, and taken up by the mammary gland to be incorporated in milk fat. Lipid supplementation in lactating cows could affect different steps in these processes, as dietary FA have been reported to inhibit (step i) microbial growth, and (step ii) de novo microbial FA synthesis in the rumen, and to increase (step iii) the uptake preformed FA from dietary origin by mammary gland. Such phenomena could reduce synthesis and secretion of OBCFA, and thereby, when cows receive high fat diets, interfere with previously established relationships between these milk FA. To assess the influence of dietary lipids on milk OBCFA, eight Holstein cows (101 ± 11 DIM) were used in a double 4 × 4 Latin-square design with 14-d periods. Treatments were infusion of: CTL) fat-free emulsion in the rumen; SBR) 450 g emulsified unsaturated FA (soybean oil) in the rumen (putative effects on steps i, ii and iii); EBR) 450 g emulsified saturated FA (EnergyBooster) in the rumen (putative effects on steps ii and iii); and EBA) 450 g emulsified saturated FA in the abomasum (putative effects on step iii). Contrasts compared CTL to SBR, SBR to EBR, and EBR to EBA. The results indicate that dietary lipids do affect expression of various milk OBCFA; these effects would need to be considered in the development of models aiming to predict rumen parameters based on milk OBCFA.

Key Words: milk fat synthesis, odd and branched chain fatty acids, dietary lipids

Table 0634. Milk fat concentrations (mg/g) of individual OBCFA

					P-value		
Fatty acid	CTL	SBR	EBR	EBA	CTL vs. SBR	SBR vs. EBR	EBR vs. EBA
iso13:0	0.31	0.26	0.24	0.25	0.01	0.23	0.79
anteiso13:0	0.22	0.16	0.22	0.15	0.05	0.02	0.01
13:0	1.24	1.04	1.05	1.00	< 0.01	0.79	0.35
iso14:0	1.36	1.47	1.40	1.74	0.20	0.40	< 0.01
iso15:0	1.90	1.66	1.68	1.79	< 0.01	0.58	0.02
anteiso15:0	8.17	7.50	7.48	7.92	0.05	0.95	0.19
15:0	12.2	10.2	10.7	10.6	< 0.01	0.18	0.69
iso16:0	3.51	3.44	3.45	4.26	0.82	0.96	0.02
iso17:0	1.12	1.27	1.24	1.30	0.04	0.64	0.34
anteiso17:0	3.34	2.85	3.49	3.53	< 0.01	< 0.01	0.71
17:0	4.80	4.28	6.21	6.18	< 0.01	< 0.01	0.81
*c*9–17:1	1.46	1.32	1.71	1.74	0.01	< 0.01	0.46
iso18:0	0.17	0.17	0.24	0.16	0.74	< 0.01	< 0.01

0635 Feeding incremental levels of ground flaxseed increased n-3 fatty acids and conjugated linoleic acids in organically-managed jersey cows.

A. F. Brito[1], J. Kraft*[2], T. L. Resende[3], A. B. D. Pereira[1], K. J. Soder[4], D. H. Woitschach[5], and R. B. Reis[3], *[1]University of New Hampshire, Durham, [2]Dep. of Animal Science, University of Vermont, Burlington, [3]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, [4]USDA–Agricultural Research Service, University Park, PA, [5]Universidade Federal de Viçosa, Brazil.*

We reported previously that feeding incremental levels of ground flaxseed (GFLAX) linearly reduced DMI, milk production, and contents and yields of milk components. Flaxseed is a high-energy oilseed rich in α-linolenic acid. It is well established the impact of flaxseed on changing milk fatty acids (FA) profile but there is limited research about the effects of GFLAX on milk FA composition, particularly in cows fed high-forage diets. In a recent needs assessment of research and educational needs of the organic dairy industry in the Northeast 84% of respondents indicated the development of value-added dairy products as one of the most pressing areas for dairy research (Pereira et al., 2013 JDS 96:7340–7348), thus justifying additional studies with flaxseed. Twenty organically managed Jersey cows (425 ± 37 kg of BW and 111 ± 62 DIM) in the beginning of the study were blocked by milk yield and parity and randomly assigned to treatment sequences in five replicated 4 × 4 Latin squares to investigate the effects of incremental levels of GFLAX (0, 5, 10, or 15% diet DM) on milk FA composition. All cows were fed TMR containing (% of diet DM): 55% alfalfa-grass baleage, 8% grass hay, and 37% concentrate; soybean meal (from 6 to 2% of diet DM) and corn meal (from 27 to 16% of diet DM) were replaced with GFLAX (from 0 to 15% of diet DM), while roasted soybean (2% of diet DM) was maintained constant across treatments. Diets were isonitrogenous (mean = 18.3% CP), but crude fat increased from 3.8 to 7.4% when replacing soybean meal and corn meal with GFLAX. Milk concentration (% of total milk FA) of total n-3 FA (0.74 to 1.42%), *t*C18:1 (1.35 to 2.63%), *c*9, *t*11 CLA (0.47 to 0.87%), total CLA (0.55 to 1.08%), total monounsaturated FA (21.9 to 34.3%), and total polyunsaturated FA (2.87 to 4.72%) increased linearly in response to increasing levels of GFLAX. Conversely, milk concentrations of n-6 FA (1.78 to 1.49%) and total saturated FA (72.7 to 58.1%), and the n-6 to n-3 ratio (2.42 to 1.06) declined linearly with increasing levels of GFLAX. Quadratic effects were observed for total n-3 FA, *t*C18:1, *c*9, *t*11 CLA, total CLA, and the n-6 to n-3 ratio. It can be concluded that GFLAX is an effective supplement to enrich milk with bioactive FA of potential health benefits for humans.

Key Words: flaxseed, organic dairy cows, milk fatty acids

0636 Lactational responses to palmitic acid supplementation when substituted for soyhulls or corn grain.

C. L. Preseault, J. P. Boerman, and A. L. Lock*, *Michigan State University, East Lansing.*

Effects of a palmitic acid-enriched fat supplement (PA; 87% C16:0) when replacing soyhulls or corn grain on feed intake and metabolic and production responses of dairy cows were evaluated. Twenty-four Holstein cows (185 ± 70 DIM) were randomly assigned to treatment sequence in a 3 × 3 Latin square design. Treatments were a control diet (CON; no added PA), 1.5% added PA with soyhulls replaced (PA-SH), or 1.5% added PA with corn grain replaced (PA-CG). Treatment periods were 21 d, with the final 5 d used for sample and data collection. The study was conducted from June through August 2013 when temperature-humidity index in the barn averaged 70.5 ± 5.7°F. The corn silage and alfalfa silage-based diets contained 20.0% forage NDF and 16.8% CP. The statistical model included the random effect of cow and fixed effects of period and treatment; preplanned contrasts evaluated the effect of PA treatments (CON vs. 1/2[PA-SH+PA-CG]) and the effect of PA-SH vs. PA-CG. The PA treatments increased milk fat concentration (3.55, 3.65, and 3.71%; $P < 0.01$) and yield (1.38, 1.49, and 1.42 kg/d; $P < 0.05$) for CON, PA-SH, and PA-CG, respectively. Compared with CON, there was no effect of PA treatments on DMI, milk yield, milk protein yield, or ECM ($P > 0.18$). However, compared with PA-CG the PA-SH treatment increased DMI 1.35 kg/d, milk yield 2.38 kg/d, milk protein yield 0.08 kg/d, and ECM 2.26 kg/d ($P < 0.05$). The PA treatments increased feed efficiency (ECM/DMI), 1.46, 1.51, and 1.50 for CON, PA-SH, and PA-CG, respectively ($P < 0.05$). Compared with CON, PA treatments increased the yield of 16-carbon milk FA by 83 g/d ($P < 0.01$) but did not affect the yield of de novo ($P = 0.38$) or preformed ($P = 0.71$) milk FA. There was a trend for increased yield of de novo (21 g/d; $P = 0.07$) and preformed (27 g/d; $P = 0.10$) milk FA for PA-SH vs. PA-CG. The PA treatments did not alter BW ($P = 0.42$) or BCS ($P = 0.99$); however, PA-SH increased BW 9.5 kg vs. PA-CG ($P < 0.05$). There was no effect of PA treatments on plasma concentrations of glucose ($P = 0.92$) or insulin ($P = 0.57$), whereas PA treatments increased NEFA (99.5, 110, and 109 uEq/L for CON, PA-SH, and PA-CG, respectively; $P < 0.01$). Treatment had no effect on rectal temperature or respiration rate ($P > 0.46$). Results demonstrate that a PA-enriched fat supplement increased milk fat concentration and yield and feed efficiency. Responses were greater when PA replaced soyhulls rather than corn grain.

Key Words: fat supplementation, milk fat, palmitic acid

0637 Interaction between culture pH and corn oil concentration on NDF digestibility and biohydrogenation of unsaturated fatty acids in batch culture. Y. Sun*, M. S. Allen, and A. L. Lock, *Michigan State University, East Lansing.*

Effects of culture pH and corn oil (CO) concentration on NDF digestibility (NDFD) and biohydrogenation (BH) of unsaturated fatty acids (FA) in batch culture were evaluated in a 2 × 3 factorial design. Cultures (4/treatment/time point) included alfalfa hay plus increasing concentrations of CO (0, 1, 2% DM) incubated at culture pH 5.8 or 6.2 for 0, 6, 12, 18, and 24 h. Effects of culture pH, CO, time, and their interactions were determined. Increasing CO in cultures increased total FA concentration which averaged 2.19, 3.36, and 4.54% DM for 0, 1, 2% CO, respectively ($P < 0.001$). Culture pH did not affect total FA concentration ($P = 0.29$). Main effects of treatments (culture pH and CO concentration) across time were significant for the response variables of interest despite significant ($P < 0.10$) interactions (both two-way and three-way interactions) for these variables. Lower culture pH reduced NDFD across CO treatments and time (11.6 vs. 21.6%; $P < 0.001$), whereas increasing CO increased NDFD across pH treatments and time (14.2, 16.9, and 18.8%; $P < 0.001$); NDFD increased over time for all treatments ($P < 0.001$). Addition of CO increased the concentration of *cis*-9, *cis*-12 18:2 across pH treatments and time (7.88, 17.4, 23.0 g/100 g FA; $P < 0.001$) and higher culture pH reduced its concentration across CO treatments and time (13.8 vs. 18.4 g/100 g FA; $P < 0.001$). Lower culture pH reduced BH extent for *cis*-9, *cis*-12 18:2 (34.4 vs. 53.0%; $P < 0.001$), which increased with time ($P < 0.001$) and was affected to a lesser extent by increasing CO (43.0, 45.3, and 42.7%; $P < 0.001$ quadratic). Lower culture pH and increasing CO reduced the concentration of 18:0 (20.1 vs. 24.9 g/100 g FA and 28.7, 21.7, and 17.1 g/100 g FA, respectively; $P < 0.001$). Lower culture pH increased the concentration of *trans*-10 18:1 (1.04 vs. 0.73 g/100 g FA; $P < 0.001$) and reduced the concentration of *trans*-11 18:1 (4.73 vs. 6.11 g/100 g FA; $P < 0.001$) across CO treatments and time. Increasing CO increased the concentration of *trans*-10 18:1 (0.72, 0.92, and 1.03 g/100 g FA; $P < 0.001$) and *trans*-11 18:1 (3.46, 5.85, and 6.95 g/100 g FA; $P < 0.001$) across pH treatments and time. In conclusion, higher culture pH increased NDFD, BH of *cis*-9, *cis*-12 18:2, and formation of *trans*-11 18:1. Increasing the inclusion of CO increased the formation of BH intermediates as well as NDFD (unexpectedly). Treatments interacted with each other and with time for all variables of interest, particularly formation of *trans*-10 and *trans*-11 18:1.

Key Words: batch culture, biohydrogenation, digestibility

0638 Feed intake and production responses of lactating dairy cows when commercially available fat supplements are included in diets: a meta-analysis. J. P. Boerman* and A. L. Lock, *Michigan State University, East Lansing.*

This analysis was performed to evaluate the effects of commercially available fat supplements on DMI and production responses of lactating dairy cows. Available data were collected from 133 peer-reviewed publications; of which 88 met our selection criteria, comprising 159 treatment comparisons. Calcium-salts of palm fatty acid distillate (PFAD; $n = 73$), saturated prilled fats (PRILLS; $n = 37$), and tallow ($n = 49$) supplemented at $\leq$ 3% diet DM were compared to nonfat supplemented diets used as controls. Analysis was performed using Comprehensive Meta Analysis v2 software to calculate the effect size as the mean difference in least square means between control and fat supplemented treatments using a random effects model. Treatment comparisons were obtained from either randomized design ($n = 99$) or crossover/Latin square design experiments ($n = 60$). There were no differences in the overall effect of fat supplementation between randomized design and crossover/Latin square design experiments for any production parameter (all $P > 0.46$). Therefore, all types of experimental design were analyzed together. Fat supplementation reduced DMI compared to control (0.30 kg/d, $P < 0.01$). However, the response was dependent on fat type; PFAD and tallow reduced DMI (0.58 and 0.44 kg/d, $P < 0.01$ and $P = 0.06$, respectively), while PRILLS had no effect ($P = 0.71$). Fat supplementation increased milk yield by 1.05 kg/d ($P < 0.01$), with differences in the magnitude of response for PFAD (1.20 kg/d, $P < 0.01$), PRILLS (1.19 kg/d, $P < 0.01$), and tallow (0.70 kg/d, $P < 0.01$). Fat supplementation increased milk fat yield by 0.04 kg/d ($P < 0.01$) with increases of 0.05 and 0.06 kg/d for PFAD and PRILLS, respectively (both $P < 0.01$) with no effect of tallow ($P = 0.72$) compared to control. There was no overall effect of fat supplementation on milk fat concentration ($P = 0.84$), although compared with control, tallow reduced milk fat by 0.08% units ($P = 0.01$), PFAD had no effect ($P = 0.25$), and PRILLS increased milk fat by 0.08% units ($P = 0.05$). Milk protein yield was unaffected by PFAD and tallow (both $P > 0.31$) and increased by 0.03 kg/d by PRILLS ($P < 0.01$) resulting in an overall increase by fat supplementation of 0.01 kg/d ($P < 0.01$). Milk protein concentration was reduced by all fat supplements ($P < 0.01$ for PFAD and tallow; $P = 0.04$ for PRILLS) for an overall reduction in milk protein concentration of 0.05% units ($P < 0.01$). In conclusion, fat supplementation has the potential to reduce DMI and increase the yield of milk and milk components. However, consideration should be given to the type of fat, as production responses were highly variable across fat supplements.

Key Words: fat supplementation, meta-analysis, production response

0639 Effect of dietary fat source on milk production and milk composition in early lactation cows in a continuous trial design. G. Ma[*1], J. H. Harrison[2], E. Block[3], and L. VanWieringen[4], *[1]Washington State University, Pullman, [2]Washington State University, Puyallup, [3]Church and Dwight Animal Nutrition, Ewing, NJ, [4]Washington State University, Sunnyside.*

This study was designed to look at two dietary fat sources (Megalac and Palmit 80) when fed at amounts to deliver fatty acids at ~ 0.22 kg/d. Twenty-four multiparous dairy cows in early lactation (average DIM = 68) were used to compare the temporal relationship of DMI, milk production, milk composition, body weight, and BCS. Cows were fed individually via Calan headgates. Data from wk 1 to 2 was averaged and used as a covariate period, and cows were fed Megalac as the only source of supplemental fatty acids. During wk 3 to 12, 12 cows were fed the Megalac diet at 1.15% DM, and 12 cows were fed the Palmit 80 diet at 0.93% DM. Milk production was obtained 2x/d and 1x/wk an AM-PM composite of milk was obtained from each cow and analyzed for composition. Data were analyzed with PROC MIXED of SAS with repeated measurements using a model that included treatment, week, treatment x week. There was no treatment x week interaction ($P > 0.1$). The covariant played a significant role in the adjustment ($P < 0.05$). In this study, there was no significant difference between sources of supplemental fat on milk production, 39.2 vs. 40.0 kg; DMI, 29.2 vs. 29.1 kg; milk fat %, 4.3 vs. 4.3%; milk protein %, 2.91 vs. 2.98% ($P < 0.09$); milk fat yield, 1.65 vs. 1.74 kg; BCS, 2.81 vs. 2.80; BW, 668 vs. 677 kg; or BW change, 11.7 vs. 9.5 kg (Megalac vs. palmit 80, $P > 0.1$). Milk protein yield was greater 1.13 vs. 1.19 kg ($P = 0.002$) when cows consumed Palmit 80. A previously reported trial of similar design (J. Dairy Sci. 96 (Suppl.E):Abstr. W29) showed higher production by cows fed Megalac vs. Palmit 80. In that trial, cows were earlier in DIM at the start of the study. A hypothesis is that cows at different stages of lactation use individual fatty acids differently due to metabolic status.

Key Words: milk fat, dietary fat, fatty acids

0640 Farm survey: Milk fatty acid composition measured by mid-infrared. D. M. Barbano[*1,2], C. Melilli[1,2], and T. R. Overton[3], *[1]Cornell University, Ithaca, NY, [2]Northeast Dairy Foods Research Center, Ithaca, NY, [3]Cornell University, Dep. of Animal Science, Ithaca, NY.*

Our objectives were: 1) measure fatty acid (FA) composition of individual herd milks using new chemometric models for mid-infrared (IR) milk analysis and 2) determine if there were correlations between milk FA composition and bulk tank milk fat and protein tests. Bulk tank milks from 430 farms were tested multiple times per month for 14 mo by mid-IR (Lactoscope FTA, Delta Instruments) for fat, protein, and FA composition. The IR instrument could test about 100 samples per hour. Data were organized in two groups: Jersey and Holstein. A variety of individual FA and groups of FA were measured. Validation of IR FA results was done by GLC. The key FA parameter that was positively correlated with bulk milk fat and protein concentration was de novo FA (g/100 g milk). Structural parameters of FA chain length (carbon number) and total unsaturation (double bonds/FA) were negatively correlated with fat and protein (g/100 g milk). This was true for both Jersey and Holstein. When de novo FA (relative % of FA) were higher, fat test was higher for both Jersey and Holstein. As de novo FA (g/100 g milk) increased, fat (g/100 g milk) increased ($P < 0.001$) at a much faster rate (i.e., higher slope) than when preformed FA (g/100 g milk) increased (slope 2.28 vs. 1.29) for Jersey and (slope 2.16 vs. 1.22) for Holstein, for de novo vs. preformed, respectively. As the proportion of de novo increased (and fat percent increased), the measured FA chain length and double bonds per FA decreased ($P < 0.001$). True protein (g/100 g milk) increased as de novo FA (g/100 g milk) increased. We hypothesize that feeding and farm management practices influenced de novo FA production and milk fat and protein (g/100 g milk). A group of 20 Jersey and 20 Holstein farms of interest that had a wide range of de novo FA (g/100 g fat) were selected for a more in-depth field study, in the next year, to determine if there are cost effective feeding and management practices that can be used to increase fat and protein tests. During the 14-m period of our study, the 10 Holstein and 10 Jersey low de novo herds averaged 3.62 and 3.97% fat and 2.99 and 3.15% true protein, while the 10 high de novo Holstein and Jersey herds averaged 3.92 and 4.80% fat and 3.09 and 3.62% true protein, respectively.

Key Words: mid-infared milk analysis, de novo fatty acids, fat and protein concentration

0641 The effects of high rates protected fat in rations of high yielding dairy cows on production efficiency and digestibility. U. Moallem[*1], E. Frank[1,2], M. Zachut[1], L. Livshitz[1], and A. Arieli[2], *[1]Institute of Animal Science, Volcani Center, Bet Dagan, Israel, [2]Faculty of Agriculture, Hebrew University, Rehovot, Israel.*

Due to the rise in grain price, there is an increased use of fat in rations of dairy cows in Israel; however, the effects of high rates have never been examined in the Israeli rations. Therefore, the objectives were to determine the effects of increasing rate of calcium soap of fatty acids (CSFA) on yields, efficiency and digestibility. Forty-two multiparous dairy cows were divided into three treatment groups according to milk, parity and days in milk (DIM), and fed diets containing: (i) low fat (LF), 4.7% ether extracts (EE; 1.7% CSFA); (ii) moderate fat (MF), 5.8% EE (2.8% CSFA), and (iii) high fat (HF), 6.8% EE (3.9% CSFA). The diets were isonitrogenous (16.5%), but energy content was 1.8 in the HF compared to

1.78 Mcal/kg DM in the LF and MF diets. Rumen samples were taken three times in 1 d (2 h pre-feeding, at feeding, and 2 h post-feeding) for pH and rumen measurements. The data were analyzed using the PROC MIXED model of SAS and the model included parity, DIM, and related covariate data. No differences were observed in milk and FCM (4%) yields or fat and lactose percentages and yields among groups. A trend of decreased protein percentage in milk with increasing EE content in diet was observed ($P < 0.08$), and higher protein yields were observed in LF and MF than in HF. No differences were observed in dry matter intake (DMI) or energy intake among groups. Efficiency of converting DMI to milk was also similar, but conversion of DMI into FCM (4%) was higher in MF and HF than in LF. Rumen pH was higher in MF and HF than in LF, with no differences in rumen ammonia concentrations. Total VFA concentration in rumen was higher in LF than in MF and HF groups, and apparent digestibility of DM and organic matter (OM) was higher in the LF than in both other groups. In conclusion, although apparent digestibility of DM and OM was lower in MF and HF, no detrimental effects of high rate of CSFA supplementation (up to 3.9% of the diet) on milk yields and efficiency were observed.

Key Words: CSFA, digestibility, efficiency

0642 Long chain fatty acids alter expression of genes involved in lipid metabolism in goat mammary epithelial cells partly through PPARγ.

W. Zhao[*1,2], M. Bionaz[3], J. Luo[1], A. Hosseini[4], P. Dovc[5], and J. J. Loor[2], *[1]Northwest A & F University, Yangling, China, [2]University of Illinois, Urbana, [3]Dep. of Animal and Rangeland Sciences, Oregon State University, Corvallis, [4]University of Bonn, Germany, [5]University of Ljubljana, Domzale, Slovenia.*

Data from dairy cows and goats indicate a prominent role of PPARγ in regulating milk fat synthesis (MFS). The PPARγ binds and is activated by long-chain fatty acids (LCFA), hence is amenable for fine-tuning MFS. Previous data in MacT cells indicated an agonistic capacity of saturated LCFA but also the potential of LCFA to act through alternative transcriptional regulators. To determine the specificity of LCFA in modulating PPARγ in goats, triplicate cultures of primary mammary cells from Saanen goats cultivated in lactogenic medium were cultured for 24 h with 50 μM of the specific PPARγ activator rosiglitazone (ROSI) or the specific PPARγ inhibitor GW9662 (GW), 100 μM of several LCFA (16:0, 18:0, t10,c12-CLA, DHA, and EPA), and a combination of GW with each of LCFA (for a total of 12 treatments excluding controls). Expression of 28 genes involved in MFS plus three internal control genes was measured using qPCR. Data were log-transformed and statistically analyzed using the GLM of SAS. The multiple comparisons were corrected using Tukey's test and significance set at $P < 0.05$. The cells treated with GW alone allowed uncovering that a minimum activation of PPARγ is essential for the expression of LPIN1, PPARG, LXRA, LPL, ACSL1, FABP3, and FABP4. The combination of the data from GW and ROSI treatments allowed identification of SCD, FADS1, NR1H3, SREBF1, INSIG1, LPL, FABP3, and FABP4 as strong PPARγ target genes. The 16:0 and 18:0 had the strongest effect on most of the measured genes and stronger than ROSI. Among the unsaturated LCFA, the CLA had the strongest effect in decreasing expression of FASN, FADS1, LPIN1, SREBF1, SREBF2, INSIG1, RXRA, NCOR1, and FABP3. The combination with GW diminished but did not completely eliminate the effect of saturated LCFA and interacted in a complex manner with the effect of unsaturated LCFA. The expression of AGPAT6, PLIN2, and CD36 increased in all treatments compared with control. The expression of NR1H3 solely responded to ROSI and GW but not to LCFA. Results allowed pinpointing true PPARγ target genes in goat mammary cells, and confirmed that saturated LCFA are potent PPARγ agonists in ruminants but that they act also through alternative transcriptional factors. Data established the lipid-depressing effect of unsaturated LCFA, particularly CLA. A complex mechanism for LCFA in regulating expression of lipid-related genes in goat mammary cells was uncovered.

Key Words: nuclear receptors, milk fat synthesis, nutrigenomics

RUMINANT NUTRITION V

0643 Methane emissions from lactating and dry dairy cows fed diets differing in forage source and NDF concentration. *K. J. Hammond*, D. J. Humphries, L. A. Crompton, P. Kirton, C. Green, and C. K. Reynolds, University of Reading, UK.*

Methane emission factors are lacking from different livestock species in various production states fed varying diets. The objectives of the present study were to measure effects of physiological state, silage type, and supplemental NDF on DMI, DM digestibility (DMD), and methane emissions of lactating and dry dairy cows using two 4 × 4 Latin squares (5-wk periods) with four lactating (114 DIM ± SEM 3.30; square 1) or four dry and non-pregnant (square 2) ruminally cannulated Holstein dairy cows. Measurements included DMI and DMD during wk 4, and methane production (respiration chambers) in wk 5. Four isonitrogenous treatment diets were fed as total mixed rations (TMR) with 50% silage (DM basis) offered ad libitum to lactating cows and at 1.2 × maintenance ME to dry cows. Silage was comprised of either 25:75 (MS) or 75:25 (GS) grass silage:maize silage on a DM basis, without or with additional NDF from chopped straw and soy hulls (+ 47 g NDF/kg TMR DM). Data for each square were analyzed using mixed models for fixed effects of silage, NDF, and their interaction, and random effects of cow and period. Data from each square were combined to test the effect of physiological state. Lactating cows fed MS had a greater DMI ($P < 0.02$; 21.1 kg/d) and methane production ($P < 0.10$; 484 g/d) and lower methane yield ($P < 0.02$; 22.8 g/kg DMI) than when fed GS (17.7, 440, and 24.9, respectively), however there was no effect of silage type on DMD. Added NDF increased methane yield for lactating cows fed MS (22.8 vs. 23.7 g/kg DMI), but not GS (silage by NDF interaction, $P < 0.02$). Except for DMI, which was higher ($P < 0.03$) for MS compared to GS diets (12.9 vs. 10.6 kg/d), diet did not affect methane production or yield or DMD for dry cows. Compared to dry cows, lactating cows had greater DMI (19.7 vs. 11.0 kg/d; $P < 0.02$), higher DMD (749 vs. 725 g/kg; $P < 0.01$), and lower methane yield (24.0 vs. 28.0 g/kg DMI; $P < 0.03$). The difference in methane yield between lactating and dry cows may be due to differences in DMI and rumen function, including digesta dynamics such as rumen outflow and retention time. Such differences may also explain why silage type affected methane yield in lactating cows, but not dry cows.

Key Words: methane, dairy cows, forage NDF

0644 Effects of cysteamine on ruminal fermentation parameters and methane production of water buffalo by in vitro gas production method. C. Zou[*1], Y. L. Huang[2], X. Liang[2], S. J. Wei[2], B. Lin[2], C. J. Yang[2], and X. W. Liang[2], *[1]Buffalo Research Institute, The Chinese Academy of Agricultural Sciences, Nanning, China, [2]Buffalo Research Institute, Chinese Academy of Agricultural Sciences, Nanning, China.*

In our previous studies, supplement cysteamine (Cs) could increase the conjugated linoleic acids content in water buffalo milk, but we do not know whether Cs could reduce the methane production. Thus, the aim of this present study was to evaluate the effect of Cs on ruminal fermentation parameters and methane production of water buffalo by in vitro gas production method. In vitro fermentations were conducted in 180-mL serum bottles with a reading pressure in vitro gas production system. The oven-dried subtrate (187.50 mg maize grain, 56.25 mg soybean meal, 196.88 mg elephant grass, 140.63 mg brewers grains, and 168.75 mg cassava pulps, DM basis) was weighted with three replicates into 90-mL buffer medium. The ratio of concentrate to forage of substrate was 32.5:67.5. Cs was supplemented in concentrate at levels of 0, 0.2, 0.4, 0.6, 0.8, and 1.0% (dry matter basis), respectively. The water buffalo rumen contents obtained were mixed and strained through four layers of cheesecloth into a flask under CO_2 in the water bath at 39°C. The pressure and methane production were measured at 6, 12, and 24 h. At the end of the incubation (24 h), the incubation fluids were sampled and samples were stored at -20°C for an analysis of NH_3–N concentration and VFA composition. There were no significant differences for NH_3–N concentration (6.40, 6.53, 6.43, 7.07, 7.24, and 6.30 mg/dL for the levels of 0, 0.2, 0.4, 0.6, 0.8, and 1.0% Cs supplement, $P = 0.652$) and acetate (20.91, 20.95, 20.86, 20.44, 21.22, and 19.42 mmol/L, $P = 0.702$), propionate (7.06, 7.08, 6.71, 6.44, 6.71, 6.20 mmol/L, $P = 0.436$), total VFA (32.77, 32.81, 31.56, 30.98, 31.85, and 29.20 mmol/L, $P = 0.499$), and acetate/propionate (2.97, 2.97, 3.11, 3.17, 3.16, and 3.13, $P = 0.086$) among each treatments. Methane production at 6 h (0.14, 0.13, 0.10, 0.10, 0.08, and 0.09 mmol/L, $P = 0.03$), 12 h (0.37, 0.36, 0.25, 0.28, 0.26, and 0.28 mmol/L, $P < 0.0001$), 24 h (0.61, 0.61, 0.49, 0.54, 0.51, and 0.58 mmol/L, $P = 0.004$) were decreased with an increasing level of Cs. Butyrate content (4.80, 4.79, 3.99, 4.09, 3.92, and 3.59 mmol/L, $P = 0.037$) at 24 h were decreased with an increasing level of Cs. The results of in vitro gas production method indicate that Cs can promote rument microbe fermentation, but decrease methane production of water buffalo when supplemental level of Cs is 0.8%.

Key Words*:* cysteamine, methane emission, water buffalo

0645 Effect of lowered pH and increased passage rate on methane and volatile fatty acid production from continuous culture. B. A. Wenner*[1], F. Batistel[2], J. D. Souza[3], T. J. Hackmann[4], and J. L. Firkins[1], *[1]The Ohio State University, Columbus, [2]University of São Paulo, Piracicaba, Brazil, [3]University of Sao Paulo, Piracicaba, Brazil, [4]University of Florida, Gainesville.*

The present study was conducted as a 2 × 2 factorial treatment arrangement in a Latin square design using continuous culture fermenters (n = 4). Treatments were control pH (CpH; 6.3 to 6.9) or low pH (LpH; 5.8 to 6.4) factorialized with solids passage rates (k_p) of either low (Lk_p; 2.5%/h) or high (Hk_p; 5.0%/h); total dilution by buffer was constant at 7.0%/h. Fermenters were fed once daily (40 g DM; a 50:50 concentrate:forage diet) and periods lasted 10 d with 3 d of sample collection. The main effect of LpH decreased (P < 0.001) aqueous hydrogen compared with CpH by 3.82 μM, but there was no effect of k_p (P > 0.10). The main effect of LpH decreased headspace hydrogen (H_2(g); escaped from culture) by 60.1 mmol/L×d, and an interaction over time (P < 0.001) was explained by H_2(g) being greater for CpH/Hk_p than for LpH (both k_p) from 5 to 24 h post-feeding, and CpH/Lk_p being greater than LpH (both k_p) from 6 to 24 h post-feeding. Further, H_2(g) was greater (P < 0.05) with CpH/Hk_p compared with CpH/Lk_p from 15 to 24 h post-feeding. There was no main effect (P > 0.10) of pH on methane production, but the main effect of Hk_p tended (P = 0.08) to decrease methane production compared with Lk_p by 880 mmol/L×d. A treatment × time interaction (P < 0.01) was explained in that CpH/Lk_p had the greatest (P < 0.05) methane production from 11 to 23 h post-feeding, whereas LpH/Lk_p was not different (P > 0.05) from CpH/Lk_p at 24 h post-feeding. Acetate molar percentage was 61.8, 59.6, 58.2, and 54.7% for CpH/Lk_p, CpH/Hk_p, LpH/Lk_p and LpH/Hk_p, respectively. Both the main effects of LpH and Hk_p decreased acetate molar percentage (P = 0.01) compared with CpH and Lk_p, respectively. Propionate molar percentage was 22.5, 24.4, 23.9, and 26.2% for CpH/Lk_p, CpH/Hk_p, LpH/Lk_p and LpH/Hk_p, respectively. The main effect of LpH increased (P = 0.02) propionate molar percentage, decreasing (P = 0.002) A:P ratio from 2.61 to 2.34 compared with CpH. The main effect of Hk_p increased (P = 0.006) propionate molar percentage, decreasing (P = 0.002) A:P ratio from 2.62 to 2.34 compared with Lk_p. There were no effects on butyrate molar percentage or total VFA production (P > 0.10). The results indicate increasing $k_p$and decreasing pH decreased A:P ratio independent of the current diet.

Key Words: hydrogen, methane, volatile fatty acids

0646 Effects of encapsulated nitrate on nitrogen utilization and enteric methane emissions in beef cattle. C. Lee*[1], R. C. Araujo[2,3], K. M. Koenig[4], and K. A. Beauchemin[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, AB, Canada, [2]GRASP Ind. & Com. LTDA, Curitiba, Brazil, [3]EW|Nutrition GMBH, Visbek, Germany, [4]Agriculture and Agri-Food Canada, Lethbridge Research Centre, AB, Canada.*

Effects of encapsulated slow-release nitrate (EN; GRASP Ind. & Com. LTDA, Paraná, Brazil) on nitrogen (N) utilization and enteric methane emissions in beef cattle were investigated. Eight ruminally cannulated beef heifers (452 ± 21 kg BW) were used in a replicated 4 × 4 Latin square design. The basal diet (55:45 forage:concentrate ratio) included encapsulated urea [EU; 1.2% of dietary DM; Prote-N; GRASP Ind. & Com LTDA] for the control diet. The EN replaced a portion of EU and limestone with 1, 2, or 3% EN (0.8, 1.5, and 2.3% nitrate) in dietary DM. The diets (iso-nitrogenous; 12.7% CP) were fed once daily ad libitum. Each period consisted of 21 d of adaptation in a stepwise manner followed by 14 d of sampling (total collection for 4 d and enteric methane measurements in environmental chambers for 3 d). Dry matter intake tended to decrease (10.4 to 10.1 kg/d; P = 0.06) slightly with increases in EN, but body weight was not affected. Enteric methane emissions and intensity were linearly reduced (183 to 145 g/d and 21.3 to 17.4 g/kg DMI; P < 0.001) with increasing dietary EN where a treatment × hour interaction was observed (P < 0.001). Methane emissions with greater treatment effects occurred 0 to 12 h after feeding when cows consumed 87% of total feed offered. Nitrogen intake was not affected by EN. Plasma urea-N was linearly decreased (12.5 to 10.9 mg/dl; P < 0.001) with increasing dietary EN. Urinary N excretion tended to linearly decrease (100.2 to 86.5 g/d; P = 0.056) and the proportion of N intake was linearly reduced (46.1 to 39.2%; P = 0.03) with increasing dietary EN. Urinary urea-N excretion and the proportion of N intake were linearly decreased (75.9 to 56.2 g/d, P = 0.019 and 35.2 to 25.4%, P = 0.015, respectively) with increasing EN level. Fecal N excretion was not affected by EN. As a consequence, total N excretion and the proportion of N intake were linearly decreased (P = 0.047 and P = 0.001, respectively) with increasing dietary EN. In conclusion, supplementary nitrate in a protected form lowered enteric methane emissions in a dose–response manner. Urinary N excretion was reduced for heifers fed EN compared with EU, due to lower urea-N excretion in urine. The study demonstrates that feeding EN as a N source is environmentally beneficial compared with EU in beef cattle.

Key Words: encapsulated nitrate, enteric methane emissions, nitrogen utilization

0647 Correspondence between in vitro and in vivo rumen methane production obtained with different starch sources and starch levels. B. Hatew[*1], J. W. Cone[1], W. F. Pellikaan[1], S. C. Podesta[1], W. H. Hendriks[1], A. Bannink[2], and J. Dijkstra[1], *[1]Animal Nutrition Group, Wageningen University, Netherlands, [2]Wageningen UR Livestock Research, Wageningen University and Research Centre, Lelystad, Netherlands.*

To investigate the relationship between in vitro and in vivo methane (CH_4) production measured simultaneously, 16 rumen-cannulated lactating dairy cows were assigned to four blocks with a 2 × 2 factorial arrangement of treatments. The treatments were based on concentrates formulated to contain starch varying in source (slowly fermentable (S) vs. rapidly fermentable (*R*); native vs. gelatinized corn grain) and level of starch (low (L) vs. high (H); 270 vs. 530 g/kg of concentrate DM). The grass silage to concentrate ratio of the total diet was 60:40 (DM basis). After 12 d of adaptation, the cows were housed in respiration chambers for 5 d to measure CH_4 production, replicated in four periods. In each period rumen fluid was obtained from each of four donor cows adapted to one of the four different diets for about 16 d. Gas production (GP) and CH_4 was measured (in duplicate per period) for each substrate from the same diet as fed to individual donor cow using automated GP system with CH_4 measured at distinct time points. Rumen fermentable organic matter (OM) in concentrates was determined by in situ technique and in grass silage estimated by NIRS analysis. In vitro CH_4 production (24 h) was lower with R than with S starch (42.9 vs. 49.5 mL/g of incubated OM; $P = 0.004$), and higher with L than with H (49.8 vs. 42.6 mL/g of incubated OM; $P = 0.002$). In vivo, an increased rate of fermentation, but not increased level of starch, resulted in a lower CH_4 production per unit rumen fermentable OM (55.6 *vs*. 61.1 L/kg of fermentable OM; $P = 0.007$). Across the diets tested, in vitro CH_4 correlated well with in vivo CH_4 production expressed per unit fermented OM ($R^2 = 0.54$; $P = 0.040$), but not with in vivo CH_4 production expressed per unit ingested OM ($R^2 = 0.04$; $P = 0.878$). These results indicate the complexity of rumen fermentation conditions needs to be considered to predict in vivo CH_4 production from in vitro measurements. In conclusion, in vitro CH_4 production was only indicative of the trend of in vivo rumen CH_4 production from different combinations of source and level of starch when in vivo CH_4production was expressed per unit rumen fermented OM, but not when expressed per unit ingested OM.

Key Words: methane, in vitro, in vivo

Table 0647. Chemical composition (g/kg DM) of total mixed diet

Diet	CP	NDF
SL-diet	156	441
SH-diet	157	385
RL-diet	156	440
RH-diet	163	378

0648 The potential benefit of corn dried distillers' grain (co)products (DDG) in the mitigation of methane production in cattle: an in vivo analysis. M. A. Fonseca[*1], L. F. L. Cavalcanti[2], J. G. L. Regadas Filho[3], T. R. Callaway[4], G. E. Carstens[1], T. A. Wickersham[1], and L. O. Tedeschi[1], *[1]Texas A&M University, College Station, [2]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, [3]Universidade Federal de Vicosa, Vicosa, Brazil, [4]USDA-ARS, College Station, Texas.*

Our preliminary in vitro study indicated that feeding high-fat diets may decrease methane (CH_4) production by cattle. The objective of this study was to determine the impact of different levels of DDG on the digestibility of OM and the production of CH_4using two open-circuit respiration chambers at the Nutrition and Physiology Center, Texas A&M University, College Station, Texas. The respiration chambers monitored the inflow and outflow of CO_2, O_2 (fuel cell oxygen, FC-1B; Sable Systems, Henderson, NV), CH_4, and water vapor continuously, and all calculations were corrected for the standard temperature and pressure of the air mass flowing through the chambers (FLOWKIT 500H; Sable Systems, Henderson, NV). Relative humidity was measured and used to calculate the dew point and water vapor pressure. Gases measurements were performed using a flow-through system (RH-100). Air from each source (chambers A and B, and baseline) were sampled every 4 min. The diets were formulated to have same level of ME (Mcal/kg) and to contain 0, 20, or 40% of DDG (DM basis). Animals were adapted to the experimental diets for 7 d outside the chambers and then brought in for a 48-h period for consecutive gas exchange measurement. The intake was restricted to 2% of BW and fed twice daily. Six Angus steers were allocated in an incomplete Latin rectangle design (two animals/diet for three periods). The R software (R Core Team, Vienna, Austria) and PROC MIXED of SAS (SAS Inst., Cary, NC) were used to analyze the data using a repeated measure design. Diets were assumed to be fixed factors, and periods and animals were random factors. The analysis of CH_4 emissions (L/d) corrected for a 24-h period and the CH_4 adjusted to BW (L/kg/d) had significant ($P = 0.0081$) linear and nonlinear decay patterns between CH_4 emissions and levels of DDG. Although the 20 and 40% DDG levels (DM basis) did not differ in reducing CH_4 emissions ($P = 0.16$), the linear relationship showed that for each percentage unit increase in DDG (DM basis) in the diet, a decrease ($P = 0.0027$) of 0.005 L/kg of BW/d of CH_4 emissions was observed. We concluded that 20% of DDG (DM basis) is sufficient to promote a significant reduction in CH_4 emission by cattle receiving DDG.

Key Words: abatement, greenhouse gas, respirometry

0649 Effects of including viginiamycin in feedlot diets containing monensin under commercial conditions in Mexico. M. Gorocica*[1], A. Gonzalez-Asif[2], and S. C. Loerch[3], [1]*Phibro Animal Health, Merida, Mexico,* [2]*SuKarne Agroindustrial, Culiacan, Mexico,* [3]*The Ohio State University, Wooster.*

A trial was undertaken to determine the effects of supplemental virginiamycin (VM) in combination with monensin (Mon) on finishing cattle performance. The trial was conducted in a large commercial feedlot in central Mexico. Upon arrival, 4874 crossbred bulls (LBW = 267.7 ± 21.32 kg) were dewormed, vaccinated against respiratory and clostridial pathogens and implanted with an estrogenic implant. At processing, cattle were randomly allotted to 84 pens with approximately 58 animals/pen. Two dietary supplement treatments were randomly allotted to the 84 pens: a corn-soybean based concentrate diet containing 400 mg/hd/d of Mon (MON), and the MON diet supplemented with 200 mg/hd/d of VM (MON+VM). Cattle were gradually adapted to their final diet (14% protein, 1.56 Mcal NEg/kg) over a 21–28 d period. When cattle were 60 DOF, they were reimplanted with a Trenbolone acetate implant (200 mg TBA + 20 mg Estradiol benzoate). Zilpaterol chlorhydrate was provided to all cattle at 0.15 mg/kg BW for 28 d and was withdrawn 3 d before harvest. Cattle in all pens were harvested after 130 DOF. At harvest, HCW were recorded. Data were analyzed using the PROC MIXED of SAS for a complete randomized design. Pen was used as the experimental unit. At reimplant, MON+VM cattle had greater ADG and G:F (both, $P < 0.01$) than MON (1.83 and 0.208 vs. 1.78 and 0.189, respectively). Hot carcass yield was greater ($P < 0.01$) in MON+VM cattle than MON (62.9 vs. 62.1% respectively). Total ADG and G:F were improved by 5% (both $P < 0.01$) when VM was included in the ration (MON+VM: 1.74 and 0.186 vs. MON: 1.67 and 0.177 for ADG and G:F respectively). Hot carcass weight was 5.2 kg greater ($P < 0.01$) in MON+VM than in MON cattle (306.0 vs. 300.8 respectively). Virginiamycin inclusion to feedlot diets containing Mon improved feedlot performance and carcass weight.

Key Words: virginiamycin, feedlot,

0650 Effects of extracts of *Perilla frutescens* (seeds) on in vitro rumen fermentation, methanogenesis, and microbial population. M. Liu*[1], J. X. Liu[2], and J. K. Wang[1], [1]*Institute of Dairy Science, Zhejiang University, Hangzhou, China,* [2]*Zhejiang University, Hangzhou, China.*

Seeds of *Perilla frutescens* are rich in linolenic and linoleic acid. An in vitro incubation was performed to investigate the effects of extracts from *Perilla frutescens* seeds on rumen fermentation, methanogenesis, and microbial population. Five-hundred milligrams of substrate (mixture of Chinese wild rye and corn meals at 70:30, w/w) were incubated in 120-mL serum bottles. The fermentation medium was 5 mL of sheep rumen fluid and 45 mL of buffer medium. The seeds of *Perilla frutescens* were extracted by 70% ethanol. To accurately add 20 mg of extracts, the freeze-dried extracts were dissolved into dimethyl sulfoxide (DMSO) to a concentration of 40 mg/ml, and then 500 mL of the DMSO solution was added to the incubation system. In the control, 500μL of DMSO was used without extracts. After 24 h of incubation at 39°C, rumen fermentation parameters were measured and absolute abundance of total bacteria, protozoa, fungi, and methanogens were quantified using real-time PCR based on the 16S, 18S rDNA and *mcr*A gene, respectively. Total volatile fatty acids and ammonia nitrogen concentrations were not affected ($P > 0.05$) by extracts, while methane production was decreased by 63.6% ($P < 0.01$), from 0.723 to 0.263 mmol/g DM substrate. Addition of extracts induced a dramatic shift in the population of rumen microbota (Table 0650), indicating the decreased protozoa (99.5%, $P < 0.01$) and fungi numbers (99.5%, $P < 0.01$) and reduced methanogens (62.2%, $P < 0.01$). These data indicate that ethanol extracts from seeds of *Perilla frutescens* have potential to reduce rumen methanogenesis by inhibiting protozoa and activity of methanogens without adversely affecting rumen fermentation.

Key Words: methanogenesis, *Perilla frutescens*, rumen fermentation

Table 0650. Effects of extracts of *Perilla frutescens* (seeds) on microbial population (copies/g centrifuged fermentation mixtures)

	Control	Extracts	SEM	*P*-value
Total bacteria ($\times 10^{11}$)	7.12	6.81	0.472	> 0.05
Protozoa ($\times 10^{7}$)	666.9	3.4	98.7	< 0.01
Fungi ($\times 10^{5}$)	1684.3	8.3	239.5	< 0.01
Methanogens ($\times 10^{8}$)	11.8	4.5	1.39	< 0.01

0651 Effect of tannin or inoculum as silage additives on silage quality and rumen fermentation kinetics. V. J. Taha*[1], J. A. Huntington[1], R. G. Wilkinson[1], and D. A. Davies[2], [1]*Harper Adams University, Newport, UK,* [2]*Silage Solutions, Aberystwyth, UK.*

Tannin has the ability to bind with different compounds including protein and carbohydrate to form complex undegradable compounds. Tannin-protein complexes form in the rumen (pH 6–7) and disassociate in the abomasum (pH < 3.5) enhancing duodenal supply of dietary protein. The in vitro gas production technique can be used to predict rumen fermentation kinetics. The effect of additional tannin (hydrolyzable, chestnut) and a bacterial inoculant as additives at ensiling on final silage quality and in vitro rumen fermentation kinetics were investigated. Whole crop grass, pea, and bean forages were harvested on July 14, 2011, and ensiled in triplicate in experimental silos (25kg). Before ensiling, each forage was treated with one of four additives: 40 g/kg fresh weight (FW) tannin (HT), 20 g/kg FW tannin (LT), an inoculant (*L. plan-*

tarum) 10^6 colony-forming units/g FW (In), or untreated (C). A standard volume of water (1 mL/kg FW) was applied to all treatments. Silos were opened after 100 d and subsamples stored (-20°C) before analysis for: pH, NH_3–N, DM, NDF, CP, and water soluble DM component (WS). Rumen fluid was collected from four mature wethers (fitted with permanent rumen cannula) fed straw plus concentrates (80:20 DM basis) with ad libitum access to water. Gas production (in vitro) was measured as described by Theodorou et al. (1994; J. Feed Sci. Tech. 48:185–197) and results fitted to an exponential decay curve (SigmaPlot12). Duplicate samples were incubated for 72 h with four experimental periods. The experiment was analyzed as 3 × 4 factorial design using Genstat 15 (VSN International, UK). The addition of tannin significantly reduced NH_3–N compared to control silages (41.60, 48.76, 55.66 and 60.01 g/kg total N for HT, LT, In, and C respectively, SED = 1.976, $P < 0.001$). Moreover, both tannin levels reduced the WS compared to In and C (197.2, 235.4, 258.5, and 263.7 g/kgDM for HT, LT, In, and C, SED = 8.154 $P < 0.001$). There was no significant effect ($P > 0.05$) on other proximate analysis. Effect of additive on rumen fermentation kinetics for mean silages showed that additional tannin reduced the total gas pressure (300.3, 329.6, 370.1, and 375.1 kPa for HT, LT, In, and C, respectively, SED = 26.32, $P < 0.05$) and the rate of fermentation (0.034, 0.037, 0.039, and 0.043, SED = 0.0046, $P < 0.05$) for HT, LT, In, and C, respectively. Addition of tannin at ensiling reduced crop protein degradation in silo and reduced rumen fermentation potentially increasing the supply of UDP to the small intestine.

Key Words: tannin, silage, gas production

0652 Improving the performance of dairy cattle with a xylanase-rich exogenous enzyme preparation. J. J. Romero*[1], E. G. Macias[2], Z. Ma[1], R. M. Martins[3], B. Y. Coy[1], F. M. Silva[4], D. H. Garbuio[4], I. A. Brody[1], C. L. Curry[1], K. J. Mills[1], M. G. Zenobi[1], C. R. Staples[1], and A. T. Adesogan[1], *[1]Dep. of Animal Sciences, University of Florida, Gainesville, [2]Dep. de Zootecnia, Universidad Nacional Agraria La Molina, Lima, Peru, [3]Dep. de Zootecnia, Universidade Federal de Viçosa, Minas Gerais, Brazil, [4]Universidade Estadual Paulista, São Paulo, Brazil.*

The objective was to compare effects of two *Trichoderma reesei* exogenous fibrolytic enzyme preparations (EFE) on the performance of lactating dairy cattle fed a bermudagrass- and corn silage-based TMR. The first EFE (MIX) had increased the efficiency of feed utilization by lactating dairy cows in a previous study and the second xylanase-rich EFE (XYL) was the best of 18 EFE candidates at improving in vitro NDFD and rumen-like fermentation of bermudagrass haylage. Endoglucanase and xylanase activities of MIX and XYL were 2087 and 2714 and 10,549 and 26,926 µmol/min per g, respectively. Sixty-six lactating Holstein dairy cows in early lactation (588 ± 75 kg; 21 ± 5 DIM) were grouped by previous milk production and parity and randomly assigned to control (CON), XYL, or MIX treatments. The XYL and MIX EFE were added to the diet just before feeding at rates of 1 and 3.4 mL/kg of TMR DM, respectively. Cows were fed experimental diets for 70 d after they were fed a common diet for an 11-d covariate period. The statistical model included effects of enzyme, parity, week and their interactions, as well as covariate milk production or DMI. The random effect was cow nested within treatment and parity. Body weight and condition score were not affected by treatment. Compared to CON, application of XYL increased ($P < 0.05$) intake (kg/d) of DM (28.6 vs. 27.4), OM (26.7 vs. 25.5), and CP (4.7 vs. 4.5), but MIX did not. Cows fed XYL had greater milk yield (kg/d) during wk 3 (41.2 vs. 39.8; $P < 0.10$), 6 (41.9 vs. 40.1; $P < 0.05$), and 7 (42.1 vs. 40.4; $P < 0.05$), as did those fed MIX during wk 6 (41.5 vs. 40.1; $P < 0.10$), 8 (41.8 vs. 40.0; $P < 0.05$), and 9 (40.9 vs. 39.5; $P < 0.10$). Cows fed XYL tended ($P < 0.10$) to produce more (kg/d) FCM (41.8 vs. 40.7) and fat yield (1.48 vs. 1.44) than those fed CON. Feeding with the EFE increased milk production by dairy cows.

Key Words: dairy cattle, enzyme, TMR

0653 Effects of feeding chitosan on nutrient digestibility in beef heifers. D. D. Henry*, F. M. Ciriaco, V. R. G. Mercadante, T. Schulmeister, D. Demeterco, A. Marin, G. C. Lamb, and N. DiLorenzo, *University of Florida, Marianna.*

The objective of this study was to determine whether adding the biopolymer chitosan would increase efficiency of beef heifers by improving apparent total tract nutrient digestibility of a low quality diet. Twenty-four crossbred heifers (318 ± 35 kg) were used in a randomized block design replicated in two experimental periods. Heifers were stratified by weight and randomly assigned to 12 pens (two heifers/pen), and pens were randomly assigned to one of six treatments in a 2 × 3 factorial arrangement. Factors included diet [a high concentrate (85% concentrate; HC), and a low concentrate (36% concentrate; LC)], and chitosan inclusion level (0.0, 0.5, and 1.0% of dietary DM). Heifers were housed in the University of Florida–Feed Efficiency Facility in Marianna, FL, where diets were offered ad libitum and individual intake was recorded by a GrowSafe system. Feed and fecal samples were collected for four consecutive days to determine apparent total tract digestibility of DM, OM, CP, NDF, and ADF using indigestible NDF (iNDF) as an internal digestibility marker. Feed samples were collected once a day, and fecal samples were collected by rectal grab twice daily (0700 h and 1500 h). Feed and fecal samples were pooled within pen and heifer, respectively. Concentrations of iNDF in feed and feces were determined by in vitro incubations conducted using a 4:1 buffer to ruminal fluid ratio for 288 h. Data were analyzed using PROC MIXED of SAS with heifer as the experimental unit, including the fixed effects of

diet and chitosan inclusion level, and the random effect of period. Orthogonal polynomial contrasts were conducted to determine linear and quadratic effects of chitosan inclusion level on nutrient digestibility. There was a diet × chitosan interaction for digestibility of DM ($P = 0.05$) and OM ($P = 0.04$). Inclusion of chitosan in LC at up to 1% diet DM linearly increased ($P < 0.05$) digestibility of DM and OM as compared to control (40.3 vs. 33.2%, and 41.1 vs. 34.5% for DM and OM digestibility, respectively). No differences ($P > 0.10$) were found for digestibility of CP, NDF, or ADF. In conclusion, adding 1% chitosan to low concentrate diets increased apparent total tract digestibility of DM and OM by 21 and 19%, respectively.

Key Words: beef, chitosan, digestibility

0654 Effect of *Saccharomyces cerevisiae* fermentation product (XP) on energetic efficiency of diet fed to high producing dairy cows during the hot season.

U. Moallem*, L. Livshitz, and M. Zachut, *Institute of Animal Science, Volcani Center, Bet Dagan, Israel.*

The objective was to test whether *Saccharomyces cerevisiae* fermentation product (XP, Diamond V, Cedar Rapids, IA) could compensate for lower energy density in diets by increasing digestive efficiency. Forty-two multiparous Israeli-Holstein dairy cows were divided into two treatment groups according to milk production, parity, DIM and BW. Treatments consisted of: 1) control, a common Israeli diet containing 1.78 Mcal NE_L/kg DM; 2) XP, a diet contained 1.75 Mcal NE_L/kg DM and supplemented with 50 g XP/cow/day. Diets were isonitrogenous and consisted of the same ingredients. The study was conducted for 14 wk during the typical hot season. Milk yield, DMI, rumination time, and lying time were recorded daily, and milk components were measured weekly. Rumen and blood samples were taken at the 12th wk of the study: -2, 0, 2, and 4 h relative to feeding time for rumen pH, VFA and ammonia, and plasma glucose and urea. Data were analyzed using the PROC MIXED model of SAS. Milk yields tended to be higher ($P < 0.1$) in control than in XP group, and FCM (4%) yields and milk components percentages and yields were similar between treatments. No treatment effect was observed for daily rumination and resting time. The energy intake was lower (48.9 and 50.5 Mcal/d, respectively; $P < 0.05$), and DMI tended to be lower ($P < 0.1$) in cows supplemented with XP than in control cows. Energy in milk per energy consumed tended to be higher ($P < 0.1$) in cows supplemented with XP, and resulted in similar feed efficiency (milk, ECM, or FCM/DMI). Plasma glucose concentrations were higher in cows supplemented with XP than in control cows (66.2 and 63.8 mg/dL, respectively; $P < 0.05$). Plasma urea concentrations were 15% lower ($P < 0.001$), and rumen ammonia concentrations were also lower in cows supplemented with XP than in control cows (125.8 and 157.2 μg/ml, respectively; $P < 0.001$). Rumen pH was higher in cows supplemented with XP than in the control group (6.76 and 6.57, respectively; $P < 0.05$). Rumen propionic, butyric, and total VFA concentrations were higher ($P < 0.05$) in control cows than cows supplemented with XP, whereas the acetic/propionic ratio tended to be higher ($P < 0.1$) in cows supplemented with XP. In conclusion, supplementation of 50 g XP/d to dairy cows fed a lower energy diet increased energy availability, potentially through improved ruminal nitrogen metabolism and increased supply of glucose for milk production.

Key Words: energetic efficiency, XP, nitrogen metabolism

RUMINANT NUTRITION VI

0655 Effect of rumen-protected lysine supplementation of corn-protein based diets fed to lactating dairy cows. N. E. Lobos*[1], G. A. Broderick[2], and M. A. Wattiaux[3], *[1]Dep. of Dairy Science, University of Wisconsin–Madison, Madison, [2]Broderick Nutrition & Research, LLC, Madison, WI, [3]University of Wisconsin–Madison, Madison.*

This trial tested whether rumen-protected Lys (RPL) supplementation would improve the nutritive value of RUP from corn protein. Thirty-two lactating Holstein cows were blocked by DIM and parity into eight squares of four cows in replicated 4 × 4 Latin squares. Treatments were all supplemental CP from: 1) Soy [67% expeller soybean meal (ESBM) plus 33% solvent soybean meal (SSBM)]; 2) Soy/Corn [33% ESBM, 17% SSBM, 25% corn gluten meal (CGM) plus 25% distillers dried grains plus solubles (DDGS)]; 3) Corn (50% CGM plus 50% DDGS); or 4) Corn/RPL [diet 3 top-dressed with RPL (125 g Ajipro/d, an estimated 20 g absorbed Lys/d)]. Diets contained (DM basis) 22% alfalfa silage, 43% corn silage, 18% ground high moisture and dry corn, 2.4% mineral-vitamin premix, 1.5–3.9% soyhulls, 15% CP, 30–32% NDF, and, as predicted by NRC (2001), equal RDP, RUP and metabolizable protein. Cows within squares were randomly assigned to treatment sequences and fed diets for 4-wk periods before switching; data from the last 2 wk were analyzed using the PROC MIXED of SAS. The Table 0655 reports LS-means. Intake was highest on diet 1, intermediate on diets 2 and 3, and lowest on diet 4; BW change was highest on diet 3, intermediate on diets 1 and 2 and lowest on diet 4. Intakes and BW changes were reflected by differences in Milk/DMI, which were highest on diets 2 and 4 and lowest on diet 3. Milk yield was lower on diet 3 than on diets 1, 2, and 4, and protein yield was highest on diets 1 and 2, intermediate on diet 4, and lowest on diet 3. These results indicated that dilution of soybean meal RUP with that from corn protein did not reduce milk yield and adding RPL to the corn-protein based diet increased milk and protein yields.

Key Words: soybean meal, corn gluten meal, corn distillers dried grains, rumen-protected Lys

Table 0655. Effect of Dietary CP Source and Rumen-Protected Lys on Production

Item	Soy	Soy/Corn	Corn	Corn/ RPL	SE	P > F
DMI, kg/d	27.7[a]	27.4[ab]	26.9[bc]	26.8[c]	0.40	< 0.01
BW change, kg/d	0.03[bc]	0.59[ab]	0.70[a]	-0.07[c]	0.23	0.04
Milk, kg/d	45.8[a]	46.1[a]	44.3[b]	45.4[a]	1.17	0.01
Milk/DMI	1.66[ab]	1.69[a]	1.65[b]	1.69[a]	0.038	0.04
Fat, kg/d	1.87	1.87	1.83	1.83	0.060	0.37
True protein, kg/d	1.36[a]	1.34[a]	1.25[c]	1.30[b]	0.029	< 0.01
MUN, mg/dL	10.6	10.6	10.8	11.1	0.25	0.06

[abc] **($P < 0.05$)**

0656 Effects of a rumen protected lysine (AjiPro-L) supplementation on peripartum disease, reproduction, and lactational performance of dairy cows. J. E. Nocek*[1], A. Haruno[2], M. Miura[2], T. Takagi[2], I. Shinzato[3], and T. Fujieda[2], *[1]Spruce Haven Farm and Research Center, Auburn, NY, [2]Ajinomoto Co., Inc.,, Tokyo, Japan, [3]Ajinomoto Heartland, Inc., Chicago, IL*

We used 108 multiparous cows to examine the effects of feeding AjiPro-L (Ajinomoto Co., Inc., Tokyo) 21 d pre- through 21 d postpartum and then withdrawal. Cows were assigned to one of four pre/postpartum regimens: a) Control:Control (C/C), b) 100 g AjiPro-L:Control (A/C), c) Control:150 g AjiPro-L (C/A), and d) 100 g AjiPro-L:150 g AjiPro-L (A/A). All cows started their treatment regime 21 d before expected calving date through 21 d postpartum (phase 1). Upon completion of the 21 d postpartum period, all cows were moved to a common group and fed the same diet without AjiPro-L (phase 2, 21–63 DIM). Individual DMI and milk yield were measured daily, and milk components weekly throughout both phases. Body weights, BCS, health incidence were recorded. During phase 1, DMI was not affected in the prepartum period by AjiPro-L inclusion. Postpartum, cows on A/C consumed more ($P = 0.05$) DM than C/C and C/A, with A/A cow not being different. Milk yield was highest ($P = 0.04$) for cows receiving A/A compared to C/C, with other treatments not being different. Milk fat yield was higher ($P = 0.04$) for cows supplemented with A/A compared to C/C and C/A, but not different from A/C. Cows receiving the C/A had higher milk protein percentage than A/C and A/A and not different from C/C. Milk fat percentage and milk protein yields were not affected by treatment regimens. During phase 2, no differences in body weight, BCS or milk yields were observed. Milk fat yield was higher ($P = 0.05$) for A/C and A/A cows compared to C/A with C/C not being different. Milk protein percentage was higher ($P = 0.02$) for C/A cows than those on C/C or A/A regime, with A/C not being different. Cows on A/C had higher ($P = 0.05$) milk fat percentage than C/C and C/A, not being different than A/A. Cows on A/C exhibited lower incidences of displaced abomasum and ketosis than other regimens. These results suggest that AjiPro-L supplementation both pre- and postpartum generally resulted in the most consistently positive production performance immediate postpartum than other regimens. It was also suggested that feeding AjiPro-L only prepartum had some specific effects on postpartum health status and production performance.

Key Words: lysine, milk production, transition period

0657 Effect of strategic ration balancing with use of Prolak and USA-Lysine on the efficiency of milk protein production and environmental impact. J. H. Harrison[1], J. Jarrett[2], Y. Chen[*3], L. VanWieringen[4], B. Chalupa[5], F. Sun[3], P. Ndegwa[3], D. Wilks[6], and H. S. Joo[3], *[1]Washington State University, Puyallup, [2]Prince Agri, Quincy, IL, [3]Washington State University, Pullman, [4]Washington State University, Sunnyside, [5]University of Pennsylvania, New Bolton Center, [6]EPL Feeds, Dixie, WA.*

The objective of this study was to evaluate the effect of a diet supplemented with a high quality protein and rumen protected lysine source on the efficiency of milk production and environmental impact in a commercial dairy herd. The general herd diet was reformulated with the Agricultural Model and Training System model and use of Prolak and USA-lysine. The control and treated diet had similar dietary CP concentration (17.7% vs. 17.6%). Cows were completely randomized to two groups with 163 cows each pen and milked three times per day. The groups had similar average days in milk (135 vs. 135) and parities (2.99 vs. 2.84) before initiation of the trial. Respective diets were fed in a 40 d switch back design trial with two periods. Milk weight (all three milkings), and milk (sample from one of three milkings) and manure samples were obtained at the end of second and third weeks of each period for analysis. Cows fed the two diets had similar pen DMI (24.2 vs. 24.1 kg/d), but the reformulated diet supported more milk yield (43.0 vs. 44.9 ± 0.15 kg/d), milk protein yield (1.27 vs. 1.33 ± 0.01 kg/d), milk fat yield (1.51 vs. 1.57 ± 0.01 kg/d), and increased ratio of milk true protein to total protein intake (29.4 vs. 31.2%) and ratio of total milk protein to total protein intake (34.3 vs. 36.5%). The concentration of MUN was higher when cows were fed reformulated diet (16.5 vs. 18.7 mg/dl). Cows fed the reformulated diet consumed 2.6% less N, but produced 4.7% more milk N, and excreted 6.2% more predicted urinary N and 24% less calculated fecal N. Manure from cows fed the reformulated diet had lower ammonia (NH3) flux (145 vs. 130 mg*h^{-1}*m^{-2}). This study illustrates that diets supplemented with high quality protein could improve efficiency of milk production and N utilization, and reduce the environmental impact.

Key Words: protected lysine, bypass protein, milk production

0658 Effect of strategic ration balancing with use of Prolak and MetaboLys on the efficiency of milk protein production and environmental impact. P. Ndegwa[1], J. H. Harrison[2], D. Wilks[3], L. VanWieringen[4], Y. Chen[*1], W. Chalupa[5], F. Sun[1], and H. S. Joo[1], *[1]Washington State University, Pullman, [2]Washington State University, Puyallup, [3]EPL Feeds, Dixie, WA, [4]Washington State University, Sunnyside, [5]University of Pennsylvania, New Bolton Center.*

The objective of this study was to evaluate the effect of reduced dietary CP concentration on efficiency of N utilization and environmental impact in a commercial dairy herd. The general herd diet was reformulated with the Agricultural Modeling and Training System model and use of Prolak and MetaboLys. Reformulation reduced the dietary CP concentration (17.4 vs. 15.9%) and resulted in a DCAD of 31.3 vs. 21.2 mEq/100 g DM. Cows were completely randomized to two groups with 155 cows each and milked three times per day, and the two groups had the same average days in milk (DIM = 149) before initiation of the study. Respective diets were fed in a 40-d switch back design trial with two periods. Milk weight, milk, and manure samples were obtained at the end of the second and third week of each period. The manure samples were incubated in closed chambers for 19 d to measure ammonia (NH3) flux. Average pen DMI was similar (25.1 vs. 25.3 kg/d). The reformulated diet supported 0.6 kg less milk production (44.3 vs. 43.7 ± 0.16kg/d), less milk protein yield (1.27 vs. 1.25 ± 0.01kg/d) and the same amount of fat yield (1.48 vs. 1.46 ± 0.01kg/d), but increased the ratio of true protein/total CP intake (28.4 vs. 30.6%) and milk CP/total CP intake (33.3 vs. 38.6%). The concentration of MUN was lower for cows fed the reformulated diet (13.4 vs. 11.56 mg/dl). When the cows were fed reformulated diet, they consumed 9% less N, produced 1% less milk N, but excreted 14% less predicted urinary N and 15.4% less calculated fecal N. The manures from the reformulated diet had a lower NH3 flux (147 vs. 137mg*h^{-1}*m^{-2}). This study illustrated that the lower N diet could improve the efficiency of N utilization and reduced the environmental impact, but may influence the milk production.

Key Words: milk protein, lysine, rumen undegradable protein

0659 Evaluation of diets formulated with soybean-based products, blood meal, or rumen-protected lysine to meet MP lysine demands of lactating dairy cows. W. D. Weich[*1], K. F. Kalscheur[1], K. J. Herrick[2], and F. R. Valdez[2], *[1]South Dakota State University, Brookings, [2]Kemin Industries, Inc., Des Moines, IA.*

Objectives were to determine if production of early to mid-lactation dairy cows was maintained when fed diets formulated to be similar in grams of metabolizable protein (MP) lysine and methionine but lower in CP. Diets were formulated using: 1) soy-based protein (positive control; PC, 17.7% CP,

204 g/d MP-lys), 2) blood meal and soy-based protein (BM; 16.4% CP, 203 g/d MP-lys), or 3) rumen-protected lysine and soy-based protein (RPL; 16.2% CP, 205 g/d MP-lys). Diets formulated to desired MP lysine (204 g/d) were compared with a negative control diet lower in MP lysine (LL; 16.2% CP, 193 g/d MP-lys) created by removing dietary RPL. Diets were formulated using AMTS (Version 3.4.7.1). Sixteen Holstein cows blocked by parity (12 multiparous) and production were assigned one of four treatments arranged in a 4 × 4 Latin square design with 28-d periods. The model included: treatment, square, treatment × square, and period. Treatments were prepared as four separate concentrate mixes that were combined with common amounts of corn silage (36% of diet DM) and alfalfa hay (19%) among diets. Milk production was similar ($P > 0.10$), comparing BM and RPL with PC or LL, but tended ($P = 0.06$) to be greater for BM over RPL. Cows fed BM and RPL had lower ($P = 0.04$) DMI than LL; however, ECM was sustained which led to an increase in feed efficiency comparing BM and RPL with LL. Performance of lower CP diets, BM, and RPL, were similar to PC, but performance from LL suggests that MP supply was sufficient across treatments.

Key Words: amino acid, lysine, metabolizable protein

Table 0659.

Item	Treatment				SEM	Contrast[1]
	PC	BM	RPL	LL		
DMI, kg/d	26.16	25.64	25.46	26.66	0.61	B
Milk, kg/d	39.47	40.44	38.81	39.50	1.08	d
ECM	39.35	40.43	39.37	39.88	1.36	–
ECMFE	1.53	1.59	1.59	1.52	0.05	a, B
Fat, %	3.47	3.54	3.59	3.55	0.12	–
Fat, kg/d	1.35	1.42	1.39	1.40	0.06	–
Protein, %	3.17	3.06	3.10	3.13	0.08	A, b
Protein, kg/d	1.25	1.23	1.20	1.23	0.05	–
MUN, mg/dL	16.59	13.92	14.03	13.46	0.33	A, b

[1] Contrasts: A = PC vs. BM + RPL; B = BM + RPL vs. LL; D = BM vs. RPL. Uppercase = $P < 0.05$, lowercase = $0.05 < P < 0.10$.

0660 The plasma free amino acid dose response technique: A proposed approach for determining lysine bioavailability of ruminally protected lysine products.

N. L. Whitehouse*[1], A. F. Brito[1], and C. G. Schwab[2], *[1]University of New Hampshire, Durham, [2]Schwab Consulting, LLC, Boscobel, WI.*

While most companies provide estimates of lysine (Lys) bioavailability for their products, values are often obtained with different techniques, and there are little to no data comparing efficacy and cost-effectiveness of different products. Our objective is to propose that the plasma free amino acid (AA) dose–response technique be accepted as the standardized method for evaluating rumen protected Lys (RP-Lys) products, because its animal-derived estimates of bioavailability are obtained under conditions similar to commercial use. Bioavailability estimates are calculated by dividing the slope of the regression line relating changes in plasma Lys to increased feeding of RP-Lys divided by the slope of the Lys infusion regression line. Eleven dose–response Latin square trials using 66 lactating, ruminally cannulated multiparous Holstein cows (d in milk = 60 through 315; milk yield = 25 to 62 kg/d at the start of the study) were conducted. Abomasally infused and fed amounts of Lys ranged from 0 to 84 g/d and periods from 4 to 21 d. The RP-Lys products were mixed with 1 kg of total mixed ration, placed in tubs, and fed 30 min before each of the three daily feedings. Product not consumed within 20 min was delivered via the ruminal cannula. Diets were formulated (NRC, 2001) to be adequate in metabolizable protein-Met but varied in predicted metabolizable protein-Lys (5.04–6.81%). One to four blood samples were taken from the tail vein for 1 to 3 d in each period. Basal plasma Lys concentrations ranged from 2.14 to 5.62% of total AA without infusions, from 2.33 to 5.67% of total AA for fed RP-Lys, and from 2.94 to 8.62% of total AA with infusions. Results corroborate previous research that showed a positive linear relationship between both infused and fed RP-Lys and plasma Lys concentrations. Regression analysis (by trial and cow) indicated the two factors that most affected the magnitude of the response slopes, and hence the technique's precision, were the cows basal level of plasma Lys (i.e., intercept, the lower the better) and the cows plasma Lys response to infused Lys (measured by the magnitude of their response to the highest level of infused Lys). Stage of lactation and milk production did not affect plasma Lys response. It is concluded that the plasma free AA dose response technique is sensitive to increasing amounts of absorbed Lys and therefore is an appropriate technique for evaluating RP-Lys supplements.

Key Words: technique, bioavailability, lysine

0661 Effects of maternal nutrition and rumen-protected arginine supplementation on pregnant and non-pregnant ewe and postnatal lamb serum amino acids.

J. L. Peine*[1], G. Jia[1], M. Kapphahn[1], S. T. O'Rourke[1], A. M. Meyer[2], L. P. Reynolds[1], and J. S. Caton[1], *[1]North Dakota State University, Fargo, [2]Div. of Animal Sciences, University of Missouri, Columbia, MO.*

Our hypothesis was that rumen-protected arginine supplementation would increase levels of serum amino acids in both non-pregnant and pregnant ewes and their offspring, and thereby help overcome negative effects of nutrient restriction during the last two-thirds of gestation. To test this hypothesis, two studies were conducted with Rambouillet ewes penned individually in a temperature-controlled facility: Study 1 was a dose titration study to determine the most effective dose of rumen-protected arginine, and Study 2 tested our hypothesis in pregnant ewes and their lambs. Study 1 used non-pregnant primiparous ewes ($n = 60$) randomly assigned to one of four treatments: a control group receiving no supplement (0), and groups receiving 90mg/kg BW (90), 180mg/kg BW (180), or 360mg/kg BW of rumen-protected

arginine supplement (360). After 15 d of supplementation, ewes receiving 180 had greater serum ornithine ($P = 0.05$) and arginine ($P = 0.05$), and tended to have greater aspartate ($P = 0.08$) than ewes receiving 90, and 180 were similar to 360 fed ewes ($P \geq 0.55$). In Study 2, multiparous ewes ($n = 32$) were allocated to trhee treatments at 54 ± 3.9 d of gestation: 100% of requirements (control, CON), 60% of control (restricted, RES), or RES plus a 180 mg/kg BW rumen-protected arginine supplement once daily (RES-ARG). Ewes were maintained on treatments through parturition, when lambs were removed from dams and reared independently. At 128 d of gestation, CON ewes weighed more ($P \leq 0.001$) than RES and RES-ARG ewes, and had greater ($P \leq 0.001$) BCS. In addition, serum ornithine, citrulline, aspartate, arginine, and methionine were greater ($P \leq 0.03$) in CON than RES and RES-ARG ewes, suggesting that arginine supplementation could not overcome differences in nutritional plane. Lambs from CON ewes had greater ($P = 0.03$) birth weights than RES, with lambs from RES-ARG ewes being intermediate and similar in weight to other treatments ($P \geq 0.08$). At birth, lambs from RES-ARG ewes had greater serum arginine ($P = 0.04$) and lysine ($P = 0.04$) than those from RES ewes, suggesting effects on amino acid transport from dam to fetus. These results support our hypothesis that maternal rumen-protected arginine supplementation could increase serum levels of amino acids in offspring. Additionally, arginine supplementation of dams may be able to increase fetal circulating arginine without altering maternal circulating arginine.

Key Words: arginine, amino acids, developmental programming

0662 Intestinal digestibility of amino acids in fluid- and particle-associated rumen bacteria determined using a precision-fed cecectomized rooster bioassay.

A. C. Fonseca[1], S. M. Fredin[*1], L. F. Ferraretto[1], P. L. Utterback[2], C. M. Parsons[2], and R. D. Shaver[1], *[1]Univeristy of Wisconsin, Madison, [2]University of Illinois at Urbana-Champaign, Urbana.*

Microbial protein represents the majority of metabolizable protein absorbed by ruminant animals. Enhanced understanding of the AA digestibility of rumen microbes will improve estimates of metabolizable protein. The objective of this experiment was to determine the digestibility of AA in fluid- (FAB) and particle-associated bacteria (PAB) using the precision-fed cecectomized rooster bioassay. Bacteria were isolated from four ruminally cannulated lactating Holstein cows fed an 89% forage diet (DM basis). Samples of FAB and PAB were fed to nine cecectomized roosters to determine standardized digestibility of AA. Data were analyzed using PROC MIXED (SAS, 2004). Bacterial N composition (average = 8.3%) was similar to previous literature values. Total AA digestibility was (mean ± SE) 76.8 ± 2.4 and 75.5 ± 2.2% for FAB and PAB, respectively. Amino acid digestibility did not differ between FAB and PAB ($P > 0.05$). There were differences in essential (EAA) and non-essential AA digestibility within bacterial type when compared with mean essential or non-essential AA digestibility values ($P < 0.05$). Arginine, His, and Met were greater than the mean EAA digestibility in FAB, whereas Trp and Val were lower. Arginine and Lys were greater than the mean EAA digestibility in PAB, whereas Phe and Val were lower. Compared with previous literature and relative to NRC (2001) estimates of AA digestibility in microbes, the precision-fed cecectomized rooster assay is an acceptable in vivo model to determine AA digestibility of rumen bacteria.

Key Words: amino acid, digestibility, rumen bacteria

0663 Performance by holstein steers offered hay and supplement with or without added methionine.

A. L. Bax[*1], J. D. Caldwell[1], L. S. Wilbers[1], B. C. Shanks[1], T. Hampton[2], S. E. Bettis[2], Y. Liang[2], and G. I. Zanton[2], *[1]Dept. of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO, [2]Novus International, Inc., St. Charles, MO.*

Recently, amino acid supplementation by forage-fed cattle has been examined in greater detail. Methionine can restrict productivity of many ruminant animals, chiefly because microbial protein, the main source of metabolizable protein in forage-based ruminant diets, is most limiting in methionine. The objective of this study was to evaluate steer performance when offered hay and a supplement with or without added methionine as MFP (MFP). On Oct. 24, 2013, a total of 90 (230 ± 2.2 kg body weight) Holstein steers were stratified by body weight within five blocks and were allocated randomly to one of two treatments: 1) control supplement (C; 15 replications) or control supplement plus MFP (15 replications). Each replication had access to a 0.4-ha pasture with limited forage available for grazing and were offered ad libitum access to medium quality hay, water, and shelter. A soybean hull and wheat middling based, pelleted supplement was offered daily at 0.5% of body weight for each replication; in addition the supplement contained minerals, and vitamins. Treatment was provided at 1.17% of supplement DM resulting in an average intake of approximately 15 g/d of MFP. Hay offered did not differ ($P = 0.62$) across treatments. Initial, d 14, and d 28 body weights did not differ ($P \geq 0.11$) across treatments, but d 42 and d 56 body weights were greater ($P \leq 0.05$) from pastures receiving MFP compared with C. Average daily gain and gain at d 14 did not differ ($P \geq 0.27$) across treatments. However, d 28 ADG and gain tended ($P \leq 0.07$) to be greater from MFP compared with C and were greater ($P \leq 0.03$) at d 42 and d 56 from MFP compared with C. Through 56 d, steers in pastures offered MFP gained 5.0 ± 2.1 kg/hd more ($P < 0.03$) body weight than steers fed C. It is concluded that, when steers were offered medium quality hay, providing a supplement that contained MFP showed improved body weights, ADG, and total gain through the backgrounding phase.

Key Words: methionine, backgrounding, steers

0664 Effects of feeding slow release NPN and microbial fermentation extracts on lactation performance of high-producing dairy cows. F. Díaz-Royón[*1], A. D. Garcia[1], K. F. Kalscheur[2], and K. Mjoun[3], *[1]Dairy Science Dep., South Dakota State University, Brookings, [2]South Dakota State University, Brookings, [3]Alltech, Brookings, SD.*

The objective of this study was to examine the effects of partial substitution of soybean meal with a product containing slow release NPN and microbial fermentation extracts [(OPT); Optimase Alltech Inc., Nicholasville, KY)] in diets with two forage concentrations. Sixteen lactating Holstein dairy cows (four primiparous and 12 multiparous) were randomly assigned to a 4 × 4 Latin square in a 2 × 2 factorial. High and low forage diets contained respectively 61% (HF) and 46% forage (LF), with (O) and without OPT (NO). Forage consisted of 75% corn silage and 25% alfalfa hay (DM basis). Experimental diets containing OPT (125 g/cow/day) were designed to partially replace soybean meal 48 (0.625 kg) with forage fiber [corn silage (0.225 kg) and alfalfa hay (0.075 kg)] and non-forage fiber [soybean hulls (0.200 kg)]. Feeding cows HF versus LF reduced DMI, milk, ECM, protein %, and protein yield, but increased fat % (Table 0664, $P < 0.05$). Feeding OPT decreased ($P = 0.033$) DMI 1.05 kg/d compared to diets without OPT. Milk yield decreased ($P = 0.046$) slightly with OPT inclusion; however, 4%FCM and ECM were not affected. Feeding OPT did not affect milk fat percentage and yield, lactose percentage, and total solids percentage and yield. Milk protein yield decreased ($P = 0.013$) 3.5% in cows fed OPT. OPT fed both in HF and LF diets as a partial replacement to soybean meal resulted in similar lactation performance (4% FCM and ECM) and feed efficiency despite a decrease in DMI and milk yield.

Key Words: slow-release-NPN, microbial fermentation extracts, dairy cows

Table 0664.

	HF		LF			*P* value[1]	
Item	NO	O	NO	O	SEM	F	O
DMI, kg/d	26.4	25.5	29.5	28.3	0.76	< 0.001	0.033
Milk, kg/d	41.2	40.0	43.5	42.5	1.44	< 0.001	0.046
4% FCM, kg/d	42.3	40.9	43.0	42.7	1.25	0.165	0.362
ECM, kg/d	44.8	43.1	46.1	45.6	1.25	0.038	0.247
Fat, %	4.22	4.20	3.96	4.06	0.13	0.024	0.648
Fat, kg/d	1.72	1.66	1.71	1.72	0.06	0.681	0.590
Protein, %	3.07	3.00	3.14	3.14	0.05	< 0.001	0.058
Protein, kg/d	1.25	1.19	1.35	1.32	0.03	< 0.001	0.013
ECM:DMI	1.71	1.70	1.57	1.61	0.04	0.001	0.624

[1] There were no interactions forage by OPT.

0665 Concentration of soluble non-ammonia nitrogen and related transporter expression in non-mesenteric gastrointestines of dairy cows. Y. M. Xie[1], Q. B. Xu[*1], Y. M. Wu[1], and J. X. Liu[2], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Zhejiang University, Hangzhou, China.*

Dietary protein is gradually degraded from peptide-bound amino acids (PBAA) into free amino acids (FAA) and ultimately into ammonia by the rumen microbes. Both PBAA and FAA are milk protein precursor, and the rumen and small intestines are the main sites where milk protein precursor is produced and absorbed. This work was designed to investigate the concentrations of PBAA, FAA and soluble protein and the expression of peptide transporter (PepT-1) and amino acid transporters in the rumen, omasum, and duodenum of dairy cows. The digesta and tissues were collected from six healthy Holstein dairy cows (BW = 643 ± 67.4 kg and milk yield = 13.4 ± 2.05 kg/d) immediately after the animals were slaughtered. The FAA was assessed by amino acid (AA) analyzer, PBAA was by quantification of AA before and after acid-hydrolysis by 6M HCl, and soluble protein was by bicinchoninic acid. Concentrations of FAA, PBAA, and soluble protein are shown in Table 0665. Concentration of all portions of non-ammonia nitrogen was the highest in the duodenum. The PBAA was the largest component of soluble non-ammonia nitrogen in all the digesta from rumen, omasum, and duodenum, indicating that peptides may be the main form absorbed in these sites. Abundance of PepT-1 mRNA was consistent with the concentrations of PBAA from rumen to duodenum. Expression of all genes was greater in the duodenum than in the rumen and omasum, suggesting that the duodenum is the major nonmesenteric site where peptides are transported and absorbed.

Key Words: gastrointestine; milk protein precursor; peptide-bound amino acids

Table 0665. Concentrations of soluble non-ammonia nitrogen (mg N/100ml) in rumen, omasum, and duodenum ($n = 6$)

	Rumen	Omasum	Duodenum	SEM	P-values
Free amino acid	22.4[B]	49.9[B]	189.8[A]	24.5	< 0.01
Peptide-bound amino acids	40.0[B]	73.3[B]	285.5[A]	35.8	< 0.01
Soluble protein	15.1[B]	34.6[B]	168.4[A]	16.4	< 0.01
Total	77.5[B]	157.7[B]	643.6[A]	65.8	< 0.01
Peptide-bound/Total (%)	51.6	46.5	44.4		

[A,B] Values with different letters differ significantly ($P < 0.01$).

0666 Role of proton-coupled oligopeptide transporter 1 in small peptide absorption in the bovine forestomach. Q. B. Xu*[1], Y. M. Wu[1], H. Y. Liu[1], and J. X. Liu[2], [1]*Institute of Dairy Science, Zhejiang University, Hangzhou, China,* [2]*Zhejiang University, Hangzhou, China.*

In this work, transepithelial transport of glycylsarcosine (Gly-Sar) in bovine forestomach cells was determined to investigate the role of proton-coupled oligopeptide transporter 1 (PEPT1) in small peptide absorption. Primary cultured omasal epithelial cell (OEC) and rumen epithelial cell (REC) monolayers derived from newborn Chinese Holstein male calves were grown in transwell set-up. The transepithelial electrical resistance of transwell model reached plateau after a week, and that of OEC monolayers was higher than that of REC monolayers (2468 ± 216 vs. 1918 ± 33 $\Omega \cdot cm^2$). Fluorescein sodium was used to measure the permeability of monolayers. After 150 min, transmittances of fluorescein sodium across OEC and REC monolayers were 0.63 and 0.19%, respectively, whereas that of control (blank filter) was 12.0%. The monolayers were then used for incubation with various concentrations of Gly-Sar in apical side at various pH values or at 37°C and 4°C for various times. In addition, mRNA of PEPT1 was detected in OECs and RECs. The cells were also incubated in absence or presence of 0.5 mM diethylpyrocarbonate, an inhibitor of PEPT1. Transportation of Gly-Sar was dependent on concentration, incubation time, temperature and pH value. Accumulation of Gly-Sar in basolateral side (pH 7.4) increased with the increasing level of Gly-Sar and reached a plateau at 5 mM. Transportation of Gly-Sar by OEC monolayers was higher at 37°C compared to 4°C ($P < 0.05$), with an optimal pH of 6.0 to 6.5, and inhibited by diethylpyrocarbonate. In addition, accumulation of Gly-Sar in basolateral side of OEC monolayers was greater than that of REC ($P < 0.05$), indicating that the OECs have greater ability to transport Gly-Sar than RECs. In summary, the PEPT1 plays an important role in small peptide absorption in bovine forestomachs.

Key Words: bovine forestomach epithelial cells, oligopeptide transporter 1, transport

RUMINANT NUTRITION VII

0667 Effect of reduced energy density of close-up diet on ruminal fermentation parameters in multiparous Holstein cows. W. M. Huang*, A. Simayi, A. Yasheng, Z. H. Wu, Z. J. Cao, and S. L. Li, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing.*

The objective of this study was to determine the effect of reduced energy density of close-up diet on ruminal fermentation parameters in multiparous Holstein cows. Fourteen dry cows were utilized in a randomized block design. Cows were blocked by their milk production in the first 3 mo of the previous parity, BW, and expected calving date and assigned randomly into one of three energy levels (6.8, 6.2, 5.4 MJ of NE_L/kg; 14.0% CP) diets to meet 100% (100NRC; n = 4), 90% (90NRC; n = 5), 80% (80NRC; n = 5) of the NRC (2001) dietary NE_L recommendation, respectively, from 21 d before expected day of calving. After parturition, all cows were fed the same lactation diet to 28 d in milk (DIM). Intake of DM (DMI) of individual cows was determined every day. Ruminal fluid was obtained at 1030 h on -21, -14, −7, 1, 3, 5, 7, 14, 21, and 28 d relative to parturition, and at 0830, 1030, 1230, 1430, 1630, and 1830 h on 7 DIM, at 0930, 1130, 1330, 1530, 1730, and 1930 h on 8 DIM. Data were analyzed by SPSS with repeated measures procedure. The reduced energy density diet decreased the average DMI prepartum ($P < 0.05$) and tended to increase the DMI postpartum ($P = 0.08$). The average ruminal pH of the 80NRC group was higher prepartum (6.88, 6.35, 6.44; $P < 0.05$) and lower (6.05, 6.21, 6.30; $P < 0.05$) during the first 4 wk of lactation compared with 90NRC and 100NRC groups. The 80NRC group had three sampling points of pH below 5.6 on 7 and 8 DIM, none for 90NRC and 100NRC groups. The reduced energy density diet depressed the average ruminal concentration of propionate (16.7, 17.9, 19.6 mmol/L; $P = 0.04$), tended to decrease butyrate (7.4, 9.4, 10.4 mmol/L; $P = 0.06$) prepartum, and increased the average concentration of total VFA (112.6, 95.8, 92.0 mmol/L; $P < 0.001$) and decreased the ratio of acetate to propionate (2.4, 2.3, 2.7; $P = 0.03$) during the first 4 wk of lactation. In conclusion, the cows fed reduced energy density diet prepartum had higher VFA concentration for energy metabolism but were more susceptible to subacute ruminal acidosis postpartum.

Key Words: Holstein cow, dietary energy density, ruminal parameters

0668 Prepartum dietary energy strategies for Holstein dairy cows: Effects on markers of negative energy balance and performance. S. Mann*[1], F. A. Leal Yepes[2], T. R. Overton[2], J. J. Wakshlag[3], and D. V. Nydam[1], *[1]Cornell University, Dep. of Population Medicine and Diagnostic Sciences, Ithaca, NY, [2]Cornell University, Depar. of Animal Science, Ithaca, NY, [3]Cornell University, Dep. of Clinical Sciences, Ithaca, NY.*

Study objectives were to compare different dry cow nutritional strategies and their influence on peripartal concentrations of β-hydroxybutyrate (BHBA) and nonesterified fatty acids (NEFA) as analytes related to negative energy balance and periparturient dry matter intake (DMI) and milk yield. Cows (n = 84) were dried off 57 d before expected calving and assigned to one of three diets: a controlled-energy diet (L) that was formulated to meet, but not greatly exceed, energy requirements for the entire dry period; a step-up approach (I) in which animals received diet L for the first 4 wk of the dry period and after that a diet supplying 125% of energy requirements until calving; and a higher energy diet (H) formulated to contain 150% of requirements for the entire dry period. Data measured over time were subjected to repeated measures ANOVA using PROC MIXED with treatment, time and parity as fixed effects (Table 0668). Energy content was 1.28, 1.35, and 1.42 Mcal NEl/kg DM for the L, I, and H diets, respectively. Animals fed L had lower concentrations of BHBA during both the prepartum and postpartum periods than cows fed H. Concentration of NEFA in cows fed L was higher prepartum compared with the

Table 0668. Least squares means for energy metabolites, DMI, and milk yield

Parameter		Treatment			Fixed effects	
		L	I	H	Treatment	Treatment x Time
		LS means ± *SE*			*P*	
BHBA, mmol/dL	prepartum	0.29 ± 0.01[a]	0.30 ± 0.01[ab]	0.34 ± 0.01[b]	0.04	0.03
	postpartum	0.63 ± 0.06[a]	0.77 ± 0.06[ab]	0.85 ± 0.06[b]	0.05	0.19
NEFA, uEq/L	prepartum	237.1 ± 12.4[a]	179.5 ± 12.7[b]	175.4 ± 12.5[b]	0.001	0.03
	postpartum	659.1 ± 36.4[a]	664.6 ± 36.7[a]	795.7 ± 39.5[b]	0.02	0.37
DMI, kg/d	prepartum	14.2 ± 0.3[a]	15.3 ± 0.3[b]	16.4 ± 0.3[c]	<0.0001	0.03
	postpartum	22.3 ± 0.6	22.4 ± 0.6	22.4 ± 0.6	0.99	0.75
Milk yield, kg/d		43.8 ± 1.2	43.6 ± 1.2	43.9 ± 1.2	0.98	0.31
ECM yield, kg/d		46.1 ± 1.2	47.0 ± 1.2	48.3 ± 1.3	0.48	0.94

[abc]Row means with different superscripts differ.

other two treatments, while being lower in cows fed L or I compared with H postpartum. Yields of milk and energy-corrected milk (ECM) were not different among treatments. Although sample size was not sufficient to study health outcomes, results suggest positive effects on metabolic health by feeding a controlled energy diet during the dry period.

Key Words: energy, peripartal, controlled

0669 Hepatic acetyl CoA concentration decreases following feeding in early-postpartum but not in late-lactation dairy cows. P. Piantoni*, C. M. Ylioja, and M. S. Allen, *Michigan State University, East Lansing.*

The relationship between hepatic acetyl CoA concentration (Ac-CoA) and dry matter intake (DMI) was determined using 28 multiparous Holstein cows. Fourteen were early-postpartum (PP; 12.6 ± 3.8 DIM), and 14 were late-lactation cows (LL; 271 ± 29.6 DIM). Cows were fed once daily, and DMI was determined for the first 4 h after feeding. Liver and blood samples were collected before feeding and 4 h after feeding. Feed intake over the 4-h period ranged from 3.2 to 9.6 kg DM and did not differ by stage of lactation. Before feeding, Ac-CoA was greater ($P < 0.0001$) for PP (mean: 36.0; range: 12.7 to 56.1 nmol/g) compared with LL (mean: 14.1; range: 7.7 to 19.4 nmol/g), and tended to decrease over the 4 h after feeding for PP only ($P < 0.10$). The range of change in Ac-CoA over the 4-h period was wide for both PP (-24.3 to 10.4 nmol/g) and LL (−5.7 to 16.1 nmol/g), and was negatively related to DMI at 4 h for PP ($P < 0.01$), but not for LL. The reduction in plasma NEFA concentration over the 4-h period was greater for PP than LL (−684 vs. −52 μEq/L; $P < 0.0001$), and was greater for PP ($P < 0.05$) and tended to be greater for LL ($P < 0.10$) as DMI at 4 h increased. Greater reductions in Ac-CoA were related to higher DMI during the first 4 h after feeding in PP ($P < 0.01$), which is contrary to our expectation if oxidation of Ac-CoA increased hepatic energy charge. However, hepatic energy charge is dependent on the relative rates of production and utilization of high-energy phosphate bonds and the rate of utilization might have been greater for cows with higher DMI. Alternatively, increased DMI over the first 4 h after feeding might have been from decreased oxidation of Ac-CoA during meals if the greater reduction in plasma NEFA concentration reduced Ac-CoA production by β-oxidation. Consistent with this is that the change in Ac-CoA was positively related to the reduction in plasma NEFA concentration for PP ($P < 0.05$). Besides oxidation, the pool of Ac-CoA is decreased by ketogenesis and hydrolysis and export as acetate. Further research is required to determine the fate of Ac-CoA within the timeframe of meals and the effects of feeding on energy charge in hepatic tissue.

Key Words: acetyl CoA, metabolic control of intake, postpartum

0670 Overconditioned prepartum cows exhibit a greater magnitude of insulin resistance and mobilize more NEFA earlier compared with lean cows. J. E. Rico*[1] and J. W. McFadden[1,2], *[1]West Virginia University, Morgantown, [2]Johns Hopkins University, Baltimore, MD.*

Overconditioned transition cows are at greater risk of developing metabolic disease compared with lean cows. Severity of metabolic disease can be augmented by the magnitude of insulin resistance. Our objective was to identify the onset of insulin resistance in overconditioned prepartum cows to delineate the progression of the disease for future predictive biomarker discovery. Multiparous Holstein cows were allocated into two treatment groups according to their BCS at d −30 prepartum: lean (LEAN; BCS < 3.25; $n = 21$) or overconditioned (OVER; BCS > 3.75, $n = 26$). Diets were formulated to meet nutrient recommendations. Blood samples were collected at d −45, −30, −15 and −7, relative to expected calving, and at d 1 and 4 postpartum. Plasma glucose, NEFA, insulin, and BHBA concentrations were measured, and the Revised Quantitative Insulin Sensitivity Check Index (RQUICKI) was calculated as an insulin sensitivity indicator. The statistical model included the random effect of cow and the fixed effects of BCS and time (relative to calving). BCS was different for LEAN and OVER at d -30 postpartum (3.04 ± 0.042 vs. 3.91 ± 0.038; $P < 0.001$). With the exception of glucose, plasma variables were affected by time ($P < 0.001$). NEFA (mM) were higher for OVER relative to LEAN at d −45, −30, −15, and −7 (+54%, $P < 0.01$; +40%, $P < 0.05$; +116%, $P < 0.001$; and +91%, $P < 0.001$, respectively) and tended to be higher at d 1 (+31%, $P = 0.07$). Insulin (μU/ml) was higher in OVER relative to LEAN at d −15 (+37%; $P < 0.05$). RQUICKI was lower for OVER relative to LEAN at d −30, -15, and −7 (−10%, $P < 0.05$; −18%, $P < 0.001$; and −9%, $P < 0.01$, respectively), and tended to be lower at d −45 and d 1 for OVER relative to LEAN (−8 and −7%, respectively, $P = 0.08$). BCS affected NEFA and RQUICKI (+44% and −9%, respectively, OVER relative to LEAN; $P < 0.001$). Glucose and BHBA were not affected by BCS. Relative to LEAN, OVER showed a negative change in BCS from d -30 to d −7 (0.13 vs. −0.10 units, $P < 0.01$). BCS had no effects on BW or milk yield. Somatic cell score was higher in OVER at d 10 (+18%, $P = 0.025$). Overconditioned cows experienced a greater magnitude of insulin resistance and mobilized more NEFA earlier compared with lean cows. Early detection of pre-onset insulin resistance in overconditioned dairy cows is needed to develop interventions aimed at reducing excessive NEFA mobilization and associated metabolic disorders.

Key Words: insulin resistance, overconditioned, transition cow

0671 Identifying biomarkers for pre-onset insulin resistance using mass spectrometry-based metabolomics: Plasma ceramides are elevated in overconditioned transition dairy cows.

J. E. Rico[1] and J. W. McFadden[*1,2], *[1]West Virginia University, Morgantown, [2]Johns Hopkins University, Baltimore, MD.*

Metabolomics is a systems biology analytical approach used to study disease phenotypes, an established field in biomedicine that is emerging in the dairy sciences. Parallel with transcriptome and proteome, the comprehensive set of small molecules in biological systems constitutes its metabolome. Because no single analytical methodology is suited to identify all metabolites, a combination of untargeted and targeted methods (measurement of any molecule that ionizes within a specific mass range, and measurement of specific metabolites, respectively) are employed using gas chromatography (GC) or liquid chromatography (LC), coupled with mass spectrometry (MS). Metabolome screening provides the opportunity to discover molecules (biomarkers) that are associated with disease progression. Similar to overweight monogastrics, overconditioned transition dairy cows experience greater insulin resistance compared with lean cows. Since insulin resistance accelerates NEFA mobilization, overconditioned dairy cattle are at greater risk of developing postpartum disease. Therefore, our objective was to screen the bovine metabolome using GC/MS and LC/MS technologies in search for metabolic phenotypes associated with decreased insulin sensitivity. Our data set included multiparous Holstein cows grouped according to BCS at d -30 prepartum: lean (BCS < 3.0; n = 10; LEAN) or overconditioned (BCS > 4.0, n = 11; OVER), with blood samples collected at d −45, −30, −15 and −7, relative to expected calving, and at d 4 postpartum. For untargeted detection, derivatized plasma methanol extracts were analyzed using GC/MS. For targeted analysis, plasma chloroform-methanol extracts were analyzed by LC/MS. Following normalization, log transformation, and median-scaling, data were analyzed using ANOVA and cluster analysis. Non-parametric spearman's correlations were used to evaluate the associations between NEFA and insulin sensitivity to ceramides. Relative to LEAN, OVER had reduced insulin sensitivity and greater NEFA mobilization at d −30, −15 and −7 prepartum (P < 0.05). GC/MS and LC/MS analysis detected lactate, urea, glycerol, amino acids, citrate, mono- and disaccharides, saturated and unsaturated free FA, uric acid, vitamin E, nonesterified cholesterol, ceramides, hexylceramides, and others. Of interest, relative to LEAN, OVER had elevated ceramides at d −15, −7, and 4 (e.g., C20:0-ceramide; P < 0.05), and mono- and dihexylceramides at d4 (P < 0.05). Multiple ceramides were positively associated with NEFA, and negatively associated with insulin sensitivity (e.g., C22:0-, C24:0-, C24:1-, and C26:0-ceramide; P < 0.05). Currently used markers (e.g., NEFA and BHBA) have limited predictive power for pre-onset insulin resistance, as they are delayed indications of metabolic stress. Metabolomics may improve our ability to predict prepartum cows at risk of developing greater insulin resistance.

Key Words: insulin resistance, metabolomics, transition cow

0672 Effects of yeast product supplementation on production, feeding behavior, and metabolism in transition dairy cows.

K. Yuan[*1], T. Liang[2], M. Muckey[1], L. Mendonca[1], L. Hulbert[1], L. Mamedova[1], C. C. Elrod[3], and B. Bradford[1], *[1]Kansas State University, Manhattan, [2]GM Powertrain, Pontiac, MI, [3]Vi-COR, Inc., Mason City, IA.*

The objective of this study was to assess the effects of supplementing a yeast product derived from *Saccharomyces cerevisiae* on production, feeding behavior, and metabolism in transition cows. Forty multiparous Holstein cows were blocked by expected calving date and randomly assigned within block to one of four treatments (n = 10) from 21 d before expected calving to 42 d postpartum. Rations were top-dressed with yeast culture plus enzymatically hydrolyzed yeast (Celmanax, Vi-COR, Mason City, IA) at the rate of 0, 30, 60, or 90 g/d throughout the experiment. Dry matter and water intake, feeding behavior, and milk production were monitored. Plasma collected on −21, −7, 1, 4, 7, 14, 21, and 35 d relative to calving was analyzed for glucose, β-hydroxybutyrate, nonesterified fatty acids (NEFA), and haptoglobin. Data were analyzed using mixed models with repeated measures over time. Pre- or postpartum DMI and water intake did not differ (P > 0.10) among treatments. There were quadratic dose effects (P < 0.05) for prepartum feeding behavior, reflecting decreased meal size, meal length, and intermeal interval, and increased meal frequency for cows received 30 and 60 g/d of yeast products. Postpartum feeding behavior was unaffected (P > 0.10) by treatments. Milk yields were not affected (P > 0.10; 45.3, 42.6, 47.8, and 46.7 kg/d for 0, 30, 60, and 90 g/d, respectively) by treatments. Tendencies toward increased ($0.05 < P \leq 0.10$) percentages of milk fat, protein, and lactose were detected for cows receiving yeast. A treatment × wk interaction (P < 0.01) was observed for somatic cell linear score (SCS), reflecting a quadratic dose effect on SCS in wk 1 (P = 0.03; 2.34, 2.85, 1.47, and 4.05 ± 0.57 units for 0, 30, 60, and 90 g/d, respectively). Yeast product increased (P < 0.01) plasma β-hydroxybutyrate and tended to decrease (quadratic P = 0.06) glucose, but did not affect NEFA or haptoglobin. Yeast product supplementation during the transition period did not affect milk production, but may modulate feeding behavior, mammary gland health, and metabolism.

Key Words: production and metabolism, transition cow, yeast

0673 Milk production performance of autumn-calving Holstein Friesian cows managed under flat-rate or feed-to-yield concentrate feeding systems.

D. C. Lawrence[*1,2], E. Kennedy[2], M. O'Donovan[2], T. M. Boland[3], A. Lawless[4], and J. Patton[5], *[1]School of Agriculture and Food Science, University College Dublin, Belfield, Ireland, [2]Teagasc, Animal and Grassland Research and Innovation Center, Moorepark, Fermoy, County Cork, Ireland, [3]School of Agriculture and Food Science, University College Dublin, Ireland, [4]Teagasc, Johnstown Castle, Co. Wexford, Ireland, [5]Teagasc, Grange, Dunsaney, County Meath, Ireland.*

This experiment was conducted to examine the effects of two feeding systems, on milk production, body condition score and feed inputs of autumn-calving cows. Autumn-calving Holstein Friesian cows (n = 84) were blocked pre-partum according to parity, body condition score, genetic merit for milk production and assigned to one of two postpartum concentrate feeding systems; feed to budget (FTB) or feed to yield (FTY); FTB cows were allocated concentrate at a flat rate, and FTY were allocated concentrate based on individual milk production. Both feeding systems were offered 14.5 kg forage DM/cow/day during the winter housing period containing grass silage and maize silage (in the ratio 2:1) plus 3.0 kg DM of concentrate. Cows on the FTB treatment received a further 3.95 kg DM of concentrate in the milking parlor; cows on the FTY treatment received 0.43 kg DM of concentrate in the milking parlor per kg of milk (based on the previous weeks mean milk production) exceeding a base milk yield 23.0 kg/cow/day. Cows were turned out to pasture on February 10. During the main grazing period (March-September) pre-grazing herbage mass was 1300 to 1500 kg DM/ha (above 4 cm), and was grazed to a residual of < 100kg DM/ha (target 4.0 cm). Where pasture supply was adequate, the FTY group was offered 0.43 kg DM concentrate per kg milk, exceeding a base yield of 25.0 kg/day as described previously. When pasture supply was below the demand, additional concentrate (plus silage if required) was allocated at a flat-rate to both treatments. Data were analyzed using a mixed model procedure in SAS v9.3 which included a repeated measure for week of experiment. Concentrate feeding system had no significant effect on milk yield, milk solids production or mean BCS during the indoor period or at grazing. In total the FTY treatment was fed 250 kg DM/cow less concentrate that the FTB ($P < 0.001$). The ratio of concentrate fed per kg of milk output was lower for FTY which indicates improved efficiency of milk production from forage.

Key Words: feed to yield, pasture, autumn calving

0674 Does concentrate allocation pattern affect the milk production of autumn calving cows at high and low feeding levels?

D. C. Lawrence[*1,2], M. O'Donovan[3], T. M. Boland[4], E. Lewis[3], and E. Kennedy[3], *[1]Teagasc, Animal and Grassland Research and Innovation Center, Moorepark, Fermoy, County Cork, Ireland, [2]School of Agriculture and Food Science, University College Dublin, Belfield, Ireland, [3]Teagasc, Moorepark, Fermoy, County Cork, Ireland, [4]School of Agriculture and Food Science, University College Dublin, Ireland.*

The objective of this experiment was to examine the effects of concentrate allocation pattern at two concentrate feeding levels, on feed intake, milk yield, and milk composition of autumn calving cows offered a base forage mix of grass silage and maize silage. The study used a randomized block design with a 2 × 2 factorial arrangement of treatments and was performed over an 11-wk period in 2011 and 2012. The treatment factors were flat (F) or variable (V) concentrate allocation pattern, at high (7.0 kg DM/cow per day (Hi)) or low (4.0 kg DM/cow per day (Lo)) concentrate feeding level. Cows (n = 108) were blocked in groups of four based on calving date, parity and the milk yield, body weight and BCS of weeks three and four of lactation. Within each treatment cows were sub-grouped as high, medium, and low milk yield based on pre-experimental milk data. The HiV cows received 8.7, 7.0, or 5.3 kg DM of concentrate/cow per day in the high, medium and low subgroups, respectively. The LoV cows received 5.3, 4.0, or 2.7 kg DM of concentrate/cow per day in the high, medium and low subgroups, respectively. Flat rate treatments received 7.0 kg DM (HiF) or 4.0 kg DM (LoF) of concentrate/cow per day. Concentrate was allocated in the base diet; 2 kg and 2.4 kg DM for Hi and Lo, respectively, and the remaining amount was allocated in the parlor. All cows remained on a fixed level of concentrate for the duration of the experiment. Data were analyzed using a mixed model procedure in SAS v9.3, which included a repeated measure for week of experiment. Cows on the Hi treatment had 2.9 kg higher total DM intake ($P < 0.001$), and 0.5 kg reduction in base feed DM intake ($P < 0.05$), compared to animals on the Lo treatment, which had a total DM intake of 15.8 kg DM and a base feed intake of 14.2 kg DM. Each additional 1 kg concentrate DM intake above the Lo treatment, resulted in a 0.43 kg increase in milk yield ($P < 0.001$) which was 25.1 kg and 23.8 kg on Hi and Lo, respectively. There was no allocation pattern by feeding level interactions for milk yield, milk composition or dry matter intake. Allocating concentrate at a variable rate had no effect on milk yield or DM intake, when compared to allocating concentrate at a flat rate.

Key Words: feed-to-yield, flat-rate: Holstein Friesian

RUMINANT NUTRITION VIII

0675 Characterization of rumen microbial community composition of buffalo fed diets varying in forage:concentrate ratio. B. Lin[*1,2], C. Zou[1], F. Cox[2], G. Henderson[2], P. H. Janssen[2], X. Liang[1], and G. Attwood[2], [1]*Buffalo Research Institute, The Chinese Academy of Agricultural Sciences, Nanning, China,* [2]*AgResearch Limited, Grasslands Research Centre, Palmerston North, New Zealand.*

Murrah and Nili-Ravi are two widely used dairy water buffalo breeds in Asian countries. In this study, we investigated the diversity of ruminal microbes in six Murrah and six Nili-Ravi water buffalos maintained in China. The buffalos were separated into two groups; each group contained three Murrah and three Nili-Ravi buffalos, and two different diets (with forage to concentrate ratios of 3.2 or 1.6) were fed to the two groups. After feeding the diets for 15 d, ruminal fluid was sampled by stomach tube before the morning feeding. The bacterial and archaeal 16S rRNA genes and the ciliate protozoal 18S rRNA genes from the 12 rumen samples were sequenced by multiplex 454 Titanium pyrosequencing, and the sequence data was analyzed using QIIME 2.0 software. Our results showed that at the phylum level, Bacteroidetes was the predominant bacterial group, accounting for 42% to 72% of total bacteria, followed by Firmicutes, Fibrobacter and Proteobacteria. At the genus level, *Prevotella* dominated, accounting for 22 to 58% of total bacteria, followed by *Fibrobacter*, *Paludibacter* and *Ruminococcus*. While there were differences between the bacterial community compositions of different animals, there was no obvious correlation of bacterial community composition, at the phylum or genus level, with the diets or with buffalo breeds. For the archaea, *Methanobrevibacter*-related organisms were the dominant group, accounting for around 80% of the total, followed by *Methanoplasmatales* (RCC, 15%) and *Methanosphaera* (3%). Similar to the bacterial community, there was no clear correlation of the archaea community profile with diet or buffalo breed. The ciliate protozoal communities differed between the samples analyzed, although *Entodinium* was the most abundant group of ciliates in every sample, accounting for more than 40% of total protozoa. The second largest ciliate group varied in different samples with *Isotricha*, *Polyplastron* or *Dasytricha* the dominant genera after *Entodinium*. In summary, the predominant genera observed in the bacterial, archaeal and ciliate protozoal communities in rumen samples of Murrah and Nili-Ravi buffalo were *Prevotella*, *Methanobrevibacter* and *Entodinium,*, respectively. Overall, the buffalo rumen microbial communities varied greatly between individual animals, regardless of the diet composition or the buffalo breed used in this study.

Key Words: buffalo, rumen, microbial community, forage to concentrate ratio

0676 Bacterial diversity associated with different primer pairs on different diets in the rumen microbiome of Kankrej cattle. D. W. Pitta[*1], N. Indugu[2], S. Kumar[1], K. B. Prajapathi[3], A. K. Patel[4], N. Parmar[4], A. B. Patel[4], B. Reddy[4], and C. Joshi[4], [1]*University of Pennsylvania, Kennett Square,* [2]*University of Pennsylvania, Kennett Square,* [3]*Sardharkrushinagar Dantiwada Agricultural University, India,* [4]*Anand Agriculture University, India.*

A comprehensive analysis of the bacterial diversity in the rumen of Kankrej cattle was investigated in this study. Two groups of four animals were assigned to two diets of Dry and Green roughage, respectively. In each dietary group, four animals (replicates) were group fed one of three dietary treatments for 6 wk each; dietary treatments were K1 (50% concentrate, 50% dry/green roughage), K2 (25% concentrate, 75% dry/green roughage), and K3 (100% dry/green roughage). The rumen samples were collected at the end of 6 wk period and separated to solid and liquid fractions. The genomic DNA was extracted from each sample and PCR-amplified for V1-V3, V4-V5, and V6-V8 hypervariable regions, sequenced on 454 Roche platform and analyzed for bacterial diversity using QIIME. A total of 600, 851 pyrotags were analyzed in this study. Differences in community composition were based on UniFrac distance metric calculated by primer, diet, treatment, fraction, and animal and analyzed by Permanova test. Different primers had a significant ($P < 0.001$) effect on community compositions. There was no difference between diets but the inclusion of concentrate had an effect on community composition ($P < 0.01$). Also community compositions between fiber and liquid fractions were different ($P < 0.01$). Phylogenetic analysis revealed significant differences in the rumen microbiome mediated by primer ($P < 0.001$). In primer pair 1 associated bacterial communities, the predominant phyla were *Bacteroidetes* and *Firmicutes* which together constituted > 90% of abundance. These two phyla were influenced by dietary treatment ($P < 0.001$) and fraction ($P < 0.05$). Among communities associated with primer pairs 2 and 3, *Firmicutes* was predominant and contributed up to 90% of the fiber fraction. Dietary treatment had an influence on the abundance of B*acteroidetes* ($P < 0.001$) and *Firmicutes* ($P < 0.001$) with K1 showing higher ($P < 0.001$) *Bacteroidetes* while K2 and K3 treatments had higher ($P < 0.001$) abundance of *Firmicutes*. Other bacterial phyla such as *Proteobacteria* and *Fibrobacter* together contributed up to 6% of the bacterial abundance that was influenced by dietary treatment ($P < 0.001$) and fraction ($P < 0.001$) across all three primer pairs. The identified repertoire of bacterial populations was dependent on the primer pair, as targeting the V1-V3 region resulted in greater diversity profiles of the rumen microbiome in this study. Within each primer pair, there were no differences between dry and green roughages. However, inclusion

of concentrate in the diet altered the community composition with noticeable shifts at the phylum level.

Key Words: rumen microbiome, Kankrej cattle, QIIME, concentrate, roughage

0677 Development of rumen microbiota in dairy calves: Impact of weaning and different weaning strategies.

S. C. Li*[1], M. A. Steele[2], P. Azevedo[1], M. Carson[2], J. C. Plaizier[1], H. Derakhshani[1], and E. Khafipour[1,3], *[1]Dep. of Animal Science, University of Manitoba, Winnipeg, Canada, [2]Nutreco Canada Agresearch, Guelph, ON, Canada, [3]Dep. of Medical Microbiology and Infectious Diseases, Winnipeg, MB, Canada.*

Weaning stress affects the establishment of rumen bacterial community in dairy calves, which is important for rumen development and future rumen physiology. This study examined the effects of different weaning strategies on the microbial composition of rumen in 24 male and 20 female Holstein dairy calves. Calves were blocked according to gender and birth weight, and randomly assigned to a step-down weaning (SW) or an abrupt weaning (AW) treatment. All calves had free access to water and starter intake throughout the experiment and 9 L/d of milk until d 36 of life and weaned on d 49 of life. Calves in SW group were weaned gradually by reducing milk intake from 9 to 4.5 L/d from d 37 to d 48 while the AW calves were abruptly weaned on d 49 by reducing milk intake from 9 to 0 L/d. Rumen fluid was sampled on d 36 (pre-weaning) and on d 54 (post-weaning) of life. DNA was extracted and V4 region of 16S rRNA gene was amplified and subjected to paired-end Illumina sequencing. The output paired-end reads were merged using PANDASeq assembler and analyzed using QIIME. The resulted operational taxonomic units were aligned to Greengenes database. Alpha-diversity of bacterial community was calculated using different richness estimators. Differences in β-diversity of microbiota across treatments and time points were tested using Permutational ANOVA. Alpha-diversity of microbiota declined post-weaning, indicating a compositional heterogeneity reduction in rumen population. Beta-diversity of microbiota differed ($P < 0.05$) between pre- and post-weaning. Different weaning strategies did not affect α and β-diversities. Predominant phyla before weaning included *Bacteroidetes* (66%), *Firmicutes* (19%) and *Proteobacteria* (11%). Another 18 phyla were present at low abundance; each below 1% of population. In post-weaned calves, *Bacteroidetes* was reduced (44%) while *Firmicutes* and *Proteobacteria* increased. However, a smaller increase in *Firmicutes* and a greater increase in *Proteobacteria* were observed after weaning in SW compared to AW calves (28% vs. 38%, and 22% vs.17%, respectively). Eighty-two out of 348 identified bacterial genera were different between pre- and post-weaned calves across AW and SW treatments, which accounted for 50% of sequences. The impact of weaning strategy was observed on several genera, including but not limited to, several members of *Alphaproteobacteria*, RF32, *Alcaligenaceae*, and *Helicobacter*. Data provided novel information on the profile of rumen microbiota associated with weaning and weaning strategy that can be used as biomarkers in future studies.

Key Words: calves, weaning, rumen microbiota

0678 The potential benefit of corn dried distillers' grain (co)products (DDG) in the mitigation of methane production in cattle: An in vitro analysis.

M. A. Fonseca*[1], D. K. A. Silva[2], H. D. Naumann[3], T. R. Callaway[4], and L. O. Tedeschi[1], *[1]Texas A&M University, College Station, [2]Federal Rural University of Pernambuco, Garanhuns, Brazil, [3]University of Missouri, Columbia, [4]USDA-ARS, College Station, TX.*

The objective of this work was to determine the impact of different levels of DDG on the digestibility of OM and the production of methane (CH_4) using an in vitro technique. Nine diets were formulated with Bermuda grass hay, ground corn, and alfalfa hay mixed with DDG (0, 10, 20, 30, 40, 50, 60, 80, and 100% of diet DM). These nine diets and alfalfa hay alone (laboratory control) were ground (1 mm), and incubated with rumen fluid (from grazing cows) and media. Blanks (rumen fluid and media only) were used to adjust the CH_4 production. Three replicates and four incubation times (3, 6, 24, and 48 h) were investigated in the bottle's headspace using a syringe for collection. Because these diets had different amounts of potentially fermentable substrate, adjusted CH_4 was computed as CH_4 concentration divided by the amounts of NDF (CH_4NDF, mM/g NDF), NFC (CH_4NFC, mM/g NFC), fermentable carbohydrate (FCHO = CHOA + CHOB1 + CHOB2) (CH_4FCHO, mM/g FCHO), OM (OM = 100– Ash) (CH_4OM, mM/g OM), and fermentable OM (FOM = OM– Ash– EE) (CH_4FOM, mM/g FOM) in the diet sample. The PROC MIXED of SAS (SAS Inst., Cary, NC) was used to analyze the data assuming a repeated measure design. Diets and incubation times were assumed as fixed factors and replicate within diet as random factor. Except for CH_4FCHO and CH_4NFC, diet effect was significant ($P < 0.001$) for all other adjusted CH_4 concentrations, suggesting that FCHO and NFC may not explain differences in CH_4 concentration. Regarding incubation time and its interaction with diet, all adjusted CH_4 concentration were highly significant ($P < 0.001$). There was a tendency to decrease CH_4 concentration as the DDG level increased, but the level of DDG in the diet had to be greater than 50% to yield significant reduction in the adjusted CH_4 concentration, CH_4FOM and CH_4OM (CH_4 per unit of OM) when the fat content was greater than 7.39% DM. Significant linear regressions for adjusted CH_4 concentration ($CH_4 = 14.5 - 0.667 \times$ Fat; $r^2 = 0.64$, RMSE = 1.48 mM, $n = 46$) and CH_4FOM (CH_4FOM $= 83.8 - 3.35 \times$ Fat; $r^2 = 0.53$, RMSE = 9.30 mM/% FOM, $n = 46$) on fat content of the diets were observed. These in vitro results suggested that under normal ru-

minal fermentation CH_4concentration will decrease as dietary fat increases if ruminal retention time is between 24 and 48 h.

Key Words: abatement, greenhouse gas, ruminant

0679 Use of avian antibodies against lipopolysaccharides to improve gastrointestinal function in early lactation dairy cows. L. Ibarbia[*1], F. Cunha[1], K. N. Galvão[1], F. Maunsell[1], A. Donovan[1], and N. DiLorenzo[2], *[1]Dep. of Large Animal Clinical Sciences; University of Florida, Gainesville, [2]University of Florida, Marianna.*

Subacute ruminal acidosis (SARA) has been associated with decreased milk production in early lactation dairy cows. During SARA, increased lipopolysaccharides (LPS) are released in the rumen from the breakdown of gram negative bacteria, increasing LPS concentrations and potential translocation to blood. Presence of LPS in the blood stream leads to activation of the acute phase response in peripheral blood, which in turn leads to a reduced DMI and milk production. An avian-derived anti LPS polyclonal antibody preparation (PAP-LPS) was developed (Camas Inc., LeCenter, MN) to use as a feed additive in dairy cattle. Our objective was to evaluate the effectiveness of PAP-LPS in decreasing the intensity of the inflammatory response and increasing milk yield on early lactation dairy cows. Primiparous (Pr; n = 174) and multiparous (Mu, n = 226) Holstein cows from one herd were randomly allocated to one of three treatments: 1) PAP-LPS (n = 55 Pr and n = 70 Mu), 2) Placebo (n = 66 Pr and 77 Mu), and 3) Control (n = 53 Pr and 79 Mu). Cows on PAP-LPS received a dose of 3 g/d of PAP-LPS via oral drench in a water suspension, while Placebo received the same dose of a PAP-LPS inactivated by an acid-shock treatment. Control cows did not receive any treatment. The PAP-LPS and Placebo treatments were administered from d 0 (calving) until 14 DIM. Milk production was recorded from d 0 to d 98 and weekly averages were used in a repeated measures analysis using the PROC MIXED of SAS and a first-order autoregressive covariate structure. The model included the fixed effects of treatment, parity and treatment x parity interactions. Feeding PAP-LPS increased (P = 0.04) total milk production on the first 98 DIM when compared with Control (3881 and 3769 kg, respectively), while only tended to increase it (P = 0.07) when compared to placebo (3785 kg). A week x treatment interaction was observed (P = 0.088) for weekly average milk production. Weekly average milk production was greater (P < 0.05) for PAP-LPS vs. Control on weeks 3, 4, and 10. On week 6, cows fed PAP-LPS had greater (P < 0.05) milk production (44.9 kg/d) when compared with both Control (43.1 kg/d) and Placebo (43.1 kg/d). In conclusion, feeding PAP-LPS increased milk production in early lactation dairy cows, likely due to a reduced inflammatory response during diet transition.

Key Words: dairy cows, LPS, avian antibodies

0680 Large-subunit rDNA based differentiation of anaerobic rumen fungi using restriction fragment length polymorphism. D. Sumit[1,2,3], S. Kumar[*2,4], D. W. Pitta[4], J. Edwards[1], T. Callaghan[1], G. Grifith[1], P. Mudgil[2], and A. Puniya[2], *[1]Aberystwyth University, Aberystwyth, UK, [2]National Dairy Research Institute, Karnal, India, [3]Agharkar Research Institute, Pune, India, [4]University of Pennsylvania, Kennett Square.*

The contribution of rumen anaerobic fungi to animal production systems is substantial despite their lower numbers in the rumen. Utilizing both cultivation-based and advanced genomic tools, several reports have described the repertoire of ligno-cellulolytic enzymes secreted by these fungi. However, characterization of anaerobic rumen fungi is a tedious process with difficulties in isolation methods, their pleomorphic nature and lack of appropriate targeted genetic markers to understand fungal diversity. Previously, we have identified a new marker, D1/D2 domain of 28S rDNA of LSU (large-subunit; LSU) region which provided a better resolution in species differentiation of genus *Orpinomyces* than internal transcribed spacer (ITS) region, a preferred genetic marker for most fungal diversity studies. In the current study, we applied the same D1/D2 marker to assess species level distribution of several fungal lineages. For this, nearly 100 isolates of known lineages (*Orpinomyces*, *Neocallimastix*, *Anaeromyces*, *Piromyces*, *Caecomyces*, *Cyllamyces*) and unknown anaerobic fungi were cultivated from the rumen of different herbivorous animals. The isolates were extracted for their genomic DNA using modified method of Cetyl tri-methyl ammonium bromide (CTAB) and also MoBio genomic DNA extraction kit. The genomic DNA samples were PCR-amplified for D1/D2 regions of LSU (≈ 780 bp) using NL1 and NL4 primers. The amplified PCR products were purified, sequenced and characterized for phylogeny. Based on the phylogenetic analysis, representative sequences from identified fungal lineages were further subjected to in silico restriction digestion that led to the identification of two restriction enzymes, *Alu*I (recognition sequence, AG▼CT) and *Hinf*I (recognition sequence, G▼ANT C). About 34 selected sequences were co-digested by these two restriction enzymes using Restriction Fragment Length Polymorphism (RFLP) assay. The RFLP analysis of electrophoretic runs revealed distinct riboprints for individual fungal lineages that were identified in this study. Sequences annotated to similar fungal lineages showed comparable riboprints, which confirmed that targeting D1/D2 region of the LSU gave repeatable results. Our study summarized that RFLP-based differentiation of fungal lineages was better accomplished when D1/D2 region of the LSU was used as a genetic marker.

Key Words: rumen, anaerobic fungi, LSU, PCR-RFLP, co-digestion

0681 Responses in rumen microbiomes of *Bos taurus* and *Bos indicus* steers fed rice straw and supplemented protein. E. A. Latham[*1], J. C. McCann[2], K. Weldon[1], T. A. Wickersham[1], J. Coverdale[1], and W. E. Pinchak[3], *[1]Texas A&M University, College Station, [2]University of Illinois, Urbana, [3]Texas A&M AgriLife Research, Vernon.*

Bos indicus typically perform better than *Bos taurus* when consuming a low-quality diet; however, the response to supplementation is generally greater in *Bos taurus*. The underlying mechanisms supporting these responses have not been elucidated. Characterization of differences in rumen bacterial populations and their role in the two subspecies may provide insight. Five cannulated Angus and Brahman steers were used in concurrent 5 × 5 Latin squares with repeated measures. Animals were offered ad libitum access to rice straw (4.7% CP). Treatments consisted of an unsupplemented control and two levels (50 and 120 mg N/kg BW) of isonitrogenous supplements (30% CP), either high (H; 74%) or low (L, 26%) in UIP. Rumen sample were collected at 0 and 4 h post-feeding, separated into liquid and solid fractions and frozen immediately in liquid N. Rumen bacterial taxa were sequenced utilizing a Roche 454 platform based on the 16s rRNA gene. At 97% sequence similarity, 97,826 OTUs were identified, which included 21 phyla, 108 families, and 255 genera. Each taxa was analyzed using PROC MIXED with period and animal as random effects. The top seven phyla accounted for > 98% of observed abundance. Six phyla differed as a function of fraction, time, and fraction × time interaction ($P < 0.05$). *Bacteroidetes* (65%) and *Firmiucutes* (28%) were dominant phyla, both tended to differ as a function of subspecies × treatment and treatment ($P < 0.06$). The top 14 families accounted for > 93% observed abundance. Unlike phyla, families were influenced more by subspecies and treatments than fraction ($P < 0.05$). *Prevotellaceae* (> 42%), *Ruminococcaceae* (> 13%), *Sphingobacteriaceae* (> 8%), and *Lachnospiraceae* (> 7%) were the dominant families. Genus abundance also varied as a complex function of subspecies, time and various associated interactions with treatment and fraction ($P < 0.05$). Twenty genera were present at > 0.8% average abundance and accounted for over 85% of total observed abundance. Dominant genera were *Prevotella* (29.5%), unknown *Prevotellaceae* (11%), unknown *Ruminococcaceae* (8.5%) and unknown *Sphingobacteriaceae* (7%). Overall bacterial community diversity was greater than expected because rice hay is recalcitrant to bacterial digestion. Similarly, consistent differences in family and genus taxa between *B. indicus* and *B. taurus* suggest important roles the symbiotic rumen microbiome may have in the capacity of *B. indicus* to utilize low-quality forage over a range of supplement types and levels.

Key Words: cattle, microbiome, supplementation

0682 Effects of dietary fat source and monensin on methane to carbon dioxide ratio, VFA profile, and performance of finishing steers. A. C. Pesta[*1], A. K. Watson[1], R. G. Bondurant[1], S. C. Fernando[2], and G. E. Erickson[1], *[1]University of Nebraska-Lincoln, Lincoln, [2]University of Nebraska, Lincoln.*

A finishing study was conducted to evaluate effects of supplemental fat type and presence or absence of monensin on methane to carbon dioxide ratio (CH_4:CO_2), ruminal VFA profile, and performance of finishing steers. Steers ($n = 60$, initial BW = 414 ± 16 kg) were individually fed for 125 d using Calan gates. Steers were stratified by initial BW and assigned randomly to one of six treatments. Four diets were designed to compare fat source: CON (corn-based diet with no added fat), MDGS (50% modified distillers grains plus solubles added), OIL (3% corn oil added), and TAL (3% tallow added). Added fat diets were formulated to provide 6.5% total dietary fat. An additional two treatments were added to factorialize presence or absence of monensin (375 mg daily) with CON or MDGS diets. At time of feeding, exhaled breath samples were collected from each animal at weekly intervals throughout the study using a custom built automated gas collection system and were analyzed for CH_4 and CO_2, using gas chromatography. Carbon dioxide was used as an internal marker and CH_4:CO_2 was used to quantify the effects of diet on methane emission. Rumen fluid collected via esophageal tubing on d 55, before feeding, was analyzed for VFA profile. Treatment differences were evaluated using pre-planned contrasts. No diet × monensin interaction was observed ($P = 0.19$). The CH_4:CO_2 for cattle fed MDGS was greater ($P = 0.03$) than CON, 0.057 compared to 0.050, respectively. No effect ($P = 0.56$) of monensin inclusion on CH_4:CO_2 was observed. Differences in CH_4:CO_2 observed may be due to composition of dietary fat, as steers fed MDGS had greater CH_4:CO_2 than those fed TAL or CON ($P < 0.03$), while those consuming OIL were intermediate. No differences were observed ($P = 0.45$) for ruminal acetate to propionate ratio (A:P) due to fat type or presence of monensin, as A:P of all diets fell between 1.08 and 1.40. Finishing performance was also unaffected as no differences in DMI ($P = 0.48$), ADG ($P = 0.37$), or G:F ($P = 0.78$) were observed. Composition of the finishing diet, particularly source of added fat does impact CH_4:CO_2.

Key Words: distillers grains, fat, methane

RUMINANT NUTRITION IX

0683 Effects of supplemental zinc, copper, and manganese concentration and source on performance and carcass characteristics of feedlot steers. E. Caldera*[1], J. J. Wagner[1], K. Sellins[1], T. E. Engle[1], S. B. Laudert[2], and J. Spears[3], [1]*Colorado State University, Fort Collins,* [2]*Micronutrients, Indianapolis, IN,* [3]*North Carolina State University, Raliegh.*

Four-hundred cross-bred steers (initial BW 335 ± 9.6 kg) were utilized to investigate the effects of supplemental Zn, Cu, and Mn concentration and source on performance and carcass characteristics of feedlot steers fed a high concentrate steam flaked corn-based finishing diet for 159 d and zilpaterol hydrochloride for the last 21 d before slaughter (5-d withdrawal). The experimental design was a randomized complete block design. Steers were blocked by weight and randomly assigned within block to one of the five treatments (eight pens/treatment; 10 hd/pen). Treatments consisted of: 1) 90 mg of Zn/kg DM from $ZnSO_4$; 17.5 mg of Cu/kg DM from $CuSO_4$; 48 mg of Mn/kg DM from $MnSO_4$; 2) 30 mg of Zn/kg DM from Zn hydroxychloride; 10 mg of Cu/kg DM from basic Cu chloride; 20 mg of Mn/kg DM from Mn hydroxychloride; 3) 45 mg of Zn/kg DM from hydroxychloride; 12.5 mg of Cu/kg DM basic Cu chloride; 29.5 mg of Mn/kg DM from Mn hydroxychloride; 4) 60 mg of Zn/kg DM from Zn hydroxychloride; 15 mg of Cu/kg DM from basic Cu chloride; 39 mg of Mn/kg DM from Mn hydroxychloride; and 5) 90 mg of Zn/kg DM from Zn hydroxychloride; 17.5 mg of Cu/kg DM from basic Cu chloride; 48 mg of Mn/kg DM from Mn hydroxychloride. Steers were individually weighed on d -1, 0, 55, 112, and pen-weighed two consecutive days at the termination of the experiment. Steers were transported to a commercial abattoir, slaughtered, and individual carcass data and liver samples were collected. Initial pen BW was used as a covariate in the statistical analysis and significance was determined at $P \leq 0.05$. No differences were observed for final body weight ($P > 0.42$). Overall ADG, DMI, and feed efficiency were similar across treatments. Hot carcass weight, dressing percentage, yield grade, LMA, adjusted fat thickness, KPH, and marbling score were similar across treatments. Concentrations of Zn, Cu, and Mn in livers and blood samples collected on d 112 and at harvest were similar across treatments. These data indicate that under the conditions of this experiment, supplemental Zn, Cu, and Mn concentration and source had no impact on performance and carcass characteristics in feedlot steers.

Key Words: cattle, feedlot, trace mineral

0684 Decreasing dietary calcium to potentiate changes in beef tenderness with zilpaterol hydrochloride supplementation. C. L. Van Bibber-Krueger*, K. A. Miller, and J. S. Drouillard, *Kansas State University, Manhattan.*

Dietary calcium concentrations were manipulated during supplementation of zilpaterol hydrochloride (ZH) to evaluate impact on feedlot performance, carcass characteristics, and beef tenderness using 96 heifers (BW 392 kg ± 3.2). We hypothesized that temporary depletion followed by repletion of dietary calcium before harvest would increase intracellular calcium concentrations, thus stimulating postmortem activity of calcium-dependent proteases. Heifers were stratified by initial BW and randomly assigned, within strata (block), to treatments consisting of a finishing diet in which calcium was added in the form of limestone (+Ca) and a diet in which the limestone had been removed (-Ca) during ZH supplementation. Cattle were fed a common diet before ZH supplementation, and 24 d before slaughter ZH was added to the diet with and without the supplemental calcium. Calcium content of the diets during ZH supplementation was 0.74% or 0.19% (diet DM) for +Ca and-Ca, respectively. Zilpaterol hydrochloride was fed for 21 d, then removed from the diet 3 d before harvest. The final 3 d before harvest, limestone was added back into the-CA diet at 0.74% of diet DM. Heifers were housed in concrete surfaced pens with eight animals per pen (six pens per treatment). At the end of the finishing phase, animals were weighed and shipped to an abattoir in Holcomb, KS. Severity of liver abscesses and HCW were collected the day of harvest, and after a 48-h chill USDA yield and quality grades, KPH, LM area, 12th rib fat thickness were determined and boneless loin section was collected for Warner-Bratzler shear force determination. Removal of calcium did not affect Warner-Bratzler shear force values ($P = 0.64$). In addition, ADG, DMI, final BW and feed efficiency were unaffected by treatment ($P > 0.05$). Carcass measurements also were unaffected by the decrease in dietary calcium ($P > 0.05$). In conclusion, temporary depletion of dietary calcium did not alter beef tenderness, live animal performance, or carcass measurements.

Key Words: calcium, zilpaterol hydrochloride, beef tenderness

0685 Optimizing phosphorus utilization by dairy cows. J. C. Plaizier*, K. H. Ominski, and E. J. McGeough, *University of Manitoba, Winnipeg, Canada.*

A survey was conducted on 10 dairy farms in Manitoba to quantify factors that affect the utilization of phosphorus (P) by lactating cows. Farms were visited once to collect samples and data, including days in milk (DIM), milk yields (MY), parities (PAR), body condition scores (BCS), and body weights from 30 Holstein cows in different stages of lactation. Feeds were analyzed for crude protein (CP), fat (FAT), ash (ASH), NDF,

starch (STARCH), P (DIETP) and acid insoluble ash (AIA). Feces were collected from the rectum and analyzed for P (FECALP) and AIA. Composite milk samples were analyzed for fat (MFAT), protein (MPROT), and P (MILKP). The apparent digestibilities of P (ADCP) of cows were determined using AIA as a marker. Dry matter intake was estimated using the equation of NRC(2001). The P utilization efficiencies (PEFF) of cows were determined as the ratio between the output of P in milk and the P intake. Descriptive statistics (Table 0685) show the considerable variation of parameters among cows. Examination of dietary and fecal P concentrations and measures of P utilization suggested that approximately half of the cows received more P than required. Linear regression models were developed between dependent variables (FECALP, PEFF, ADCP) and independent diet and cow variables. Independent variables with a significance level greater than 0.25 were stepwise removed.

Regression models were:

$$ADCP = -152.9 + 1.00 \times PAR - 2.06 \times MFAT + 2.22 \times CP + 3.63 \times FAT + 1.18 \times ASH + 2.52 \times NDF + 114.06 \times DIETP \ (R^2 = 0.39)$$

$$PEFF = 45.91 - 0.45 \times PAR - 0.04 \times DIM + 0.34 \times MY - 2.64 \times MFAT + 313.80 \times PMILK - 82.37 \times DIETP \ (R^2 = 0.79)$$

$$FECALP = 1.21 + 0.0005 \times DIM + 0.03 \times CP - 0.10 \times FAT + 0.06 \times ASH - 0.01 \times STARCH - 0.04 \times NDF \ (R^2 = 0.25)$$

Correlations among independent variables, including PDIET and other dietary variables, complicated assessing relationships between variables. The models show the complexity of factors that determine the efficiency of P for milk production, and generally suggest that this efficiency decreases in later stages of lactation when and milk yield decreases and diets are formulated accordingly.

Key Words: phosphorus, efficiency, dairy

Table 0685. Descriptive statistics

	Average	SD	Min.	25th perc.	50th perc.	75th perc.	Max.
PAR	2.37	1.41	1	1	2	3	8
DIM	170	97	15	74	166	259	464
Milk yield, kg/d	35.6	9.0	9.5	28.7	34.4	41.3	65.1
Milk P, %	0.09	0.07	0.07	0.09	0.09	0.10	0.11
Milk P eff., %	34.6	8.3	16.1	28.3	33.3	39.5	61.4
CP, %DM	16.9	0.9	15.1	16.4	16.8	17.6	18.3
NDF, %DM	34.1	3.6	29.7	30.7	33.8	35.8	41.0
P, %DM	0.41	0.04	0.34	0.37	0.41	0.45	0.47
Feces P, %DM	0.70	0.19	0.30	0.55	0.69	0.83	1.28
ADC P, %	35.1	13.2	15.9	24.0	31.7	48.1	59.7

0686 Effect of supplementary copper source on copper status in growing beef heifers offered a diet naturally high in copper antagonists. S. J. Whelan[1], T. M. Boland[1], V. P. Gath[2], J. C. Jacquier[1], and K. M. Pierce[*1], *[1]School of Agriculture and Food Science, University College Dublin, Ireland, [2]School of Veterinary Medicine, University College Dublin, Belfield, Ireland.*

The bioavailability of Cu sources fed to ruminant animals has been the subject of many research articles due to its essentiality in bodily processes and the complexities between Cu and other minerals such as Mo, S, and Fe, rendering Cu unavailable to the animal. As many of these complexes occur within the rumen, an attractive method of improving Cu bioavailability is to offer Cu sources which bypass the rumen digestive process and are subsequently digested and absorbed in the abomasum and small intestine, respectively. This experiment evaluated the effect of three Cu sources on animal Cu status where diets naturally high in antagonists are fed. Sixty beef heifers (*Bos taurus*) were used in a randomized block design based on liver Cu content and offered one of four dietary treatments (n = 15). These were: Control (Con), $CuSO_4$, Bioplex (Bio), and a novel Cu complex (NCu). The Con contained 20 mg Cu/kg DM whereas the other diets contained 54 mg Cu/kg DM. Animals were offered their basal diet of grass silage and concentrate (minerals: Fe, Cu, Mo, and S at 703, 17, 5, and 1400 mg/kg DM). Treatments were fed individually on a daily basis while blood sampling and weights were taken on a weekly basis with a liver biopsy harvested at the beginning (d −7) and end (d 56) of the trial. There was no effect of treatment on live weight (404 kg, P = 0.77). However, animals offered NCu gained more weight (+ 0.18 ± 0.11 kg/d, P = 0.03) than those offered Con. Similarly, liver Cu at d 56 was higher (+132.5 ± 25 mg/kg DM, $P < 0.01$) for animals offered NCu than those offered Con; animals offered Bio and $CuSO_4$ were not different from other treatments. Plasma Cu levels were in the normal biological range for cattle and were lower in Bio supplemented animals compared to other groups (-0.16 ± 0.03 mg/L, $P < 0.01$). Similarly, caeruloplasmin was within the normal range for cattle but was higher for animals offered $CuSO_4$ than those offered Bio (+3.41 ± 0.85 U/ml, $P < 0.01$). These results suggest that animals offered Con may have mobilized liver Cu to maintain Cu homeostasis in the blood as measured by caeruloplasmin and plasma Cu. The NCu complex gave the highest liver Cu concentration and weight gain, demonstrating the role of rumen protection of Cu in improving Cu bioavailability and animal performance.

Key Words: copper

0687 Evaluation of liver mitochondrial oxygen consumption of lactating Holstein dairy cows supplemented with Cobalt, Copper, Manganese and Zinc in organic and inorganic forms. G. Acetoze*[1], J. Champagne[2], J. J. Ramsey[3], A. M. Gehman[4], K. A. Dawson[5], and H. A. Rossow[6], *[1]University of California–Davis, Tulare, [2]VMTRC–UC Davis, Tulare, [3]University of California–Davis, Davis, [4]Alltech, Inc., Nicholasville, KY, [5]Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech, Nicholasville, KY, [6]VMTRC, University of California, Tulare.*

Production of reactive oxygen species (ROS) at mitochondrial level may cause membrane damage impacting energetic efficiency by yielding less ATP. The objective of this study was to evaluate the impact of different concentrations of organic and inorganic forms of Co, Cu, Mn, and Zn (Bioplex Co, Cu, Mn, and Zn; Alltech, Inc.) on liver mitochondrial respiration of lactating dairy cows at a commercial dairy. Fifty lactating Holstein dairy cows (70 DIM) were randomly assigned to five treatments: Control, Organic75, Organic100, Organic125, Inorganics ($CuSO_4.5H_2O$, $MnSO_4.H_2O$, and ZnSO4.H_2O supplemented at the same amount as Organic100) (Table 0687). Minerals were supplemented on top of control diet to individual cows daily with an oral solution of the mineral for 28 d (24 d for adaptation and 4 d of sample collection). On the last day of treatment, 1 g of liver tissue was biopsied to measure O_2 consumption in isolated mitochondria. Statistical analysis was performed in R (version 2.15.1) using ANOVA. State 3 respiration (maximum ATP stimulated respiration), State 4 respiration (maximum leak-dependent respiration), and respiratory control ratio (RCR = State 3/State 4) did not differ among treatments ($P = 0.72$, $P = 0.38$, and $P = 0.76$, respectively), which may be related to high variation in mitochondrial respiration among cows. Numerically, Organic100, 75, and inorganics had the greatest oxygen consumption for ATP production and the greatest rates of oxygen consumption during proton leak dependent respiration. If only considering oxygen consumption results, greater mitochondrial efficiencies would be expected for cows with less oxygen consumption during State 4 and greater oxygen consumption during State 3 respiration. In the present study, supplementation of Co, Cu, Mn, and Zn in Organic125 and control cows had the least oxygen consumption during State 4 respiration, however data on individual cow's feed intake may change these results. Concentration of minerals for Organic125 could be acting as antioxidants by decreasing the incidence of ROS and protecting mitochondria from oxidative damage. Limiting oxidative damage by feeding greater concentrations of antioxidants may prevent mitochondrial membrane damage increasing the efficiency of ATP production and potential increase on milk production and feed efficiency.

Key Words: dairy, mitochondria, minerals

Table 0687. Amount of minerals supplemented on top of control diet for each treatment

	Control	Organic75	Organic100	Organic125	Inorganics
			(mg/d)		
Co	2.96	14.70	19.60	24.50	19.60
Mn	354.00	125.07	166.76	208.45	166.76
Cu	472.00	215.07	286.76	358.45	286.76
Zn	1409.00	375.88	501.18	626.48	501.18

0688 Cobalt-lactate inclusion in a high forage total mixed ration fed to late lactation dairy cows. J. P. Pretz*[1], H. T. Purvis[2], D. Davis[2], B. Trautman[2], J. L. Anderson[1], K. F. Kalscheur[1], and D. Casper[1], *[1]South Dakota State University, Brookings, [2]Ralco Nutrition, Marshall, MN.*

Cobalt-lactate is a highly soluble source of Co in the rumen. Prior research evaluating higher Co feeding rates has been shown to increase ruminal fiber digestion. Feeding high forage rations to late lactation dairy cows to improve income over feed cost could potentially benefit from feeding higher ruminal soluble Co rates to enhance ruminal fiber digestion and nutrient digestibility. Twenty-four late-lactation (238 ± 68.8 DIM and 36.5 ± 5.4 kg milk) Holstein dairy cows (10 primiparous and 14 multiparous), were blocked by milk yield, DIM, and parity and randomly assigned to one of two treatments. Treatments included: 1) CONTROL diet containing cobalt carbonate fed at 58 mg/cow/d, and 2) TEST diet being the same basal diet but including an additional 5 g/cow/d of a 1% Co-lactate product (Co-Max) to increase levels of cobalt by 50 mg/cow/d. Rations were 70% forage and 30% of the respective experimental grain mix on a DM basis with the forage blend consisting of 60% alfalfa baleage and 40% corn silage (DM basis). Cows were fed the CONTROL ration during the covariate period of 7 d followed by 4 wk of data collection when CONTROL and TEST diets were fed. Milk production (26.2 and 25.8 kg/d for CONTROL and TEST, respectively throughout results) was similar ($P = 0.72$). Dry matter intakes (22.9 and 23.1 kg/d) were similar ($P = 0.8$). Concentration of milk fat (4.13 and 4.13%), milk protein (3.53 and 3.40%), and lactose (4.68 and 4.71%) were similar ($P = 0.98$, $P = 0.21$, and $P = 0.66$, respectively). Body weights (684 and 673 kg) were not different ($P = 0.11$). Feeding additional Co as cobalt-lactate did not influence milk production, milk composition, dry matter intake, or body weight for lactating dairy cows fed a high forage ration.

Key Words: dairy cattle, cobalt-lactate, high-forage diet

0689 Supplemental trace minerals (Zn, Cu, and Mn) as sulfates, organic amino acid complexes, or hydroxy trace mineral sources for shipping-stressed calves. A. W. Ryan*[1], E. B. Kegley[1], J. Hawley[1], J. A. Hornsby[1], J. L. Reynolds[1], and S. B. Laudert[2], [1]*Dep. of Animal Science, University of Arkansas Div. of Agriculture, Fayetteville,* [2]*Micronutrients, Indianapolis, IN.*

The objective of this study was to evaluate the effect of trace mineral supplementation from sulfate, organic amino acid complexes, or hydroxy sources on growth performance, morbidity and immune response to bovine viral diarrhea (BVD) vaccination in newly received stocker cattle. Crossbreed calves (n = 350; average BW = 240 ± 1 kg) were obtained from regional livestock auctions. Within each arrival set (block, n = 4), calves were stratified by BW and sex, and allocated into one of eight pens (10 to 12 calves/pen). Pens were assigned randomly to one of three treatments consisting of supplemental Zn (360 mg/d), Cu (125 mg/d), and Mn (200 mg/d) from sulfate (n = 2 pens/block), organic complexes (Availa4, Zinpro Corp., Eden Prairie, MN; n = 3 pens/block), or hydroxy (IntelliBond, Micronutrients, Indianapolis, IN; n = 3 pens/block) trace mineral sources fed over a 42- (block 4) to 45-d (blocks 1, 2, 3) backgrounding period. Cattle were observed daily for signs of morbidity from bovine respiratory disease (BRD) and treated according to a preplanned protocol if rectal temperature exceeded 40°C. Serum samples for BVD antibody titer analysis were obtained on d -1, 14, 28, and final day from the calves in 2 blocks (n = 175). Data were analyzed using the PROC MIXED of SAS with treatment as a fixed effect, block as a random effect, and pen as the experimental unit. When dead (n = 1) and chronic (n = 6) calves were removed from the dataset, final BW did not differ among treatments (280 ± 4 vs. 283 ± 3 vs. 280 ± 3 kg for sulfate, organic complexes, and hydroxy, respectively; P > 0.55) or ADG (0.94 ± 0.05 vs. 0.99 ± 0.04 vs. 0.93 ± 0.04 kg for sulfate, organic complexes, and hydroxy, respectively; P = 0.51). For all calves, dietary treatments had no effect on the number treated once (P = 0.93), twice (P = 0.71), or three times (P = 0.53) for BRD, or on the number of calves classified as chronic (P = 0.55). Trace mineral source had no effect (P = 0.78) on average medical cost per calf. Antibody titer response to BVD vaccination was not affected by trace mineral source (treatment × day, P = 1.00). Based on results from this experiment, source of trace mineral supplementation did not affect total weight gain, ADG, morbidity, medical costs, or antibody titer response to BVD vaccination during the receiving phase in shipping stressed calves.

Key Words: beef cattle, trace mineral

0690 Effect of inorganic or organic selenium supplementation during gestation and lactation on cow and pre-weaning calf performance. C. R. Muegge*[1], K. M. Brennan[2], R. P. Lemenager[1], and J. P. Schoonmaker[1], [1]*Purdue University, West Lafayette, IN,* [2]*Alltech Inc., Nicholasville, KY.*

Angus x Simmental cows (n = 48, BW = 594 kg, BCS = 5.26, Age = 2.7), pregnant with male fetuses, were used to determine the effect of selenium (Se) source during the last 80 d of gestation and first 105 d of lactation on cow and calf performance. At 203 d in gestation, cows were allotted to one of three treatments based on body weight, breed composition, and calf sire: no Selenium, organic Se, or inorganic Se. Diets contained corn silage, corn stover, haylage, dried distiller grains solubles, and mineral and were formulated to contain 10.4% CP and 0.90 Mcal/kg NEg during gestation and 12.1% CP and 1.01 Mcal/kg NEg during lactation. Diets were fed daily as a total mixed ration and none, 0.30 mg/kg Se as sodium selenite, or 0.30 mg/kg Se as Sel-Plex were top-dressed daily. Treatment diets were fed through 105 d post-partum (DPP). At 105 DPP cow-calf pairs were commingled until weaning at 210 DPP. At 68 DPP milk production was calculated using the weigh-suckle-weigh procedure, and a milk sample was collected to determine composition. Cow weight and BCS and calf birth weight did not differ at the beginning of the trial ($P \geq 0.55$). Cow BW and BCS ($P \geq 0.85$) did not differ between treatments at any time point during the study. Milk production, milk fat %, and total solids % ($P \geq .38$) did not differ among treatments. Milk protein % tended to increase in the inorganic Se diet compared to organic Se diet (P = 0.07) and milk lactose % tended to be greatest in the organic Se cows (P = 0.10). Conception to AI and overall pregnancy rates did not differ between the diets ($P \geq 0.39$). Calf weights and ADG did not differ for the 105 d experimental period ($P \geq 0.77$) or for the entire pre-weaning period ($P \geq 0.33$). In conclusion, dietary Se source did not affect cow performance, milk production, or reproductive ability. Organic Se decreased milk protein and increased milk lactose, but did not alter pre-weaning performance of the progeny.

Key Words: beef, cow/calf, selenium

0691 Effects of calf age at weaning on cow and calf performance and feed utilization in an intensive production system. J. M. Warner*[1], K. H. Jenkins[2], R. J. Rasby[1], M. K. Luebbe[2], G. E. Erickson[1], and T. J. Klopfenstein[1], [1]*University of Nebraska, Lincoln,* [2]*University of Nebraska, Scottsbluff.*

A 2-yr experiment compared the feed utilization of producing a weaned calf to 205 d of age between early and normal weaning in an intensive beef cow-calf production system. Multiparous, crossbred (Red Angus x Red Poll x Tarentaise x South Devon x Devon), lactating beef cows (n = 163) with

summer-born calves at side were blocked by prebreeding BW (H, M, L), stratified by calf age and assigned randomly to one of four treatments within strata. The experiment was a randomized complete block design with a 2 × 2 factorial arrangement of treatments with three replications (pens) per treatment per year (total $n = 24$). Treatment factors were: 1) location: eastern (ARDC) or western (PHREC) Nebraska, and 2) calf age at weaning: 91 ± 18 (EW) or 203 ± 16 (NW) d of age. Regardless of location, EW cows and calves and NW pairs were fed a common diet (60:40 distillers grains:crop residue [yr 1]; 40:40:20 corn silage:distillers grains:crop residue [yr 2], DM basis) from the time of early to normal weaning. EW cows were limit-fed (6.9 kg DM/cow daily), while EW calves were offered ad libitum access to feed (4.0 kg DM/calf daily). NW pairs were limit-fed the equivalent amount of DM consumed by EW cows and calves (10.8 kg/pair daily). All cattle were managed in earthen feedlot pens, with pen serving as the experimental unit. By design, BW and BCS at early weaning were similar ($P \geq 0.27$) between EW and NW cows. At normal weaning time, EW cows had greater BW than NW cows, and BW change from early to normal weaning was 17 kg greater ($P \leq 0.01$). Cow BCS at normal weaning time was not impacted ($P = 0.42$) by weaning management. Likewise, calf age at weaning had no impact on BCS change. As intended, calf BW at the time of early weaning was not different, but remained similar ($P = 0.38$) at normal weaning time. NW and EW calves gained 0.85 and 0.82 kg daily, respectively. Similar feed energy intake resulted in comparable performance between weaning regimens. These data indicate early weaning has minimal effect on reducing the feed energy needed to maintain a cow-calf pair. Thus, decisions regarding early weaning should be made on the basis of management rather than feed efficiency.

Key Words: cow, efficiency, weaning

0692 Can treatments of barley grain with lactic and citric acid improve performance of male calves?

K. Rezayazdi[*1], M. Nematpoor[2], and M. Dehghan Banadaky[1], [1]*Dep. of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran,* [2]*University of Tehran, Karaj, Iran.*

Thirty Holstein male calves with an initial body weight 308 ± 22 Kg were used in a completely randomized design with 3 treatments and 10 replicates in each treatment for 100 d. Rolled barley grain steeped in an equal quantity (i.e., in a ratio of 1: 1, wt/vol) of either tap water alone, 0.5% lactic acid solution, or 1% citric acid solution was added to rations. Therefore, dietary treatments included: 1) control (with rolled barley), 2) rolled barley treated with citric acid, and 3) rolled barley treated with lactic acid. The rations were formulated according NRC beef (1996) guidelines. Calves were housed in tie stalls and fed individually. Dry matter intake was measured daily, and weight gain was measured every 4 wk. All of data were analyzed with PROC MIXED of SAS. Final body weight differed across treatments ($P < 0.05$) being 424, 439, and 442 kg to the treatment 1, 2, and 3, respectively. Average daily gain was greater in treatment 2 and 3 vs. 1 ($P < 0.05$, 1.30, 1.48, and 1.50 kg/d, respectively). Dry matter intake was not different among treatments. Gain-to-feed ratio increased due to lactic or citric acid treatment compared with control ($P < 0.05$; 0.162, 0.167, and 0.144, respectively). Overall, feeding feedlot cattle with rolled barley grain treated with lactic or citric acid improved growth performance of calves.

Key Words: barley treated with acid, feedlot cattle, performance

---

0693 Starter crude protein concentrations on growth and intake of dairy calves.

S. A. McCullough[1], B. Houin[2], and T. D. Nennich[*1], [1]*Purdue University, West Lafayette, IN,* [2]*Homestead Dairy, Plymouth, IN.*

The objective of this study was to determine the effects of starter CP levels on growth, intake, feed efficiency, and plasma urea nitrogen (PUN) concentrations of dairy calves on a commercial dairy. In this randomized complete block design, 120 Holstein heifers (BW = 40.3 ± 4.9 kg) were blocked by birth date. Heifers were assigned to starter CP levels of 18, 20, 22, or 24% (as fed). Calves were fed whole milk and allowed ad libitum access to starter. All calves were fed milk 3x/day and received 5.7 L/d for 14 d, 6.7 L/d from d 15 to 21, and 7.6 L/d from d 22 to 1 wk before weaning when calves were reduced to 1.9 L once/d. Calves were weighed at birth and measured every 3 wk for BW, hip height, heart girth circumference (HGC), and hip width. Blood samples were taken at wk 12 and analyzed for PUN. Data were analyzed as repeated measures using the PROC PROC MIXED of SAS. At 12 wk, BW was greater ($P < 0.01$) for 24% compared to 18% calves (106.9 and 101.4 kg, respectively) with 20% and 22% (103.7 and 104.1 kg, respectively) being similar to all treatments. Overall average daily gain (ADG) for 20% and 22% (0.74 and 0.75 kg/d, respectively) were similar to 18 and 24%, but 18 and 24% (0.72 and 0.78 kg/d, respectively) were different ($P < 0.05$). Starter intake over the study was similar among treatments at 0.80, 0.83, 0.87, and 0.91 kg/d for 18, 20, 22, and 24%, respectively ($P > 0.23$). Overall feed efficiency was similar ($P > 0.45$) among treatments at 1.78, 1.83, 1.92, and 2.0 kg DM intake/kg gain, respectively. Hip height and HGC were similar among treatments ($P > 0.55$), but hip widths at 12 wk were greater for 22 and 24% ($P < 0.05$). As CP levels increased from 18 to 24%, PUN concentrations increased among treatments (11.8, 13.1, 15.2, and 16.4 mg/dL, respectively; $P < 0.001$). Feeding calves increasing levels of CP in starter did not result in differences in skeletal growth, feed efficiency, or overall starter intake. At 12 wk, feeding calves 24% CP starter resulted in greater BW than feeding 18% CP, but was similar to feeding 20 or 22% CP starter. Feeding 18, 20, or 22% CP starter resulted in similar ADG.

Key Words: dairy calves, starter, protein

0694 Influence of dietary carbohydrate fractions on growth and development of prepubertal dairy heifers. T. S. Dennis*, J. E. Tower, A. M. Mosiman, and T. D. Nennich, *Purdue University, West Lafayette, IN.*

The objective of this study was to evaluate the effects of altering dietary non-fiber carbohydrates (NFC) on heifer growth, dry matter intake (DMI), feed efficiency, and blood and rumen metabolites. Ninety Holstein heifers (145.3 ± 25.4 kg, 144 ± 26 d of age) were randomly allocated by body weight (BW) to one of 15 pens. Pens were randomly assigned to dietary treatments of high NFC (HNFC; 40.7% of diet DM), low NFC (LNFC; 31.4% of diet DM) and low NFC plus fat (LNFC+; 31.9% of diet DM). Diets were formulated to be isonitrogenous, with lower calculated ME for LNFC compared with HNFC and LNFC+. Heifers were fed diets for 112 d, and forage:concentrate ratios were increased from 35:65 to 60:40 on d 57 of the study. Body weights were taken every 2 wk, and hip and withers heights, body condition score (BCS), heart girth, hip width, and blood samples were collected monthly. Rumen fluid was collected esophageally 6 h after feeding from 10 heifers/treatment (two heifers/pen) to determine pH and volatile fatty acids (VFA) monthly. Data were analyzed as repeated measures using PROC MIXED of SAS with pen as the experimental unit. Feeding LNFC+ resulted in heifers that were 4.8 kg ($P < 0.10$) and 8.8 kg heavier ($P < 0.01$) at the end of the study compared with HNFC and LNFC, respectively. Average daily gains ($P < 0.01$) and feed efficiency ($P < 0.10$) were greatest for LNFC+ from d 0 to 56; however, no treatment differences were observed from d 57 to 112. Intake as a percent of BW was greatest for HNFC (3.3%) compared with LNFC (3.1%) and LNFC+ (3.1%) throughout the study ($P < 0.01$). Heifers fed LNFC+ were taller at the hip and withers than heifers fed HNFC ($P < 0.05$) and LNFC ($P < 0.01$) on d 112. Additionally, feeding LNFC+ resulted in greater BCS compared to LNFC ($P < 0.01$), but not HNFC ($P > 0.10$). Rumen pH was lower for HNFC from d 0 to 56 ($P < 0.05$), but similar among treatments at d 84 and 112. Proportions of acetate and butyrate were least and greatest, respectively ($P < 0.01$), for HNFC from d 57 to 112. Unexpectedly, increasing dietary NFC did not improve growth compared to lower NFC diets despite increased DMI, indicating that energy availability may have greater impacts on growth than dietary carbohydrates.

Key Words: heifer, carbohydrates, growth

RUMINANT NUTRITION: THE GLEN BRODERICK SYMPOSIUM – IMPROVING NITROGEN UTILIZATION IN DAIRY COWS

0695 Opening remarks and overall impact of Dr. Glen Broderick on research around the world.
A. Faciola*, *University of Nevada, Reno, NV.*

Dr. Glen Broderick has been an ADSA member since 1968. Glen has been an ad hoc reviewer for JDS since 1975 and is currently a collaborator with the USDA-ARS and emeritus professor at UW-Madison. Glen received his B.S., M.S., and Ph.D. degrees from UW–Madison. Glen served as an assistant and associate professor of animal science at Texas A&M University from 1972 to 1980. In 1981, he returned to Madison to work at the USDFRC and was appointed as professor of dairy science at UW–Madison. His research focused on protein nutrition of the lactating cow, with emphasis on enhancing utilization of feed nitrogen for milk production and reducing nitrogen excretion. This work involved developing strategies to minimize dietary CP without losing milk or protein yield, identifying factors influencing microbial protein synthesis in the rumen, and perfecting methodologies for quantifying ruminal protein degradation both in vivo and in vitro. Glen's research has generated more than 135 peer-reviewed publications, of which over 100 are in JDS and JAS alone. Glen's major contributions to dairy science include: 1) understanding ruminal microbial metabolism utilizing isotope marker techniques, 2) improvements of in vitro methodologies for assessing ruminal microbial growth and ruminal protein degradation, 3) in vivo quantification of ruminal nitrogen metabolism, and 4) improving overall nitrogen utilization and reducing the environmental impact of milk production. According to the Web of Science, Glen's research articles have been cited more than 4580 times, with an average of at least 105 citations per year. According to the same source, Glen's most cited article is Broderick and Kang. 1980. J. Dairy Sci. 63: 64–75, which has been cited over 600 times. Moreover, in addition to teaching and mentoring of graduate students at UW–Madison and other universities around the world, he has served on the editorial boards of several journals, including JDS, JAS (1981–1993), and Animal Feed Science & Technology (1999–2013), among others. Glen presented a number of invited papers at meetings in more than 25 different countries and mentored over 50 graduate students, postdocs, and visiting scientists. He did sabbaticals at the Rowett Research Institute (1985–1986) in Aberdeen, Scotland, and the Swedish Agricultural University in Uppsala (1997–1998 and 2013). Glen was named a "highly-cited researcher" by the Web of Knowledge in 2005 and received the Nutrition Research Award of the American Feed Industry Association presented by the American Dairy Science Association (1997).

Key Words: dairy cow nutrition

0696 Conundrums of protein and peptide metabolism in the rumen.
R. J. Wallace*, *Rowett Institute of Nutrition and Health, Aberdeen, UK.*

Nitrogen retention in ruminants is inefficient due to rumen microbial activity. Protein in forages is particularly vulnerable, because a high proportion of forage carbohydrate comprises cellulose or hemicellulose, which are slowly degraded, in contrast to the soluble protein, which degrades rapidly. The release of energy-yielding sugars, which enables ruminant microbes to trap the forage protein N, therefore does not match the availability of amino acids, which are degraded excessively, leading to high N emissions by the animal. Protein supplements are almost as vulnerable. The problem with supplements is that they tend to be variable in their degradation rate; thus, diet formulation relies on knowledge of their rate of degradation in the rumen. How to assess protein degradation and the chemistry and microbiology of the process have long been interests of Glen Broderick. It was therefore natural that Glen might want to spend time at the Rowett Research Institute, where Bob Orskov and I shared this interest. Malt whiskies and old Scottish castles also had their part to play! Bob was a committed advocate of the nylon-bag method, a technique that Glen abhorred. I sat on the fence on that one. It might seem like a trivial thing to do, to develop a method to assess the rate and extent of protein degradation. Many have tried to develop in vitro incubations that enable the determination of those characteristics, soon finding that something simple, like the release of ammonia, was vastly in error. Protein supplements are not comprised entirely of protein, indeed starchy carbohydrate even exceeds protein in some supplements. Thus, an enzyme system is fraught with difficulty. The physical form of the supplement is an issue: to grind or not to grind? Furthermore, when ruminal digesta is used as an inoculum for protein degradation assays hydrolyses in vitro, microbes mop up the released amino acids and ammonia as they ferment the carbohydrate. Glen and his colleagues devised an in vitro system that overcame these problems and at the same time revealed some fundamental properties of ruminal protein metabolism. Peptides as an intermediate of the proteolysis cascade were a contentious topic when Glen first arrived on Scottish shores. He and I had great fun in establishing the sequence characteristics that dictate microbial degradation rates of peptides— particularly the importance of the N-terminal amino acids and whether the peptide was basic or acidic.

Key Words: proteolysis, peptide metabolism, rumen

0697 Dr. Glen Broderick's contributions to in vivo quantification of ruminal nitrogen metabolism using the omasal sampling technique. P. Huhtanen*, *Swedish University of Agricultural Sciences (SLU), Umea, Sweden.*

Dr. Glen Broderick has made a significant contribution to improve understanding of protein and amino acid nutrition of dairy cows with the aim of improving overall nitrogen utilization and reducing the environmental impact of milk production. Development of in vitro method to determine ruminal protein degradability was one of his main contributions at earlier stages of career. More recently, he has focused on studying ruminal N metabolism in lactating dairy cows, with the main emphasis in optimizing the efficiency of microbial N synthesis. In these studies Dr. Broderick and his PhD students have applied and developed omasal sampling technique. The method is now widely replaced more invasive duodenal sampling technique, but it also allows studying ruminal N metabolism in more detail as sampling takes places before hydrolysis in the abomasum and endogenous contribution is less. Applying omasal sampling technique Dr. Brodrick demonstrated that the flow of soluble NAN fractions has an important contribution to feed N flow from the rumen. Soluble feed amino acid (AA) flow accounted approximately 10% of omasal total AA flow indicating substantial escape of dietary soluble AA from ruminal degradation. This calls into question the use of in situ estimations of protein degradation to predict RUP flow. Oligopeptides had the greatest contribution of soluble feed AA flow. The study investigating gradual replacement of solvent extracted soybean meal (SBM) with lignosulfonate-treated SBM concluded that NRC (2001) overestimated the supply of RUP from treated SBM. The other important conclusion from this study was decreased microbial protein synthesis with increased proportion of RUP in dietary protein. Consistently with this, replacement of solvent extracted SBM with urea and lignosulfonate-treated SBM decreased NAN and microbial N flow at the omasum demonstrating that microbial protein synthesis is stimulated by true protein RDP compared with NPN. Comparison of red clover and alfalfa silages supported the conclusions from previous studies; increased RUP supply from red clover was counteracted by reduced microbial protein synthesis. Meta-analysis of the data from omasal sampling studies indicated usually smaller residual variance of digesta flow estimates compared with studies applying duodenal sampling, probably reflecting more the marker system applied to estimate digesta flow than sampling site per se. The results suggested that the NRC (2001) system underestimates microbial N flow and overestimates the supply of RUP. The contributions Dr. Broderick emphasize the need for re-evaluation of the feed protein systems.

Key Words: Dr. Broderick, omasal sampling, dairy cow

0698 Glen Broderick's contributions to improving in vitro methodologies for assessing ruminal microbial growth and ruminal protein degradation. P. Udén*, *Swedish University of Agricultural Sciences, Uppsala, Sweden.*

Dr. Broderick has supervised numerous graduate students during his career, been a very active contributor to scientific meetings throughout the world, and also published 126 full papers in refereed journals (Web of Knowledge, Jan. 16, 2014) of which 28 have "in vitro" in the title. The most cited (707) paper of them is so far Broderick and Kang (J. Dairy Sci. 63:64–75, 1980), describing an automated method to analyze ruminal ammonia and amino acids. This method was essential for enabling use of the inhibited in vitro (IIV) system, previously developed by Broderick (J. Nutr. 108:181–190, 1978), to measure release of ammonia and amino acids. He subsequently compared the IIV method with solubility estimates (Broderick and Craig, J. Nutr. 110:2381–89, 1980) and against in sacco estimates (Broderick et al., J. Anim. Sci. 66:1739–45, 1988). In sacco rates were only 36% of those of IIV due to an immediate loss of more rapidly degradable protein in soluble and fine particle forms. This, however, did not prevent adoption of the in sacco method as a standard method for protein evaluation, at least in Europe. The theory of the IIV method is elegant: to inhibit microbial protein synthesis without affecting protein hydrolysis and to estimate degradation as the sum of microbial extra- and intracellular metabolism. The latter feature is attractive as casein data from Broderick and Craig (J. Dairy Sci. 72:2540–48,1989) suggested that uptake of amino acids and peptides is too slow to be ignored. So far, this methodological feature is only shared with the gas-in vitro method of Raab et al., Br. J. Nutr. 50:569–82, 1983). However, the use of inhibitors has limited the use of long incubation times ($> \sim 4$ h) due to a concomitant loss of microbial activity. Nevertheless, the IIV method seems to give biologically sensible degradation rates for sufficiently rapidly degrading proteins. Dr. Broderick has also been involved in developing a 15N based in vitro method to estimate microbial growth (Hristov and Broderick, J. Dairy Sci. 79:1627–37, 1994). An important finding of this study was that microbial protein synthesis is positively related to protein degradation which implies a compensatory effect of low-escape proteins by an increased supply of microbial amino acids to the duodenum.

Key Words: in vitro, protein, dairy cow

0699 Dr. Glen Broderick's contributions to protein and amino acid nutrition of the dairy cow. A. N. Hristov*, *Dep. of Animal Science, The Pennsylvania State University, University Park.*

Dr. Broderick's interest in amino acid (AA) nutrition of the dairy cow started as early as the 1970s, stemming from his

M.S. and Ph.D. studies at the University of Wisconsin under the supervision of the late Dr. Larry Satter. In these early experiments, Dr. Broderick demonstrated that abomasal infusion of casein plus Met in cows fed a 16% crude protein diet increased milk protein content and yield. In his thesis work, Dr. Broderick utilized the concept that an essential AA will not accumulate in plasma, if it is limiting, but will start to accumulate once demands for it in the tissues are met. Using this approach, he concluded that Met, Val, and Lys were most likely limiting AA for milk production in dairy cows. Dr. Broderick's interest in Met continued throughout his career resulting in a number of key publications on production responses to rumen-protected Met (RPMet) products. These experiments demonstrated that, under some circumstances, supplemental RPMet may alleviate the negative impact of decreased dietary protein on milk production and composition with the additional benefit of drastically reducing N excretion in urine and manure. His protein and AA research branched into investigating sources of rumen-undegraded protein (RUP) for the high-producing dairy cow. Early experiments in this challenging area showed increased milk production with roasted soybeans compared with solvent-extracted soybean meal. By comparing forages in the basal diet, it was concluded that resistant protein sources may have a greater value with diets containing alfalfa silage than corn silage-based diets. Working at the U.S. Dairy Forage Research Center, Dr. Broderick's research was focused exclusively on the nutritional aspects of feeding forages, specifically alfalfa, to dairy cows. A series of studies was conducted to assess the feeding value of alfalfa silage vs. hay, with or without preservatives, and the benefit of protein supplementation of alfalfa silage-based diets. This work confirmed that alfalfa silage-based diets may benefit from RUP supplementation and identified the effectiveness of various protein feeds as RUP sources supplying limiting AA postruminally. Other forages, including tanniferous plants, were also investigated as dairy feeds. Research on urea vs. true protein sources established maximum urea supplementation levels. Studies on the interaction of fat and RUP challenged the concept that fat-supplemented diets would benefit from RUP supplementation. These numerous contributions have made Dr. Broderick one of the world's foremost experts in protein nutrition of the dairy cow.

Key Words: Glen Broderick, amino acid, dairy cow

0700 Exploring milk urea-N excretion as a nutritional and environmental management tool for the dairy industry. M. A. Wattiaux* and P. M. Crump, *University of Wisconsin–Madison, Madison.*

In controlled experiments, concentration of urea-N in milk, commonly referred to as milk urea-N (MUN), has been highly correlated with dietary CP level, N use efficiency (NUE, milk-N/intake-N) and urinary urea-N excretion (UUNE). However, under field conditions, variations due to non-nutritional factors (e.g., sampling type, frequency of milking, milk production) and lack of information about N intake the day of DHI testing have lessened the value of MUN as a management tool. This study explored the use of milk urea-N excretion (MUNE) as a UUNE predictor, and the use of MUNE per unit of milk protein yield (PY) as an indicator of NUE. Using DHI (AgSource-CRI) records from 2005 to 2013, we determined the association between PY and MUN or MUNE (calculated as MUN x milk production, regardless of sampling type). Then, we studied the relationship between MUNE/PY and NUE, and between MUNE and UUNE with data of a 128-cow nutritional study. Finally, we compared the MUNE/PY of DHI herds to the values obtained from the nutritional study. Regression analysis of approximately 1.5 million test-day MUN records of 529 DHI herds indicated no linear ($P = 0.08$) relationship between PY and herd-level MUN, but the relationship between PY (g/d) and MUNE (mg/d) was described as: PY = 0.173 + 4.19xMUNE ($r^2 = 0.995$, $P < 0.001$) for PY in the range of 600 to 1300 g/d. In the nutritional study, MUNE was calculated as average morning and evening MUN weighted by milk production at each milking. The relationship between UUNE and MUNE was described as: UUNE (g/d) = 26.8xMUNE ($r^2 = 0.991$, $P < 0.001$) for UUNE in the range of 40 to 125 g/d. Furthermore, MUNE/PY increased from (mean ± SE) 1.1 ± 0.3, to 2.2 ± 0.3, 3.6 ± 0.5, and 4.3 ± 0.3 mg/g as NUE decreased linearly ($P < 0.01$) when mid- to late-lactation cows were fed diets of 11.8, 13.1, 14.6, and 16.2% CP (DM basis), respectively. In the DHI database, however, MUNE/PY averaged 4.6 ± 0.01 mg/g, but ranged from 2.5 to 6.7 mg/g for the 47 herds for which MUNE could be calculated as in the nutritional study. In conclusion, MUNE may be used as a reliable predictor of UUNE and indicator of NUE. Comparing MUNE/PY of the nutritional study to MUNE/PY of selected Wisconsin dairy herds suggested that producers could feed cows to increase NUE and lower UUNE simultaneously across a wide range of PY. Additional research is needed to ascertain the usefulness of MUNE and MUNE/PY as management tools.

Key Words: protein nutrition, nitrogen, environment.

RUMINANT NUTRITION X

0701 Evaluation of 2013 survey of beef producers in Nebraska. M. Jones*, *University of Nebraska–Lincoln, Lincoln.*

Methane is a type of greenhouse gas (GHG) that can capture heat in the atmosphere 21 times more efficiently than carbon dioxide, illustrating its potency as a GHG. Enteric fermentation by ruminants is a known contributor to methane production. A survey was sent to 3391 Nebraska cattle producers with a 19% response rate. The objective of the survey was to evaluate producer opinions regarding beef cattle, climate, and their interaction to direct extension education at reducing GHG emissions in intensive and extensive beef systems. Data were analyzed using the chi-squared method in SPSS. Before accounting for size and type of operation, overall findings were not significant even though numerical differences were evident for many questions. When asked whether they agree or disagree with the statement "methane production impacts cattle performance," 48.1% of all respondents neither agreed nor disagreed. Almost half (45.6%) disagreed with the statement "cattle diet influences methane production." The majority of respondents believed cattle had a positive impact on the environment and reported their confidence in methane production as "not very confident" or "somewhat confident" (34.9 and 45.1%, respectively). After accounting for size and type of operation, significant variables were found using a 99% confidence interval. Feedlots of all sizes tended to agree they were likely to adopt practices that would improve animal performance ($\chi^2 = 45.8$). Veterinarians tended to neither agree nor disagree with methane production being a concern to the environment ($\chi^2 = 22.0$). Producers who obtain livestock production information from the government and other sources tended to agree that cattle diet influences methane production ($\chi^2 = 29.0$). An open-ended question was included in the survey, and responses contained themes on how methane production by cattle was a minor issue, cattle impact on the environment outweighs any negative effects by methane production, and an acknowledgement of a lack of knowledge on the subject. While survey analysis has shown differences among groups for many of the questions, there does not appear to be one specific target group in need of outreach activities. Therefore, extension outreach efforts should focus on current management practices that improve profitability of the operation while also including information about how to reduce methane production in intensive and extensive systems.

Key Words: greenhouse gases, methane, beef cattle, education

0702 Meta-analysis of concentrate supplement effects on voluntary intake in high and low quality pastures. J. R. R. Dórea and F. A. P. Santos*, *University of Sao Paulo, Piracicaba, Brazil.*

The objective was to evaluate the effects of level of supplementation and forage quality on forage and total dry matter intake (DMI). Individually intakes from 1153 beef animals reported in 45 articles published from 1974 to 2011 were compiled. Forage was classified as high quality (more than 9% of CP) and low (less than 9% of CP). A meta-analysis approach was used according to St. Pierre (2001). For high quality pastures forage DMI decreased linearly as the supplementation level increased (-0.651% BW for energy 1% BW supplementation level) ($P < 0.05$). However, total DMI increased linearly ($P < 0.05$) as supplementation level increased (0.348% BW for energy 1% BW supplementation). On the other hand, for low quality pastures forage DMI was increased up to 0.25% BW supplementation level and it was decreased ($P < 0.05$) with high levels of supplementation. Total DMI was increased linearly ($P < 0.05$). The positive effect of supplementation fed up to 0.25% BW on low quality forage intake is due to the high CP content of these supplements supplying RDP to microbes. The negative effect of supplementation on forage DMI occurs when doses are greater than 0.25% BW, and energy is included in the supplement.

Key Words: pasture, protein, supplementation

Table 0702. Best-fit equations for simple regression of response to concentrate supplementation on voluntary intake in different pastures quality

Pasture quality	Variable	Intercept	SE	Slope β1	SE	β2	SE	β3	SE	r^2	RMSE
High	TI	2.35	0.15	0.348	0.242	–	–	–	–	0.66	0.462
	FI	2.35	0.15	-0.651	0.242	–	–	–	–	0.35	0.465
Low	TI	1.70	0.13	0.900	0.122	–	–	–	–	0.65	0.338
	FI	1.63	0.14	1.732	0.789	−5.281	2.670	3.384	2.126	0.30	0.372

FI = forage intake, TI = total intake, SE = standard error, RMSE = root means square error.

0703 Determining the preference and in situ digestibility of a microalgae co-product for beef cattle. M. L. Van Emon*, S. L. Hansen, and D. D. Loy, *Iowa State University, Ames.*

Two experiments were conducted to determine preference (Exp. 1) and in situ digestibility (Exp. 2) of dried, mechanically de-oiled, milled microalgae co-product (ALG) in beef steers. In both experiments, three ruminally cannulated steers (998 ± 103 kg BW) and four treatments were utilized: 1) dry rolled corn-based diet (CON), 2) 15% ALG as a DM replacement of corn (ALG15), 3) 30% ALG (ALG30), and 4) 45% ALG (ALG45). Exp. 1 was performed in a 3 × 6 Latin square design with six 5-d periods and six paired diet combinations. Steers were fed the CON diet for 3 d. On d 4, each steer was offered two diets, placed in either side of a bunk divider in-tubs. Steer diet preference was determined based on DM disappearance for the 4-h immediately post-feeding. On d 5, paired diets were again offered to each steer, on the opposite side of the divider. Exp. 2 was conducted in a 3 × 4 unbalanced Latin square design with three diets fed each period and four 14-d periods. Steers were limit-fed at 2% of BW and adapted to diets for 12 d. On d 13, Dacron bags containing samples of dried and ground corn, soyhulls, or ALG were incubated in the rumen for 6, 12, 24, or 36 h to determine DM disappearance. Data were analyzed using Glimmix and PROC MIXED of SAS for Exp. 1 and 2, respectively. In Exp. 1, the proportion of total DM consumed by steers during the 4-h period was affected ($P = 0.01$) by the paired diet combination. Intake of ALG45 was lesser ($P \leq 0.008$) when offered in combination with the ALG15 or ALG30 diets, but not when offered with CON ($P = 0.76$). No other paired diet combinations altered ($P \geq 0.23$) DMI. In Exp. 2, inclusion of ALG in the diet did not affect ($P \geq 0.12$) rate of, or overall digestibility of, corn, soyhulls, or ALG (71.5 ± 0.83% DM disappearance for ALG at 24 h). Additionally, DMI was linearly decreased ($P = 0.05$) as ALG increased in the diet due to lesser intake ($P = 0.05$) by ALG45 compared with CON, while ALG15 and ALG30 did not differ from CON ($P \geq 0.19$). In summary, steers readily consumed the microalgae co-product but preferred concentrations of less than 45% of diet DM under the conditions of these experiments.

Key Words: beef, digestibility, microalgae

0704 Digestibility of traditional and adding cellulosic ethanol wet distillers grains in finishing lambs. E. L. Lundy*, M. L. Van Emon, D. D. Loy, and S. L. Hansen, *Iowa State University, Ames.*

The feeding value of further processed distillers grains is unclear. A new, secondary fermentation process for converting corn kernel fiber into cellulosic ethanol, including a pretreatment with cellulosic enzymes, yeast, and heat, results in a novel wet distillers grain (WDG) called Adding Cellulosic Ethanol WDG (A-WDG). The study objective was to evaluate the impact of increasing inclusion of WDG from traditional WDG (T-WDG) or A-WDG on nutrient digestibility in lambs. Ten wethers (34.1 ± 0.74 kg) were used in a replicated 5 × 5 Latin square with 15-d periods, including 10-d of diet adaptation and 5-d of fecal and urine collection. Lambs received one of five diets per period: a corn-based control containing 7.5% each of T-WDG and A-WDG (CON), and 30% and 45% inclusion of T-WDG (30T-WDG or 45T-WDG) or A-WDG (30A-WDG or 45A-WDG) on a DM basis. Data were analyzed using PROC MIXED. Dry matter intake (DMI) was not affected ($P \geq 0.25$) by concentration of T-WDG. However, DMI was quadratically affected ($P = 0.02$) by increased concentration of A-WDG, due to lesser DMI by lambs fed 30A-WDG. Digestibility of DM tended to decrease quadratically ($P = 0.09$) in lambs fed T-WDG diets (80.6, 80.0, and 77.4%, SEM 0.57 for CON, 30 and 45T-WDG, respectively). Digestibility of DM linearly decreased ($P < 0.01$) as A-WDG inclusion in the diet increased (78.3 and 75.3%, for 30 and 45A-WDG, respectively). Diet NDF concentration linearly increased ($P < 0.01$) with increasing inclusions of A-WDG (24.6, 31.0, and 33.6%, SEM 0.83 for CON, 30A-WDG, and 45A-WDG, respectively). Diet NDF concentration quadratically increased ($P = 0.03$) with increasing inclusions of T-WDG (26.9 and 32.2%, for 30T-WDG, 45T-WDG, respectively). Digestibility of NDF and ADF did not differ ($P \geq 0.25$) with increased inclusion of A-WDG in the diet. A linear increase in NDF and ADF digestibility was observed with increased inclusion of T-WDG ($P < 0.05$; 50.8, 51.8, and 55.1%, SEM 1.04 for NDF digestibility, and 50.2, 51.8, and 57.2%, SEM 1.74 for ADF digestibility of CON, 30T-WDG, and 45T-WDG, respectively). In this study, WDG from a novel, secondary fermentation process appeared to be an effective substitute for corn in finishing diets, with similar fiber digestibility and a slight decrease in DM digestibility as inclusions increased. With traditional WDG, fiber digestion was linearly improved with increasing inclusions and DM digestibility was decreased only at the highest inclusion.

Key Words: cellulosic ethanol, digestibility, wet distillers grains

0705 Effect of sugarcane fiber digestibility and mode of conservation on intake and ruminal short chain fatty acids of growing steers. *D*. Sousa[*1], B. Mesquita[1], J. Diniz-Magalhes[1], F. Rodriguez[2], I. Bueno[1], and L. F. P. Silva[2], *[1]University of São Paulo, Pirassununga, Brazil, [2]University of Sao Paulo, Pirassununga, Brazil.*

Effect of sugarcane stalk fiber digestibility (NDFD) and method of conservation on intake and ruminal short chain fatty acids (SCFA) was evaluated. Eight ruminally cannulated steers (275 ± 20 kg BW) were used in a duplicated 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments. Two sugarcane genotypes with differing stalk

NDFD were used: IAC86–2480 with higher NDFD (33.7% 30h-NDF digestibility), and SP91–1049 with lower NDFD (29.6% 30h-NDF digestibility). Treatment diets contained 40% sugarcane (DM basis) as sole roughage source given as freshly-chopped or as silage. All diets were formulated with 14.8 CP to provide daily gain of 1.2 kg/d. Animals were housed individually in tie-stalls with free access to water, and fed ad libitum allowing 10% orts. Periods lasted for 14 d, with 10 d for adaptation and 4 d for sample collection. Dry matter intake was determined on d 10, 11, and 12, and rumen fluid samples were collected at six times: 0, 1, 3, 6, 9, and 12 h after feeding on d 14. Samples were taken from three areas of the rumen, filtered through a 1-mm nylon mesh, and centrifuged at 6500×g for 15 min. A 2-mL subsample of the supernatant was taken, mixed with 0.4 mL of formic acid for SCFA determination by gas chromatography. Main effects of sugarcane genotype (GEN), method of conservation (CONS), and their interaction were tested by PROC MIXED. Feeding sugarcane with higher NDFD increased DM intake (5.6 vs. 4.5 ± 0.5 kg/d, $P = 0.01$), however the interaction GEN x CONS was significant ($P = 0.01$). The effect of greater NDFD on DMI was only significant when feeding sugarcane as silage ($P < 0.01$), having no effect on DMI when sugarcane was fresh ($P = 0.53$). Total concentration of SCFA was higher for fresh sugarcane compared with silage (114 vs. 99 ± 12 mM, $P = 0.05$). Conserving sugarcane as silage resulted in greater acetate proportion in the rumen, when compared with fresh sugarcane (58.7 vs. 55.8 ± 1.6% of total SCFA, $P = 0.01$). Proportion of propionate was also effect by conservation method, with greater proportion for diets with fresh sugarcane than sugarcane silage (24.2 vs. 20.6 ± 1.6% of total SCFA, $P = 0.01$). There was no effect of GEN of SCFA in the rumen. Increased in vitro NDFD improved intake, but only when given as silage. Feeding sugarcane ensiled decreased total SCFA and propionate proportion and increased acetate proportion.

Key Words: sugarcane silage, cattle, NDF digestibility, short chain fatty acids.

0706 Evaluation of a mixture of crude glycerol and molasses as an energy supplement for beef cattle consuming bermudagrass hay.

F. M. Ciriaco*, D. D. Henry, V. R. G. Mercadante, T. Schulmeister, G. C. Lamb, and N. DiLorenzo, *University of Florida, Marianna.*

The objective of this study was to evaluate the effects of a crude glycerol:molasses supplement on forage digestibility and cattle performance. Twenty-four Angus crossbred heifers (380 ± 31 kg) were used in the study. On d 0, heifers were weighed after 16-h feed withdrawal, stratified, blocked by initial BW (2 blocks: lightest and heaviest), and randomly assigned to one of four treatments: 0.00, 0.45, 1.36, and 2.27 kg/d of a 50:50 liquid mixture of crude glycerol:molasses. Heifers were housed in individual pens for 28 d and had ad libitum access to ground Tifton 85 bermudagrass hay (13.0% CP, 56% TDN, DM basis). Individual intake of hay was monitored using a GrowSafe feed intake monitoring system. The liquid supplement was weighed and offered daily to each individual animal. Any unconsumed amount of supplement was weighed and recorded. Feed (hay and liquid) and fecal samples were collected starting on d 22 and d 23, respectively, for four consecutive days to determine apparent total tract digestibility of DM, OM, CP, NDF, and ADF. Fecal samples were collected twice daily at 0800 h and 1600 h from the ground, inside the pen, immediately after the animal defecated. Feed and fecal samples were pooled within heifer and indigestible NDF (iNDF) was used as an internal indigestible marker. Concentrations of iNDF in feed and feces were determined by in vitro incubations conducted for 288 h. Data were analyzed as a generalized randomized block design using heifer as the experimental unit and the model included the fixed effects of treatment, and the random effect of block. Orthogonal polynomial contrasts were conducted to determine the effects of supplementation level on animal performance or nutrient digestibility. There was a linear effect ($P \leq 0.05$) of liquid feed supplementation level on ADG, total DMI, and G:F measured using hay DMI only. No effect on G:F ($P = 0.70$) was observed using total DMI (hay plus supplement). The ADG was 1.31, 1.37, 1.39, and 1.56 kg for 0, 0.45, 1.36, and 2.27 kg/d, respectively. Apparent total tract digestibility of DM, OM, NDF, and ADF increased linearly ($P \leq 0.05$), while that of CP decreased linearly ($P = 0.01$) as the level of supplementation increased. The inclusion of up to 2.27 kg/d of a mixture of crude glycerol:molasses supplement may favor forage fiber digestion, improving performance of beef cattle.

Key Words: crude glycerol, molasses, forage digestibility

0707 The effects of dietary energy density and intake restriction on apparent maintenance energy requirements of beef cows.

L. A. Trubenbach*, T. A. Wickersham, and J. E. Sawyer, *Texas A&M University, College Station.*

Intensification of cow calf systems may offer a mechanism to increase land use efficiency of beef production. To determine effects of dietary energy density and intake restriction on energy requirements of beef cows, 32 crossbred cows were individually fed using Calan gates. Cows were fed either a high energy density (H; 1.54 Mcal NEm/kg) or low energy density (L; 1.08 Mcal NEm/kg) diet at each of two levels of intake to achieve 80 or 120% of maintenance energy requirements as predicted by the NRC model. Cows were blocked by BW and treatments were applied in a 2 × 2 factorial to yield four treatment combinations (H80, H120, L80 and L120). After initial treatment application (d −7), cows were weighed daily for 7 d to detect measurable fill change. To accommodate initial fill differences, BW gain was measured from d

−4 to d 42. On days −7 and 42, 12th rib fat thickness was measured via ultrasound. Equations from the NRC model were utilized to calculate heat energy (HE) for individuals. All responses were analyzed as a randomized block design with a factorial treatment arrangement. No energy density by intake level interactions were observed for any response ($P > 0.14$). While there was a difference ($P < 0.01$) in initial body weight between energy density groups due to differential fill loss before d −4, neither diet energy density ($P = 0.09$) nor intake restriction ($P = 0.13$) affected change in BW over the 46-d observation period. Similarly, change in rib fat was not affected by diet energy density ($P = 0.48$) or intake restriction ($P = 0.24$). Cows fed H had 11.6% lower ($P < 0.01$) HEd^{-1} and 9.9% lower maintenance requirements (daily HE/kg $BW^{0.75}$; $P < 0.01$) than cows consuming L. Cows fed 80 had 28.7% lower ($P < 0.01$) HEd^{-1} and 29.1% lower maintenance requirements ($P < 0.01$) compared to cows fed 120. When predicted NEm requirements were based on the equation: 0.077Mcal NEm per $BW^{0.75}$, apparent maintenance requirement deviations were greater (more negative) in both H ($P < 0.01$) and 80 ($P < 0.01$). These results suggest that the additive effects of increasing diet energy density and restricting intake reduce apparent maintenance requirements of beef cows. Substantial gains in efficiency of maintaining beef cows in intensive systems can be achieved by limit feeding an energy dense ration.

Key Words: cow energy requirements

0708 Comparison of the effects of pectin and starch on the rumen fermentation, growth performance, and microbial populations in sheep. J. Liu*[1], M. Liu[1], and J. X. Liu[2], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Zhejiang University, Hangzhou, China.*

Supply of available energy is important for microbial synthesis in the rumen. Pectin and starch are two primary sources of soluble carbohydrates, but remarkably different in digestion and fermentation characteristics. This study was conducted to compare the effects of pectin and starch on rumen metabolism, growth performance, and microbial populations in sheep. Forty-five male sheep (40.2 ± 3.16 kg) were divided into five groups of nine animals each according to body weight, with three pens of three sheep in each group, and then assigned to five dietary treatments with supplementation of 0, 2.5, and 5% pectin or corn starch, respectively, to a basal diet consisted of corn stover and concentrate mixture (50:50, DM basis). The trial lasted 5 wk, and feeds offered and refused were recorded for two consecutive days every week. Body weights were measured at the beginning and end of the feeding trial for two consecutive days. At the end of the trial, two-thirds of experimental sheep were slaughtered before morning feeding to collect samples of rumen contents. Dry matter intake was increased quadratically or decreased linearly with the increasing level of pectin or starch, respectively. Increasing level of pectin led to a linear increase ($P < 0.01$) in microbial protein synthesis and daily weight gain, with highest values at 5% pectin among all treatments ($P < 0.01$). Total volatile fatty acids concentration in the rumen was linearly increased ($P < 0.01$) by inclusion of either pectin or starch, but the ratio of acetate to propionate was not affected. Abundances of *Treponema* genus and *Treponema saccharophilum* quantified by real-time PCR were positively stimulated ($P < 0.01$) only by pectin, suggesting their specific role on pectin digestion. On the contrary, abundances of typical rumen amylolytic bacteria such as *Succinivibrio dextrinosolvens*, *Ruminobacter amylophilus*, *Succnimonas amylolytica* were higher ($P < 0.05$) when starch was supplemented. Both pectin and starch increased ($P < 0.01$) the population of *Treponema bryantii*. Increasing the level of pectin led to a linear decrease ($P < 0.01$) of the rumen lipolytic bacterium *Anaerovi briolipolytica*, whereas starch stimulated the growth of the species. Because *A. lipolytica* cannot utilize starch but lactate as substrate, the growth of *A. lipolytica*in starch treatments may be attributed to the lactate accumulation. A better understanding of microbial populations that accompany dietary differences will expand our knowledge of ecological importance of bacteria in the rumen and may further lead to beneficial strategies to improve ruminant production performance.

Key Words: soluble carbohydrate, microbial protein synthesis, bacterial populations

---

0709 Effect of dietary starch at similar energy intake during backgrounding on subsequent finishing performance and carcass characteristics in beef cattle: a meta-analysis. *P. A. Lancaster*, C. R. Krehbiel, and G. W. Horn, Oklahoma State University, Stillwater.*

Intramuscular fat is reported to utilize glucose for fatty acid synthesis rather than acetate, but inconsistent results have been reported on the effect of dietary starch on marbling in beef cattle. The objective of this study was to use meta-analysis methods to determine the effect of dietary starch during backgrounding on subsequent finishing performance and carcass characteristics in beef cattle. Following a literature search, 14 studies were identified where diets differing in grain inclusion level were fed to normal-weaned steers such that energy intake was controlled for similar ADG. All treatments within a study were fed the same finishing diet. Treatments within study were classified as low, medium, or high starch based on grain inclusion level of the diet. This resulted in subdividing the dataset to analyze comparisons of high (HI1) vs. medium (MED) starch (9 studies) and high (HI2) vs. low (LOW) starch (seven studies); not enough studies had a medium vs. low starch comparison. Data were analyzed using a linear mixed model (PROC MIXED of SAS) that included diet as a fixed effect and intercept as a random effect with the unstructured option and study as the subject. Least square means

were computed using the inverse of the squared standard error for the dependent variable as a weighting factor. The mean grain inclusion level, calculated NEg concentration, and growing phase ADG were 79.4 and 45.2% of DM, 1.42 and 1.02 Mcal/kg DM, and 1.07 and 1.12 kg/d for HI1 and MED, respectively, and were 72.8 and 16.4% of DM, 1.42 and 1.03 Mcal/kg DM, and 1.30 and 1.26 kg/d for HI2 and LOW, respectively. Growth rate, DMI, and G:F were similar ($P > 0.05$) between HI1 and MED and HI2 and LOW. Likewise, HCW, LM area, and 12th–rib fat thickness were similar ($P > 0.05$) between HI1 and MED and HI2 and LOW. Marbling score was similar ($P > 0.05$) between HI1 and MED (427 and 436 ± 17; 400 = Small[00]) and HI2 and LOW (443 and 434 ± 19). These data indicate that dietary starch inclusion level at similar energy intake during the growing phase does not impact subsequent finishing performance or carcass characteristics.

Key Words: backgrounding, dietary starch, marbling

0710 Evaluation of MegaFerm Fiber to enhance ruminal fermentation and nutrient digestibility of a total mixed ration using an in vitro gas production measurement system. D. Casper*[1], I. P. Acharya[1], and D. Miller[2], [1]*South Dakota State University, Brookings,* [2]*Miller-Casper Life Sciences, Brookings, SD.*

The addition of specific feed additives to a total mixed ration (TMR) has the potential to enhance the rate and/or extent of ruminal fermentation and nutrient digestibility. MegaFerm Fiber (MFF) is a unique blend of nutritional technologies that enhances the ruminal fermentation and nutrient digestion of a TMR fed to lactating dairy cows. A standard TMR consisting of alfalfa haylage, corn silage, and a grain mix was dried at 55°C and ground through an ultracentrifuge mill having a 1.0-mm screen. One g of ground TMR was placed in a 50 µm dacron bag, heat sealed, and then placed in a 500 mL Ankom Gas Fermentation Bottle (GFB) to measure rate of gas production and digestion. Treatments were: Control (C) and MFF fed at 3 rates to equate to a feeding rate of 5, 10, and 15 g/cow/d. Each treatment was replicated six times as individual GFB. Rumen fluid was collected from a ruminally cannulated lactating dairy cows fed the same TMR. The rumen fluid was strained through four layers of cheesecloth and 20 mL were added with 200 mL of buffer to each GFB. Bottles were incubated in a circulating water bath at 39°C and gas measurements were collected every 5 min for 30 h. At the completion of 30 h fermentations, Dacron bags were removed and dried to calculate dry matter disappearance and then analyzed for NDF concentrations to calculate NDF digestibility. The rate of gas production was linearly improved ($P < 0.07$) with the addition of MFF to the C TMR (8.0, 8.2, 9.0, and 8.6%/h for C, and MFF at 5, 10, and 15 g/cow/d, respectively). The extent of digested dry matter (76.8, 76.7, 75.8, and 75.2%) was similar ($P > 0.09$) for all treatments. The pH at 30 h was similar for all treatments (6.45, 6.45, 6.46, and 6.49). The pH decline from 0 to 30 h was similar for all treatments (-0.069, -0.073, -0.097, and -0.089 pH units). This study demonstrated that MFF can enhance the rate of digestion by increasing the rate of gas production, but the extent of nutrient digestibility was not affected. The enhanced rate of nutrient digestibility could possibility enhance the milk production of lactating dairy cows

Key Words: gas production, nutrient digestibility, MegaFerm Fiber

---

0711 Application of fecal NIRS profiling to predict diet characteristics and voluntary intake in beef cattle. J. R. Johnson*[1], G. E. Carstens[1], S. D. Prince[2], K. H. Ominski[3], K. M. Wittenberg[3], M. Undi[3], J. A. Basarab[4], T. D. Forbes[5], A. N. Hafla[6], and D. R. Tolleson[7], [1]*Texas A&M University, College Station,* [2]*Texas A&M AgriLife Research, Temple,* [3]*University of Manitoba, Winnipeg, Canada,* [4]*Alberta Agriculture and Rural Development, Lacombe, Canada,* [5]*Texas A&M Agrilife Research, Uvalde,* [6]*USDA–Agricultural Research Service, University Park, PA,* [7]*University of Arizona, Camp Verde.*

Objectives of this study were to evaluate the use of fecal near-infrared reflectance spectroscopy (fecal NIRS) to predict dietary characteristics and voluntary DMI in beef cattle. Fecal samples and phenotype data were collected from 11 growing cattle trials for which intake was measured individually (Calan-gate or GrowSafe systems), and residual feed intake (RFI) calculated. For each trial, animals were fed diets containing at least 70% roughages (1.9 to 2.7 Mcal ME/kg DM), and composite fecal samples were analyzed using a Foss NIRS 6500 monochromator. Modified partial least squares approach was used to develop calibration equations to predict CP, NDF, and DMI using fecal NIRS spectra as independent variables, and CP, NDF, or DMI as dependent variables. Calibration accuracies (SE calibration; SEC and R^2 of calibration; R^2_c) were 0.61 and 0.90 for prediction of CP, 2.35 and 0.85 for NDF, and 11.3 and 0.76 for DMI. Validation of equations was accomplished by cross-validation and evaluated using SE cross-validation (SECV) and R^2 of cross-validation (R^2_{cv}). Validation accuracies (SECV and R^2_{cv}) for prediction of CP and NDF were acceptable and in agreement with previous studies, further indicating that fecal NIRS is a capable tool for predicting dietary CP and NDF. Validation accuracy for prediction of DMI was less accurate than for prediction of dietary CP and NDF. However, the results were comparable to those reported for the prediction of individual-animal intake by fecal NIRS and n-alkane methods in previous studies. Additionally, the fecal NIRS prediction equation for DMI in this study was able to predict individual-animal DMI for the evaluation of divergent RFI groups. Across studies, low RFI animals consumed 12% less ($P < 0.01$) than high RFI animals based on observed intakes (107.8 vs. 122.4 ± 2.2 g/BW$^{0.75}$), and 10% less ($P <$

0.01) based on fecal NIRS predicted intakes (108.9 vs. 120.9 ± 2.13 g/BW$^{0.75}$). Results from this study indicate that fecal NIRS profiling may be useful in predicting animal variance in diet characteristics and DMI.

Key Words: beef cattle, fecal NIRS, feed intake

Table 0711. Statistical performances of fecal NIRS calibrations

					Calibration		Validation	
Item	N	Outliers[1]	Mean	SEL[2]	SEC	R^2_c	SECV	R^2_{cv}
CP, % DM	408	22	13.14	0.10	0.61	0.90	0.67	0.88
NDF, % DM	408	15	55.21	0.31	2.35	0.85	2.46	0.82
DMI, g/BW$^{0.75}$	408	20	109.1	1.18	11.3	0.76	11.8	0.73

[1] Identified by "GH" statistic $\geq$ 8.0 or "T" statistic $\geq$ 2.5.
[2] SEL: SE laboratory.

RUMINANT NUTRITION XI

0712 A comparison between propylene glycol and a multiple component drench on energetic variables in early lactating Holstein cows.

M. Abuajamieh*[1], S. K. Stoakes[1], M. V. Sans-Fernandez[1], J. S. Johnson[1], P. J. Gorden[1], D. M. McKilligan[2], and L. H. Baumgard[1], [1]*Iowa State University, Ames,* [2]*TechMix LLC, Stewart, MN.*

Gluconeogenic precursors are therapeutically administered to treat ketosis in early lactation dairy cows and frequently provided as a standard management practice on all fresh cows. Study objectives were to compare and contrast a multiple component drench (MCD) containing glycerol, propylene glycol, calcium propionate, and water to propylene glycol (PG) on circulating glucose, insulin, NEFA, and β-HBA. Lactating Holstein dairy cows (n = 24, 11.6 ± 1 DIM; parity 1 to 7) were utilized in a replicated experimental design. Cows were randomly assigned to receive one of four treatments: 1) control (300 mL water), 2) 300 mL of PG (Propylene Glycol USP/EP, Dow Chemical Company, Midland MI), 3) 300 mL (M-MCD; TechMix, Stewart MN), and 4) 360 mL (H-MCD; TechMix, Stewart MN). The PG and H-MCD treatments were designed to provide a similar amount of gluconeogenic precursors. Cows were fasted for 4 h and then received a rumen drench of their respective treatment at 0800 h. All products were administered using an orogastric tube to assure successful rumen delivery and chased with 100 mL of warm water. Blood samples were collected via a jugular catheter at -15, 0, 15, 30, 60, 90, 120, and 150 min relative to treatment administration. Metabolite and hormone responses were calculated as area under the curve (AUC) by linear trapezoidal summation between time coordinates after subtracting their respective baseline values. Compared to controls, PG, M-MCD, and H-MCD all increased ($P < 0.01$) circulating glucose following the drench, but the glucose AUC did not differ between treatments. The insulin response peaked at +30 min in the PG, M-MCD, and H-MCD; the overall response was similar amongst treatments. Compared to controls, PG, M-MCD, and H-MCD all markedly decreased ($P < 0.05$) NEFA (42% at +120 min) and NEFA nadir occurred 60 min following treatment administration. Compared to controls, all three treatments decreased β-HBA, but PG tended ($P < 0.09$) to decrease ketones more than M-MCD and H-MCD. In summary, although variable, all three gluconeogenic precursor treatments influenced energetic variables, and thus the MCD product appears to be a viable strategy to manage energetic deficits in early lactation.

Key Words: dairy cow, propylene glycol, multiple component drench

0713 A comparative analysis of metabolomics and transcriptomics from prepartal liver of cows developing ketosis postpartum and healthy cows supplemented with Smartamine M and MetaSmart during the transition period.

K. Shahzad*[1], J. S. Osorio[1], D. N. Luchini[2], and J. J. Loor[1], [1]*University of Illinois, Urbana-Champaign, Urbana,* [2]*Adisseo S.A.S., Alpharetta, GA.*

Cows overfed energy during the dry period are most susceptible to developing ketosis postpartum. Supplementation with Smartamine M (SM) and MetaSmart (MS) during the transition period improves postpartal dry matter intake and resulted in fewer cases of clinical ketosis postpartum. Metabolomics (GC–MS, LC-MS; Metabolon Inc.) and transcriptomics (45K-whole-transcriptome microarray; Agilent) analyses were performed in liver tissue harvested at -10 d relative to parturition from cows that were healthy on 7 d postpartum or were diagnosed with clinical ketosis (K, n = 8). From -21 d to calving all cows consumed a higher-energy diet without (developed K) or with SM (n = 8) and MS (n = 8) (clinically healthy). From 313 identified biochemical compounds, metabolomics analysis ($P \leq 0.10$) revealed 34 or 33 affected in the comparison of K vs. SM or K vs. MS. Comparing profiles in K vs. SM revealed 13 compounds up-regulated and 21 downregulated. Among the up-regulated compounds most belong to bile acid, fatty acid, branched-chain amino acid, and arginine and proline metabolism. Among the downregulated compounds, there were several lysolipids and di-carboxylic acids along with components of pentose, purine, and sphingolipid metabolism. Citrate was markedly lower in liver of K vs. SM. In the comparison of K vs. MS, seven compounds were up-regulated and 26 were downregulated. The up-regulated compounds are intermediates of glycolysis/gluconeogenesis/pyruvate, histidine, glycine/serine/threonine, and fatty acid metabolism. Among downregulated compounds, seven were lysolipids, but also citrate, squalene, several pentoses, and purines were affected. Analysis of transcriptomics data resulted in 834 or 1261 differentially expressed genes (DEG, $P \leq 0.05$) in K vs. SM or K vs. MS. Bioinformatics analysis using the Dynamic Impact Approach (DIA) revealed a strong activation in K vs. MS of Notch, Hedgehog, and TGF-β signaling pathways along with "steroid biogenesis." In contrast, "synthesis and degradation of ketone bodies" was markedly inhibited. The pathway response in K vs. SM was less pronounced in part due to the fewer number of DEG. For example, the Hedgehog signaling pathway was highly impacted but moderately activated; whereas, the "renin-angiotensin system" was the most impacted and markedly inhibited. Preliminary data analysis suggests that supplemental MS and SM elicit distinct metabolomics and transcriptomics responses in liver before calving. Cows developing K postpartum also had a distinct molecular phenotype compared with those supplemented with methionine. The functional relevance of these differences remains to be determined.

Key Words: ketosis, transition cows, metabolomics

0714 The effect of subacute ruminal acidosis on milk fat synthesis and relative expression of key lipogenic enzyme genes in liver tissue in dairy cows. Y. Guo[*1,2], S. L. Li[1], Z. J. Cao[1], X. Xu[1], and Y. Zou[1], [1]*State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing,* [2]*Shijiazhuang Academy of Agriculture and Forestry Science, Shijiazhuang, China.*

The aims of this study were to: 1) determine the variation of performance and relative expression of lipid anabolism related genes in liver tissue triggered by induced subacute ruminal acidosis (SARA), and 2) evaluate the ability of pelleted beet pulp (BP) as a substitute for ground corn to alleviate SARA. Eight mid-lactation Holstein cows were fed four diets during four successive 17-d periods: 1) total mixed ration (TMR) containing 0% finely ground wheat (FGW) (W0), 2) TMR containing 10% FGW (W10), 3) TMR containing 20% FGW (W20), and 4) TMR containing 10% BP as a replacement for 10% ground corn (BP10). The SARA induction protocol reduced the mean ruminal pH from 6.37 to 5.94 ($P < 0.01$), and the minimum ruminal pH decreased from 5.99 to 5.41 from baseline to challenge period. Mean ruminal pH increased from 5.94 to 6.05, and minimum pH increased from 5.41 to 5.63, when BP was substituted for corn. Dry matter intake and milk yield were not affected by the dietary treatments; however, milk fat percentage and yield were reduced ($P < 0.01$) in the W20 and BP10 treatments than the W0 treatment. Cows fed the W20 diet had a lower ($P < 0.01$) plasma concentration of triglyceride and total cholesterol, and a higher ($P < 0.01$) plasma concentration of glucose and insulin than cows fed the W0 diet. Liver tissue relative expression of acetyl-CoA carboxylase α (ACACA) ($P = 0.03$), FA synthase (FASN) ($P = 0.05$), sterol-response element binding protein 1 (SREBF1) ($P < 0.01$) was increased in cows fed the W20 diet, but there were no significant differences among the W10, W20, and BP10 diets. Our results indicate that the SARA could decrease of milk fat synthesis and increase of relative expression of lipid synthesis key genes in liver tissue. The substitution of pelleted BP for ground corn in a high-concentrate diet could reduce the risk of SARA in dairy cows.

Key Words: subacute ruminal acidosis, milk fat, key lipogenic enzyme

0715 Effect of 2-hydroxy-4-(methylthio)butanoate (HMTBa) on risk of diet-induced milk fat depression. M. Baldin[*1], J. Y. Ying[1], G. I. Zanton[2], and K. J. Harvatine[1], [1]*Penn State University, University Park,* [2]*Novus International, Inc., St. Charles, MO.*

Dietary polyunsaturated fatty acids (FA) and diet fermentability are key risk factors for diet-induced milk fat depression (MFD). A role for HMTBa in increased milk fat yield has been proposed, but the interaction of HMTBa and dietary risk factors for MFD have not been investigated. The objective was to evaluate the effect of HMTBa (ALIMET feed supplement, Novus International, Inc., St. Charles, MO) on milk fat synthesis when feeding diets with increasing risk for MFD. Thirty multiparous Holstein cows [227 ± 88 DIM, producing 38 ± 17 kg milk/d (Mean ± SD)] were used in a randomized block design. Treatments were control (corn carrier) and HMTBa (HMTBa fed at 0.1% of the diet DM provided with a corn carrier). The experiment was 70 d and included a 14-d covariate period followed by three phases that fed diets with increasing risk of MFD. During the low-risk phase (28 d) the base diet was balanced to 33.5% NDF and had no exogenous oil, during the moderate-risk phase (14 d) the diet was balanced to 31% NDF and contained 0.75% soybean oil, and during the high-risk phase (14 d) the diet was balanced to 28.5% NDF and contained 1.5% soybean oil. Milk yield, DMI, and BW were measured daily. Milk was sampled every 7 d and analyzed for fat and protein concentration. Data were analyzed using PROC MIXED with repeated measures and the effect of treatment was tested at each time point. There was no overall effect of treatment or treatment by time interaction for DMI, BW, milk yield, and milk protein concentration and yield. A treatment by time interaction was observed for milk fat concentration ($P = 0.02$) and yield ($P = 0.01$). HMTBa increased milk fat percent during the high-risk phase on d 63 (2.83 vs. 3.55, $P < 0.0001$) and d 70 (2.91 vs. 3.43%, $P = 0.005$) and increased milk fat yield on d 63 (821 vs. 1093 g/d, $P = 0.002$) and d 70 (771 vs. 951 g/d, $P = 0.018$). In conclusion, HMTBa increased milk fat yield when cows were fed a diet with a high risk of diet-induced MFD.

Key Words: HMTBa, milk fat depression

0716 Time-course of changes in select ruminal microbes during induction and recovery from diet-induced milk fat depression in dairy cows. D. E. Rico*, S. H. Preston, and K. J. Harvatine, *Penn State University, University Park.*

Diet-induced milk fat depression (MFD) results from bioactive fatty acids produced in the rumen during altered biohydrogenation, and changes in the rumen microbial population are commonly proposed as a key factor in development of the condition. An experiment was conducted to characterize the changes in select rumen microbes during induction and recovery from diet-induced MFD. Eight ruminally cannulated cows were used in repeated design and fed a low fiber, high PUFA diet (Induction; 29.5% NDF and 3.7% PUFA; DM basis) for a period of 21 d, and then switched to a high fiber, low PUFA diet (Recovery; 36.9% NDF and 1.1% PUFA) for 21 d. The control was the high fiber, low PUFA diet. We have previously reported decreased milk fat yield by d 7 and near maximal MFD by d 13 during induction, and a progressive increase in milk fat yield with full recovery by d 15. Ruminal digesta samples were collected 8 h after feeding on Days 0, 4,

8, 12, and 20, and select ruminal microbes were quantified by Real-time PCR. Data were analyzed by PROC MIXED with the repeated statement and treatments compared at each time point. Treatment by time interactions were observed for most taxa ($P < 0.05$). *Megasphaera eldesnii* and *S. ruminantium* (lactate using bacteria) increased progressively > 170% until d 12 of induction and decreased progressively during recovery. *Streptococcus bovis* (amilolytic bacteria) peaked at 350% higher than control on d 4 of induction ($P < 0.01$) and rapidly decreased during recovery. *Prevotella bryantii* (amilolytic bacteria) decreased 66% from d 8 to 20 of induction compared with the control and increased to control levels by d 12 of recovery. *Ruminococcus albus* (fibrolytic bacteria) and *P. ruminicola* (fibrolytic bacteria) were nearly constant during induction and recovery. However, *F. succinogenes* (fibrolytic bacteria) decreased 97% compared to control by d 4 of induction and increased progressively to an equal extent during recovery. The *Butyrivibrio/Pseudobutyrivibrio* group (*t*11–18:1 producer) decreased progressively during induction and increased during recovery, whereas the *Butyrivibrio hungatei* group (*t*11–18:1 producer) was not affected by treatment. Both ciliate protozoa and total fungi decreased progressively by > 90% during induction and increased during recovery. Rapid adaptation of most of the observed microbes occurred during both induction and recovery from diet-induced MFD, and the time-course of adaptation matches the time-course of changes in biohydrogenation intermediates and inhibition of milk fat.

Key Words: dairy cows, milk fat depression, ruminal microbes.

0717 The effect of length of adaptation to a high-grain diet and acidosis challenge and recovery on rumen papillae mRNA expression of genes relating to barrier function, inflammation, and short-chain fatty acid transport in beef heifers.

K. M. Wood*[1], T. Schwaiger[1], J. C. Plaizier[2], K. A. Beauchemin[3], and G. B. Penner[1], *[1]University of Saskatchewan, Saskatoon, Canada, [2]University of Manitoba, Winnipeg, Canada, [3]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Ruminal acidosis induced by high-grain diets can have serious negative effects on animal health and performance. The objective of this study was to investigate if the duration that ruminally cannulated beef heifers were fed a high-grain diet influences mRNA expression of genes relating to barrier function, immune response and short-chain fatty acid (SCFA) absorption in rumen papillae. Heifers were assigned to one of four blocks and randomly allocated to be long adapted (LA; 34 d; $n = 8$) or short adapted (SA; 8 d; $n = 8$) from a backgrounding diet to a high-grain (81% barley) finishing diet before inducing ruminal acidosis. Ruminal acidosis was induced by restricting DMI to 50% for 24 h followed by an intra-ruminal dose of barley grain (10% of DMI). Rumen papillae from the ventral sac were collected and stored in RNA later during the baseline period (BASE; 6 d of before challenge), 24 h after challenge (Recovery1; REC1), and 8 d after challenge (REC2). Total mRNA was isolated from papillae using TriZol and quantitative real-time PCR was conducted to quantify relative expression of genes relating to gut barrier function (zonula occluden 1, claudin 1, and occuldin), immune response (TNF-α, Toll-like receptor 4;TLR4), and intracellular pH regulation and SCFA metabolism (Na^+/H^+ exchanger 1 and 3, monocarboxylate transporter 1 and 4; MCT1 and 4 respectively, and 3-hydroxy-3-methylglutaryl-CoA synthase 1 and 2; HMGS 1 and 2 respectively). Expression of mRNA were normalized for expression of GAPDH and β-actin and expressed as normalized relative fold-change. Data were analyzed using PROC MIXED in SAS and mean separation conducted using Tukey post-hoc separation test. Dietary treatment ($P \geq 0.19$) and the treatment × period interaction ($P \geq 0.06$) did not influence mRNA expression of genes of interest. Total mRNA expression was affected by period ($P \leq 0.03$) for TLR4, ZO1, claudin, occludin, MCT1 and MCT4. In general, REC1 showed least expression and expression during REC2 returned to values similar (TLR4, claudin 1, and occludin) or intermediate (ZO1, MCT1, and MCT4) to BASE. These results indicate that length of dietary adaptation used in our study was not sufficient to differentially influence the expression of mRNA for key genes influencing barrier function, immune response and SCFA transport following an acidosis challenge. However exposure to ruminal acidosis generally reduced mRNA expression with values returning to baseline conditions within 8 d.

Key Words: barrier function, cattle, immune response, rumen acidosis, short-chain fatty acids

---

0718 Induction of subacute ruminal acidosis affects the rumen microbiome.

J. C. McCann*, S. A. Alqarni, S. Luan, P. Cardoso, and J. J. Loor, *University of Illinois, Urbana.*

Subacute ruminal acidosis (SARA) negatively impacts the dairy industry by decreasing milk production, efficiency of milk production, and increasing culling rate and death loss. Six lactating Holstein cows were used in a replicated 2 × 2 Latin square design to determine the effects of SARA induction on the rumen microbiome. Experimental periods were 10 d with d 1 through 3 for ad libitum intake of control diet, followed by 50% feed restriction on d 4, and ad libitum access on d 5 of the control diet (control) or control diet + 4.6 kg of a 50:50 wheat/barley pellet (challenge). Ruminal samples were collected on d 1 and 6 of each period before morning feeding and separated into liquid and solid fractions. Bacterial DNA was extracted from the solid fraction after physical homogenization. Real-time quantitative PCR was used to determine SARA challenge effects on culturable bacterial species. *Butyrivibrio proteoclasticus* was observed in the greatest rela-

tive abundance of the evaluated species (0.4 to 0.2%) with a treatment × day effect ($P < 0.01$). For the control treatment, *Butyrivibrio proteoclasticus* increased ($P = 0.04$) from d 1 to d 6, but there was a tendency to decrease ($P = 0.08$) for the challenge treatment from d 1 to d 6. *Anaerovibrio lipolytica* remained stable during the challenge treatment; however, relative abundance increased ($P < 0.01$) decidedly on control d 6. A primary cellulolytic species, *Fibrobacter succinogenes*, was decreased ($P < 0.02$) from d 1 to d 6 of the control and challenge treatment. While *Selenomonas ruminantium* and *Eubacterium ruminantium* decreased ($P \leq 0.03$) from d 1 to d 6 of the challenge treatment, both species were unaffected by control treatment. Relative abundance of *Prevotella bryantii* increased ($P < 0.01$) on d 6 of the challenge treatment, but no effects of the control treatment were observed. Similarly, the lactate-utilizing species, *Megasphaera elsdenii*, had a tendency to increase ($P < 0.06$) on d 6 of the challenge treatment, yet populations remained stable during the control treatment. Overall, results indicate the challenge treatment caused greater shifts within the rumen microbiome and are likely linked to the onset of SARA.

Key Words: acidosis, SARA, microbiome

0719 Effects of feeding a negative DCAD diet prepartum for varied lengths of time on serum metabolites and performance.

Z. Wu*[1], J. K. Bernard[1], K. P. Zanzalari[2], and J. D. Chapman[3], *[1]University of Georgia, Tifton, [2]Prince Agri Products, Inc., Franklin, IN, [3]Prince Agri Products, Inc., Quincy, IL.*

Forty-five multiparous Holstein cows and 15 springing heifers were used in a completely randomized design trial to determine the effect of length of feeding a negative DCAD diet prepartum on serum metabolites, DMI, milk yield and composition. After training to eat through Calan doors, cows within parity were assigned randomly to negative DCAD diets for 3 (3WPC), 4 (4WPC) or 6 wk (WPC) before predicted calving. Actual days cows were fed negative DCAD diets were 19.2 ± 4.1, 27.9 ± 3.1, and 41.5 ± 4.1d for 3WPC, 4WPC, and 6WPC, respectively. All cows were fed a diet formulated for late gestation (14.6% CP, 42.3% NDF, 20.5% starch, 7.1% ash, and 0.97% Ca) supplemented with Animate (Prince Agri Products, Inc., Quincy, IL) with a resulting DCAD (Na + K– Cl–S) of -21.02 mEq/100 g DM. After calving, cows were fed a diet formulated for early lactation (18.0% CP, 36.4% NDF, 24.2% starch, 8.1% ash, and 0.94% Ca) for the following 6 wk with a DCAD of 20.55 mEq/100 g DM. Urine pH was not different ($P > 0.10$) among treatments before calving and averaged 6.36. No differences ($P > 0.10$) were observed in prepartum DMI which averaged 11.4, 11.5 and 11.7 kg/d for 3WPC, 4WPC, and 6WPC, respectively. Prepartum serum total protein ($P = 0.03$), albumin ($P = 0.01$), Ca ($P = 0.02$), and anion gap ($P < 0.01$) were within normal limits, but decreased linearly with the increasing time cows were fed a negative DCAD diet. No differences were observed in serum metabolite concentrations on the day of calving. After calving, serum total protein ($P = 0.04$) and globulin ($P = 0.02$) increased linearly with the increasing time cows were fed a negative DCAD diet. No differences were observed in postpartum DMI, milk yield, or concentration of fat or protein among treatments: 19.1, 40.6, 4.30, and 2.80; 19.6, 41.5, 4.50, and 2.90; and 18.6 kg/d, 41.0 kg/d, 4.30% and 2.73% for 3WPC, 4WPC, and 6WPC, respectively. Results of this trial indicate that extending the length of time cows are fed a negative DCAD diet does not negatively affect serum metabolites or resulting performance.

Key Words: DCAD, serum metabolites, milk yield, milk composition

---

0720 Effect of pre-calving dietary cation anion difference on milk production: A meta-analysis.

I. J. Lean[1], R. Rodney[1], P. J. DeGaris[2], D. M. McNeill[3], and E. Block*[4], *[1]SBScibus, Camden, Australia, [2]Tarwin Veterinary Group, Leongatha, Australia, [3]University of Queensland, Gatton, Australia, [4]Church and Dwight Animal Nutrition, Ewing, NJ.*

The effects of dietary cation anion difference (DCAD) of pre-calving diets on milk production. A total of 15 studies and 34 comparisons were identified and analyzed (Stata 13.0 Statacorp, Texas) using a random effects model. A weighted mean difference between treated and control was also calculated. Meta-regression analysis evaluated whether parity of the cattle, difference in DCAD between treatment and the control diet and estimated energy density, crude protein, crude fat, neutral detergent fiber, non-fiber carbohydrates, DCAD, calcium, magnesium, phosphorus, potassium, and content of the control diet influenced responses. The average ± SE days of exposure to transition diets was 29 ± 3, and the DCAD of controls and treated cows was 232 ± 37 and -27 ± 33 meq/Kg, respectively. Only the parity of the cow ($P = 0.003$) and NDF of the control diet ($P = 0.02$) influenced responses with milk production increased in cows ($P = 0.0001$) and lowered in heifers ($P = 0.027$). The effect size (ES) for milk production of studies in cows was positive (0.629 95% CI 0.292 to 0.965). Estimated responses in milk or fat corrected milk over 65 ± 14 d of lactation were 1.153 (95% CI 0.335 to 1.971) L per day. In heifers, milk production responses were ES of -1.211 (95% CI -2.288 to -0.135) and the weighted mean difference was -1.482 (95% confidence interval -1.872 to -1.093) L per day. The I^2 was 77.1 for cows and 87.2 for heifers, indicating very considerable variability in responses. The effect size response was lower with higher NDF diets. The lower response to DCAD in high NDF studies may indicate a role for ruminal outputs to influence acid-base status. Critically, other sources of variation, as indicated by the high I^2, were not identified, despite the large number of covariates tested. Reference: Lean IJ, DeGaris PJ, McNeil DM, Block

E (2006) Hypocalcemia in dairy cows: Meta-analysis and dietary cation anion difference theory revisited. *Journal of Dairy Science*. 89: 669–684.

Key Words: dietary cation anion difference, pre-calving diet, meta-analysis

---

0721 Evaluation of choline metabolites in milk as potential biomarkers for choline absorption in the lactating dairy cow. V. M. Artegoitia*[1], C. L. Girard[2], H. Lapierre[2], S. R. Campagna[1], F. Harte[1], and M. J. de Veth[1,3], *[1]University of Tennessee, Knoxville, [2]Agriculture & Agri-Food Canada, Sherbrooke, QC, [3]Balchem Corporation, New Hampton, NY.*

Choline is an essential nutrient for growth and performance of production animals, and an established symptom of choline deficiency in periparturient cattle is fatty liver. Dietary choline is extensively degraded in the rumen, and although rumen-protected choline (RPC) has been found to reduce the extent of hepatic fat infiltration, no biomarkers have been established to assess the efficacy of RPC supplements in dairy cows. Secretion of total choline in milk could be a potential biomarker; however, choline is secreted in milk in many metabolic forms and some specific metabolites in milk may be more closely associated with choline absorption than total choline secretion. The objective of this study was to evaluate secretion of choline metabolites in milk as potential biomarkers of choline absorption. Five lactating Holstein cows (237 ± 17 DIM) were used in a 5 × 5 Latin square design, with 5-d treatment periods and a 2-d interval between periods. Treatments were 1) control (0 g/d choline), 2) RPC- low dose (RPC-L), 3) RPC-high dose (RPC-H), 4) abomasal infusion (ABO)– low dose (ABO-L), 5) ABO– high dose (ABO-H). The low and high doses of RPC (Reashure, Balchem Corp.) and ABO each supplied 12.5 and 25 g choline/d, respectively. Milk samples from d 5 were analyzed for acetylcholine (AC), betaine (Bet), free choline (Cho), glycerophosphocholine, lysophosphocholine, phosphatidylcholine, phosphocholine (PC), and sphingomyelin, using liquid chromatography-tandem mass spectrometry. Although total choline secretion in milk was not affected by ABO, Cho and Bet secretion increased ($P < 0.01$) in a dose dependent manner with ABO by 74% and 171%, respectively, with ABO-L and 146% and 278%, respectively, with ABO-H. The amounts of Cho and Bet secreted in milk increased from 0.54 to 0.94 and 1.33 g/d and from 0.14 to 0.38 and 0.53 g/d, respectively for the low and high doses. Increases in the yields of AC and PC were also observed ($P = 0.04$), although only with ABO-H. The other metabolites were not changed by ABO ($P > 0.12$), nor were any changes observed in secretion of individual choline metabolites with RPC. Multiple regression indicated the changes in milk PC and Bet secretion could be explained to a large degree by the ABO dose of choline ($P = 0.01$; $R^2 = 0.72$). The results of this study suggest that some choline metabolites may be more sensitive biomarkers than total choline for absorption of supplemental choline.

Key Words: choline, bioavailability, dairy cow

0722 Association of plasma ghrelin concentrations with feed intake in beef cattle. A. P. Foote*, K. E. Hales, C. A. Lents, and H. C. Freetly, *USDA-ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Active ghrelin is an acylated peptide produced in the gastrointestinal tract of animals that is thought to stimulate appetite. Cattle used in this experiment were sired by bulls representing five breeds in the United States, including Hereford, Angus, Limousin, Charolais, and Gelbvieh. Steers ($n = 128$) and heifers ($n = 133$) were fed a finishing diet and individual intake was recorded for 84 d. Blood samples were collected via jugular puncture at 113 d on feed. Active ghrelin was protected by acidifying the blood plasma and adding a protease inhibitor. Active ghrelin was quantified using a commercial RIA specific for the acylated form of ghrelin. The mixed model procedure of SAS was utilized to determine factors influencing active ghrelin levels. Fixed effects included sex, sire breed, dam breed, total dry matter intake (TDMI), and BW at time of blood collection. Sire nested within sire breed was included as a random effect. A mixed model was also used to determine if concentrations of active ghrelin could be used to predict TDMI. Fixed effects included concentrations of active ghrelin, sire breed, dam breed, sex, BW, and sire nested within sire breed was included as a random effect. Concentrations of active ghrelin were positively associated with TDMI ($P = 0.012$) when sex and breed effects were accounted for in the model. Regardless of breed, heifers had lower TDMI than steers ($P = 0.012$) but tended to have greater concentrations of active ghrelin ($P = 0.099$). Gelbvieh-sired cattle had the greatest concentrations of active ghrelin and Angus, Limousin, and Charolais had the lowest concentrations while concentrations of ghrelin in Hereford-sired cattle were intermediate ($P = 0.003$). Angus-sired cattle had the highest TDMI, while Limousin-, Charolais-, and Gelbvieh-sired cattle had the lowest TDMI with Hereford cattle intermediate ($P < 0.001$). Modeling the data showed that active ghrelin concentrations had a positive association with TDMI; however, both the sex and sire breed effects indicate that cattle with lower intakes (e.g., heifers and Gelbvieh-sired cattle) tend to have greater concentrations of active ghrelin than cattle with higher intakes. Data indicate there is a genetic effect on active ghrelin levels that may affect the association with intake. *USDA is an equal opportunity provider and employer.* *Funded in part by NIFA Grant 2011–68004–30214 through the National Program for Genetic Improvement of Feed Efficiency in Beef Cattle.*

Key Words: breed differences, feedlot cattle, gut peptides

0723 Effects of ruminal dose of sucrose, lactose, and starch on ruminal fermentation and expression of genes in ruminal epithelial cells. M. Oba*, J. Mewis, and Z. Zhu, *University of Alberta, Edmonton, Canada.*

The objective was to evaluate effects of ruminal dose of sucrose (SUC), lactose (LAC) and cornstarch (STA) on ruminal fermentation and expression of genes in ruminal epithelial cells. Six ruminally cannulated non-lactating non-pregnant Holstein cows (BW = 725 ± 69.6 kg) were fed a diet containing whole crop barley silage and dry ground corn (dietary NDF and CP contents: 41.8 and 13.2% at DM basis, respectively), and assigned to treatments in a 3 × 3 Latin square design with 7-d periods; 1 d for data and sample collection followed by a 6-d washout period. Treatment was a pulse-dose of SUC, LAC, and STA (3.0, 3.0, and 2.85 kg DM, respectively, to provide similar amount of hexose across the treatments) through the rumen cannulas. All treatments were given with alfalfa silage (1.75 kg DM) to prevent acute rumen acidosis. Rumen pH was continuously monitored, and rumen fluid was sampled at 0, 30, 60, 90, 120, 150, and 180 min after the dose. In addition, ruminal papillae were sampled from the ventral sac at 180 min after the dose. Ruminal dose of SUC and LAC, compared with STA, increased ($P < 0.05$) ruminal total VFA concentration and molar proportion of butyrate since 60 min after the dose, and expression of genes for sodium hydrogen exchanger 1 and 2, and ATPase-1 in ruminal epithelial cells. Ruminal dose of SUC, compared with LAC and STA, decreased ($P < 0.05$) rumen pH since 120 min after the dose and molar proportion of acetate in ruminal fluid from 60 to 150 min after the dose, and increased ($P < 0.05$) molar proportion of propionate in ruminal fluid from 60 to 150 min, and expression of genes involved in butyrate metabolism (3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1) and anion exchange across ruminal apical cell membrane (putative anion transporter 1). These results suggest that replacing dietary starch with sugar may affect ruminal fermentation, and metabolism regulating intracellular pH and fermentation acid absorption in ruminal epithelial cells, and that these effects can be greater for SUC than LAC.

Key Words: sucrose, lactose, starch

SMALL RUMINANT

0724 Rumen microbial species associated with feed efficiency in sheep fed a forage-based diet.
K. M. Cammack*[1], M. Ellison[2], G. C. Conant[3], W. R. Lamberson[3], R. Cockrum[4], and K. J. Austin[1], *[1]Dep. of Animal Science, University of Wyoming, Laramie, [2]University of Wyoming, Laramie, [3]University of Missouri, Columbia, MO, [4]Virginia Polytechnic Institute and State University, Blacksburg.*

The rumen microbial ecosystem plays a dominant role in fermentation of consumed feeds in ruminant livestock and therefore influences the efficiency of feed utilization. Determination of rumen microbial species important to feed efficiency may ultimately lead to development of technologies to aid producers in selecting more efficient seedstock. Our objective was to identify rumen microbial species associated with variation in feed efficiency in lambs fed a forage-based diet. Briefly, growing wethers (initial BW = 51.5 ± 1.7 kg; n = 38) of Rambouillet, Suffolk, and Hampshire breed backgrounds were administered a forage-based pelleted diet and individual feed intake was collected using a GrowSafe system over a 7-wk period. Residual feed intake (RFI) was estimated for each lamb and subsequently used to rank lambs for feed efficiency. The most efficient (low-RFI; n = 4) and the least efficient (high-RFI; n = 4) lambs were selected for sequencing of DNA isolated from respective rumen fluid samples. Pair-end reads were filtered, quality trimmed and compared with a database of known 16S rDNA genes. Operational taxonomic units (OTU) were defined as sequence clusters with ≥ 97% identity. Abundance of 28 OTUs differed (P < 0.05) with feed efficiency status, with the majority (n = 18) of these being *Prevotella* species. Of particular interest were *Ruminococcus flavefaciens* and *Ruminococcus albus*, two predominant rumen fibrolytic bacterial species involved in cellulose digestion. Unexpectedly, these two bacteria were in greater (P < 0.001) abundance in high-RFI lambs (3.2-fold greater for *R. flavefaciens*; 1.5-fold greater for *R. albus*). This may be due to differences in diet quality and form (i.e., pelleted), as previous studies have indicated that changes in abundance of such fibrolytic species can be associated with diet differences. Data from this study suggest that rumen microbial populations differ with feed efficiency status; however, certain species may be prone to variations in diet quality and presentation.

Key Words: feed efficiency, microbes, rumen, sheep

0725 Rationing late gestation ewes using a net energy or metabolisable energy rationing system: Impacts on ewe and lamb performance.
F. Campion*, F. McGovern, A. G. Fahey, and T. M. Boland, *School of Agriculture and Food Science, University College Dublin, Ireland.*

Ewe body reserves, colostrum, and milk production, lamb birth weight, lamb vigour and lamb survival are influenced by late gestation nutrition. Net energy (NE) rationing systems are purported to more accurately define the requirements of the animal relative to metabolisable energy (ME) systems. The objective of this study was to investigate the effect of rationing ewes to ME or NE during late gestation on ewe and lamb performance. Twenty-six twin-bearing ewes (n = 13) were rationed to either 100% of ME (MER) or 100% of NE requirements (NER) for the final 5 wk of gestation. Ewes were rationed on an individual basis and offered a grass silage diet supplemented with concentrate to 100% of requirements. Ewe live weight and body condition score (BCS) were recorded at Day 85 of gestation, parturition, 5 wk postpartum and weaning (14 wk postpartum). Colostrum production was measured at 1, 10, and 18 h postpartum along with lamb colostrum intake. Lamb live weights were collected at birth, weekly during the first 7 wk postpartum and fortnightly from 9 wk postpartum to slaughter. Lamb growth rate was calculated by regression of live weight on time. Carcass weight was obtained at slaughter and kill-out percentage calculated. Statistical analysis was performed using generalised least square means in SAS v9.4. Energy intake expressed as both NE and ME was lower for the MER ewes (P < 0.01). Live weight loss of MER ewes during the same period was higher (P < 0.05) reflecting their lower energy intake. No difference was observed in ewe live weight loss from parturition to weaning (P > 0.05). Ewe BCS did not differ between treatments throughout the study (P > 0.05). Total colostrum production to 18 h postpartum tended to be greater for NER ewes (P < 0.1). This difference was not mirrored in lamb colostrum intake to 18 h postpartum (P > 0.05) indicating both treatments produced sufficient colostrum to meet requirements. Lamb live weight, growth rate, carcass weight, and kill-out percentage did not differ between treatments (P > 0.05). This uniformity in postnatal performance appears to have resulted from increased body reserve mobilization by the MER ewes, thus countering potential negative effects of the reduced energy intake. For ewes in the correct BCS in late gestation, either the NE or ME rationing system used in this study are appropriate for dietary formulation.

Key Words: energy postpartum performance

0726 Determining growth performance implications on meat goat kids fed soybean hull or corn-based pelleted diets. A. C. Vesco*, C. K. Jones, L. C. Grimes, T. H. Fountain, B. R. Faris, and A. K. Sexten, *Kansas State University, Manhattan.*

The meat goat industry is rapidly expanding, yet there is limited knowledge on feeding kids to market weight, providing opportunities for research in this area. This study investigates the option of an alternative energy source to corn for a growing kid ration. Eighty-four Boer × Spanish kids (30 kg; 8 mo) were used in a randomized complete block design to determine the effects of a soybean hull based diet on growth performance and blood serum mineral composition. Kids were blocked by sex and randomly assigned to one of two treatments: 1) corn and soybean meal based pellet (Corn) or 2) soybean hull and soybean meal based pellet (Soyhull). Kids were allowed a 10-d pen and diet adaptation period. Feed was delivered once daily at 0600 with daily intake adjustments to maintain ad libitum intake of pellets and brome hay for 70 d. There were 7 pens per treatment with six head per pen; sex was divided equally between treatments. Weights for all kids were recorded every 2 wk. Pellet and hay grab samples were collected daily, composited by 2-wk period, oven-dried, and ground to be analyzed for DM, Ash, N, NDF, and ADF. Blood samples were taken on d 0, d 28, and d 70, and serum was analyzed for levels of Na, K, Cl, Ca, P, and Mg. Initial body weight was similar ($P = 0.24$) between treatments. Body weights remained similar ($P \geq 0.12$) between treatments for each weigh date for the entire 70-d feeding period. Overall gain and ADG were likewise not different ($P \geq 0.18$) between treatments. Kids consuming the Soyhull diet had greater ($P \leq 0.001$) DMI throughout the study compared to kids consuming the Corn diet. Overall DMI averaged 1.37 $kg \cdot hd^{-1} \cdot d^{-1}$ vs. 1.06 $kg \cdot hd^{-1} \cdot d^{-1}$ for the kids consuming the Soyhull and Corn diets, respectively. No differences ($P \geq 0.44$) were observed for blood serum mineral composition between treatments. Based on these results soybean hulls are a viable alternative feed source to corn for growing meat goats when protein requirements are met.

Key Words: meat goat, soybean hulls, mineral

0727 Early supplementation of alfalfa to starter diets improves the pre- and post-weaning performance of lambs. B. Yang*[1], B. He[1], S. S. Wang[1], J. X. Liu[2], and J. K. Wang[1], [1]*Institute of Dairy Science, Zhejiang University, Hangzhou, China,* [2]*Zhejiang University, Hangzhou, China.*

The objective of this study was to determine the effects of alfalfa supplementation to starter diets of artificial reared lambs on pre- and posting performance. Twelve Hu lambs at the age of 10 d, with an initial body weight of 3.87 ± 0.564 (SD) kg, were randomly divided into two equal groups and allocated to two dietary treatments: cereal feeding (CF, milk replacer, and pelleted starter) and forage feeding (FF, milk replacer, pelleted starter, and alfalfa). All animals were fed the same milk replacer at 880 mL/d on d 1, and milk replacer was then reduced at a rate of 30 mL/d until d 24. The lambs were then fed at 180 mL milk replacer per day from d 24 to 28 (weaning). During this period, the pelleted starter (16.8% NDF) was offered to all animals, but alfalfa (38.6% NDF) was only to group FF ad libitum. After weaning, the animals were offered with 300 g/d cereal powder (21.5% NDF) and had free access to alfalfa. Feed offered and refused, and body weights were recorded for two consecutive days at 0800 every week during the 4-wk feeding trial after weaning. On d 57, blood samples were obtained to determine serum concentration of glucose and β-hydroxybutyrate. After slaughtered, rumen pH and weight of carcass and forestomachs were determined immediately. Average alfalfa intake was 118 g/d before weaning, and 345 and 289 g/d ($P = 0.365$) for FF and CF after weaning, respectively. Starter intake was not affected by early supplementation of alfalfa ($P = 0.195$), but intake of cereal powder tended to be higher in FF group than in CF (258 vs. 209 g/d, $P = 0.051$). Average daily gain was 69% ($P = 0.001$) and 12% ($P = 0.006$) higher in FF than that in CF before and after weaning, respectively. Forage feeding before weaning resulted in higher carcass weight compared to cereal feeding (5.76 vs. 4.57 kg, $P = 0.005$). No significant difference was observed in abomasum and reticulum weight between CF and FF ($P > 0.05$), but rumen weight tended to be higher in FF than in CF (292 vs. 247 g, $P = 0.059$), and omasum weight increased by 24% ($P < 0.05$) in FF than in CF. Differences in rumen pH and serum concentration of glucose and β-hydroxybutyrate were not observed between two treatments ($P > 0.05$). From the present study, it is inferred that supplementation of alfalfa in starter diets is beneficial to growth performance and forestomach development in weaned lambs.

Key Words: alfalfa, lamb, starter

0728 Performance and reproductive measurements of Katahdin ewes and fall-calving Angus cows grazing stockpiled toxic tall fescue under a mixed or sequential grazing scheme: 2-yr summary. R. E. Daugherty Jr.*, J. D. Caldwell, B. C. Shanks, C. L. Boeckmann, C. A. DeOrnellis, and A. L. Bax, *Dep. of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO.*

Multi-species grazing has several potential advantages and ultimately may improve performance for one or both species. With renewed interest in multi-species grazing, there is value in evaluating mixed versus sequential grazing schemes. However, there has been little research evaluating hair sheep and cattle grazing stockpiled toxic tall fescue (E+) either mixed or sequentially. Our objectives were to determine performance and reproductive measurements of Katahdin ewes and fall-

calving Angus cows grazing stockpiled E+ under a mixed or sequential grazing scheme. Katahdin ewes (n = 81; 27 ± 3.6 kg initial BW; 3 ± 0.07 initial BCS) and fall-calving Angus cows (n = 40; 471 ± 23.5 kg initial BW; 6 ± 0.6 initial BCS) were stratified by BW and age within species and were allocated randomly to one of four groups representing two treatments: 1) mixed grazing (four replications) or 2) sequential grazing (four replications). In the sequential grazing treatment, cows always followed ewes. Each group had access to a 0.68-ha paddock and were rotated based on available forage. A total of 8.16 ha were grazed over 40 d for all groups. Initial weight and BCS from ewes and cows did not differ ($P \geq 0.83$) across treatments. Average daily gain, total gain, end weight, and end BCS from ewes and cows did not differ ($P \geq 0.35$) across treatments. Cow pregnancy rate, calf birth date, and calf birth weight did not differ ($P \geq 0.56$) across treatments. Calf start weight, end weight, average daily gain, and total gain did not differ ($P \geq 0.26$) across treatments. Ewe pregnancy rate, lamb birth date, and lamb counts did not differ ($P \geq 0.11$) across treatments. A treatment × sex interaction tendency (P = 0.06) was detected for lamb birth weight and a treatment × sex interaction (P = 0.01) was detected for lamb weaning weight. Mixed grazing ram lambs tended to be heavier at birth compared with mixed grazing ewe lambs, and mixed grazing ram lambs were heavier compared with sequentially grazed ram lambs at weaning. Therefore, utilizing sequential grazing with Katahdin ewes and fall-calving Angus cows may not increase performance or reproductive measurements; thus, managing a multi-species, sequential grazing regime relative to mixed grazing may not be warranted.

Key Words: fescue, mixed grazing, sequential grazing

0729 Reducing dietary cation-anion difference increased gastrointestinal calcium binding proteins-D9k expression level of transition goats for plasma calcium absorption. W. X. Wu* and Y. Yang, *College of Animal Science, Guizhou University, Guiyang, China.*

The mechanism to explain why reducing dietary cation-anion difference (DCAD, mEq/kg DM) could prevent hypocalcemia in transition dairy cows remains unclear. Calcium binding protein-9 kDa (CaBP-D9k) was the main biological factor highly associated with Ca absorption in the gastrointestinal tract (GIT; rumen, reticulum, omasum, abomasum, jejunum, ileum, colon, cecum, and rectum). This study was conducted to clarify the mechanism by investigating the influence of varying DCAD level on CaBP-D9k expression level in GIT and plasma Ca concentration of transition goats, which had similar anatomy and metabolic process relative to dairy cows. Twenty-seven transition goats were randomly allocated to one of three treatments and were fed one of three diets with varying DCAD levels: +300 (HD), +150 (CON), and −50 (LD), respectively. Goats were bled on d 10 before lambing, d 0 for lambing, and d 3 after lambing to determine plasma ions contents; and were slaughtered to detect the CaBP-D9k expression level, respectively. Dry matter intake was unaffected by DCAD treatments ($P > 0.05$). Urine pH was reduced with decreasing DCAD level ($P < 0.05$). The LD diet level induced higher plasma Cl^- and Ca^{2+} concentrations relative to CON and HD diets ($P < 0.05$). Greater CaBP-D9k mRNA expression level was observed in whole GIT of LD-fed goats except for ileum, cecum, and rectum compared with goats in two other groups ($P < 0.05$). Moreover, feeding LD diet moderated the decline of CaBP-D9k mRNA expression level in abomasum, jejunum, and colon after lambing ($P < 0.05$). In conclusion, reducing DCAD could up-regulate CaBP-D9k expression level in stomach, proximal intestine and colon, which was accompanied with higher plasma Ca concentration for transition goats. This result would be the possible mechanism of low DCAD enhancing blood Ca homeostasis during periparturient period to prevent hypocalcemia of transition dairy animals.

Key Words: dietary cation-anion difference, calcium binding protein-9 kDa, transition goats

---

0730 Hematological and serum chemical profiles in lambs fed sericea lespedeza. M. Acharya*[1], J. M. Burke[2], J. E. Miller[3], T. H. Terrill[4], E. Smyth[1], G. Huff[5], E. B. Kegley[6], K. P. Coffey[1], and C. F. Rosenkrans[1], *[1]University of Arkansas, Fayetteville, [2]USDA-ARS, Booneville, AR, [3]Louisiana State University, Baton Rouge, [4]Fort Valley State University, Fort Valley, GA, [5]USDA, Agriculture Research Service, Fayetteville, AR, [6]Dep. of Animal Science, University of Arkansas Division of Agriculture, Fayetteville.*

Sericea lespedeza (SL) is plant-grazed or fed to small ruminants for parasite control. Condensed tannins in SL may lead to unintended consequences such as changes in production. The objective was to determine the effect of SL with or without molybdenum supplementation on changes in BW, hematology, and serum chemistry in lambs. Thirty Katahdin or Katahdin × Romanov lambs weaned in May (84 ± 1.5 d of age; 27 ± 1.1kg) were blocked by BW, breed, and parasite resistance, and assigned randomly to be fed 900 g of 75% alfalfa pellets (CON; n = 10) or 75% SL pellets (n = 20) for 104 d. Supplements were isonitrogenous, ioscaloric, and similar in trace mineral concentrations. Within the SL group, half of the lambs were administered ~ 70 mg/Lamb of sodium molybdate daily to ameliorate a reduction in serum molybdenum (SL+MO) observed previously. Lamb BW was obtained and blood collected every 14 d to determine hematological and serum chemical profiles. Data were analyzed using a mixed model with repeated measures. Mean packed cell volume, number of platelets, lymphocytes, monocytes, eosinophils, and hemoglobin were similar among diets ($P > 0.10$). White blood cell count ($P < 0.05$) and number of neutrophils ($P < 0.001$) were greater in CON than SL lambs.

Red blood cell count was greater in CON and SL+MO than SL lambs ($P < 0.03$). However, mean corpuscular volume ($P < 0.08$) and corpuscular hemoglobin ($P < 0.06$) tended to be greater in SL than CON lambs ($P < 0.08$). Serum concentrations of albumin ($P < 0.001$) and aspartate aminotransferase ($P < 0.003$) were lower in SL than CON lambs. Serum concentrations of creatinine were greater for CON and SL+MO than SL lambs ($P < 0.04$), and total protein was greater in CON and SL than SL+MO lambs ($P < 0.001$). Serum concentrations of uric acid were similar among diets ($P > 0.10$). There was a treatment × time interaction for BUN in that values were greater in CON lambs between d 14 and 42 than SL fed lambs, and otherwise similar ($P < 0.001$). Lambs BW was similar among diets ($P = 0.11$). Since most hematological and serum chemical profiles were within a normal range, any changes in animal health or production associated with condensed tannins in SL observed in previous studies likely were not related to these variables examined.

Key Words: hematology, lambs, molybdenum, sericea lespedeza

0731 Comparison of white blood cell phagocytic efficiency in two genotypes of Katahdin sheep.

S. Azarpajouh*, T. Wuliji, and A. L. Bax, *Dep.of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO*

The production and deployment of phagocytic cells are central functions of the hematopoietic system. Neutrophils, the most abundant type of white blood cells in mammals, are an essential part of the innate immunity. The objective of this study is to compare the phagocytic efficiency of neutrophils in two genotypes of footrot resistant and susceptible Katahdin sheep. Fourteen Katahdin ewes, seven in each of high resistant footrot gene markers (HR) and low resistance (LR) were selected and blood sampled, weekly for 8 wk. Blood samples were collected in vacutainer tubes (2 × 10 mL) contained EDTA. Blood smears were made on glass slides to determine the percentage of neutrophils in whole blood. Neutrophils were isolated using a Percoll gradient technique, and stained with 0.8 mM Trypan Blue to determine the percentage of viable cells. Subsequently, 1 mL of freshly isolated neutrophils was inoculated with 1 mL of Lactobacillus casei (2×10^7/mL) in PBS and incubated with rotation at 37°C for three time periods at 20 min, 40 min and 1 h. Control samples were incubated in PBS with neutrophils alone to account for bacterial growth during the assay. At specific intervals of 20, 40, and 60 min the number of surviving bacteria in the supernatant (extracellular) was determined by culture plate colony counting to estimate the phagocytic efficiency of the neutrophils. The data were analyzed by using mixed model procedures of SAS and $P < 0.05$ was considered as significant. The average viability of extracted neutrophils was 95% in each individual specimen at inoculation. The percentage of neutrophils in whole blood was not significantly different ($P = 0.57$) in HR vs. LR genotypes. There were no significant differences ($P = 0.63$) among the numbers of bacterial colonies after addition of neutrophil and incubation periods in HR vs. LR genotypes. The number of bacterial colonies significantly decreased after 20, 40, and 60 min of incubation ($P < 0.001$). The interaction of time and gene marker groups was not significant ($P = 0.23$). No bacterial colony growth was observed in control samples. There is no difference in phagocytic efficiency of the white blood cells in footrot resistant and susceptible genotypes of Katahdin sheep.

Key Words: neutrophil, phagocytic efficiency, sheep

0732 Short-term effects of divergent selection for parasite resistance in F_1 Kiko × Boer doe progeny.

C. L. Thomas*[1,2], B. C. Shanks[1], J. D. Caldwell[1], L. S. Wilbers[1], K. L. Basinger[1], B. Weaber[3], and W. R. Lamberson[2], *[1]Dep. of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO, [2]University of Missouri, Columbia, [3]Kansas State University, Manhattan.*

Future prospects of the goat industry appear optimistic as demand for goat meat has consistently overwhelmed domestic supply in recent years. However, parasitism is arguably the most serious economic restriction limiting goat production in the United States. One approach to combat internal parasites is utilizing the host animal's natural immunity in a selection program to increase the level of parasite resistance in a herd. The objective of this study was to evaluate the short-term effects of divergent selection for parasite resistance in F_1 Kiko × Boer doe progeny. First generation Kiko × Boer progeny ($n = 41$) from two lines of does selected for high resistance to internal parasites (HL; $n = 22$) or low resistance to internal parasites (LL; $n = 19$) were compared. Fecal egg counts (FEC), FAMACHA scores (FAM), and packed cell volumes (PCV) were measured at weaning, 28 d post-weaning, pre-breeding, during breeding, and at end of breeding. No differences ($P \geq 0.12$) were found between HL and LL for FEC, FAM, or PCV at all measurement times except for PCV at 28 d post-weaning, which tended ($P = 0.09$) to be higher for HL vs. LL. Consequently, number of times dewormed and survival rates were similar ($P \geq 0.19$) between lines. Reproductive rate, litter size, kidding date, and F_2 kid birth weight did not differ ($P \geq 0.23$) across lines. A sex effect ($P \leq 0.04$) was detected, with males weighing more vs. female kids. Correlations between FEC and FAM were significant ($P < 0.05$) and positive for LL ($R = 0.26$), but were insignificant ($P = 0.74$) for HL; correlations between FEC and PCV were significant ($P < 0.01$) and negative for LL ($R = -0.30$), but were insignificant ($P = 0.25$) for HL; correlations between FAM and PCV were significant ($P < 0.001$) and negative for LL ($R = -0.46$) and tended to be significant ($P = 0.10$) and negative for HL ($R = -0.16$). Short-term effects of divergent selection for parasite resistance re-

sulted in minimal differences in parasitism, survival rate, and reproductive performance. Associations between indicators of parasitism were moderate in some cases, but varied by doe line. This research is part of an ongoing long-term selection project for parasite resistance.

Key Words: divergent selection, F_1 Kiko × Boer, parasite resistance

---

0733 Milk production and characteristics of lactation curve in dairy sheep and their crosses in Mexico.

J. C. Angeles Hernandez*[1], D. A. Solis Guzman[2], M. Gonzalez Ronquillo[3], A. H. Ramirez Perez[4], and S. Angeles campos[2], *[1]Universidad Nacional Autonoma de México, México City, [2]Universidad Nacional Autonoma de México, México City, [3]Universidad Autonoma del Estado de México, Toluca, [4]Universidad Nacional Autonoma de México, Mexico City.*

The use of appropriate genotypes for milk production in dairy sheep herds allows maximizing the use of natural resources, obtain adequate milk yields and promotes their economic viability. The aim of this study was analyze the milk yield and the characteristics of the lactation curve of sheep of local breeds, dairy breeds and their crosses. Lactation records used were obtained from dairy herd located in Mexico. We used 863 weekly milk records of sheep of six genotypes: 12 East Friesian (EF), 12 Native (Nt), 6 EF1/2Native1/2 (EF50Nt50), 16 EF3/4Native1/4 (EF75Nt25), 15 Suffolk1/2Native1/2 (SF50Nt50), and 8 Corriedale sheep. Sheep were milked mechanically, and milk production was recording weekly from the fourth day after lambing; the first 60 d of lactation, sheep were milked once a day with a partial weaning, lambs were separated from sheep during the night and milked in the morning (0800). At d 60 post-lambing, full weaning was complete, and sheep began to be milked twice daily (0800 and 1800). For analysis of the lactation curve and their parameters, we used the Wood (WD) model: $Y_t = at^b e^{ct}$. Where Y is the milk production at time *t,* and *a, b,* and *c* are the parameters describing the curve shape, these were estimated individually for each lactation using a nonlinear regression. Using WD model, we calculated total milk yield observed (TMY^{obs}) and adjusted to 180 d (TMY^{180}), peak yield (PY), peak time (PT), and persistence (Per). Genotype influenced significantly ($P < 0.05$) in the TMY^{obs} and TMY^{180}, where EF50Nt50 sheep had the best performance. With respect to parameters of WD model, differences between genotypes were observed only in the parameter *b,* being higher ($P < 0.05$) in SF50Nt50, EF50Nt50, and EF sheep. PY was higher ($P < 0.05$) in sheep EF50Nt50, also PY showing a positive correlation with TMY ($r = 0.582$) and negative with Per ($r = -0.176$). PT was positively correlated ($P < 0.01$) with TMY^{180} and Per ($r = 0.479$ and 0.525 respectively). There was a positive effect on the TMY^{obs}, TMY^{180} and shape of the lactation curve in EF50Nt50 sheep. EF and EF75Nt25 sheep showed lower TMY compared with EF50Nt50, who show the best productive performance, which may be associated with better adaptation to the agroclimatic conditions and the lower adaptation to the environmental conditions of animals with a higher proportion of EF genes. The crossing EF50Nt50 is a viable option in dairy sheep herds with similar climatic conditions to those of the present study.

Key Words: dairy sheep, crossbreeding

0734 Goats of Arkansas and Missouri: A production survey.

K. F. Cole*[1], B. M. Onyango[1], J. A. Pennington[2], C. A. Clifford-Rathert[3], C. Hoegeman[1], and E. L. Walker[1], *[1]Missouri State University, Springfield, [2]Lincoln University, Jefferson City, MO, [3]Dep. of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO.*

A survey of goat producers in Arkansas and Missouri was conducted to assess the current state of the goat industry. Production data from 206 producers (response rate of 21%) were examined to determine areas needed for education, future research, and outreach activities. An introductory email was sent to 1087 producers before the survey followed by reminder email sent after the survey was delivered. Undeliverable and inapplicable targets were removed from the original listing. Producer addresses and emails were obtained from registry organizations and extension personnel. The survey was conducted primarily as Web-based via email through Survey Monkey with a hard-copy option. Survey questions focused on farm characteristics, farm management protocols, product marketing, informational sources, and personal demographics. Of the 206 responding farms, 30.6% were from Arkansas and 69.4% from Missouri, with 24.7% raising both meat and dairy, 41.8% raising only dairy, and 33.5% only meat goats. An estimated 57% of producers were between the ages of 41 and 60. Respondents reported a source of income (58.9%) and personal consumption (54.3%) as major incentives to raise goats. Over 94.3% of respondents use anthelmintics as a part of their deworming program, whereas 38.3% use culling and animal selection. Years of experience influenced deworming strategies ($P \leq 0.05$). Educational attainment ($P \leq 0.05$) also influenced producer willingness to use services provided by extension and university personnel. Producers with less than 5 yr of experience use other goat producers ($P \leq 0.05$) for information; whereas, producers between 61 and 70 and 71 and 80 are more likely ($P \leq 0.05$) to use group meetings as an informational sources. Dairy goat producers are less likely to use farm visits ($P \leq 0.05$), farm field days ($P \leq 0.05$), group meetings ($P \leq 0.05$), and university/extension staff ($P \leq 0.05$) as informational sources than meat goat producers. Dairy producers are also more likely ($P \leq 0.05$) to use the internet as a source of information and consider food safety regulations a limiting factor in selling their products ($P \leq 0.05$). Based on our results, producers need to lower their reliance

on anthelmintics to reduce internal parasite resistance and rely more on more sustainable production practices. Understanding how age, education level, years involved, and farm type influence the type of resources used to gain further knowledge of new practices and informational sources could allow the development of education programs more suited for the population. Awareness of current production practices will assist educators, extension, and industry collaborators in conducting appropriate educational programming.

Key Words: goats, survey, production

SMALL RUMINANT: SUSTAINABLE SMALL RUMINANT PRODUCTION STRATEGIES TO MEET GLOBAL DEMANDS

0735 Pasture development and sustainable grazing management.

S. P. Hart*, *American Institute for Goat Research, Langston University, Langston, OK.*

Because grazed forage is the cheapest source of nutrients for small ruminants, grazing systems should be planned around maximizing use of grazed forages and minimizing that of hay and purchased feedstuffs. From 4 wk before parturition until weaning, the doe or ewe will consume 60% of the nutrients required in a year; therefore, it is important to provide as much nutrition as possible during this time from grazed forages. This may be accomplished by adjusting the lambing/kidding season and/or utilizing appropriate forage species that provide grazing during this period. Soil type (series), fertility, and rainfall (amount and distribution) are major determinants of forage production. A soil survey and soil test determine limitations in selection of forage species. Local/state level expertise is very important for planning a forage production system. Planting new forage species is expensive, although no-till drills reduce the cost. However, it can be cost-effective to establish forages that provide grazing during critical periods, such as cool-season forages for kidding/Lambing or warm-season forages for summer grazing. Overseeding forages, especially cool-season legumes and grasses, can be quite cost-effective. Forage plant structure (bunch vs. sod forming) and tannin-containing plants can facilitate control of internal parasites. Control of internal parasites is often a more important factor in pasture management than maximizing forage production. Inclusion and/or maintenance of woody species in the goats' grazing system is beneficial. Woody species may be leguminous, provide high quality forage, tolerate drought, and enable animals to graze away from the soil, reducing parasite challenge. Nonetheless, the inclusion of woody species in grazing systems is limited by lack of information. Rotational grazing is important for the control of internal parasites, uniform utilization of available forages, weed control, and pasture persistence. Timely provision of supplements such as minerals and/or protein can increase intake and digestibility of available forage, mitigating need for additional supplementation. Fencing costs can be a major constraint of small ruminant pasture management, but electric fencing may be a cost-effective solution. Shade is necessary in humid areas, and a windbreak is necessary during cold weather to reduce stress in grazing animals. A well-planned water distribution system will facilitate a rotational grazing program. Predator control is essential for an effective small ruminant grazing program. An appropriate forage management plan will reduce internal parasite problems and costs of production, thereby improving profitability of the small ruminant enterprise.

Key Words: pasture management, grazing system, internal parasite

0736 Internal parasite anthelmintic resistance and control.

J. E. Miller*, *Louisiana State University, Baton Rouge.*

Gastrointestinal nematodes are major pathogens of small ruminants, and control has relied almost exclusively on the frequent use of anthelmintics. Nematodes, especially *Haemonchus contortus*, have developed resistance to all approved anthelmintics. *H. Contortus* is a problem in warm/wet environments like the southeastern United States (year-round) and is now a seasonal (summer) problem in the rest of United States. For the past 50+-plus years, recommended control strategies maximized benefits of treatment and ignored resistance issues. Resistance is the ability of nematodes to survive treatments that are generally effective at the recommended dose. Treatment eliminates those whose genotype renders them susceptible and those that are resistant survive and pass on their "resistant" genes. Resistant nematodes accumulate and finally treatment failure occurs. For anthelmintics to remain effective, refugia must be preserved. Refugia is the proportion of the population that is not selected by drug treatment and provides a pool of susceptible genes to dilute resistant genes in that population. Targeted selective treatment is a concept based on the unequal distribution of nematodes in the animal population. A small proportion of animals in a population harbor most of the nematodes and are responsible for most of the egg output and thus pasture contamination. Targeting only those animals for treatment will provide refugia in the untreated animals. Monitoring with FAMACHA and/or fecal egg counts are proven concepts to identify those animals needing treatment. Once identified, smart use of anthelmintics and incorporating alternative control measures into an integrated control program are essential for sustainability.

Key Words: small ruminant nematodes, anthelmintic resistance, control

0737 Genetic selection for enhanced production efficiency.

D. F. Waldron*, *Texas A&M AgriLife Research, San Angelo.*

The objective of this presentation is to cover issues related to using genetic selection to enhance production efficiency of small ruminants. Efficiency of production is a function of outputs and inputs. Meat and fiber production are the most economically important outputs. Outputs may be expressed as a function of number of breeding animals, amount of feed utilized, amount of land area, amount of time or labor required, or some other input factor. Genetic means of improving production efficiency should start with selection of the proper breed(s) for the production environment. Sheep and goat production can be thought of as a means of harvesting and con-

verting forage or grains to meat and fiber. Small ruminants can be productive in a variety of environmental conditions. The efficient breed(s) is one that fits the environment. Clarifying selection objectives is an important first step in developing a selection program. Selection for traits that have high heritability and can be measured early in life can yield results in a short period of time. Improvement in traits that can only be measured later in life and/or have a lower heritability take longer to yield results. An effective selection program must be adopted by enough breeders to have an impact on the larger population. The segmented nature of the meat and fiber industries does not lend itself to efficient communication of economic incentives for improvements in production. Breeders and producers may not realize the importance of traits that are crucial at the processing stage. Improvement in information flow via economic incentives will provide breeders with the information needed to set breeding goals. Improved knowledge of relative importance of traits, in all segments of the industry, will lead to design of more effective selection programs. Designing an effective selection program requires knowledge of genetic and phenotypic relationships among traits and relative economic values of output traits. Selection programs must also account for substantial changes in relative values of input traits.

Key Words: sheep, goats, genetics

0738 Efficiency of small ruminant reproductive management. M. Knights*, *West Virginia University, Morgantown.*

Productivity of the female small ruminant is below its true potential in part due to suboptimal reproductive performance. Lifetime reproductive performance of the ewe is influenced by age at first lambing, frequency of lambing and prolificacy. Replacement females comprise 20 to 30% of the breeding flock but their pregnancy rates, embryonic survival and prolificacy are lower than that of their adult flock mates, which reduces overall reproductive efficiency. Strong correlations exist between weight at first breeding and variables contributing to lambing rate. A positive correlation also has been reported between fertility and genetic potential for growth of the ewe lamb. These findings indicate that fertility of replacements can be improved through nutritional management and selection without delaying the age at first breeding. Additionally, pre-treatment with progestogen and gonadotropins enhances fertility and should be integrated in management of replacements. Seasonality of reproduction restricts lambing to once per year in temperate latitudes. Frequency of lambing can be accelerated by increasing the proportion of females bred out -of-season through light management, selection and breeding, and the use of the male effect in combination with pre-treatment with progestogens. These approaches are less effective in fall-born ewe lambs and lactating ewes, but genetic selection may improve fertility in these categories. Development of efficient, low-cost weaning systems, and approaches that increase the fertility of the lactating ewe during seasonal anestrous are needed to increase lifetime reproductive performance. Maintaining an appropriate ratio of parous to non-parous breeding females, synchronization of estrus, and pregnancy diagnosis will increase the proportion of ewes lambing and assist in controlling the timing of births to facilitate accelerated lambing programs. Wide variation in ovulation rate and prolificacy exists between and within breeds and across parity, and, lower prolificacy is observed in ewe lambs and ewes bred out-of-season. Optimum prolificacy can be achieved through a combination of selection and breeding, nutritional management and by maintaining an appropriate parity distribution in the breeding flock. Pharmacological treatments, including use of gonadotrophic hormones and immunization against protein and steroid hormones can increase prolificacy, but the response is limited by increasing prenatal losses as ovulation rate is increased. Cost effectiveness of such treatments needs to be evaluated further. In conclusion, our current understanding of reproduction provides an opportunity to make incremental changes to age at first lambing, pregnancy rate, frequency of lambing and prolificacy and thereby increase lifetime reproductive performance of the ewe.

Key Words: reproductive efficiency, small ruminants

0739 Managerial steps to alleviate the effects of heat stress, water deprivation, and low pasture quality in small ruminants. P. Y. Aad*[1] and S. Abi Saab[2], [1]*Notre Dame University, Zouk Mosbeh, Lebanon,* [2]*Lebanese University, Faculty of Agricultural Sciences, Dekwaneh, Lebanon.*

Global environmental challenges as depicted by increased ambient temperature by 0.7°C, decreased rainfall, and unpredictable weather patterns are associated with global warming. Such changes are translated by an increase in heat stress amplitude and duration, less water, and more solar radiation, resulting in slower pasture growth, higher soil erosion, and overgrazing. Therefore, small ruminants will be exposed to more days outside thermal neutral zone, less available water, and poorer pasture quality. Unfortunately, in most parts of the world threatened by global warming, small ruminants are managed extensively and walk long distances for pastures and water access. Heat stress in sheep and goat is associated with both lower feed intake and performance. Intensive small ruminant production could benefit from highly digestible and denser energy diets as supplemented by fats or isoflavonoids, and temperate water with modulated salt content. Moreover, in extensively managed animals, proper pasture rotation to prevent overgrazing, and the use of mixed pasture such as legume and grass could provide proper feeding under heat stress conditions. Furthermore, traveled distance modulation, timing of sheering, shade, ventilation and sprinkles provide good management to alleviate solar radiation intensity and heat stress and additionally improve follicular and semen quality

and prevent early embryonic loss. Breeding strategies and the usage of locally adapted breeds should be promoted alongside planned breeding for animals with lower environmental impact. Small ruminants, when properly managed, have the potential to be good energy converters and could provide a viable solution for food security in a globally warming world.

Key Words: heat stress, gobal warming, small ruminant management

---

0740 Global demand for small ruminant products.

G. W. Williams* and D. Anderson, *Texas A&M University, College Station.*

A dynamic world market continues to evolve for the products of small ruminants. Small ruminants, for this paper, are restricted to sheep and goats. While we may focus on lamb and sheep meat, other products including goat meat, wool, mohair, and cashmere remain important. Several factors are at work in today's global market for small ruminant products. As usual, they are the classic factors that affect the demand for any product: the product's own price, consumer incomes, the prices of competing goods, and changing tastes and preferences. Fueled by growth of the Chinese economy and incomes, Chinese sheep meat imports have surged in recent years. In 2012, China overtook France as the world's largest importer of sheep meat by volume. China imports primarily lower value cuts so that the average value of the Chinese sheep meat imports is lower than that of Northern European and U.S. markets. Nevertheless, the average value of Chinese sheep meat imports is growing. A better picture of the changing market requires a look at supply as well as demand factors impacting the market. Global sheep flock numbers remain just below the 2007 peak of about 1.1 billion head, although some growth in flocks did begin to occur again in 2011. China has the world's largest flock at 139 million head. Global sheep meat production has grown by 20% over the last decade, however, due to increases in productivity. The major meat exporting countries of Australia and New Zealand are in the top 10 ranking by flock size. Production in those countries has been hampered by drought, volatile prices, and the profitable economics of competing enterprises like dairy and milk production. U.S. sheep meat production has declined by 35% over the last decade. Although decreased global wool production has led to higher prices in recent years, those prices have been tempered by the effects of the worldwide recession on demand. The demand for relatively high priced fibers has struggled during the recession and economic recovery. Overall, the global market for small ruminant market continues to evolve. Trade flows between countries are changing as incomes rise and production patterns shift.

Key Words: sheepmeat, wool, China

SWINE SPECIES: MINI-SYMPOSIUM: OPPORTUNITIES AND CHALLENGES WITH THE USE OF CARBOHYDRASE AND PROTEASE ENZYMES IN SWINE FORMULATIONS

0741 Opportunities and challenges with the use of carbohydrase and protease enzymes in swine formulations.

R. T. Zijlstra[*1], T. A. Woyengo[1], Z. Nasir[1], and E. Beltranena[1,2], *[1]University of Alberta, Edmonton, Canada, [2]Alberta Agriculture and Rural Development, Edmonton, Canada.*

Co-products from crops processed for the food, biofuel, or bio-industry are attractive feed ingredients to manage feed costs per unit of gain in pigs. Compared with crops from which they are derived, alternative feed ingredients may contain more anti-nutritional factors such as phytate, fiber, and indigestible proteins that may limit nutrient digestibility. Together with feed processing technologies and advanced feed quality evaluation techniques, supplemental feed enzymes are important parts of a strategy to mitigate the risks associated with high dietary inclusion of co-products and reduce feed cost per unit of gain. Supplementation of feed enzymes to cereal-based diets has been studied. Recently, feed enzyme technology has been applied to co-products. Among feed enzymes, phytase inclusion has one of the most consistent effects on increased nutrient digestibility, especially for P. For fiber-degrading enzymes (carbohydrases) and proteases, some important considerations are: 1) the substrate for the enzyme must be the main limitation for digestibility of the nutrient of interest, 2) processing technology may affect the content and functional characteristics of fiber in the co-product, and 3) age and thus gut development may affect responses to enzyme supplementation. Generally, carbohydrases increase energy digestibility, but their effects on AA and P digestibility are variable depending on trial conditions. Protease enzymes appear to have less consistent effects on nutrient digestibility in grower pigs. Due to the alterations made in nutrient flow through the intestinal tract, supplemental enzymes may also alter nutrient availability to intestinal microbes, and hence alter microbial populations. Thus apart from opportunities, a major challenge for using carbohydrases and proteases is to obtain effects as consistent as observed for phytase. If solved, application of enzyme technology combined with modern feed processing and feed quality evaluation technologies may then provide the pig with additional energy, AA, and P resulting in cost-effective, predictable growth performance and carcass quality.

Key Words: enzyme, feed ingredient, pig

SWINE SPECIES: REPRODUCTION AND MANAGEMENT

0742 Betaine supplementation in maternal diet modulates the epigenetic regulation of hepatic gluconeogenic genes in neonatal piglets.

D. Cai*, Y. Jia, H. Song, S. Sui, J. Lu, Z. Jiang, and R. Zhao, *Nanjing Agricultural University, China.*

Maternal gestational nutrition provides a critical window in which neonates are predisposed to metabolic syndrome in adult life. Betaine as a methyl-donor nutrient is critical for fetal development and it donates methyl donors for DNA and protein methylation through methionine metabolism, which is critical for the epigenetic regulation of gene expression. However, direct evidence regarding the effects of betaine supplementation in maternal diet during gestation on hepatic gluconeogenic genes in neonatal offspring are lacking. In this study, gestational sows were fed control or betaine-supplemented diets (0.3% w/w) throughout the pregnancy, and we are aiming to elucidate if maternal dietary betaine affects offspring hepatic gluconeogenic genes through epigenetic mechanisms. Neonatal piglets born to betaine-supplemented sows had significantly higher serum and hepatic betaine contents ($P < 0.05$), together with significantly enhanced expression of methionine metabolic enzymes ($P < 0.05$) in the liver. Interestingly, significantly higher serum concentrations of lactic acid ($P < 0.05$) and glucogenic amino acids, including serine ($P < 0.05$), glutamate ($P < 0.05$), methionine ($P < 0.05$) and histidine ($P < 0.05$) were detected in betaine-exposed piglets, which coincided with higher hepatic glycogen content ($P < 0.05$) and greater protein expression of gluconeogenic enzymes, pyruvate carboxylase (PC) ($P < 0.05$), cytoplasmic phosphoenolpyruvate carboxykinase (PEPCK1) ($P < 0.05$), mitochondrional phosphoenolpyruvate carboxykinase (PEPCK2) ($P < 0.05$) and fructose-1, 6-bisphosphatase (FBP1) ($P < 0.05$). Moreover, maternal betaine significantly changed the methylation status of both CpGs and histones on the promoter of gluconeogenic genes. The decreased *PEPCK1* mRNA was associated with DNA hypermethylation ($P < 0.05$) and increased repression histone mark H3K27me3 ($P < 0.05$), while the up-regulated *PEPCK2* and *FBP1* mRNA was associated with DNA hypomethylation ($P < 0.05$) and increased activation histone mark H3K4me3 ($P < 0.05$). Furthermore, hepatic expression of miRNAs predicted to target *PC* and *PEPCK1* was also affected by maternal betaine supplementation. Two out of seven miRNAs targeting *PC* and 6 out of 7 miRNAs targeting *PEPCK1* were detected to be dramatically suppressed ($P < 0.05$) in the liver of betaine-exposed piglets. Our results provide the first evidence that maternal betaine supplementation affects hepatic gluconeogenic genes expression in newborn piglets through enhanced hepatic methionine metabolism and epigenetic regulations which involve DNA and histone methylations, as well as miRNAs-mediated post-transcriptional mechanism.

Key Words: betaine, epigenetic regulation, gluconeogenic genes expression

0743 Rearing system affects the efficiency of oleic acid deposition in Duroc x Iberian pigs.

D. Solà-Oriol[1], S. López-Vergé*[1], E. Varella[2], A. C. Barroeta, and J. Gasa[1], *[1]Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Tecnología & Vitaminas, S.L., Alforja, Spain.*

The aim of the study was to evaluate the impact of the rearing system (intensive 2.5 m^2/pig vs. semi-extensive 30 m^2/pig) used during the growing-finishing period on PUFA deposition by using an oleic enriched diet during the finishing period. The Iberian pig regulations require a minimum of 51% of oleic acid in fat (10 cm from the caudal basis) at slaughter to be considered for cured ham. Therefore, the effect of the rearing system on the time spend to reach the oleic acid proportion was also evaluated. A total of 16 barrows (Duroc x Iberian) were selected at 90 kg of BW ($n = 8$ per system) and offered the same growing and finishing diets. A diet based on barley–wheat–oats and soybean–sunflower meal to contain 14.7 MJ/kg ME; 5.7 g/kg Lys; 60.9 g/kg ether extract and 34.3 g/kg oleic acid was fed for the finishing period. Back fat samples were collected from each pig on Days 0, 14, 28, 62, and 85 (slaughter) of the finishing period. Back fat samples were collected by an automatic cut/extraction system with a needle (8 mm Ø), and fatty acid profile was analyzed by the direct transesterification method and the percentage of oleic acid content calculated. The deposition response of the oleic acid was fitted by linear regression using the REG procedure of SAS. The comparison of slopes and times were analyzed with ANOVA by using the GLM procedure of SAS. The oleic acid deposition response for the semi-extensive reared pigs was y = 46.6 + 0.054(t) ($R^2 = 0.84$), while for the intensive reared pigs was y = 47.5 + 0.071(t) ($R^2 = 0.83$). Higher efficiency for oleic acid deposition was observed for the animals reared in the intensive system ($P = 0.013$). Therefore, a reduction of the days spent to reach the required level of oleic acid (51%) was observed for the animals reared in the intensive system than those reared in a semi-extensive system (49.0 vs. 80.4 d SEM = 5.24; $P = 0.003$). However, although higher efficiency on oleic acid and PUFA deposition was observed for the animals reared in the intensive system, the higher subcutaneous and inter-muscular but not intramuscular (marbling) fat content of the semi-extensive reared pigs has to be taken into account. It is concluded that the rearing system has a high impact on the efficiency of oleic acid deposition.

Key Words: Iberian, oleic acid, rearing system

0744 Effects of sugar beet pulp on reproductive performance of gestation sows. Z. Cheng*, D. Hou, Y. Chen, H. Zhang, B. Wang, Y. Wang, S. Bai, H. Lei, S. Jiang, and W. Jin, *Animal Nutrition & Feed Center, COFCO Nutrition and Health Institute, Beijing, China.*

Sugar beet pulp is widely used as feed ingredient in dairy feeds. However, its use in sow feeds may benefit sows because of its high level of fiber. The purpose of the study was to investigate the use of sugar beet pulp to see if there is any benefits for gestation sows fed sugar beet pulp. One hundred gestation sows were divided into three treatments with 33, 34, and 33 sows per treatment, they were fed diets containing 0, 7.5, or 15% of sugar beet pulp at breeding, respectively, for 3 mo. The diets contained the same calculated levels of crude protein and digestible energy. On d 91, they were fed the same lactating sow diets for another 25 d until farrowing. Total number of pigs born were 12.48 ± 2.44, 12.28 ± 2.21, and 13.24 ± 2.26 for sows fed diets containing 0, 7.5, or 15% of sugar beet pulp, respectively. Total pigs born live weight were 17.66 ± 2.87 kg, 17.86 ± 3.82 kg, and 18.45 ± 2.98 kg, for sows fed diets containing 0, 7.5, or 15% of sugar beet pulp, respectively. There were no significant differences in total pigs born and total pigs born live weight among all treatments ($P = 0.063$). Total number of pigs born alive were 11.76 ± 2.23, 12.00 ± 2.08, and 13.05 ± 2.40, for sows fed diets containing 0, 7.5, or 15% of sugar beet pulp, respectively; total number of pigs born alive were significantly increased ($P < 0.032$) by supplementing 15% sugar beet pulp into gestation sow diets as compared to control sow diets.

Key Words: sugar beet pulp, gestation sows, reproductive performance

0745 Utilizing meta-analyses to generate prediction equations for pork carcass back, belly, and jowl fat iodine value. C. B. Paulk*[1], J. R. Bergstrom[2], M. D. Tokach[1], S. S. Dritz[1], D. D. Burnett[1], J. M. DeRouchey[1], R. D. Goodband[1], J. L. Nelssen[1], and J. M. Gonzalez[1], *[1]Kansas State University, Manhattan, [2]DSM Nutritional Products, Inc., Parsippany, NJ.*

Iodine value (IV) is a measure of unsaturated fatty acids and is currently the industry standard for assessing pork fat quality. The objective of this meta-analysis was to use data from existing literature to generate equations to predict back, belly, and jowl fat IV of finishing pigs. The final database resulted in 24 papers with 169 observations for backfat IV, 21 papers with 124 observations for belly fat IV, and 29 papers with 197 observations for jowl fat IV. Some observations (back $n = 36$, belly $n = 37$, and jowl $n = 45$) changed dietary fatty acid composition during the experiment (i.e., switching from higher to lower or lower to higher iodine value product diet), where initial diets (I) were defined as those fed before the change in diet composition and final diets (F) were defined as those fed after the change in diet composition. The predictor variables tested were divided into five groups: 1) diet fat composition (dietary percent C16:1, C18:1, C18:2, C18:3, EFA, and unsaturated fatty acids, and iodine value product) for both I and F diets; 2) duration of feeding of the I and F diets; 3) ME or NE content of the I and F diet; 4) performance criteria (initial BW, final BW, ADG, ADFI, and G:F); and 5) carcass criteria (HCW and backfat thickness). PROC MIXED (SAS institute, Inc., Cary, NC) was used to develop regression equations, and experiment within paper was included as a random effect. Statistical significance for including terms in the models was determined at $P < 0.10$. Evaluation of models with significant terms was then conducted based on the Bayesian Information Criterion (BIC), where the lowest BIC were preferred. Optimum equations to predict back (BIC = 739), belly (BIC = 558), and jowl (BIC = 758) fat IV were: backfat IV = 84.83 + (6.87 × I EFA) − (3.90 × F EFA) − (0.12 × I d) − (1.30 × F d) − (0.11 × I EFA × F d) + (0.048 × F EFA × I d) + (0.12 × F EFA × F d) − (0.0060 × F NE) + (0.0005 × F NE × F d) − (0.26 × backfat depth); belly fat IV = 106.16 + (6.21 × I EFA) − (1.50 × F d) − (0.11 × I EFA × F d) − (0.012 × I NE) + (0.00069 × I NE × F d) − (0.18 × HCW) − (0.25 × BF); and jowl fat IV = 85.50 + (1.08 × I EFA) + (0.87 × F EFA) − (0.014 × I d) − (0.050 × F d) + (0.038 × I EFA × I d) + (0.054 × F EFA × F d) − (0.0066 × I NE) + (0.071 × I BW) − (2.19 × ADFI) − (0.29 × backfat depth). These regression equations may be used to predict the back, belly, and jowl fat IV of finishing pigs fed different diets.

Key Words: Iodine value, meta-analysis, pork quality

0746 The effects of copper source (copper sulfate or methionine hydroxy analogue chelate; Mintrex) on growth performance, carcass characteristics, and barn cleaning time in finishing pigs. K. F. Coble*[1], J. M. DeRouchey[1], M. D. Tokach[1], S. S. Dritz[1], B. Lawrence[2], J. Escobar[2], J. C. Woodworth[1], R. D. Goodband[1], and N. Boettger[2], *[1]Kansas State University, Manhattan, [2]Novus International, St. Charles, MO.*

Copper source and feeding duration on growth performance, carcass characteristics, and pen wash time were determined using 1196 pigs (initially 25.7 kg BW) in a 111-d study. Pigs were allotted to one of six dietary treatments, based on initial pen weight in a randomized incomplete block design with 26 pigs/pen and seven to eight pens/treatment. A negative control diet was supplemented with 17 ppm Cu from the basal trace mineral. Remaining diets were formulated by supplementing the negative control with 50 ppm Cu from $CuSO_4$ or Mintrex, or 125 ppm Cu from $CuSO_4$. The 50 ppm Cu as CuSO4 diet was fed for 111 d. The 50 ppm Mintrex and 125 ppm CuSO4 diets were fed for either 42 or 111 d. Diets were formulated 0.05% below the estimated standardized ileal digestible Lys

Table 0746. Copper source, level and duration for finishing pigs

Cu source		$CuSO_4$	Mintrex Cu	$CuSO_4$	Mintrex Cu	$CuSO_4$		
Added Cu, ppm		50	50	125	50	125		Treatment,
Duration, d	0–111	0–111	0–42	0–42	0–111	0 -111	SE	$P <$
d 111 BW, kg	122.7	124.6	124.3	122.5	125.3	125.0	1.33	0.16
ADG, kg	0.890	0.907	0.901	0.883	0.909	0.901	0.008	0.12
ADFI, kg	2.25[c]	2.33[a]	2.26[bc]	2.25[c]	2.30[abc]	2.31[ab]	0.027	0.02
G:F	0.397[ab]	0.389[c]	0.399[a]	0.393[abcc]	0.396[abc]	0.390[bc]	0.003	0.04
HCW, kg	89.0	89.3	88.9	89.4	89.7	90.2	0.92	0.71
Wash time, s	345	332	323	365	324	352	15.2	0.26

[1] Means within row with different superscripts differ, $P < 0.05$.

requirement. Average daily gain was not affected ($P > 0.12$). Pigs fed either 50 or 125 ppm of Cu from $CuSO_4$ from d 0–111 had greater ADFI ($P < 0.02$) than pigs fed the control or diet with 50 ppm of added Cu from Mintrex from d 0–42. Feed efficiency was poorer ($P < 0.04$) for pigs fed either 50 or 125 ppm of added Cu from $CuSO_4$ fed throughout compared with those fed 50 ppm of Cu from Mintrex from d 0 to 42. There were no differences in final BW, HCW, or pen wash time. In summary, pigs fed 50 ppm of Cu from Mintrex for the first 42 d of the finishing period had improved G:F compared with pigs fed 50 or 125 ppm of Cu from $CuSO_4$ for the complete finishing period; however, G:F for those pigs was not improved when compared to those not fed added Cu.

Key Words: finishing pig, copper, wash time

0747 Immunocastration affects testicular mass, serum concentrations of testosterone, and average daily gain of boars. D. Lugar*[1], S. Clark[2], S. Callahan[1], L. Wittish[1], and M. Estienne[3], *[1]Virginia Tech, Blacksburg, [2]Virginia–Maryland Regional College of Veterinary Medicine, Blacksburg, VA, [3]Virginia Tech, Suffolk.*

The objective of this study was to determine the effects of an immunological castration product (Improvest, Zoetis) on reproductive steroid hormones, reproductive organs, and growth. A total of 72 Landrace x Yorkshire boars (69 d of age, 22.76 ± 4.64 kg BW) were used in two successive replications. This study was a randomized design with three treatment groups: single injection (SI) of Improvest at 10 wk of age, double injection (DI) of Improvest at 10 and 15 wk of age, and intact controls (no Improvest; CNT) (n = 24 per group). At wk 10, 15, 20, and 25, blood was collected and serum harvested to evaluate testosterone concentrations via RIA, and BW were determined. At wk 25, 18 pigs (n = 6 per group) were sacrificed and testicles were removed, weighed, and measured for length, width, and circumference. Statistical analysis was performed using JMP Pro 10. Testosterone concentrations at wk 20 and 25 were less ($P < 0.0001$ and $P = 0.0003$, respectively) for DI (0.065 ng/mL and 1.178 ng/mL, respectively) compared to SI (1.589 ng/mL and 6.372 ng/mL, respectively) and CNT (1.356 ng/mL and 5.920 ng/mL, respectively). Testosterone concentration for wk 10 and 15 were similar ($P = 0.5332$ and $P = 0.7875$, respectively) among the three treatments. Body weights were greater ($P = 0.017$) for DI compared to CNT at wk 25 (122.0 kg and 117.6 kg, respectively), while SI (120.1 kg) was not different ($P = 0.398$) from DI and tended ($P = 0.119$) to be greater than CNT. The ADG from birth to the initiation of the treatments (10 wk of age) was not different ($P = 0.7631$) among treatments; ADG from 10 to 25 wk of age was greater ($P = 0.0093$) for DI compared to CNT and there was a tendency ($P = 0.067$) toward a greater ADG for SI compared to CNT. Both left and right testicle length, width, and circumference were less ($P < 0.0001$) for DI compared to SI and CNT. Testicle wt (g/kg BW) was less ($P < 0.0001$) for both the left and right testicles for DI compared to SI and CNT. The results of the current study indicate that immunological castration has a major impact on ADG and that a single injection tended to cause a greater ADG when compared to intact males

Key Words: boars, immunocastration, swine

0748 New perspectives to the enterotoxigenic *E. coli* F4 infection model in weanling piglets in relation to the susceptibility genotypes and bacterial shedding. P. J. Roubos*, R. H. G. M. Litjens, J. W. Resink, and Y. M. Han, *Nutreco Research & Development, Boxmeer, Netherlands.*

Post-weaning diarrhea caused by enterotoxigenic *E. coli* (ETEC) is a major problem in weaner piglets. Responses of individual animals to ETEC infection are very different and show high varieties in animal experiments with ETEC infection. The aim of this study was to optimize the ETEC F4ac infection model in piglets by combining the genotype susceptibility with performance and bacterial shedding.

Before weaning 120 male piglets (individual housed) were tested for susceptibility or resistance towards ETEC O149:F4ac by a DNA marker based test. After weaning (27 ± 2-d-of-age) the piglets were orally infected with 5 mL of an inoculum suspension (containing $1.5*10^8$ CFU/ml ETEC F4ac in a 2.5% sucrose solution) at d 7, 8, and 9 after weaning. Fecal bacterial shedding was determined at d 7 (before challenge), 10, and 13 by spreading on CBA plates. Hemo-

lytic colonies were confirmed by an agglutination test with an ETEC F4ac specific antiserum. In the first week after challenge all (n = 4) homozygote sensitive (SS) animals died. During the same period, feed efficiency (FE) was significant lower ($P < 0.001$) in heterozygote sensitive (RS)-animals (FE = 0.67; n = 61) compared with the homozygote resistant (RR) animals (FE = 0.8; n = 55). After this week the animals started to recover and the feed efficiency differences became less. Diarrhea incidence was significantly different ($P < 0.001$) between genotypes SS (91%) compared to RS (67%) and RR animals (47%) in the first week after challenge. Furthermore while ETEC was hardly detected in the fecal material of the RR animals, they were found in most of the RS animals and in all SS animals (see Table 0748). In conclusion, susceptible animals (RS and SS) compared to resistant animals (RR) animals showed poorer feed efficiency, higher diarrheal incidence and higher numbers of ETEC fecal shedding in the first week after challenge. The DNA marker based test can be used to select animals that are susceptible for ETEC for inclusion in the ETEC infection model.

Key Words: ETEC F4, infection model, genotype

Table 0748. Detection of ETEC in fecal material at Day 10 and 13 as grouped by genotype

Genotype	Positive both days	Negative	Positive at Day 10	Positive at Day 13	ND	Total
RR	0	51	2	2	0	55
RS	35	10	9	6	1	61
SS	4	0	0	0	0	4
						120

ND = not determined

SYMPOSIUM: PROCEDURES AND METHODOLOGY FOR DETERMINING STANDARD ILEAL DIGESTIBILITY (SID) AMINO ACID DIGESTIBILITY AND ENERGY OF FEEDSTUFFS

0749 Procedures and methodology for determining standard ileal digestibility (SID) amino acid digestibility of feedstuffs. H. H. Stein*, *University of Illinois at Urbana-Champaign, Urbana.*

Since results of the first digestibility experiments with animals and humans were published more than 250 yr ago, it has been known that not all nutrients that are ingested by an animal are absorbed. The early work with AA digestibility was based on determining apparent total tract digestibility of AA in individual feed ingredients using rats or chickens as models. It was soon recognized that to avoid the contribution of microbial protein to AA output, AA digestibility is more correctly determined as ileal digestibility. The first procedure to collect digesta from the distal ileum, the reentrant ileal cannula, was described in 1962 and in 1974 the first description of the intestinal T-cannula was published. With this technique, it became possible to collect fluids from the distal ileum and by subtracting the ileal output of AA from the intake of AA it is possible to calculate the ileal digestibility of individual AA. In addition to dietary AA that enter the intestinal tract, there is also a contribution of endogenous AA that are secreted in the form of mucins, enzymes, bile acids, etc., and because of the contribution of endogenous AA to the ileal output, digestibility values that are calculated by subtracting the ileal output of AA from the intake are called apparent ileal digestibility (AID) values. The practical consequence of the endogenous contribution of AA is that values for AID that are measured in individual feed ingredients often are not additive in mixed diets. The endogenous AA may be divided into AA that are non-specific to the diets, also called basal endogenous AA, and AA that are secreted in response to the diet that is being fed. Basal endogenous AA and are not needed for calculation of digestibility values that characterize specific feed ingredients and may be determined after feeding a protein-free diet. By disregarding the basal endogenous losses in the calculation, values for standardized ileal digestibility (SID) are calculated. This concept was first proposed in 1995 and later publications documented that values for SID of AA are additive in mixed diets when fed to pigs. Because practical diet formulation relies on the assumption that values for AA digestibility in individual ingredients are additive in mixed diets, diets are most correctly formulated based on values for SID of AA.

Key Words: amino acids, ileal digestibility, pigs

0750 Procedures and methodology for determining the net energy content of feedstuffs. C. M. Nyachoti*, *University of Manitoba, Winnipeg, Canada.*

Feed is the single most expensive input in commercial pork production and a large portion of the cost associated with feed is related to supplying energy. Thus, there have been concerted efforts to develop methods and systems for evaluating the energy content of feed. In this regard, the net energy (NE) system, which takes into account the metabolic utilization of energy, has been proposed as a superior system for characterizing the energy value of feeds. Furthermore, the NE system allows for a more effective use of high fiber feedstuffs and may lead to reductions in feed cost. Various procedures and methods have been used to determine NE in feeds and feedstuffs, the most common ones being the comparative slaughter (CS) and indirect calorimetry (IC) methods. Each of these methods has its advantages and disadvantages. For instance, although the CS method is regarded as the gold method, it is labor-intensive and requires a large number of animals. The IC method requires fewer animals, takes a relatively short period of time and can be used for repeated measurement of energy balance, but it also requires sophisticated and often expensive equipment for the required gaseous exchange measurements. Nonetheless, the IC method is the most commonly used method for determining the NE content in swine feed and feedstuffs and require accurate estimation of energy lost as heat and the energy required for maintenance. These estimates, which are influenced by several factors including physiological status and activity level, have direct impact on the NE estimates obtained, and therefore it is critical that these are accurately determined. For routine estimation of NE content, however, prediction equations based on chemical composition measurements of feeds and feedstuffs have been suggested, although questions of acceptability for such equations still exists. In this presentation, the procedures and methods for estimation of NE in feeds and feedstuffs and considerations for design of experimental diet will be discussed. Results of recent studies comparing determined and predicted NE values will be highlighted.

Key Words: net energy, methodologies, feeds, feedstuffs, pigs

0751 Procedures for determining digestible and metabolizable energy contents of feedstuffs. O. Adeola*, *Department of Animal Sciences, Purdue University, West Lafayette, IN.*

A pig derives energy for cellular processes by oxidation of carbohydrates, amino acids, and fatty acids contained in feeds, and thus the resulting energy is equal to the sum of the energy produced from oxidation of these feed nutrients. The utilization of energy in a feed for pigs may be determined by total collection method in which pigs are fed test diet over a period of time and then feces and urine are collected for

subsequent chemical analysis. Depending on the collected energy-containing components (feces and urine), either apparent digestible (DE) or metabolizable energy (ME) can be determined. Total quantitative collection of feces and urine from pigs fed the diet or ingredient is achieved by placing pigs in metabolism cages with feed intake and feces and urine output commonly determined over a 5-d period that is preceded by an adaptation period of 5 to 10 d. Ensuring that the feces collected originate from the feed provided during the 5-d collection period requires a marker that is added to the feed at the beginning and end of the collection period to signal the start and end of feces collection, respectively. Urine collection during the period when feces are collected starts and ends at the time of marker addition to the feed at the beginning and end of the collection period. The difference between the gross energy (GE) in the feed and that in the feces is DE. Subtracting the GE in urine from the DE of the diet gives ME. For most pig feed, the ME is between 92 and 98% of the DE.

Key Words: digestible energy, feed, metabolizable energy, pig

SWINE SPECIES:
SWINE SPECIES NUTRITION

0752 Apparent and standardized ileal amino acids digestibility for different protein feedstuffs fed at two dietary protein levels for growing pigs.
A. O. Adebiyi[1], D. Ragland[2], L. Adeola[2], and O. A. Olukosi[*1], *[1]Scotland's Rural College, Ayr, UK, [2]Purdue University, West Lafayette, IN.*

This study determined the apparent and standardized ileal amino acids digestibility (AID or SID) for growing pigs fed three protein feedstuffs with different fiber types at two dietary crude protein (CP) levels. Twenty boars (Yorkshire × Landrace) with 35 kg body weight and fitted with a simple T-cannula at the distal ileum were used. The treatments were three protein feedstuffs [soybean meal (SBM), canola meal (CM) or corn distillers dried grains with solubles, (cDDGS)] and two dietary CP levels (18 or 14%). Eighteen pigs were allocated to the experimental diets using a replicated 6 × 2 Youden square design. In each of the two experimental periods, two pigs were offered a nitrogen free diet to determine basal endogenous amino acid flow. Digesta was collected for 2 d after 5 d of adaptation. Reducing dietary CP level by 4% did not affect AID of DM and AA or SID of AA. Except for Met, Trp, Cys and Pro, AID for all the other AA were greater ($P < 0.05$) in the SBM diet compared with the CM diet. Apparent ileal digestibility for Gly and Asp was greater ($P < 0.05$) for the SBM diet compared with the DDGS diet. The AID for Ile, Leu, Phe, Val, Ala, Tyr and Asp was greater ($P < 0.05$) in the DDGS diet compared with the CM diet. There was protein feedstuff × protein level interaction ($P < 0.05$) for AID of Lys because in the diets with 18% CP, the AID of Lys was greater ($P < 0.05$) in the SBM and cDDGS diets compared with the CM diet, whereas the AID of Lys was not different among the protein feedstuffs in diets with 14% CP. Standardized digestibility was greater ($P < 0.05$) in the SBM diet compared with the CM diet for all AA except Trp and Pro, whereas the SID of Gly and Asp were greater ($P < 0.05$) in the SBM diet compared with the cDDGS diet. Standardized digestibility for Ile, Leu, Val, Ala, Tyr and Asp were greater in the cDDGS diet compared with the CM diet. It was concluded that differences in AA digestibility observed for the pigs were related to differences in chemical, including fiber, profiles of the protein feedstuffs used but independent of dietary CP level.

Key Words: amino acids, protein feedstuff, protein level

0753 Effects of high levels of nicotinic acid on growth, carcass traits, and meat quality of finishing pigs.
J. R. Flohr[*1], J. M. DeRouchey[1], J. C. Woodworth[1], M. D. Tokach[1], S. S. Dritz[1], R. D. Goodband[1], T. A. Houser[1], C. A. Fedler[2], and K. J. Prusa[2], *[1]Kansas State University, Manhattan, KS, [2]Iowa State University, Ames, IA*

A total of 1232 pigs (PIC 337 × 1050; initially 27.0 ± 0.51 kg) were used in a 98-d study to determine the influence of high doses of added nicotinic acid (NA) on growth, carcass traits, and meat quality of finishing pigs during the summer months. Average daily high, mean, and low temperatures were 27.5, 23.9, and 20.5°C, respectively. There were 28 pigs per pen and 11 replications per treatment. Four dietary treatments were made by adding 0, 350, 700, or 1050 mg/kg NA (Lonza, Allendale, NJ) to a corn-soybean meal basal diet that contained 30 mg/kg of added NA. Diets were fed in four phases with the same NA concentrations in each phase. On d 98 of the study, two pigs per pen (one barrow and one gilt) were transported to a commercial abattoir. Carcass traits and pH decline (45 min, 3, and 21 h) were measured at the abattoir. Afterward, a 40-cm segment of boneless LM was used to determine purge loss and ultimate pH following a 10-d aging period. Then 2.5-cm boneless chops were cut and used to measure subjective color and marbling, objective color (L*, a*, b*), 24-h drip loss, and NA concentration. Overall (d 0 to 98), increasing NA had no effect on ADG or G:F; however, ADFI tended ($P = 0.07$) to increase. Carcass traits were not influenced by NA. Forty-five min and 21 h pH were decreased with increasing NA ($P < 0.01$), but ultimate pH was not different. Purge loss, drip loss, and NA concentrations were not influenced by treatment. The a* and b* were increased ($P < 0.05$) with increasing NA; however, subjective color scores were not different among treatments. Overall, high doses of NA had little influence on growth, carcass traits, and meat quality of finishing pigs raised in a commercial setting.

Key Words: finishing pigs, niacin, nicotinic acid

Table 0753. Effects of added dietary NA on growth and meat quality of finishing pigs

	Dietary NA, mg/kg					Probability, $P <$	
Item	30	380	730	1080	SEM	Linear	Quadratic
d 0 to 98							
ADG, kg	0.82	0.82	0.83	0.82	0.005	0.40	0.50
ADFI, kg	2.03	2.08	2.10	2.07	0.017	0.07	0.71
G:F	0.404	0.395	0.393	0.398	0.003	0.15	0.90
L*	53.12	54.67	54.56	54.16	0.82	0.54	0.21
a*	18.20	18.30	18.89	19.05	0.39	0.05	0.58
b*	16.05	16.45	16.88	17.09	0.40	0.04	0.89

0754 Effects of sugar beet pulp and expansion on performances of lactating sows and nursery piglets. Z. Cheng*, D. Yuan, D. Hou, Y. Chen, H. Zhang, Y. Wang, W. Jin, B. Wang, H. Lei, Q. Li, S. Jiang, S. Bai, and Z. Zhang, *Animal Nutrition & Feed Center, COFCO Nutrition and Health Institute, Beijing, China.*

Ninety-six PIC lactating sows were divided into six treatments with 16 sows per treatment. They were fed diets containing 0, 5, or 10% of sugar beet pulp for 21 d. Three treatment diets were pelleted, and the other three diets were expanded and then pelleted. The diets contained the same calculated levels of CP and DE, sows were fed three times daily. On d 21, piglets were weaned and performances of lactating sows and nursery piglets were recorded. Results indicated that total weaning weight of piglets per litter and average daily weight gain of piglets were 50.47 ± 6.14 kg/Litter and 201.70 ± 30.17 g/piglet; 51.07 ± 11.04 kg/Litter and 189.04 ± 45.89 g/piglet; and 53.43 ± 12.31 kg/Litter and 207.27 ± 41.79 g/piglet for sows fed diets containing 0, 5, or 10% of pelleted sugar beet pulp, respectively; and total weaning weight of piglets per litter and average daily weight gain of piglets were 62.19 ± 12.56 kg/Litter and 222.38 ± 36.75 g/piglet; 47.97 ± 10.63 kg/Litter and 198.13 ± 47.15 g/piglet; and 53.75 ± 7.35 kg/Litter and 193.81 ± 36.30 g/piglet for sows fed diets containing 0, 5, or 10% of expanded and then pelleted sugar beet pulp, respectively. Results also indicated that expansion has significant effects on sow feed intake, total weaning weight of piglets per litter and average daily weight gain of piglets ($P < 0.05$), feed intake was 3.26 ± 0.90 kg/d and 4.77 ± 0.71 kg/d, for sows fed pelleted and expanded diets, respectively; total weaning weight of piglets per litter was 50.47 ± 6.14 kg/Litter and 62.19 ± 12.56 kg/Litter for sows fed pelleted and expanded diets, respectively; and average daily gain of piglets was 201.70 ± 30.17 g/d and 222.38 ± 36.75 g/d for sows fed pelleted and expanded diets, respectively. There were no internations between sugar beet pulp and diet forms ($P > 0.05$).

Key Words: sugar beet pulp, pellet, expansion, lactation sows, piglets

0755 The evaluation of narasin in grow-finish swine diets. L. Greiner[1], R. Barrett[1], A. Graham[*1], and J. Connor[2], *[1]Carthage Innovative Swine Solutions, Carthage, IL, [2]Carthage Veterinary Service, Ltd, Carthage, IL.*

A total of 1180 pigs were placed on study at approximately 27.0 ± 2.6 kg in a wean-to-finish barn to determine if feeding narasin improves feed conversion and average daily gain during the grow-finish period. Pigs were sorted by gender, with the lower 10% being sorted off and the rest gate-cut into a total of 48 test pens. Pens were randomly allocated to one of three treatments: control, narasin included at 15 ppm (S1), or narasin included at 20 ppm (S2). Treatments were randomly assigned within a block. Narasin was fed from d 0 to d 63. Diets consisted of 20% dried distillers grain with solubles (DDGS) from d 0 to 42, 20% DDGS from d 42 to 63, and then 0% DDGS from d 63 to market. Diets met or exceeded NRC (2012) recommendations. Pen weights and feed intake information were collected at each diet phase change to allow for calculation of ADFI and G:F by period. Data that were collected and analyzed included: wean-to-finish mortality (non-value pigs), full value pigs, non-full value pigs/culls (sub-standards at weaning and culls sold to secondary market), finishing ADG (pens), finishing ADFI (pens), G:F (pens), and days to 90 kg HCW. Data were analyzed as an incomplete block design using PROC MIXED, and starting average pig weight was used as a covariate. Data were reported as LSMEANS. The feeding of narasin resulted in no differences in ADG, ADFI, or G:F from d 0 to 21 of the study, regardless of inclusion rate. However, feeding narasin at both 15 and 20 ppm inclusion improved G:F from d 21 to 42 (0.431, 0.443 and 0.440, respectively; $P < 0.003$). Narasin inclusion improved G:F from d 0 to 63 (0.428, 0.435, 0.434, respectively; $P < 0.01$). Once narasin was removed from the diet at d 63 (approximately 89 kg BW), there were no differences in performance. After the removal of narasin from the diet, there were no further improvements or residual impacts on growth performance. Overall, from d 0 to 63, the feeding of narasin at either 15 or 20 ppm improved G:F when compared to control-fed pigs.

Key Words: grow-finish, narasin, pigs

0756 Replacement value of maize offal in diets of weaned pigs supplemented with chicken offal meal. A. O. K. Adesehinwa[*1], E. O. Akinfala[2], and O. O. Adeleye[3], *[1]Institute of Agricultural Research & Training, Obafemi Awolowo University, Ibadan, Nigeria, [2]Dep. of Animal Sciences, Obafemi Awolowo University, Ile-Ife, Nigeria, [3]Federal University of Agriculture, Abeokuta, Nigeria.*

Young pigs have been reported in earlier studies to utilize up to 13.66% maize offal (MO) (a by-product of maize milling consisting mainly of the aleurone layer and some adulterants of germs and endosperm), as replacement for 25% maize in a 54.62% maize-based diet supplemented with chicken offal meal (COM) (ground dried poultry processing by-product comprising heads, viscera, feathers, beaks, etc.) but not 50% replacement of maize with 27.26% MO. Seventy-two weanling pigs (8.84 ± 0.2 kg body weight) were therefore randomly allotted to six dietary treatments of 0, 13.66, 16.34, 19.03, 21.70, and 24.39% MO representing 0, 25, 30, 35, 40, and 45% replacements of maize in 53.34% maize-based diet (containing 20% crude protein) enriched with COM to determine the replacement value of MO for maize in a complete randomized design. There were three pigs per pen and four replicate pens per treatment group. Weekly record of feed intakes and weight gains were taken for the 56-d trial period.

Two pigs/replicate were randomly selected and bled at the first and last weeks of the trial to determine the serum total proteins, albumin, globulin, creatinine, urea, cholesterol, and glucose. All statistical data were subjected to ANOVA, and, where statistical significance were observed, the means were compared using the Duncan's multiple range test (SAS). The results indicated that the increasing levels of MO resulted in increased levels of crude fibre (5.83, 6.57, 6.83, 7.05, 7.27, and 7.38%) and decreased levels of predicted metabolizable energy (ME) contents of the diets (3531.01, 3459.51, 3447.60, 3416.08, 3410.05, and 3372.47 Kcal ME/kg), while the dry matter intake (0.85, 0.84, 0.80, 0.82, 0.87, and 0.85 kg) was not ($P > 0.05$) affected for the 0, 25, 30, 35, 40, and 45% MO levels, respectively. The diets and the constituent nutrients were efficiently utilized in terms of G:F (0.56, 0.54, 0.58, 0.54, 0.56, and 0.54), ME intake per gain (6361.82, 6277.67, 5991.78, 6382.28, 6067.30, and 6199.02 Kcal ME) to support comparable ($P > 0.05$) gains (0.47, 0.49, 0.48, 0.47, 0.51, and 0.48 kg), though slight variations were observed with the ME intake. The performance of pigs fed up to 45% MO replacement of maize were comparable ($P > 0.05$) to those fed the maize-based control diet.

Key Words: maize offal, weaned pigs, non-conventional feedstuff

0757 The effects of standardized ileal digestible lysine level with or without tribasic copper chloride on growth performance, carcass characteristics, and fat quality in finishing pigs. K. F. Coble*[1], S. S. Dritz[1], J. L. Usry[2], J. E. Nemechek[1], M. D. Tokach[1], J. M. DeRouchey[1], R. D. Goodband[1], J. C. Woodworth[1], and G. M. Hill[3], *[1]Kansas State University, Manhattan, [2]Micronutrients, Social Circle, GA, [3]Michigan State University, East Lansing.*

A total of 1248 pigs (initially 28.9 kg BW) were used in a 120-d study to determine the effects of added tribasic copper chloride (TBCC; IntelliBond C; Micronutrients, Indianapolis, IN) and increasing standardized ileal digestible Lys on growth performance, carcass characteristics, liver Cu concentration, and carcass fat quality in finishing pigs. Pens of pigs were allotted to one of six dietary treatments, balanced on average pen weight in a randomized complete block design with 26 pigs per pen and eight replications per treatment. Treatments were arranged in a 3 × 2 factorial with main effects of SID Lys (85, 92.5, and 100% of the estimated requirement) and added Cu (0 or 150 ppm) from TBCC. All diets were corn-soybean meal-based with 30% distiller's dried grains with solubles, 15% bakery meal and 17 ppm Cu from $CuSO_4$ provided from the trace mineral premix. There were no TBCC × SID Lys interactions observed for growth performance or liver Cu concentrations. Increasing SID Lys increased ($P < 0.01$) ADG, G:F and final BW (Table 0757). Pigs fed 150 ppm TBCC tended ($P < 0.10$) to have increased ADG, G:F and final BW. Liver Cu concentrations were greater ($P < 0.01$) in pigs fed TBCC and tended to decrease (quadratic; $P < 0.09$) as SID Lys increased. In pigs fed TBCC, jowl fat iodine value (IV) calculated from the fatty acid analysis of all three fat layers, increased with increasing SID Lys but not in pigs fed diets without TBCC (Lys × TBCC interaction; $P < 0.03$). In summary, SID Lys did not influence the response to TBCC is this experiment.

Key Words: finishing pig, copper, lysine, iodine value

0758 Effects of hard red winter wheat particle size on finishing pig growth performance and caloric efficiency. J. A. De Jong*, J. M. DeRouchey, M. D. Tokach, R. D. Goodband, and S. S. Dritz, *Kansas State University, Manhattan.*

A total of 288 pigs (43.8 kg BW) were used in an 83-d trial to determine the effects of hard red winter wheat particle size on finishing pig growth performance and caloric efficiency. Caloric efficiency (CE) was calculated using the ingredient energy values from NRC (2012) ME and INRA (2004) NE. Pigs were allotted to one of three dietary treatments with six pens/treatment and eight pigs/pen. The same wheat–soybean meal-based diets were used for all treatments. Diets were fed in mash form. The three dietary treatments included hammer-mill ground wheat to particle sizes of) 728, 579, and 326 µm, respectively. From d 0 to 40, decreasing wheat particle size decreased (linear; $P < 0.03$) ADFI (2.29, 2.24, 2.20 kg), but improved (quadratic; $P < 0.01$) G:F (0.400, 0.413, 0.409) and

Table 0757. Dietary SID Lys level with or without tribasic copper chloride in finishing pigs

	TBCC, ppm						Probability, $P <$ [1]		
	0			150				SID Lys	
SID Lys, %	85.0	92.5	100.0	85.0	92.5	100.0	TBCC	Linear	Quadratic
d 120 BW, kg	122.8	125.4	126.2	123.7	125.8	129.0	0.07	0.01	0.76
ADG, kg	0.80	0.81	0.82	0.80	0.82	0.84	0.10	0.01	0.74
ADFI, kg	2.18	2.20	2.19	2.19	2.19	2.23	0.65	0.23	0.95
G:F	0.365	0.370	0.373	0.365	0.374	0.380	0.09	0.01	0.58
Liver Cu, ppm	13	13	12	33	33	26	0.01	0.18	0.09
Jowl IV[2]	84.2	84.6	83.6	82.7	83.6	85.5	0.74	0.16	0.87

[1]SEM were 1.52, 0.007, 0.032, 0.004, 3.3, and 0.801 for d 120 BW, ADG, ADFI, G:F, liver Cu, and jowl IV, respectively.
[2]Linear TBCC × Lys interaction ($P < 0.03$).

CE (7.89, 7.65, 7.72 Mcal ME/kg) and (5.84, 5.66, 5.71 Mcal NE/kg) basis, with no change ($P > 0.24$) in ADG (0.92, 0.93, 0.90 kg/d). From d 40 to 83, decreasing wheat particle size increased (quadratic; $P < 0.01$) ADG (0.92, 0.90, 0.95 kg/d), and improved (linear; $P < 0.01$) G:F (0.319, 0.322, 0.336) and CE (9.92, 9.83, 9.44 Mcal ME/kg and 7.45, 7.38, 7.08 Mcal NE/kg), with no change ($P > 0.23$) in ADFI (2.87, 2.80, 2.84). Overall from d 0 to 83, reducing wheat particle size improved (linear; $P < 0.01$) G:F and CE on both an ME and NE basis, with no difference in ADG or ADFI. Fine grinding wheat was detrimental to feed intake in early finishing but improved ADG in late finishing and G:F for both periods and overall.

Key Words: finishing pig, particle size, wheat

Table 0758. Effects of hard red winter wheat particle size on finishing pig growth performance and caloric efficiency

	Wheat particle size, µm				Probability $P <$	
d 0 to 83,	728	579	326	SEM	Linear	Quadratic
ADG, kg	0.92	0.91	0.93	0.01	0.47	0.50
ADFI, kg	2.59	2.53	2.53	0.03	0.13	0.43
G:F	0.354	0.361	0.367	0.002	0.01	0.82
Caloric efficiency, Mcal/kg gain						
ME	8.94	8.76	8.62	0.06	0.01	0.75
NE	6.67	6.53	6.43	0.05	0.01	0.75

0759 The effects of dietary zinc oxide and chlortetracycline on nursery pig growth performance.

J. A. Feldpausch*, J. A. De Jong, M. D. Tokach, S. S. Dritz, J. C. Woodworth, R. G. Amachawadi, H. M. Scott, J. L. Nelssen, and R. D. Goodband, *Kansas State University, Manhattan.*

A total of 240 weaned pigs (PIC 1050; initially 6.08 ± 0.60 kg) were used in a 47-d study to compare the effects of added Zn from ZnO, alone or in combination with a low or high dose of chlortetracycline (CTC) on nursery pig growth performance. Pigs were allotted to pens at weaning (d 0) and fed a common starter diet with no antimicrobial for 5 d before the start of the experiment. On d 5, pens of five pigs were allotted to one of six dietary treatments, balanced on average pen weight in a randomized complete block design with eight replications per treatment. Dietary treatments were arranged in a 2 × 3 factorial with main effects of added ZnO (0 vs. 2500 ppm of Zn) and CTC (0, 55, or 441 mg/kg feed). Pigs were fed experimental diets from d 5 to 26 after weaning followed by a common corn-soybean meal-based diet without antimicrobial from d 26 to 47. Pigs on the 55 mg/kg treatment received CTC continuously from d 5 to 26; however, to comply with FDA guidelines, CTC was removed from the diets of pigs fed 441 mg/kg CTC on d 15, then added again from d 16 to 26. All diets contained at least 110 ppm of Zn from ZnO in the trace mineral premix. No ZnO × CTC interactions were observed. Pigs fed added ZnO had increased ($P = 0.001$) ADG, ADFI, and BW during the treatment period but decreased G:F ($P = 0.025$) from d 26 to 47 when a common diet was fed. Overall (d 5 to 47), pigs fed added ZnO had increased ($P < 0.05$) ADG and ADFI. Pigs fed CTC had increased (linear, $P < 0.05$) ADG, ADFI, and BW during the treatment period. Overall, pigs fed CTC tended to have increased (linear, $P < 0.10$) ADG and ADFI, but G:F tended (quadratic, $P = 0.070$) to increase then decrease as CTC increased. In summary, ZnO and CTC increased ADG and ADFI but had a minimal effect on feed efficiency.

Key Words: nursery pig, zinc, chlortetracycline

Table 0759. Effect of zinc oxide and chlortetracycline on pig growth

Added Zn, ppm	0	0	0	2500	2500	2500	
CTC, mg/kg	0	55	441	0	55	441	SEM
d 5 to 26							
ADG, g	355	378	386	397	397	417	7.9
ADFI, g	504	514	528	549	542	570	11.9
G:F	0.705	0.737	0.731	0.725	0.734	0.732	0.0128

0760 Efficacy of Biomin BBSH 797 to biotransform deoxynivalenol to the metabolite de-epoxy-deoxynivalenol in serum of pigs.

S. Schaumberger*[1] and U. Hofstetter[2], [1]*BIOMIN Holding GmbH, Herzogenburg, Austria,* [2]*Biomin Holding GmbH, Herzogenburg, Austria.*

The mycotoxin deoxynivalenol (DON) and its metabolites are important biomarkers to demonstrate the efficacy of DON deactivating products in vivo. The aim of this study was to prove the capability of Biomin BBSH 797 to detoxify DON to the metabolite de-epoxy-deoxynivalenol (DOM-1) in the gastrointestinal tract of pigs. Therefore, DON and DOM-1 were measured in the serum of pigs. A total of 124 weaned piglets (mixed sex, approx. 28 d) were adapted for 2 wk. After adaption, 24 animals were randomly assigned to three experimental groups, according to weight, gender and overall condition. Control group received no DON and no BBSH 797. The second group only received 2 µg/kg of naturally DON contaminated wheat and the third group received two µg/kg DON and 1.7 × 10^8 cfu BBSH 797/kg feed. During the experimental phase, piglets were fed restrictively twice a day. Serum samples of all animals in all groups were taken on four consecutive days. Sample 1 (blank serum sample) was taken before feeding the experimental diets. All other serum samples were taken 1.5, 4, 10, and 24 h after feeding the experimental diets. Serum samples were analysed for DON and DOM-1 concentrations by LC/MS-MS method. There were no significant differences in blank serum samples between the three groups. Due to the presence of DON in the standard diet, small amounts of DON and DOM-1 produced by the native intestinal flora were also found in the blank samples. On d 3 of the trial, DON concentration 1.5 h after feeding was more than four times higher in serum of the DON group compared to the control and the DON+BBSH group ($P = 0.02$). DOM-1 concentrations in serum (d 3, 1.5 h) were

highest in the DON+BBSH group and differed significantly ($P = 0.00$) from the control as well as the DON group. To conclude, biomarker analysis of pig serum samples revealed a significant reduction of DON concentration and a simultaneously significant increase of the metabolite DOM-1 in Biomin BBSH 797 treated animals. These results demonstrate the efficacy of Biomin BBSH 797 to detoxify DON in vivo.

Key Words: Biomin BBSH, deoxynivalenol, biotransformation

0761 The effect of superdosing phytase on inositol and phytate concentration in the gastrointestinal tract and its effect on pig performance. P. Wilcock[1], C. L. Bradley*[1], J. J. Chewning[2], and C. L. Walk[1], [1]*AB Vista Feed Ingredients, Marlborough, UK,* [2]*Swine Research Services, Inc., Springdale, AR.*

Dietary phytate has been shown to be detrimental to piglet performance and the use of superdosing levels of phytase can improve performance through phytate destruction rather than phosphorus provision. This extra phosphoric effect of superdosing phytase has not been widely tested in older pigs and therefore this trial was conducted to determine if increasing phytase (Quantum Blue) levels would improve performance in grower pigs (22.8 to 56.5 kg). In addition, inositol and phytate (IP6) levels were measured in the stomach and duodenum to determine if these were correlated to phytase dose and performance. Pigs ($n = 300$) were allocated to one of five treatments (five pigs per pen and 12 replicate pens per treatment): T1, commercial diet formulated to meet the pigs nutrient requirements, except AVP and Ca were reduced 0.15% and 0.16% (equivalent of 500 FTU/kg phytase matrix), respectively; T2 was T1 with the addition of 500 FTU/kg phytase to target an AVP (0.32%) and Ca (0.71%) adequate diet; T3, T4 and T5 were T1 with, 1000, 1500, and 2000 FTU/kg phytase, respectively. All pigs were fed a two-phase feed program (0 to 21 d and 21 to 35 d) with gain, feed intake and FCR determined for the complete feeding period. At 35 d, six pigs per treatment of average BW were selected, penned individually and fed twice per day with the same treatment feed as previously fed. At 42 d each pig was fed 1.5 kg for 30 min, and after an additional 60 min pigs were slaughtered and stomach and duodenum contents were removed for phytate and inositol analyses. There was a linear increase in ADG ($P < 0.01$) and ADFI ($P < 0.01$) and a linear improvement in FCR ($P < 0.01$) as phytase dose increased. There was a linear increase in inositol ($P < 0.01$) in the stomach/duodenum and a quadratic ($P < 0.01$) decrease in IP6 with increasing levels of dietary phytase. There is a good relationship between gastrointestinal phytate breakdown ($R^2 = 0.95$), inositol production ($R^2 = 0.93$), and FCR improvement. In conclusion supplementing grower diets with dietary phytase to doses exceeding commercial levels (> 500 FTU/kg) linearly improved performance (T1, 51.8 kg; T2, 54.5 kg; T3, 55.1 kg; T4, 55.7 kg; T5, 56.5 kg) and feed conversion (T1, 2.07; T2, 1.95; T3, 1.94; T4, 1.89; T5, 1.88) which may be linked to IP6 breakdown and inositol production in the gastrointestinal tract.

Key Words: phytase, phytate pig

TEACHING: UNDERGRADUATE AND GRADUATE EDUCATION

0762 The effects of learning communities and pro-active advising on performance of first semester students.

S. L. Schaake*, A. K. Sexten, T. L. Douthit, D. A. Nichols, J. M. Kouba, D. W. Moser, B. W. Schurle, and M. R. Hay McCammant, *Kansas State University, Manhattan.*

Learning communities in higher education are not new, but they have received increased attention as universities look to enrich student learning. The objective of this study was to determine if students are more engaged and perform better academically when in an environment designed to foster stronger relationships with faculty advisors, course instructors, and peer students. First semester pre-veterinary freshmen at Kansas State University with ACT scores ranging from 21 to 28 (n = 122) were assigned to one of four treatment groups: 1) pro-active advising, learning community, and advisor as instructor; 2) learning community only; 3) pro-active advising only; 4) no intervention beyond standard advising. Students who were pro-actively advised were requested to meet with their faculty advisors a minimum of five times. Learning community students were enrolled in four common courses (eight credit hours). Students were monitored for academic performance, attendance in courses and advisor meetings. Additionally, students were required to complete a survey at the end of their first semester. Pro-actively advised students had a greater (P = 0.01) first semester grade point average (GPA) than students who were not pro-actively advised. Participation in the learning community alone or in addition to pro-active advising did not affect first semester GPA. Students whose faculty advisor was also one of their classroom instructors had a greater first semester GPA (P = 0.05) than students with an advisor they did not have as a classroom instructor. Grades for the Principles of Animal Science course, enrollment n = 147, were greater for students in treatment groups 1, 2, and 3 compared to students without intervention. There were no differences in course attendance between treatment groups. Treatment group 1 reported attending more (P < 0.0001) advisor meetings than students in treatment group 3. Treatment group 2 reported attending a similar number of advisor meetings to students in treatment group 4. More friendships (P < 0.0001) among peers were reported among students in treatment group 1 than any of the other treatment groups. Engagement of students with faculty and their peers seems to be greater when students participated in both the learning community and pro-active advising compared to students who only engaged in one or none of these activities. Increased engagement in the classroom and academic advising may be the reason for improved academic performance.

Key Words: learning community, pro-active advising, student performance

0763 Changes in the perceptions of students involved in a traditional meat science course.

M. J. Anderson*, J. L. Lucia, K. J. Stutts, M. M. Beverly, and S. F. Kelley, *Sam Houston State University, Huntsville, TX.*

Many students have an interest in their food, but the idea of participating in or observing the slaughter and fabrication processes concerns them. However, the effect of participating in slaughter and fabrication on the perceptions of students taking a meat science course is relatively unknown. The objective of this study was to evaluate changes in student perceptions concerning fabrication and slaughter practices after participating in a traditional meat science course and laboratory. Students were surveyed at the beginning and end of the meat science course at SHSU. Survey questions centered on students' perceptions of sanitation during slaughter and fabrication, U.S. slaughter practices, and the students' current and desired level of knowledge about food production. All questions were measured using a 15-cm line scale with the lowest numerical value representing the most negative perception and the greatest numerical value representing the most positive perception. Averages of the paired pre- and post-course surveys were analyzed using the TTest procedure in SAS. When asked how sanitary the processes of slaughter and fabrication were, the responses in the post-course survey were greater (P < 0.01) for both questions. Results of the post-course survey indicated that students believed they were significantly more knowledgeable about the meat products that they consume compared to before taking the course. However, no differences (P = 0.29) were detected in the overall level of knowledge that students desired to gain about their food products. After taking the course, students had a more positive (P < 0.01) outlook toward slaughter practices in the United States. When asked which in step of slaughter that beef cattle go from being an animal to a product, no differences (P = 0.52) were detected between the pre- and post-course surveys. These results indicate that involving students in slaughter and fabrication did not change students' interest in the meat industry or their perceptions on when an animal becomes a product. However, it improved their overall perceptions of the meat industry and their overall level of knowledge, leading us to the conclusion that participating in and observing slaughter and fabrication continues to be a valuable teaching instrument despite student concerns.

Key Words: meat science, fabrication, slaughter

0764 Student and evaluator perceptions of an oral equine "speed selling" exercise. J. S. McCann*, *Virginia Tech, Blacksburg.*

Evaluation skills taught in animal science curriculums often serve as foundation education for judging competitors that may be required to deliver oral reasons. The formality and structure of the oral reasons may be a deterrent to some students' enrollment. Thus, a class of 43 students in an equine conformation and biomechanics class were required to apply their knowledge in two oral "speed selling" exercises for a grade. Students were required to select an outstanding horse with photos and/or video and construct a maximum 90-sec presentation designed to sell the horse on its merits. A panel of evaluators familiar with oral reasons volunteered to score students on a scale range from 1 to 5 for eye contact, voice strength, confidence, terminology, and analysis depth. Students were required to present twice for the first exercise and had the option to present two or three times for the second exercise (top two scores recorded). Class average grade recorded for the first exercise was 41.6 ± 4.7 points, while an improvement was evident when compared to the average 46 ± 2.8 points for the second exercise. To prepare, 70% of the students searched through a minimum of four to 10 horses (Internet sales or farm sites) to find a suitable horse. Most students (81%) elected to practice their oral presentation more than three times, either alone or in front of others. Nervousness decreased from the first exercise (84% either agreed or strongly agreed they were nervous) to 56% on the second exercise. All but three students felt the 90-sec time frame was appropriate for the exercise, and 77% felt the exercise enhanced their verbal skills, a value similar to the 77% who felt they ultimately spoke more like a horseman. When asked if the exercise should be included in future classes, 86% responded positively. Among the volunteer evaluators, 67% were comfortable with scoring within three students. Most evaluators (83%) preferred a 60-sec review time with the student to explain the scores given and agreed the exercise was worth their time. Among the traits scored, evaluators indicated confidence was the trait most important in earning a higher score. Oral speed selling scores were attained for the entire class within a 45-min time frame, and the positive reception to the exercise from students and evaluators has ensured the future implementation of the exercise.

Key Words: equine, instruction, reasons

0765 Efficacy of *i*CEV incorporation into a general animal science undergraduate classroom. R. J. Rathmann* and R. A. Ritz, *Texas Tech University, Lubbock.*

The purpose of this study was to evaluate the effectiveness of utilizing online media technology (*i*CEV; CEV Multimedia, Ltd., Lubbock, TX) as opposed to a traditional textbook to enhance learning in a general animal science undergraduate course. *i*CEV is an online media library of over 40,000 edited minutes of content specific to courses taught in agriculture and especially disciplines in animal science. A customized playlist was created which was linked to the instructors' syllabus online. The playlist allowed students to easily identify and view the segments required by the instructor before attending lecture in the classroom. The instructor administered accountability quizzes at the beginning of the lecture period to ensure that students viewed the material. The objective was to efficiently enhance learning through visual exposure to industries and experts across disciplines in animal science to engage students at a deeper level. The instructor developed a 16-item instrument to survey students after completion of the course. A convenient sample of students (n = 37) were asked to indicate their level of agreement with each statement by using a four point Likert-type scale (strongly agree, agree, disagree, strongly disagree). Participation of subjects was voluntary and data was collected in confidentiality. Descriptive statistics were generated with SPSS (IBM SPSS, Chicago, IL; 20.0 software). Twenty percent of the respondents indicated they spent less than an hour weekly viewing *i*CEV, 52.5% spent one to 2 h, 25% spent two to 3 h, and 2.5% spent more than 3 h. Of the respondents, a total of 83.3% strongly agreed or agreed that viewing *i*CEV increased their interest in the animal science field of study and a total of 94.4% strongly agreed or agreed that viewing *i*CEV increased their awareness of career paths. Seventy-five percent of the respondents either strongly agreed or agreed that they preferred learning from online media compared to learning from a textbook. A total of 94.6% of the respondents indicated that they either strongly agreed or agreed that utilizing online media for course reference materials increased learning. Collectively, it would appear that incorporation of *i*CEV in replacement of a traditional textbook in an undergraduate general animal science course was preferred by students to stimulate the learning process.

Key Words: online multimedia, *i*CEV, teaching

0766 Impact of the male on meat production: A case scenario in swine. J. J. Parrish* and J. L. Susko-Parrish, *University of Wisconsin, Madison.*

To target global competencies in animal sciences, a case scenario exploring climate impacts on swine production was developed. Case scenarios differ from case studies in that the former are guided explorations around a topic, while the later are more open ended. The project had three major objectives: 1) development of technical skills related to understanding male physiology, semen collection, analyzing data, and processing semen for artificial insemination; 2) learning outcomes related to impact of climate on male reproduction, solutions to climate impact on boars, understanding how decisions related to boar management impact society differently in the United States and Philippines, relationship of theory to real world in male reproduction, and role of infrastructure in

livestock production; and 3) general goals of global awareness or competency, issues in global agriculture, critical thinking to solve real world problems, understand issues that would place the United States in a more favorable position to compete in global agriculture. The case scenario can be found at: http://www.ansci.wisc.edu/jjp1/pig_case/html/firstjob.html and involves a student graduating and being hired by a swine production facility in the Philippines as the boar stud manager. Student teams worked through interactive and Web-based scenarios to achieve the objectives. The case scenario replaced two lab periods in a general reproductive physiology course that is a core component of the animal science major. Several written documents (3), analysis of data (3), and class discussions were required of students. A survey was used to evaluate the project with the scoring system being on a 1-to-5 scale, with 1 being not successful, 3 being somewhat important, and 5 being very successful (n = 82), and data is presented as the mean ± sem. The attainments of six technical skills were individually evaluated, but overall the average was 4.08 ± 0.04. The six learning outcomes were also individually evaluated and were very high overall, with an average score of 4.43 ± 0.03. There were four general goals individually evaluated, but overall results were high, with an average score of 4.03 ± 0.06. A Wordle approach was used to examine the usage of words within an assignment to describe the role of the swine industry in the Philippines for a company newsletter. Students were able to demonstrate relationships between, meat, the male, meeting demand, a commercial setting and quality. Overall, the project succeeded in achieving the objectives and demonstrates how international content can be incorporated into core classes within animal sciences.

Key Words: boar, international, climate

0767 Incorporating writing-intensive assignments in an animal science production course.

S. J. Trojan*[1], C. Meyers[2] and N. Hudson[2], *[1]Texas Tech University, Dep. of Animal and Food Sciences, Lubbock, [2]Texas Tech University, Lubbock.*

Writing skills are pivotal for effective communication and are not well-developed among a majority of college students, particularly students in the field of animal science. At a southwestern university, upper-level undergraduate animal science production classes are required to be writing-intensive. In an effort to improve writing skills and as a component of course writing requirements, weekly in-class writing assignments based on prompts related to the week's lecture material were integrated into a dual-listed feedyard management course. Assignments represented 25% of the student's grade and were evaluated using a rubric for individualized feedback. To assess effectiveness of this assignment, students completed a pre-test and post-test to gauge writing apprehension. An instrument was also completed at the end of the semester for student reflection. Total course enrollment was 40; seven graduate students and 27 undergraduate students completed all assessments. A paired t test was used to analyze writing apprehension; after completing writing assignments, students indicated they were better able to express ideas through writing (P < 0.05); were more confident in expressing ideas clearly through writing (P < 0.05); stated that writing helps them think more thoroughly through concepts (P = 0.06); and felt more confident in their ability to write (P < 0.05). The majority of students (56%) indicated the writing assignments helped them to better understand the course material; felt the writing assignments allowed them to be more comfortable with the material (53%); and thought the assignments were useful and relevant (63%). The reflection instrument also revealed that writing assignments helped students learn to organize their thoughts better (57%), and that the individualized feedback for each assignment was adequate to help students to make improvements in their writing approach (67%). Based on the feedback received, this assignment will be used again, but with more detail provided throughout class on the writing process.

Key Words: animal science, production course, writing

0768 Improved student achievement through gamification and the flipped classroom.

C. J. Mortensen* and A. M. Nicholson, *University of Florida, Gainesville.*

Emerging teaching strategies for educating informational-age students include gamification and the flipped classroom. Use of game design elements in non-game contexts are thought to not only make the classroom more enjoyable for students, but also assist them in mastering knowledge. Game design elements can also potentially increase critical thinking skills based on gaming elements utilized. The flipped classroom as a pedagogy is defined as students viewing asynchronous lectures on their own and participating in learning activities during scheduled meeting times. For this experiment, students enrolled in an Introduction to Equine Science course were instructed in a flipped classroom learning environment and participated in weekly educational games over the course of a 16-wk semester. Students were administered the Cornell Critical Thinking Test (CCTT: Level X) on the first and last day of the semester. Students' exam scores and overall course grades were compared to the previous three course offerings taught in traditional lecture format. Finally, students were asked to evaluate their experiences based on a 5-point Likert scale: 1 (strongly disagree), 2 (disagree), 3 (neutral), 4 (agree), and 5 (strongly agree). For CCTT, students' scores (n = 67) increased mean 50.5 ± 0.76 from the pretest to a 55.8 ± 0.78 for the post-test (P < 0.001). When given similar exams, students' scores increased a mean 5.6% ± 1.1 for Exam 1 (P < 0.001), a mean 4.8% ± 0.9 for Exam 2 (P < 0.01), and a mean 3.8% ± 1.1 for Exam 3 (P < 0.05) compared to the previous 3 yr (n = 166). Overall course grades improved 4.0% ± 1.1 (P < 0.05) compared to the previous three class grades. Students

(n = 55), when asked to evaluate their experience, ranked the "flipped classroom has been enjoyable" as mean 4.5 ± 0.09, "flipped classroom is an effective teaching strategy" as mean 4.25 ± 0.08, "I would prefer to watch lectures online and do learning activities in class" as 4.43 ± 0.12, "in-class activities are a wise use of class time" as 4.43 ± 0.08, "this course encourages independent, creative and critical thinking" as 4.45 ± 0.09, and "I would recommend this course to a friend" as 4.67 ± 0.07. Gamification was viewed as an excellent teaching tool, particularly as review before an exam. Overall, the flipped classroom as a teaching strategy led to greater student critical thinking, achievement, and satisfaction.

Key Words: flipped, gamification, critical thinking

0769 Impact of student engagement activities on student performance on a short assessment.

O. N. Genther* and S. L. Hansen, *Iowa State University, Ames.*

Cooperative learning techniques such as Turn To Your Partner (TTYP) offer opportunities to engage an entire classroom while encouraging learners to think more deeply about a topic. A question is formulated to promote deeper understanding of a lecture concept. Students are challenged to think about the question multiple times—individually, with a partner, and during classroom discussion where individuals are randomly held accountable for thinking. To assess the value of this activity on achievement in a challenging senior-level animal science class, 47 students were enrolled in a blinded study comparing the number of TTYP activities in a class period (0, 1 or 2) with student performance on a short five-point quiz at the beginning of the following lecture period. The experiment was conducted twice during the semester, with each treatment (0, 1, or 2 TTYP) conducted during the first exam period (P1) and again during the second exam period (P2). Only scores from students that were in attendance during both experimental and assessment lectures were included in analysis (n = 35 to 42 students). Data were analyzed using the PROC MIXED of SAS, with the fixed effects of period and number of TTYP, and the random effect of student. There was a tendency for a TTYP × period interaction (P = 0.08) where during P1, 2 TTYP scores (3.47 ± 0.177) were greater (P = 0.004) than 0 TTYP scores (2.81 ± 0.183), and tended to be greater (P = 0.07) than 1 TTYP scores (3.05 ± 0.192). Scores between 0 TTYP and 1 TTYP did not differ (P = 0.30). However, during P2 there were no differences (P > 0.33) between scores for 0, 1, or 2 TTYP, (3.43 ± 0.187, 3.20 ± 0.191, and 3.38 ± 0.185, respectively). After the use of TTYP during P1, scores improved, possibly because material in this period is biochemistry-based and typically less interesting to students. However, by P2 the students may be more interested in the material and have a better understanding of expectations, such that TTYP number did not impact overall performance. This experiment suggests that utilizing simple techniques to engage learners during lecture may be beneficial to encourage participation early during the semester, as well as promote thinking during presentation of difficult material. Student evaluations at the end of the semester were overwhelmingly positive in response to both the TTYP exercises and the quiz assessments.

Key Words: student, cooperative learning, engagement

0770 The impact of implementing interactive exam review strategies on student satisfaction and exam scores.

D. T. Masser, J. M. Falk, and A. Ahmadzadeh*, *University of Idaho, Moscow.*

Interactive teaching increases students' satisfaction and performance in college courses. These strategies require time and effort from the instructor. Due to student personality differences, there is no guarantee that students are satisfied with the teaching methods of the instructor. The objective was to investigate the impacts and relationship between student personalities, the type of course review strategy on exam scores, and student satisfaction. The population consisted of 53 students enrolled in the spring 2013 Animal Reproduction and Breeding course at the University of Idaho. The Real Colors Personality Indicator (RCPI) was administered to assess and describe students' personality. For Exam 1, students were assigned randomly to one of the two review session methods: quiz bowl (QB) question-answer or lecture review (LR), with both methods facilitated by the course instructor. The groups were then switched for Exam 2. For the final exam, students chose the review method session or attended both. After attending review sessions, student satisfaction of the review type was measured using a researcher-created, (scale of 1 to 4). Data from the RCPI, satisfaction questionnaires, and exam scores were analyzed using the Statistical Package for the Social Sciences. The class was 80% animal science majors. Overall, students were more satisfied with the QB review method (M = 3.24, SD = 0.74; M = 3.52, 0.45) than the LR review method (M = 2.50, SD = 0.35; M = 2.64, 0.32) for both Exam 1 and 2, respectively. Data also revealed that students who attended the QB review session scored greater on Exam 1 (M = 79.5, SD = 13.6) than the group of students who attended LR (M = 71.6, SD = 13.0) or did not attended review session (M = 62.4, SD = 14.7). For the final exam, students attending both review methods had a greater score than those who did not attend any review sessions. When exam scores of the four personality groups were compared, students with a green personality scored the highest on all three exams. Green personalities tend to be logical intellectuals who are curious and irritated by drill and routine. It appears that interactive review sessions improve student information retention. It is recommended that college professors provide review sessions and perhaps incorporate interactive review strategies, like quiz bowl. By improving teaching methods, and awareness of student personality differences, improvements can be made in student's course performance and satisfaction.

Key Words: learning styles, review strategies, teaching

0771 Integrating teaching and extension: Swine production. H. M. Zaleski*, *University of Hawaii at Manoa, Honolulu.*

Swine Production is a senior capstone course in which students integrate concepts learned in courses such as nutrition, genetics and reproduction and apply them to practical swine production. Most animal science students at the University of Hawaii at Manoa are urban students interested in veterinary medicine, with little knowledge of or interest in swine production. The departmental learning objectives include applying principles to livestock production, but having students engage in learning this material is a challenge. The extension specialist teaching the course tried a new approach in fall 2013, integrating instruction and extension. Instead of traditional classroom instruction and written reports, teams of three students were sent out to work with cooperating farmers. Each team described their farm using a list of required information on general farm description, breeding program, feeding program, housing, waste management, health program, production management, and economics. The farms were carefully selected to represent different management approaches including varying use of local food waste and agricultural byproducts in the swine rations and different types of housing and waste management. The teams presented the results of farm visits and farmer interviews in class presentations and written reports, which were revised before being submitted in final form to both the instructor and the farmer. The course was designated as developing both oral and written communication skills. Course evaluations indicated that 78% of the students felt that the farm visits and interactions with the farmers were the most valuable part of the course, and 44% mentioned hands-on laboratories (artificial insemination and baby pig processing), while others mentioned constructive feedback, small class size, having to think, oral presentations, and writing. Student journals indicated a strong rapport with and a very positive view of the farmers and farm practices. The farmers changed some of their practices based on student recommendations, most notably adjusting feeding according to condition score. Student grades were equal to or better than in more traditional learning environments. The new structure had some challenges. Students were required to sign liability waivers and confidentiality agreements. Students had to use their own cars and to find times when all team members were available for farm visits. The relative contributions of the team members to the group reports were evaluated by all members of each team. Students indicated that the amount of work justified four rather than three credits for the course.

Key Words: swine production, undergraduate teaching, extension

0772 Teaching companion animal management: Perspective from a livestock nutritionist. J. L. Wahrmund*, *Texas A&M University–Commerce, Commerce.*

Many students enrolling in animal science programs aspire to attend veterinary school and find there are few courses in their course catalogs focused on their primary interest, companion animals. Institutions have recognized this demand, and some have created companion animal management courses to help satisfy students' wants and needs. However, few institutions employ animal science professors specializing in companion animals. At Texas A&M University–Commerce, there are two animal science professors, both of whom specialize in beef cattle. One was tasked with teaching companion animal management, and this abstract outlines the approach utilized to effectively develop and deliver this course. The course was taught online during the summer with an enrollment of 17. At the beginning of the course, students were asked to identify which species most interested them, other than dogs and cats, and which topics they were most eager to learn. Species interests included rabbits (n = 5), reptiles (n = 4), fish (n = 3), ferrets (n = 2), chinchillas (n = 1), and birds (n = 1), with one student indicating interest in all species. Topics of greatest interest included nutrition (n = 12), health (n = 11), anatomy (n = 4), and reproduction (n = 3). Other topics covered in addition to these included breeds, behavior, training, showing, geriatrics, business management, careers, and managing unwanted animals. All topics covered were presented with dogs and cats as the primary models. Other species were presented in specific lectures for that species and covered basics of nutrition, reproduction, health, and housing. The textbook *Companion Animals: Their Biology, Care, Health, and Management* by Campbell and Campbell was used as the primary guide for presentation of information. Other sources of information were obtained from the American Veterinary Medical Association, the American Kennel Club, and the Cat Fanciers' Association, to name a few. At the end of the course, students were asked to indicate their favorite and least favorite aspects of the course. Generally, students enjoyed learning about a wide variety of species and disliked that the course was offered during a short summer session online, which eliminated possibilities of hands-on learning. Student course evaluations were unanimously positive. Instructors teaching management courses outside their species of expertise can employ numerous resources. Allowing students to provide input regarding topics to be covered can help provide rewarding educational experiences for both students and the instructors.

Key Words: companion animals, teaching, undergraduate education

0773 A comparative veterinary course for pre-veterinary students. *A. P. Fidler*, University of Arkansas, Fayetteville.*

Students entering veterinary school are expected to adapt to a new learning environment and begin retaining volumes of information very quickly. These students arrive with learning strategies developed during their undergraduate studies, which may not prove adequate for the speed and volume of learning required in veterinary school, and some subject areas might be quite foreign depending on the students' academic background. Problems resulting from unfamiliar material being met with deficient learning strategies often become evident in first-year anatomy courses. To address this issue, a Comparative Veterinary Anatomy course has been developed at the University of Arkansas for junior and senior pre-veterinary students. The objectives of this course are to familiarize students with anatomical structures of domestic animals, as well as to develop critical learning strategies for success in future scientific careers, graduate programs, and professional school. The course utilizes didactic lectures, illustrative reference materials, and hands-on laboratory experiences with live animals, preserved specimens, and fresh cadavers. Course topics are reinforced by examinations requiring identification of anatomical structures in illustrations as well as on specimens. The course objectives, modes of instruction, and student evaluation are meant to closely resemble a first-year veterinary curriculum's anatomy course to prepare students to succeed in such a course. In the two semesters the course has been offered, it has reached maximum capacity at 20 students. A survey was administered following the conclusion of the first semester asking students to describe the most valuable learning experiences during and outside of class. Nineteen of 20 students responded (95.0%). Eighty percent (80.0%) of respondents indicated that laboratory time spent examining live, preserved, and fresh dead specimens was the most valuable learning experience during class time. Sixty percent (60.0%) of respondents indicated that reviewing and/or recreating illustrations from the textbook was the most valuable learning experience outside of class.

Key Words: veterinary, anatomy

TRIENNIAL LACTATION SYMPOSIUM

0774 Utilizing 'omic' techniques to understand energy balance in the lactating dairy cow.
J. R. Roche*[1], C. V. Phyn[1], T. M. Grala[2], C. G. Walker[2], M. A. Crookenden[2], S. Meier[1], J. K. Kay[1], and J. J. Loor[3], *[1]DairyNZ, Hamilton, New Zealand, [2]DairyNZ, Auckland, New Zealand, [3]University of Illinois, Urbana.*

Nutrigenomics describes how the amount and/or type of feed an animal receives, relative to its genetic and physiological requirements, affects its molecular phenotype, thus changing production, energy balance, reproduction, and health. For example, Holstein-Friesian cows (HF) bred almost exclusively for milk production have a more prolonged and severe negative energy balance in early lactation than HF cows bred on an index that includes traits related to longevity and health. This is due, in part, to a greater uncoupling of the somatotropic axis and the level and duration of this uncoupling can be influenced by diet. In addition, the decline in reproductive success in recent decades has been associated with the increased negative energy balance associated with genetic selection for milk production. However, differences in the endometrial transcriptome indicate that genetic selection for milk production is also associated with a failure to recognize pregnancy as well as inadequate suppression of the local immune system and nourishment of the embryo, which are not necessarily related to energy balance. Nonetheless, some of the genes involved are epigenetically regulated and could be altered by nutrition. Factors that influence energy balance, such as nutrition and milking frequency, have different effects on the metabolism of the mammary gland, liver, and adipose tissue. For example, although once-daily milking and greater feeding levels improve energy balance, once-daily milking lowers milk production through reduced secretory cell activity and number, whereas, greater feeding levels increase milk production through the provision of more nutrients. These effects are independent and at least partially additive; if both strategies are used, the outcome is a combination of the two. Experimental results indicate that the molecular changes underpinning these effects can persist beyond the period of treatment. Less frequent milking results in an earlier recoupling of the somatotropic axis post-partum and adipose accretion, physiological changes that are also influenced by energy balance, but are dependent on feed type as well as availability. A greater understanding of the effects of nutrition on the molecular phenotype is required to optimize cow management for productivity and welfare.

Key Words: nutrigenomics, energy balance, reproductive failure, genotype

0775 Systems biology of regulatory mechanisms of nutrient metabolism in lactation.
J. P. McNamara*, *Washington State University, Pullman.*

The role of the dairy cow is to help provide high-quality protein and other nutrients for humans. We must select and manage cows with the goal of reaching the greatest possible efficiency for any given environment. We have increased efficiency tremendously over the years, yet the variation in productive and reproductive efficiency among animals is still quite large. In part this is because of a lack of full integration of genetic, nutritional, and reproductive biology both in research and management decisions. However, integration across these disciplines is increasing as biological research findings show more specific control points at which genetics, nutrition, and reproduction interact. An ordered systems biology approach that focuses on why and how cells regulate nutrient use and on how and why organs interact by endocrine and neurocrine mechanisms will speed improvements in efficiency. Nutrient metabolism is controlled by a number of factors, including type and amount of intake, stage of lactation, and amount of milk production, through a complex system of neurocrine and endocrine regulation. In turn, nutrient metabolism in the brain, liver, splanchnic organs, and muscle directly affect the efficiency of the animal. The metabolic efficiency of the mammary gland runs at its thermodynamic maximum unless there is a physiological disease or a massively imbalanced ration. The variation in efficiency of animals is a result of variations in metabolism in non-mammary tissues; including nutrient metabolism in the liver, protein turnover in the muscle, and lipid turnover in the adipose tissue. These metabolic paths are allotted to maintenance costs in practical application. Thus, using a systems biology modeling approach, we can design experiments specifically to integrate our knowledge on tissue metabolism, food intake, milk production and overall efficiency. Data from genomic studies, transcriptional arrays, endocrine and neural signals, tissue metabolism and animal level experiments can be integrated to clearly indicate which are the controlling factors. This approach can help focus our research to make faster and large advances in efficiency and show directly how this can be applied on the farms.

Key Words: systems biology, lactation, metabolism

0776 Insights provided by nutrigenomics into the effect of diet on metabolism and milk production.
K. J. Harvatine*, *Pennsylvania State University, University Park.*

The impact of diet on metabolism and milk production has been well-appreciated by dairy nutritionist for many years. Nutrigenomics has provided tools and experimental approaches critical to identifying the functional mechanism of nutrients. First, nutrigenomics has led to the discovery of basic mechanisms using cell culture and rodent models that provide strong candidate

mechanisms for testing in the cow. Second, the application of nutrigenomics approaches in the cow has provided direct insight into novel mechanisms of the cow. The presentation will focus on the application of nutrigenomics to understanding diet-induced milk fat depression and dietary regulation of the circadian rhythm of the mammary gland. Milk fat depression is caused by specific intermediates of ruminal biohydrogenation of polyunsaturated fatty acids and is a clear example of nutritional regulation of metabolism. Advances in lipid analysis and chemistry allowed identification of the bioactive conjugated linoleic acid isomers, but nutrigenomic approaches were key to identification of mechanism. Specifically, microarray analysis identified candidate systems and transgenic approaches have allowed demonstration of the functional mechanism. Nutrient intake also entrains the daily rhythm of metabolism through regulation of a transcriptionally regulated biological clock. Although the exact nutrient is not clear, nutritional entrainment of the mammary gland clock has been demonstrated. Understanding the mechanisms of bioactive nutrients has allowed development of targeted nutritional strategies and has great future potential as an experimental approach.

Key Words: nutrigenomics, milk fat depression, gene expression

---

0777 Nutrigenomics in dairy cows. *M. Bionaz*[*1] *and J. J. Loor*[2], [1]*Oregon State University, Corvallis,* [2]*University of Illinois, Urbana.*

Nutrigenomics is defined as the study of the genome-wide influences of nutrition altering the expression and/or structure of an individual's genetic makeup. Nutrigenomics can be performed in a reductionist way, with the intent to dissect the nutritional effect on a limited part of the genome (e.g., expression of few genes) or using a systems biology approach, where a holistic view of the nutritional effect on the genome is studied. Nutrigenomics in dairy cows is a relatively new area of research. Among all nutritional factors able to affect cell biology by changing gene expression, dietary energy, fatty acids, and amino acids have the strongest potential. The level of dietary energy has a powerful and broad transcriptomics effect. This was evidenced by data generated in liver and adipose tissue, especially in peripartal dairy cows. Profound nutrigenomics effects of amino acids are emerging, particularly during the process of milk protein synthesis. The most powerful nutrigenomics dietary components are fatty acids, particularly long-chain fatty acids (LCFA). In relation to dairy production, the effect of trans10,cis12-conjugated linoleic acid on depressing milk fat synthesis via effects on few well-studied enzymes was among the first and likely the best-known nutrigenomics example tied to LCFA. The LCFA can affect expression of genes primarily because of their capacity to modulate activity of specific transcriptional factors. Among those the most sensitive to LCFA and best studied are the peroxisome proliferator-activated receptors (PPARs). Emerging data support a role of PPARs in ruminant physiology and metabolism, including the regulation of milk fat synthesis. In addition, at least in vitro, there is a strong agonistic effect of LCFA, particularly the saturated fatty acids, in activating PPARs in ruminants. The capacity of LCFA to modulate PPARs (and likely other transcriptional factors such as LXR) offers the possibility to fine-tune the biology of dairy animals, including milk synthesis. The emerging data on PPARs in ruminants allowed proposing a dynamic model where activation of PPARs in several major tissues at distinct physiological stages could improve the adaptation of dairy cows to lactation. We are at the frontier of the nutrigenomics era in ruminants and initial data strongly indicate that this scientific branch can play a critical role in future strategies to feed dairy cattle. Outputs from nutrigenomics research can help improve efficiency of high-producing dairy cows and modifying milk quality for an ever-growing number of consumers demanding "healthy" food.

Key Words: nutrigenomics, dairy cow, transcription factors

0778 Systems biology and the role of nutrition in coordinating adaptations to lactation. J. J. Loor[*1] and M. Bionaz[2], [1]*University of Illinois, Urbana,* [2]*Oregon State University, Corvallis.*

The advent of genome- and metabolome-enabled technologies (e.g., microarrays, RNA-sequencing) constituted a setback to the use of reductionism in livestock research. Those tools along with bioinformatics were essential for the advent of modern systems biology. Systems biology is a field of study widely-used in model organisms (e.g., rodents, yeast) to enhance understanding of the complex biological interactions occurring within cells and tissues at the gene, protein, and metabolite level. Application of systems biology concepts is ideal for the study of interactions between nutrition and physiological state with tissue and cell metabolism and function during key life stages of mammalian organisms, including the transition from pregnancy to lactation (i.e., the peripartal period). Within that framework, the use of a single time point to study NutriPhysioGenomics is reductive and insufficient to capture the dynamism of biological adaptations; therefore, implementation of time-course experiments must be undertaken. Modern bioinformatics tools complement the ever-increasing ability to generate large molecular and metabolite datasets. The Dynamic Impact Approach (DIA) was conceived to help interpret in a more biologically relevant manner the longitudinal physiological adaptations to lactation occurring simultaneously in several tissues such as liver, adipose, and mammary. This tool along with gene and transcriptional factor (TF) network analyses using software suites, such as the popular Ingenuity Pathway AnalysisÒ, are ideally suited for understanding high-throughput datasets. Results utilizing our own and publicly available datasets demonstrate that the DIA is robust for physiological systems analysis of complex transcriptome datasets within a tissue or among tissues. Simultaneous visualization of the complex inter-tissue adapta-

tions to physiological state and nutrition can be discerned. An example of this approach using liver, mammary, and adipose tissue during late-pregnancy and early lactation is presented. Furthermore, we present examples of new knowledge generated through the application of functional analyses and gene network tools on transcriptome and metabolome datasets encompassing nutritional management of dairy cattle, e.g., plane of dietary energy prepartum or the supplementation of amino acids or long-chain fatty acids. Overall, we demonstrate that the integrative approach across and within tissues provides a more holistic understanding of the complex dynamic physiological adaptations during lactation. The longitudinal analyses of functional and TF networks within adipose and liver in response to nutrition may prove useful for fine-tuning nutritional management of dairy cattle. An important goal during this process is to uncover key molecular players involved in the tissue's adaptations to physiological state or nutrition.

Key Words: bioinformatics, nutritional science, omics

0779 Nutrient partitioning during intramammary inflammation: A key to severity of mastitis and risk of subsequent disease? K. M. Moyes*, *Dep. of Animal and Avian Sciences, University of Maryland, College Park.*

In early lactation, susceptibility to disease is greatest, impacting cow health, productivity, and leading to economic losses. Mastitis is the most economically costly disease to the dairy industry and is most frequent at this time. Glucose and amino acids (especially glutamine) are the primary fuels used by leukocytes in other species and are essential substrates for optimal leukocyte function, but have not been elucidated in bovine leukocytes. Yet, because these substrates are in high demand to support milk synthesis in early lactation, their supply to leukocytes may be compromised. Production-related metabolic diseases during early lactation, such as ketosis and hepatic lipidosis, can also adversely affect health and productivity. Risk of subsequent disease for cows during mastitis is unknown. During an inflammatory response, increases in circulating non-esterified fatty acids and glucose during an IMI in dairy cows have been reported. Previous work indicates that hepatic expression of key genes associated with gluconeogenesis (e.g., PCK1 and G6PC), ketogenesis (e.g., HMGCS2) and fatty acid metabolism (e.g., SREBF1 and PPARA) are downregulated after intramammary infection (IMI). These results suggest a potential link between mastitis and the risk of subsequent metabolic disease for dairy cows during lactation. This presentation will discuss the complex relationships between metabolism and immune function, and how these immunometabolic interactions relate to susceptibility to mastitis and increase the risk of subsequent disease during early lactation. New strategies to prevent or control mastitis development and reduce the risk of subsequent disease during early lactation will also be discussed.

Key Words: cow, mastitis, metabolism

0780 Nutritional effects on immunology and inflammation in dairy cattle. E. Trevisi*, P. Grossi, and A. Minuti, *Università Cattolica del Sacro Cuore, Piacenza, Italy.*

Optimal health is of paramount importance for an acceptable life of farm animals, mainly during the pivotal phases of their life cycle, such as parturition and weaning. Nutrition is one of the most important players of the health status and can influence onset of clinical diseases or mild malaise (subclinical diseases). A large portion of the host resistance to infection involves the immune system and, mainly at the gastro-intestinal level, represents a crucial site of the body for the relationship among nutrients, microbes and host. Balanced diets guarantee that nutrient requirements are met and simultaneously can: 1) counteract the survival of infectious pathogens in the gastro-intestinal tract (as occurs with diets too high in fermentable carbohydrates), 2) prevent damage of the gut epithelium, 3) improve the host resistance to the pathogens, and 4) reduce tissue damage due to metabolic disorders associated with deficiencies (e.g., ketosis, liver lipidosis) and excesses (e.g., milk fever, obesity) of nutrients. A wide variety of nutritional compounds (e.g., macro and micronutrients, secondary metabolites of plants) are involved in aspects of immuno-regulation, but mechanisms are only partly known. The physiological conditions of the animals also play a relevant role in the regulatory effects of the nutrients on immune and metabolic systems. In dairy cows, the transition period represents the most vulnerable physiological life stage, in which the nutrition can influence the immune and inflammatory responses. The tremendous physiologic changes taking place during this period make the diagnosis of the nutritional-management causes challenging. Nevertheless, the immune-metabolic profiling appears as a valuable tool in the management of health of transition dairy cows, particularly for direct diagnosis of sub-clinical diseases (metabolic and infectious). Recently, growing evidence suggests that inflammation around calving is responsible for reduced performance and is associated with decreased production, efficiency and fertility. In particular, composite indices based on multiple variables associated with inflammation (e.g., Liver Functionality Index) are promising for use as an aid in the diagnosis and correction of management and nutritional problems on dairy farms. Nutritional improvements in the periparturient period not only reduce the frequency of inflammatory events, but also minimize their intensity and duration. In particular, some nutrients and compounds (e.g., omega-3 fatty acids, Conjugated Linoleic Acid, methionine, plant extracts) have demonstrated to improve the immune function and the inflammatory response around calving, underscoring a need for further studies of the interactions between nutrition, immunity and inflammatory response.

Key Words: nutrition, immunology, transition cow

WORKSHOPS: **CRAFTING USAID'S LIVESTOCK RESEARCH AGENDA– ANIMAL SCIENCE PRIORITIES UNDER FEED THE FUTURE**

0781 Feed the Future research strategy and USAID's global livestock investments. S. Moon Chapotin* and J. Turk, *U.S. Agency for International Development, Washington, DC.*

This presentation will outline major program areas under the Feed the Future research strategy, which encompasses global investments in aquaculture, poultry, and livestock production systems. It will summarize recent and current livestock research and value chain investments by USAID. USAID is currently conducting priority setting for livestock value chain research aimed at informing future investments. This presentation will also describe how stakeholders can provide input and advice about the research priorities as well as the role of U.S. universities and colleges in USAID-supported research activities.

Key Words: USAID, livestock research, value chain

0782 Nutritional value of animal source foods. L. Iannoti*, *Institute for Public Health, Washington University, St. Louis, MO.*

Animal source foods (ASF) reinforce household food security. One of the most difficult and least accounted values of livestock is their nutritional value. From the early 1970s to the 1990s, meat and milk consumption in developing countries grew by more than twice the rate in developed countries. On a global basis, foods of animal (including fish) origin provide about 17% of the energy and more than 35% of the dietary protein for humans. Most importantly, the biological value of protein in animal source foods is about 1.4 times that of foods from plants and animal proteins are 20 to 30% more digestible than plant proteins (96 to 98% vs. 65 to 70%). In rural areas of developing countries, diets of children are primarily crop-based and often deficient in vitamin A, vitamin B-12, riboflavin, calcium, iron and zinc— vitamins and minerals that are essential for human health and are more bio-available in animal source foods. Vitamin A in its usable form and vitamin B-12, for example, critical for the normal functioning of the brain and nervous system, are present only in animal-source foods. Iron is more easily absorbed by humans from meat than from vegetables, zinc has a role in the metabolism of RNA and DNA, riboflavin plays a key role in energy metabolism, calcium is an essential nutrient for cell physiology and bone mineralization, and iron is necessary for hemoglobin and myoglobin production.

Key Words: animal source foods, nutritional value, protein

0783 Research needs for inclusive livestock markets in developing countries. J. Yazman*, *U.S. Agency for International Development, Washington, DC.*

The global population is predicted to reach 9.6 billion by 2050. Nearly all of future population growth will be in urban areas, with some 50% of the developing world's population living in more than 425 cities with 1 million residents or more. Urban families in developing countries, with higher average incomes, generally consume diets higher in animal-source foods (ASF) than rural families. ASFs in developing countries reach consumers through various market value chains, often with weak enforcement of public health regulation. Disease hazards and risks inherent in traditional ASF food marketing systems are not well-understood. These challenges, along with complex trade pathways, will make traceability by developing world livestock producers difficult and prevent engagement in the growing global trade in ASFs. Increasingly consumers across the globe are linking their food choices to environmental and social equity attributes and, specifically with respect to ASFs, assurance of humane treatment of animals at farm level through to harvest. End market intermediaries often enforce private standards that associate their ASFs with a range of best management practices or adhere to accepted global standards. USAID's Feed the Future Initiative seeks to link smallholder and pastoralist livestock producers to increasing local, regional and global ASF demand. Research supported by Feed the Future will enable increased competitiveness and market linkage through new technologies and improved management practices of herds and flocks that incorporate environmental standards, reduce greenhouse gas generation, and eliminate health hazards and risks all along ASF value chains.

Key Words: animal source food (ASF), Feed the Future, USAID

0784 The indispensable role of mixed small holder systems in global food and nutritional security. J. Smith*, *International Livestock Research Institute, Washington, DC.*

By the time global population stabilizes at around 10 million in the 2050, about 60% more food will be needed than is produced now, and about 75% of that must come from intensification as the agriculture land frontier has been largely reached. In this quest to produce much more food sustainably, small holder mixed crop livestock systems, where more than half of the food in the developing world is currently produced, will play a critical role. Studies by ILRI (2009) show that globally these mixed systems produce about 50% of the cereals, and 60% and 70% of the meat and milk, respectively. Once connected to markets, small holder mixed systems respond rapidly to the application of new interventions— both technical and institutional. It is such mixed systems that are expected to undergo the greatest transition (growth/intensification) in

the coming decades, transforming to more market-oriented systems and at the same time presenting a major opportunity to ensure that the transition is positive not only for food security but for livelihoods, economies, people's health, and the environment. Because of increasing natural resource scarcity and the effect of increasing climate variability, meeting global food and nutritional security will be extremely challenging, but the transformation of mixed crop livestock systems also offers an enormous opportunity for poverty reduction and rural transformation through stronger participation of small holders in the global food economy.

Key Words: food security, nutritional security, global population

0785 Africa livestock futures and one health.
D. Carroll*, *U.S. Agency for International Development, Washington, DC.*

The current trend of a rapid increase in the demand for animal products in Africa is not yet matched by a similar trend of increased production. The increase in demand will grow in the next three decades— at least. There will be efforts to produce more animal products to fulfill the demand. At the same time, livestock are critical to people's nutrition, food security, livelihoods and resilience in many parts of Africa. There would be widespread benefits if marginal farmers were to be able to respond to (and profit from) the increased demand. An unmanaged increase in production, as witnessed in Asia between 1960 and 2000, could bring adverse consequences, including pressure on natural resources such as water and land, increased greenhouse gas emissions, and increased threats of zoonotic diseases. If animal-derived pathogens are readily transmissible between humans and cause illnesses with high fatality rates, serious outbreaks— or even pandemics— will occur. This session will examine work underway to assess options for livestock futures in Africa based on plausible assumptions of growth through 2050 of 1) consumption of animal origin foods, 2) production of livestock and products (i.e., both demand and supply sides), 3) possible consequences and risks of the different scenarios, and 4) policy options that could, if applied, reduce or mitigate the potential adverse consequences of each scenario.

Key Words: Africa, food security, livestock

0786 The role of new technologies in increasing livestock production.
D. Nkrumah*, *Bill and Melinda Gates Foundation, Seattle, WA.*

In the next 30 yr, the world's population is projected to grow by nearly 2 billion and will become more urbanized, with a more skilled workforce. The good news is that global prosperity and affluence will increase. The challenge is that food supply will need to more than double to meet the increasing demand. Specifically, the demand for animal-sourced foods needs to more than double to meet the demands of the newly affluent. With fewer and fewer people engaged in agriculture, and for the sake of the planet, animal production growth cannot continue to come from the deployment of more animals and land. Some have argued that current organic systems may be for the rich and curious and could not produce enough food to feed the world in the future. Past technologies that allowed us to advance productivity may not be enough to bring about future intensification, especially for small holders who live in areas that require attention to climatic adaptability and disease resiliency. Instead, changes in total factor productivity needs to occur through significant changes in current techniques. To transform current near-subsistence small holder production systems, we need technological innovation to drive the needed sustainable productivity increases. We require collaborative global research teams to come up with new ways of developing and adapting modern concepts in biotechnology to create the next-generation of animal genetics, health, and livestock nutrition systems. These technologies will then have to be deployed affordably through context-relevant mobile communication and digital platforms to increase accessibility.

Key Words: livestock production, food supply, biotechnology

ADSA-SAD UNDERGRADUATE ORIGINAL RESEARCH POSTER COMPETITION

0787 (M001) Characterization of serotonin (5-HT) and glucose patterns and their hepatic receptor profiles during the transition period in dairy cows.

M. Olsen*, J. Laporta, A. P. Prichard, S. A. E. Moore, B. P. Schnell, S. R. Weaver, C. R. Cronick, and L. L. Hernandez, *University of Wisconsin–Madison, Madison.*

The liver is crucial for metabolism and partitioning of nutrients to the mammary gland during lactation. Recent evidence suggests that non-neuronal serotonin (5-HT) participates in glucose metabolism, but little is known regarding 5-HT actions in the liver during the transition period in dairy cattle. Our objective was to explore glucose and 5-HT circulating patterns and to characterize the 5-HT and glucose receptor profiles in the liver during the transition from pregnancy to lactation in dairy cows. Multiparous pregnant Holstein cows (n = 6, avg. lactation = 3.5) were utilized to collect daily blood samples from 7-d pre-calving (−7 d) through 7d post-calving (+7 d), and liver biopsies were performed at −7 d, +1 d and +7 d. Total RNA was extracted and cDNA was synthetized to measure mRNA expression of 5-HT receptors (HTR, isoforms 1A, 1B, 1D, 1F, 2A, 2B, 2C, 5A, and 7) and glucose transporters (SGLT-1, Glut-1, -2, −5, −8, −9, and 10) by RT-PCR. Glucose concentrations decreased pre-calving (−7 to -1 d, 72 vs. 57 ± 3.5 mg/dl, P = 0.045), increased post-calving (+1 and +3 d, 74 ± 4.1 mg/dl, P = 0.008), decreasing again and reaching lowest concentrations at +7 d (50.2 ± 1.7 mg/dl, P = 0.0012). Serum 5-HT concentrations decreased abruptly pre-calving (−7 to −5 d, 916 vs. 90 ± 35 ng/ml, P = 0.001), remained low until +3d (160 ± 35 ng/ml, average for -3, -1, and +1 d), and increased again at +5 and +7 d (355 ± 27, average for +5 and +7 d). Hepatic mRNA expression of HTR-1D, -2D, and −7 were decreased, while HTR-2A was increased at +1 d compared to −7 d (P < 0.045). Only HTR-1F increased 2.5-fold at +7 d, compared to both −7 and +1 d (P < 0.048). HTR-4 mRNA expression was undetectable at +7 d, and HTR-2C was undetectable at +1 d. HTR-5A was not expressed at all in the liver. Hepatic expression of Glut-2, Glut-5, and SGLT1 were decreased on both +1 d and +7 compared to −7 d, while Glut-1 was increased twofold at +7 d compared to −7 d (P < 0.04). These results indicate that 5-HT can potentially play a role in liver glucose homeostasis during the transition period in dairy cows, possibly through the modulation of specific receptors. Additional research is needed to further explore the functional role of these HTRs in the liver during the transition from pregnancy to lactation.

Key Words: 5-hydroxytryptamine, liver, lactation

0788 (M002) Inhibitory factors of casein synthesis In mammary tissue of lactating dairy cows.

R. L. Garnett*, A. Felock, W. K. Ray, R. F. Helm, S. I. Arriola Apelo, and M. D. Hanigan, *Virginia Polytechnic Institute and State University, Blacksburg.*

Excess nitrogen waste excreted from dairy cows causes numerous harmful effects on the environment, such as air and water pollution. Nitrogen efficiency can be improved by feeding low protein diets and supplementing with select essential AA (EAA), as is practiced in the swine industry. However, AA metabolism within dairy animals must be further understood to achieve this goal. The objective of this study was to determine α-S1 casein synthesis responses to the cell signaling inhibitors rapamycin and AICAR and high and low concentrations of essential AA in mammary tissue. Three lactating Holstein cows from the Virginia Tech herd were slaughtered at a processing facility on campus. Mammary tissue from an uninfected rear quarter was collected, and tissue slices (120 ± 30 mg) were prepared and incubated 4 h at 37°C in 5ml of treatment media enriched with [$^2H_5$] Phe. Experiment 1 examined the interaction of 3 concentrations of rapamycin and EAA in a 2 × 3 factorial design. Essential AA were included at either 5 or 100% of normal Dulbecco's Modified Eagle Medium (DMEM) concentrations. Rapamycin was added to the medium at 0, 0.5, or 10 μM. Experiment 2 consisted of a 2 × 3 factorial design with the EAA at 5 and 100% of DMEM and AICAR at 0, 0.4, and 4.0 mM. Experiment 3 tested the interaction between six nonessential AA and protein synthesis rates. Following incubation, samples were homogenized, and a 4.6 pH precipitate was isolated. [$^2H_5$] Phe enrichment of the 34-NLLRFFVAPFPE α-S1 casein peptide was determined in the precipitate via MALDI-TOF-TOF, and α-S1 casein fractional synthesis rate (CFSR) was determined. Experiment 1 revealed no effect of rapamycin, EAA, or their interaction on CFSR. AICAR tended to reduce CFSR. There was no effect of EAA on synthesis rate, nor any interaction between the two factors. These responses were consistent with the marginal changes in mTOR signaling changes caused by these drugs. Experiment 3 revealed no interaction between non-essential AA supply and CFSR. Further study is needed to determine other possible factors regulating CFSR beyond cell signaling and amino acid substrate supply.

Key Words: casein synthesis, rapamycin, AICAR

0789 (M003) Health of Holstein bull calves fed a fermentation extract of *Aspergillus oryzae*. R. M. Townsley*, T. T. Yohe, E. M. Dudash, Y. Roman Garcia, A. R. Gibson, K. M. O'Diam, and K. M. Daniels, *Dep. of Animal Sciences, Ohio State University, Wooster.*

The objective was to determine whether dietary inclusion of a fermentation extract of the fungus *Aspergillus oryzae*, commonly used as a direct fed microbial, would improve measures of health in Holstein bull calves (n = 52) from birth through 1wk post weaning. Calves were randomly assigned to a slaughter age, 4 wk (n = 16) or 8 wk (n = 36), and treatment, control (CON**;** n = 27), or direct fed microbial (DFM; n = 25). Calves averaged 43.2 ± 1.0 kg BW and 2.8 ± 0.3 d of age at the beginning of the experiment. Calves were housed and fed individually; no bedding was used. Calves assigned to DFM were fed 2 g of DFM daily. Liquid DFM was delivered in milk replacer for the first 4 wk of the trial; solid DFM was top-dressed on texturized grain thereafter. Calves were fed nonmedicated milk replacer twice daily (22.0% CP, 20.0% fat DM basis; 680 g/d) and were weaned on consumption of 0.91 kg of grain (20% CP, 2.0% fat; medicated with decoquinate) for 3 consecutive days or on d 45 of the study, whichever came first. Calves had ad libitum access to grain and water throughout the trial. Calf fecal scores were recorded daily, then averaged across treatment. On a weekly basis, DFM calves scoured more frequently than CON. All medical interventions (including oral electrolytes) were recorded. Treatment for respiratory ailments were more frequent in CON than DFM. Medical costs were calculated on a calf basis, then averaged by treatment. Medical costs for calves from 0 through 4 wk ($43.01 ± 2.40) and 5 through 8 wk ($11.18 ± 2.40) did not differ by treatment. For 8-wk calves, jejunal lymph nodes were collected on slaughter for flow cytometric analysis of CD4 and CD8 T cell populations as a measure of immune function. The CD4 cell population as a percentage of total observed cells was greater in DFM calves. Treatment did not affect CD8 cell population as a percentage of total observed cells. Flow cytometric results indicate that DFM may affect the adaptive immune system through effects mediated by CD4 positive cells. In conclusion, calves fed DFM scoured more frequently, but a lesser percentage of DFM calves were treated for respiratory ailments, leading to no effect on medical costs. Interestingly, CD4 cell population of jejunal lymph nodes was greater in DFM calves, which warrants further research.

Key Words: dairy calf, direct fed microbial, T cells

0790 (M004) Fecal score evaluation of pre-weaned dairy calves in group housing. M. Kittell*, J. Augustine, and S. I. Kehoe, *University of Wisconsin–River Falls, River Falls.*

Group housing for pre-weaned dairy calves has gained popularity among farmers because it reduces time and labor. Automatic calf feeders allow calves to receive increased milk intake multiple times a day. However, this increased milk consumption may cause an increase in fecal score, which is the common method for dairy calf managers to identify a sick calf. The purpose of this study was to evaluate whether increased fecal scores in group-housed calves were indicative of illness. A local calf raiser was used to evaluate a total of 61 calves from arrival at approximately 3 to 5 d of age through 3 wk of age. Once a week, a blood sample was analyzed for serum protein and hematocrit concentration to assess dehydration. A fecal sample was obtained and scored using a scale of 1 to 4 with 1 being solid and 4 being watery with little to no solids (Larson et al., 1977). Nasal and ocular discharge were recorded, and the skin tent test was performed. Rectal temperature was taken, and respiration, umbilical area, and overall attitude were evaluated. Weight data and medication records were obtained from the calf grower. Data was analyzed using a multiple logistic regression model in SAS 9.3 (2010). Variables were eliminated using backward stepwise regression to obtain a minimal model containing only significant variables ($P < 0.05$). All variables were eliminated from the model except nasal and ocular discharge and serum protein ($P < 0.001$). These results indicate that a higher fecal score is not a good diagnosing tool in group-housed calves receiving higher amounts of milk. Therefore, additional research is needed to distinguish effective methods for identifying sick calves in group housing with increased milk intake.

Key Words: calves, group housing, health

ANIMAL BEHAVIOR & WELL-BEING I

0791 (M005) Free range pork production system on savanna pasture in Brazil. *L. S. Murata*, F. L. da Silva, L. R. Roos, L. S. Fonseca, I. Fontana, C. A. da Silva Júnior, F. N. Gomes da Costa, C. G. D. Q. Roriz, L. H. N. Ribeiro, A. P. Santana, and S. L. S. Cabral Filho, University of Brasilia, Brazil.*

An alternative pork breeding system to traditional confined pork breeding has been implemented in the Midwest of Brazil on native savanna pasture mainly concerning welfare and product quality to small family farmers. A free-range pork production, separated by solar electric fences, was implemented in a 4.5-ha area on the University of Brasilia's farm in Brasilia, Federal District. The pregnancy and farrowing sectors are run in a cycle system, divided into 25 and 20 paddocks, respectively, both with a management central area. Native pasture is basically composed by *Trachypogon* spp., *Schyzachririum scoparium*, *Paspalum eriantum,* and *Echinolaena inflexa*. Monthly rotation grazing is used, providing a 4-mo pasture recovery period. The maximum density range in pregnancy and farrowing paddocks is 5 and 1 sows, and the available area/paddock is aproximately 1000 m^2 and 280 m^2, respectively. Boars paddocks are composed by eight individual paddocks with 200 m^2 separated by solar electrical and wire-framed fences. The nursering sector has four paddocks with 160 m^2 each and the growing sector has eight paddocks with 80 m^2. T gestation paddock has a collective metallic shelter covered with a straw and plastic roof as well as shade-providing shelters. The farrowing area has an individual shelter similar to the one used for gestation. It contains farrowing sow restraint bars, and females can make a nest with the available provided straw. There is also a shade-providing structure. The livestock is composed of 21 sows and 3 boars in a monthly pork production system, with five groups of females. Artificial insemination is used for reproduction, and the boar's ejaculate is processed at the farm. The semen is collected with the gloved-hand method weekly, and, when needed, later diluted with the commercial BTS diluent. Sows are inseminated three times each heat with 100 mL of diluted semen with $3x10^9$ sperm cells. Ten days before farrow, the pregnant sows are moved to the farrowing paddock. Weaning of piglets occurs after 30 d of lactation. The piglets are slaughtered weighing approximately 23 kg each.

Key Words: behavior, outdoor pork porduction, welfare

0792 (M006) Behavioral laterality, facial hair whorls, and heart rate variability in horses. C. B. Shivley*, T. Grandin, and M. Deesing, *Colorado State University, Fort Collins.*

The objective of this study was to test for an association between facial hair whorl characteristics and behavioral responses to a fear-inducing stimulus as well as heart rate variability in horses. This was a pilot study in which a small sample size was used. Nineteen well-trained riding horses (7 to 30 yr old) were categorized based on their facial hair whorl height (high, medium, or low), lateral location (right or left of midline), and rotation (clockwise or counterclockwise). Each horse was subjected to a novel object test where an umbrella was suddenly opened as a person approached the horse from the front. The turning response (right or left) was recorded. A Polar RS800CX heart rate monitor was used to continuously measure heart rate and heart rate variability. The standard deviation of the inter-beat interval (SDNN) was used for analysis of heart rate variability. Two horses had double facial hair whorls, and analysis was done both including them in the category of the dominant hair whorl and excluding them. Facial hair whorl rotation showed a correlation with turning response to the fear-inducing stimulus with $P = 0.04$ including the double hair whorls and $P = 0.11$ excluding the double hair whorls. Clockwise hair whorls were associated with turning to the right and counterclockwise hair whorls were associated with turning to the left. There were no significant correlations between facial hair whorl lateral location or height and direction turned ($P > 0.05$). All horses showed a decrease in the SDNN after the presentation of the fear-inducing stimulus ($P = 0.0024$). Horses with high facial hair whorls showed a tendency for a greater decrease in SDNN compared to horses with medium/low facial hair whorls ($P = 0.06$). There was no significant correlation between rotation of facial hair whorl or lateral location and heart rate variability ($P > 0.05$). In conclusion, facial hair whorls are associated with turning response and heart rate variability in horses. Facial hair whorls may be used as a noninvasive method to predict how a horse will respond when frightened and how stressful the event will be. Further studies are needed to develop this method for use by horse owners and trainers.

Key Words: facial hair whorls, behavioral laterality, heart rate variability

0793 (M007) Effects of rearing system and stocking density on growth performance, carcass quality, and welfare of male Arbor Acres broilers. W. Chang*, J. Tang, G. Liu, and H. Cai, *Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing, China.*

This trial was to investigate effects of rearing system and stocking density on growth performance, carcass quality, and welfare of broilers. A total of 936 1-d-old male Arbor Acres

Table 0793.

Items		0~21d				22~42d			
RS	SD	ADFI(g/d)	ADG(g/d)	FGR	BW(g)	ADFI(g/d)	ADG(g/d)	FGR	BW(g)
WFR	LSD	64.07 ± 1.32ab	44.79 ± 1.60b	1.43 ± 0.03b	947 ± 16.66^{b}	109.80 ± 1.93^{b}	67.43 ± 1.35^{b}	1.63 ± 0.01^{b}	2829 ± 22.51^{b}
	HSD	57.69 ± 1.86a	42.70 ± 1.22a	1.35 ± 0.04a	897 ± 14.67^{a}	120.90 ± 3.33^{c}	64.87 ± 1.64^{a}	1.87 ± 0.02^{c}	2721 ± 39.40^{a}
LFR	LSD	69.83 ± 1.52b	47.21 ± 1.51c	1.48 ± 0.03b	992 ± 18.71^{c}	103.20 ± 3.53^{a}	65.20 ± 1.75^{a}	1.58 ± 0.01^{a}	2802 ± 27.24^{ab}
	HSD	62.56 ± 1.94ab	46.13 ± 1.70bc	1.35 ± 0.03a	969 ± 13.50^{b}	119.20 ± 2.53^{c}	64.48 ± 1.38^{a}	1.85 ± 0.01^{c}	2779 ± 21.00^{ab}
Main effects									
SD	LSD	66.95 ± 1.78a	46.00 ± 1.37a	1.45 ± 0.05b	969 ± 12.20 ^{b}	106.50 ± 2.83^{a}	66.3 ± 1.50 ^{b}	1.61 ± 0.05^{a}	2815 ± 26.80^{a}
	HSD	60.13 ± 1.83b	44.42 ± 1.47b	1.35 ± 0.07a	932 ± 11.71 ^{a}	120.10 ± 3.13^{b}	64.67 ± 1.38 ^{a}	1.86 ± 0.07^{b}	2750 ± 22.13^{b}
RS	WFR	60.88 ± 1.73a	43.74 ± 1.51a	1.39 ± 0.04a	921 ± 12.16 ^{a}	115.30 ± 3.03^{b}	66.15 ± 1.52 ^{b}	1.75 ± 0.14^{b}	2775 ± 24.22
	LFR	66.20 ± 1.71b	46.67 ± 1.56b	1.42 ± 0.03b	980 ± 12.52 ^{b}	111.20 ± 3.22^{a}	64.83 ± 1.41 ^{a}	1.72 ± 0.15^{a}	2790 ± 21.55
P-value									
SD		< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	0.019	< 0.001	0.042
RS		< 0.001	0.005	0.147	< 0.001	0.007	0.045	0.002	0.574
SD*RS		0.543	0.260	0.254	0.082	0.066	0.136	0.050	0.160

broilers were randomly allocated to four treatments with six replicates by a 2 × 2 factorial design, including two rearing types (wire floor rearing and litter floor rearing) and two stocking densities (low stocking density of 8 birds/m^2 and high stocking density of 18 birds/m^2). The results showed that during 0~3 wk, high stocking density (HSD) significantly decreased average daily gain (ADG), average daily feed intake (ADFI), and feed/gain (F/G) of broilers than low stocking density(LSD); wire floor rearing (WFR) significantly improved ADG and ADFI than litter floor rearing(LFR). During 4~6 wk, LFR significantly decreased ADG ($P < 0.05$), ADFI ($P < 0.01$) and F/G ($P < 0.01$) of broilers than WFR; HSD lowered ADG ($P < 0.05$), increased ADFI and F/G ($P < 0.01$) than LSD. There was no obvious interaction on growth performance of broilers between stocking density (SD) and rearing system (RS) ($P > 0.05$). HSD significantly decreased eviscerated weight ($P < 0.01$), breast muscle ($P < 0.01$), and thigh muscle weights ($P < 0.05$) of broilers than LSD. There was interrelationship for meat yield between SD and RS ($P > 0.05$), with an exception of eviscerated weight and thigh muscle weight ($P < 0.05$). WFR and LSD groups had higher score of feather damage, pododermatitis, and hockburn; lower foot felt temperature (litter or net) and mortality; and higher uniformity than LFR and HSD groups, respectively. In conclusion, LSD-WFR was the most superior in growth performance, carcass quality and welfare of broilers; oppositely HSD-LFR was the most inferior.

Key Words: broiler, rearing system, stocking density

0794 (M008) Comparison of three acute stressors in horses. A. J. Bachman, A. Berzas, and C. E. Ferguson*, *McNeese State University, Lake Charles, LA.*

Stress in horses can be caused by any number of things: a new pasture mate, trailer ride, unexpected loud noise, or even strenuous exercise. The objective of this study was to test three stressors (air horn, firecracker, and exercise), to determine their effect on heart rate (HR) and time from elevated heart rate to return to baseline heart rate. A total of six horses were used in this study: three mares, two fillies, and one gelding. The horses were used in a crossover design over a 2-m period where each horse received each stressor every 7 d. The horses remained in a stall while the Pre-Stress HR was measured every 30 sec for 5 min to determine baseline. Once baseline was established, the horse was brought to a round pen and exposed to a specific stressor. The exercise stressor required the horse to trot or canter for 10 minutes: 5 min clockwise and 5 min counterclockwise. The air horn and firecracker stressors lasted between 5 and 10 sec during each exposure. Immediately following being exposed to the stressor, the Stressed HR was recorded every 30 sec for 90 sec. The horse was then returned to original stall, and the Post-Stress HR was recorded every 30 sec for 15 min. Statistical differences in treatments were determined using the Proc GLM in SAS. There were no differences between the mean Pre-Stress HR of each of the stressors. The mean Stressed HR for the air horn (89 ± 14) was significantly higher ($P < 0.06$) than firecracker (58 ± 5) but not different from exercise (72 ± 4). There was no significant difference among the stressors' Post-Stress HR means. At the immediate Stressed HR measure, the one with the greatest effect ($P < 0.03$) on HR was the air horn (109 ± 19) compared with exercise (77 ± 4) and the firecracker treatment (66 ± 5). At the second immediate Stressed HR measure (60 sec following end of stimulus) the HR was not different between the air horn (86 ± 14) and exercise (71 ± 4), but both were greater ($P < 0.07$) than firecracker (57 ± 5). There were no differences in the mean Post-stressed HR between treatments. These results indicated that the short-term use of an air horn will elevate a horse's HR greater than 10 min of exercise but only for a short duration. Also, the use of a firecracker to induce short-term stress is not effective.

Key Words: horse, stress, heart rate, air horn, stressors

0795 (M009) Effect of social housing on pre- and post-weaning intake and performance of dairy calves.

E. K. Miller-Cushon*[1], R. Bergeron[2], K. E. Leslie[3], G. J. Mason[3], and T. J. DeVries[1], *[1]University of Guelph, Kemptville, ON, Canada, [2]University of Guelph, Alfred, ON, Canada, [3]University of Guelph, ON, Canada.*

This study investigated how pre-weaning housing environment affects intake and performance of dairy calves during the milk-feeding stage and once group-housed after weaning. Twenty Holstein bull calves were housed either individually (IH; n = 10) or paired and housed in pens (PH; n = 5) from birth until 49 d of age. Calves were offered grain concentrate (23% CP) and milk replacer (26% CP, 16% fat, 150 g DM/L) ad libitum and weaned by incrementally diluting the milk replacer from 39 to 49 d of age. Post-weaning, IH calves were paired within treatment, and all calves were offered a complete pelleted diet (21% CP) ad libitum and followed until 84 d of age. Feed intake was recorded daily and calves were weighed 2x/wk. Data were summarized by week and analyzed in a repeated measures general liner mixed model. Intake of milk replacer was similar between treatments (9.84 L/calf/d, SE = 0.82, P = 0.9). Pre-weaning concentrate intake was subject to a treatment × wk interaction (P = 0.014), with PH calves increasing solid feed intake to a greater extent over time (in wk 5–6, 0.17 vs. 0.051 kg/d, SE = 0.031). During the 10 d of weaning, PH calves had greater concentrate intake than IH calves (0.69 vs. 0.30 kg, SE = 0.11, P = 0.039). Growth was similar between treatments before weaning (1.05 kg/d, SE = 0.10, P = 0.5), but PH calves had greater ADG during the 10 d of weaning (0.67 vs. 0.41 kg/d, SE = 0.07, P = 0.02). Once all calves were pair-housed after weaning, there was no effect of pre-weaning housing environment on intake (3.3 kg/d, SE = 0.15, P = 0.9) or ADG (1.21 kg/d, SE = 0.07, P = 0.2). These results indicate that social housing for dairy calves encourages solid feed intake during the milk-feeding stage, resulting in improved intake and weight gain during the weaning period.

Key Words: dairy calf, social housing, feed intake

0796 (M010) Associations of stall design, behavior, and hygiene of lactating dairy cows.

M. A. Overvest* and T. J. DeVries, *University of Guelph, Kemptville, ON, Canada.*

Free stall standing behavior is typically indexed to improve cow and stall hygiene using stall designs that are often restrictive to the cow. The objective of this observational study was to determine the association of stall design, cow hygiene, and lying behavior in lactating Holstein dairy cows (n = 23; parity = 3.0 ± 1.3; mean ± SD). Cows were part of a group of 40 ± 3 cows, housed in a free-stall barn with 52 free stalls (head-to-head), and designed for free cow traffic to an automated milking system. Each stall was 1.93 m long (from rear of curb to brisket board), 1.22 m wide, and the stationary neck rail was 1.26 m above the stall bedding surface (water mattress bedded with wood shavings), and 1.91 m from the rear curb. Cows were observed for four 2-wk periods. During periods 1 and 3, a swinging PVC neck guard (located 0.92 m from the base of the stall and 2.22 m from the curb) was installed in the free stalls. Cows were hygiene scored (flank, udder, and lower leg; scale of 1 = very clean to 4 = very dirty) on the last 7 d of each period. Stalls were hygiene scored using a grid system (# contaminated 0.15 × 0.15 m squares in a 1.20 × 1.60 m grid). Electronic data loggers were used monitor lying behavior. Data were analyzed in multivariable mixed-effect regression models. Lying duration tended (P = 0.1) to decrease when cows were kept with the neck guard (-0.6 h/d; SE = 0.4), and was decreased (P < 0.05) in primiparous cows (-1.2 h/d; SE = 0.5), with higher production (-0.07 × kg/d; SE = 0.03), and when stalls were dirtier (−9.4 × stall hygiene score; SE = 4.5). Flank hygiene was worse when cows were kept with the neck guard (P = 0.001), in multiparous cows (P = 0.04), when stalls were dirtier (P = 0.002), and tended to be worse when cows spend less time lying down (P = 0.1). Udder hygiene was worse in multiparous cows (P = 0.03), when cows spend less time lying down (P = 0.002), and tended to be worse when stalls were dirtier (P = 0.06). Lower leg hygiene was worse in multiparous cows (P = 0.006), when cows spend less time lying down (P = 0.04), and tended to be worse in earlier lactation cows (P = 0.07). In summary, these results show that cow lying duration may be negatively impacted when free-stall design imposes restrictions on usage and when stalls are dirty. Further, cow hygiene is affected by lying behavior patterns of cows and by the cleanliness of the cow's environment.

Key Words: hygiene, behavior, stall design

0797 (M011) Time budget and rumen development of dairy calves around the time of weaning.

M. A. Overvest*, E. K. Miller-Cushon, and T. J. DeVries, *University of Guelph, Kemptville, ON, Canada.*

The objective of this study was to develop tools to aid in the evaluation of the success of weaning programs for dairy calves, including physiological and behavioral measures and daily time budgets for calves at this stage of life. The study followed 10 ad libitum milk-fed Holstein calves for 24 d: pre-weaning (d 33 to 39 of age), during weaning (d 40 to 49 of age), and post-weaning (d 50 to 56 of age). During weaning, milk replacer was incrementally diluted on d 40, d 43, d 46, and d 49 by 25, 50, 75, and 100%, respectively. Calves were individually housed until weaning was complete (d 49), at which time each calf was paired. Feed intakes were recorded daily. Calves were weighed 2x/wk. Rumination time was observed by live 60-sec scans between 1200 and 1300 h on alternate days beginning on d 34 and ending on d 56. Blood β-hydroxybutyrate (BHBA) concentration was recorded daily, using a

calf-side test, on the same schedule. Electronic data loggers continuously recorded standing and lying behavior for the duration of the trial. A mixed effect regression model provided insight on changes from pre- to post-weaning. Starter DMI increased from pre-weaning to post-weaning (51.7 to 3984.5 g DM/calf/d, SE = 160.0; $P < 0.001$). BHBA increased from pre-weaning to post-weaning (0.003 to 0.133mmol/L, SE = 0.01; $P < 0.001$) as consumption of concentrate increased. Rumination time decreased from pre-weaning to post-weaning (7.9 vs. 2.9 min/h, SE = 1.4; $P < 0.043$). Standing time increased (5.95 to 8.03h/d; SE = 0.16), while both lying time (18.1 to 17.2 to 16.0h/d; SE = 0.16) and lying bouts (21.7 to 18.1 to 16.9 bouts/d; SE = 0.46) decreased from pre-weaning to weaning and again from weaning to post-weaning ($P < 0.001$). The results indicate that these physiological and behavioral measures accurately assess rumen capabilities, daily time budgets, and calf comfort around the time of weaning. Further, BHBA measurements show promise in indicating rumen development in dairy calves.

Key Words: dairy calf, weaning, time budget

0798 (M012) Use of peripartum period cud chewing and activity data for diagnosis of health disorders.

D. N. Liboreiro*[1], K. S. Machado[1], P. Basso Silva[2], M. M. Filho[1], G. Franco[1], A. E. Barreto[1], M. I. Endres[2], and R. C. Chebel[1], *[1]Dep. Veterinary Population Medicine, University of Minnesota, St Paul, [2]University of Minnesota, Saint Paul.*

Objectives of the current experiment were to develop strategies to use peripartum cud chewing and activity for diagnosis of peripartum disorders within 72 h after calving. Holstein animals (nulliparous = 77, parous = 219) were fitted with cud chewing/activity monitors from -17 to 17 d relative to calving. Blood sampled weekly from 0 to 20 d relative to calving were used for determination of β-hydroxybutyrate (BHB) concentration and incidence of ketosis (BHB > 1400 mmol/L). Blood sampled on d 0, 1, and 2 relative to calving were used for determination of total Ca concentration and incidence of sub-clinical hypocalcemia (Ca < 8.5 mg/dl). Cows were examined for retained placenta (RP) and metritis by study personnel. After analyzing cud chewing and activity data according to occurrence of peripartum diseases, cud chewing data from individual cows was used to diagnose disease using the receiver operator characteristics. Formulas involving cud chewing to diagnose disease are not disclosed because of intellectual property considerations. Prevalence of stillbirth, RP, sub-clinical hypocalcemia, metritis, and ketosis were 6.1%, 13.2%, 37.8%, 21.2%, and 7.6%, respectively. The criterion used for diagnosis of stillbirth resulted in sensitivity and specificity of 50 and 79.7%, respectively. There were no criteria that could be used for diagnosis of RP before the day of calving. Two criteria could be used for diagnosis of sub-clinical hypocalcemia on the day of calving. One of the criterion resulted in 66.7 and 61.3% sensitivity and specificity, respectively. The second criterion resulted in sensitivity and specificity of 82.7 and 49.6%, respectively. Metritis could be diagnosed 72 h after calving with a sensitivity and specificity of 75 and 93.1%, respectively. Among cows that were diagnosed with RP within 24 h after calving, the cud chewing criterion resulted in sensitivity and specificity of 70.8 and 75%, respectively. Cud chewing could not be used for diagnosis of ketosis. Activity data was not useful in the diagnosis of any of the health disorders evaluated in this experiment. We conclude that cud chewing data may be used for diagnosis of stillbirth, sub-clinical hypocalcemia, and metritis.

Key Words: transition cow, health disorder, diagnosis

0799 (M013) Effect of stall size, tie-rail position, and chain length on cow injuries and cleanliness in Eastern Canadian tie-stall farms.

V. Bouffard*[1,2], A. M. de Passille[3], J. Rushen[3], E. Vasseur[4], D. B. Haley[5], and D. Pellerin[1], *[1]Université Laval, Québec, QC, Canada, [2]Valacta, Ste-Anne-de-Bellevue, QC, Canada, [3]University of British Columbia, Agassiz, [4]University of Guelph–Campus d'Alfred, ON, Canada, [5]University of Guelph, ON, Canada.*

Lying stall configuration affects cow comfort. Lack of space for the cow may result from old facilities (stall size) and from efforts to keep the cow cleaner (tie-rail position). To evaluate effects of not following recommendations for stall configuration on cow comfort, 40 lactating Holstein cows from each of 100 tie-stall dairy farms (Quebec, $n = 60$; Ontario, $n = 40$) were measured (hip height and hook bone width) and evaluated for neck, knee, and hock injuries, and udder, flank, and leg cleanliness. Data collected about stall configuration included bed length, stall width, tie-rail height and position, tie-chain length, and manger wall height, and these were compared with Canadian recommendations. Data were analyzed using Proc GLIMMIX of SAS with a binomial distribution. Only 21.1% of cows had a tie-chain long enough to meet recommendations. A standard tie-rail forward position ($\geq$ 35 cm compared to the bed length) was observed for 16.8% of cows. Each 10-cm increase of stall width closer to the recommendation decreased odds of neck injury by 11.6% ($P = 0.008$) but increased odds of flank and leg dirtiness by 35.6% ($P = 0.0006$) and 16% ($P = 0.0006$), respectively. Each 10-cm increase in bed length tended to decrease odds of knee injuries by 10.4% ($P = 0.08$) but increased odds of udder dirtiness by 35.6% ($P = 0.02$). Increasing tie-rail height by 10-cm closer to the recommendation increased odds of neck injuries by 22% ($P = 0.008$). Each 10-cm move forward of the tie-rail decreased odds of neck and knee injuries by 41.8% ($P = < 0.0001$) and 17.2% ($P = 0.0001$), respectively, but increased by 20.2% ($P = 0.03$) odds of udder dirtiness. Each 10-cm lengthening of the tie-chain decreased odds of neck (8.3%, $P = 0.02$), knee (9.9%, $P = 0.002$), and hock (8.3%, $P = 0.003$) injuries. A higher than recommended manger wall was not

related to cow injuries ($P > 0.1$) but increased by 3.7% ($P = 0.02$) odds of udder dirtiness. Although recommendations for tie-rail height need further testing, these results suggest that, even if associated with decrease in cleanliness, simple modifications by dairy producers to stall configuration (forward tie-rail position and increased tie-chain length) to meet current recommendations would result in a decrease in neck, knee and hock injuries and increasing cow welfare.

Key Words: tie-stall, injuries, cleanliness

0800 (M014) Evaluation of cow cleanliness and fly avoidance behaviors among cows with docked, switch-trimmed, and switch-intact tails.

E. A. Morabito*, D. T. Nolan, and J. M. Bewley, *University of Kentucky, Lexington.*

Tail docking has become a contentious issue in the dairy industry because of concerns related to pain and inhibition of natural fly avoidance behaviors. The TailWell Power Tail Trimmer (Shoof International LTD, Cambridge, New Zealand) is a cordless drill attachment with circular blades to trim a cows' switch quickly and easily. The objective of this study was to evaluate cow cleanliness and fly avoidance behaviors between 64 cows trimmed with the Tailwell Power Tail Trimmer (T), 89 previously docked cows (D), and 53 cows with intact switches (S). Cow cleanliness was evaluated bi-weekly with separate scores recorded for the flank, leg, and udder using a scoring system ranging from light (L) to very heavy (VH). Individual teat scores were recorded using a scoring system ranging from 0 (no dirt) to 4 (filthy). Fly avoidance behaviors were monitored for 2 min/cow at each sampling. The PROC MIXED of SAS (SAS Institute Inc., Cary, NC) was used to evaluate the effects of tail status, scoring period, herd, and interactions on udder, flank, leg, and teat cleanliness. Stepwise backward elimination was used to remove nonsignificant interactions ($P \geq 0.05$). No significant differences were observed among tail status for flank, udder, or leg scores ($P \geq 0.05$); however, significant differences were observed for scoring period, herd, and the interaction of scoring period × herd ($P < 0.05$). Herd was a significant predictor of teat scores ($P \geq 0.05$), however tail status was not ($P \geq 0.05$). The GENMOD procedure of SAS was used to evaluate fly avoidance behaviors. Cows with docked tails were 2.01 and 2.21 times more likely to have a higher tail swing score than cows with switch-trimmed and intact-switch tails, respectively ($P < 0.01$). The lack of differences among cleanliness supports existing literature suggesting that docking tails does not improve cow hygiene. The observed increase in fly avoidance behavior among docked cows suggests behavioral deprivation for these cows. The Tailwell Power Trimmer provides a way to relieve dairy worker concerns related to intact switches without the perception aspects of tail docking.

Key Words: tail trimming, fly avoidance, cow hygiene

0801 (M015) Effect of reduced hair coat on performance of feedlot steers during summer heat stress.

A. K. Curtis*, B. Scharf, W. J. Sexten, and D. E. Spiers, *University of Missouri, Columbia.*

Heat stress in cattle reduces well-being and performance. The challenge is to develop effective procedures for heat stress mediation over the entire summer period. This necessitates the identification and development of reliable predictors of heat strain in the animal. A 94-d study, using crossbred Angus steers ($n = 36$; average body weight = 284 ± 29kg) was conducted during summer 2013. Animals were stratified by weight, housed in groups of nine among four different pens with ~ 50% shade coverage, and hair scored (1 to 4 scale; with higher values indicating a shorter coat). Hair coat was carefully removed using the standard "torched" procedure from half of the steers, with those remaining being unaltered (average hair score: 1.9). Ambient temperature (T_a) and relative humidity were recorded using Hobo H8 Pro data loggers (Onset Computer, Bourne MA) in sun and shade. Range of T_a was 12.2 to 36.6°C, and calculated temperature humidity index was 54.4 to 85.3. Steers were provided a corn-based feedlot diet and water ad libitum, and core temperature (T_{core}) measured hourly using intraruminal telemetric boluses (Smartstock, Pawnee, OK). Electronic ID tags (Allflex US Inc., Dallas-Fort Worth, TX) connected to a GrowSafe FI system (GrowSafe Systems Ltd., Airdrie, AB, Canada) provided feed intake (FI) data. Respiration rates (RR) were measured at 0800 and 1700 h on select days throughout the study, with measurement frequency increasing with heat events. Data analysis was conducted using ANOVA, (JMP Statistical Software; SAS Institute; Cary, NC) to determine the effect of a reduced hair coat on FI, feed efficiency (FI/ADG), RR, and T_{core}. Analysis revealed no effect of torching on daily FI ($P = 0.85$), but an increase in feed efficiency in non torched versus torched ($P < 0.01$). Analysis of mean daily T_{core} over the entire period by animal and hour of day showed a 0.21°C lower T_{core} value for torched versus non-torched animals ($P < 0.01$). Likewise, maximum daily T_{core} was 0.25°C lower in torched versus non-torched animals, with no difference ($P > 0.10$) in daily minimum T_{core}. Torching appeared to have no significant effect on average daily respiration rates ($P = 0.89$). These results indicate that reducing the hair coat of steers during summer months may offer a cosmetic benefit along a reduction in core temperature due to an increase in cutaneous heat loss. However, overall feed efficiency was slightly reduced as a result of this procedure. Additional studies are needed to determine the reason for this reduction.

Key Words: heat, stress, steers

ANIMAL BEHAVIOR & WELL-BEING II

0802 (W001) Relationship between hair cortisol concentration and previous performance and feeding behavior in holstein bulls fed high-concentrate diets. M. Verdu[*1], A. Bach[2], and M. Devant[3], *[1]IRTA–Dep.t Ruminant Production, Caldes Montbui-Barcelona, Spain, [2]Dep. of Ruminant Production, IRTA, Caldes de Montbui, Spain, [3]IRTA–Dep. of Ruminant Production, Caldes De Montbui, Spain.*

One main hormone produced during stress responses is cortisol. Hair can be used as matrix to measure cortisol levels in beef. Hair specimen could reflect average hormone levels over months and can be used to assess cortisol long-term variations. High cortisol concentrations stimulate breakdown of body tissues to release energy and protein to further support the stress response, and therefore it may impair animal growth. Thus, the hypothesis of the present study was that hair cortisol concentration should be negatively correlated with previous ADG, feed efficiency or feeding behavior parameters. Thirty-seven Holstein bulls (129 ± 2.9 kg BW and 110 ± 2.0 d age) housed in two pens were used to obtain hair samples (1 g) from the forehead by clipping. On d 7, hair was clipped to reflect the new cortisol incorporation in the following hair specimens, which were collected on d 120 and 216 of the study. The relationships between each previous performance and feeding behavior parameters and hair cortisol were evaluated by regression analyses using a fit model procedure of JMP with animal as random effect. Hair cortisol concentration was positively correlated ($P < 0.01$) with ADG ($r = 0.28$), feed efficiency ($r = 0.34$), and coeficient of variation of concentrate intake ($r = 0.36$), whereas hair cortisol concentration was negatively correlated ($P < 0.01$) with average concentrate intake ($r = -0.37$). Hair cortisol concentration tended ($P = 0.10$) to have a negative association with meal size ($r = -0.30$), number of visits ($r = -0.16$), and concentrate eating rate ($r = - 0.21$). In contrast to the hypothesis, the relationship between hair cortisol and ADG and feed efficiency was not negative. Incorporation of cortisol to the hair matrix assumes that blood-borne substances enter the hair through passive diffusion and subsequently become deposited in the hair shaft; however, other possible mechanisms of entry are proposed like the diffusion from sweat or sebum secretions. Probably, hair cortisol concentration needs to be greater to negatively impact ADG and feed efficiency. The negative relationship between meal size and eating rate and hair cortisol concentration may be related with its impact on digestive tract health. In conclusion, weak correlations were obtained between hair cortisol concentration with 3 mo previous data of performance and feeding behavior.

Key Words: bulls, hair cortisol, performance

0803 (W002) Competition in the milk-feeding stage affects post-weaning feeding behavior of pair-housed dairy calves. E. K. Miller-Cushon[*1], R. Bergeron[2], K. E. Leslie[3], G. J. Mason[3], and T. J. DeVries[1], *[1]University of Guelph, Kemptville, ON, Canada, [2]University of Guelph, Alfred, ON, Canada, [3]University of Guelph, ON, Canada.*

This study investigated the effect of competition during the milk-feeding stage on post-weaning feeding behavior and response to a competitive feeding challenge. Twenty Holstein bull calves were pair-housed and provided milk replacer (MR) and grain concentrate ad libitum via either: 1) one teat and feed bucket/pen (competitive feeding: CF) or 2) two teats and feed buckets/pen (non-competitive feeding: NCF). Calves were weaned during wk 7 of life by incrementally diluting the MR. Post-weaning, all pens were managed similarly and offered a complete pelleted diet ad libitum via two feed buckets/pen (non-competitive feeding) in Period 1 (wk 8 and 9) and Period 3 (wk 12 and 13) and one feed bucket/pen (competitive feeding) in Period 2 (wk 10 and 11). Post-weaning feeding times and competitive interactions were recorded 2 d/wk from video. Meal criteria were used to calculate daily meal frequency, meal time, and synchronized meal time (the percentage of meal time when calves within the pen were engaged in simultaneous meals). Data were summarized by week and analyzed in a repeated measures general liner mixed model. Post-weaning, calves raised in CF pens displaced one another more frequently (6.6 vs. 1.5 displacements/d, SE = 1.9, $P = 0.02$) and had fewer overlapping meals than calves raised in NCF pens (34.5 vs. 40.7% of meals, respectively). In Period 1 (non-competitive feeding), calves in previously CF pens had ($P = 0.03$) more frequent meals than calves in previously NCF pens (10.8 vs. 9.8 meals/d, respectively) and tended to have ($P = 0.09$) greater rates of intake (44.3 vs. 38.9 g/min). Likewise in Period 3 (2 buckets/pen), previously CF pens had ($P < 0.04$) more frequent meals (11.3 vs. 9.9 meals/d) and greater rates of intake (87.8 vs. 72.0 g/min). In Period 2 (competitive feeding with 1 bucket/pen), meal frequency and rate of intake were subject to treatment × week interactions ($P < 0.004$), increasing to a greater extent in previously NCF pens compared to previously CF pens. Feeding behavior across treatments was affected by the competitive feeding challenge in Period 2 ($P < 0.04$): feeding time decreased by 18%, meal synchrony decreased by 16%, and displacement frequency increased 1.7x. These results indicate that behavioral responses to pre-weaning competition, such as competitive displacements, degree of feeding synchrony, and rate of intake, may persist once developed.

Key Words: dairy calf, competition, feeding behavior

0804 (W003) Effect of exposure to individual ration components on feed sorting of dairy heifers.

E. K. Miller-Cushon*[1], J. P. Vogel[1,2], and T. J. DeVries[1], [1]*University of Guelph, Kemptville, ON, Canada,* [2]*Dalhousie University, Truro, NS, Canada.*

This study investigated the effect of exposing heifers to individual feed components on extent and pattern of feed sorting on transition to a novel ration. Twelve Holstein heifers (403.3 ± 17.3 d old, weighing 409.8 ± 11.3 kg), consuming a familiar mixed silage-based ration (FMR; 41% corn silage and 59% haylage) ad libitum, were transitioned to a novel total mixed ration (NTMR; 41.6% haylage, 36.5% corn silage, 14.6% high moisture corn, and 7.3% protein supplement, DM basis) according to one of two treatments: direct transition to NTMR (DIR) or exposure to NTMR components individually before receiving NTMR (COM). Heifers were tested in replicates of six and fed individually with automated feed bins. During adaptation (d 1 to 4), all heifers were offered FMR. During transition (d 5 to 12), DIR heifers received NTMR, whereas COM heifers received NTMR components offered separately, in amounts according to NTMR composition (target 15% orts). After transition, all heifers received NTMR (d 13 to 20). Feed intake and feeding time were determined daily. Fresh feed and individual orts were sampled every 2 d for particle size analysis and NDF content. The particle size separator consisted of three screens (18, 9, and 1.18 mm) and a bottom pan resulting in four fractions (long, medium, short, and fine). Sorting activity for each fraction was calculated as actual intake as a percentage of predicted intake. Data were summarized by period and treatment and analyzed in a general linear mixed model. There was no effect of treatment on intake (10.6 kg DM/d, SE = 0.58, $P = 0.46$) or feeding time (172.3 min/d, SE = 4.2, $P = 0.75$) across the study. After transition to NTMR, COM heifers sorted to a greater extent than DIR, sorting against long particles (95.4 vs. 98.9%, SE = 0.5, $P < 0.001$) and for short particles (101.7 vs. 100.6%, SE = 0.4, $P = 0.04$). Heifers fed COM also tended to sort for fine particles more (102.4 vs. 100.7%, SE = 1.0, $P = 0.09$). Differences in sorting resulted in COM heifers tending to have lower NDF intake, as a % of predicted intake (98.9 vs. 100.5%, SE = 0.6, $P = 0.07$). These results suggest that degree of feed sorting in heifers may be influenced by method of transition to a novel ration.

Key Words: dairy heifer, feed sorting, feed presentation

0805 (W004) Relationships of temperament, behavior, and growth of performance tested bulls.

S. A. Lockwood*, H. G. Kattesh, P. D. Krawczel, J. B. Wilkerson, J. D. Rhinehart, D. Kirkpatrick, and A. M. Saxton, *University of Tennessee, Knoxville, TN.*

Flighty cattle can be dangerous to personnel and may threaten the longevity of equipment. The aim of this study was to explore objective criteria for evaluating temperament in bulls while examining relationships between temperament, behavior, and performance. Consigned bulls arrived at the University of Tennessee Bull Testing Station on d -14 ($n = 65$) and were reared into six pens based on age and weight. Bulls (three pens, $n = 30$) were selected to receive dataloggers to measure activity which included: total time lying, total steps taken, number of lying bouts, and lying duration from d 3 to 27 and d 59 to 84 (± 3 d). Pen scores (1, docile to 5, very aggressive) were assigned based on bull reactivity to a human observer on d -1, 27, 55, and 83 (± 3 d). Weight and exit velocity (m/s) were measured along with the time it took the bull to leave the chute once the head gate opened on d 0, 28, 56, and 84 (± 3 d). The average of pen score and exit velocity were used to evaluate overall temperament ratings. A correlation analysis was performed in SAS on temperament, exit velocity, and pen score and their relationship with the behavioral patterns and performance data with moderate and strong correlations of interest ($r > 0.3$, $r < -0.3$). Temperament, exit velocity, time to exit chute, time to cover 1.83 m, and total lying time were repeatable over the testing period ($r = 0.353$ to 0.759, $P < 0.05$) while the order of bulls through the chute showed low repeatability ($r = 0.108$ to 0.307, $P = 0.014$ to 0.394). After d 28, heavier bulls were less active and on d 84, pen score had a negative moderate correlation with bull order through the chute. Based on these data, performance and pen score were better related to behavior than temperament and growth performance.

Key Words: bull, temperament, performance

Table 0805. Relevant correlations between behavior, performance, and temperament

		Day (± 3)	Correlation	*P*-value
Weight	Total Steps	0	0.521	0.003
Exit Velocity	Time to Exit Chute	28	-0.340	0.006
Pen Score	Exit Velocity	28	0.376	0.002
Pen Score	Total Steps	56	0.370	0.044
Weight	Total Lying Time	56	0.302	0.105
Weight	Total Steps	56	-0.438	0.016
Weight	Lying Duration	56	-0.431	0.017
Weight	# Lying Bouts	56	0.531	0.003
Pen Score	Order Through Chute	84	-0.328	0.008
Pen Score	Time to Cover 1.83m	84	-0.343	0.006
Pen Score	Exit Velocity	84	0.343	0.006
Weight	Total Steps	84	-0.330	0.075
Weight	Lying Duration	84	-0.379	0.039
Weight	# Lying Bouts	84	0.513	0.004

0806 (W005) The efficacy of bridging stimuli during acquisition of an operant task and the use of food-based positive reinforcement training on unwanted oral investigative behaviors in horses, *Equus caballus*. M. R. LaFollette*, K. A. Cloonan, and K. W. Walter, *Truman State University, Kirksville, MO.*

This study sought to determine the impact of food-based positive reinforcement training (PRT) on frequency and severity of unwanted oral investigative behaviors (UOIB) in horses. It also investigated the influence of various bridging stimuli (BS) on time and number of reinforcements to behavioral acquisition of an operant task. Eighteen horses were used in a randomized complete block design, where they were split into six blocks by age and assigned to one of three treatments at random. Treatments consisted of mechanically produced BS, human-produced BS, or no BS. A standardized training protocol was used to train each individual to touch a target. Lag time between BS and food delivery was minimal. Before and after training, all horses were evaluated for number and type of UOIB (nose, lips, or teeth on skin, clothes, or treat bag) at 10-sec intervals for 5 min. These UOIB were later given a numerical value based on type and summed to evaluate overall severity. These data were analyzed using PROC MIXED of SAS. Treatment did not influence time to behavioral acquisition (TBA) ($P = 0.7682$) or number of reinforcements ($P = 0.8881$). However, the youngest block had the shortest TBA ($P = 0.0599$) and received the most treats per minute ($P = 0.0207$). Before training, the youngest and oldest blocks tended to have fewer UOIB ($P = 0.0692$) and less overall severity ($P = 0.0653$) UOIB compared to the rest of the blocks. Analysis using a two-tailed *t* test showed that, after training, horses had an average of 4.4 fewer UOIB ($P = 0.0311$) as well as a reduction in overall severity of UOIB ($P = 0.0473$). Our data indicates that use of food-based PRT decreased number and overall UOIB, which suggest that proper delivery of food rewards can allow for successful task acquisition without causing UOIB. The lack of treatment influence on TBA could be due to minimal lag time between BS and presentation of the food reward. Future research evaluating if the presence of a BS with a lag time in food delivery influences TBA is recommended.

Key Words: operant conditioning, food rewards, clicker training

0807 (W006) Towards a better understanding of foraging behavior to boost the expression of conditioned preferences for low-quality foods. F. H. Catanese*[1], R. A. Distel[1], and J. J. Villalba[2], *[1]Universidad Nacional del Sur, Bahia Blanca, Argentina, [2]Utah State University–Agricultural Experiment Station, Logan.*

Our objective was to explore the impact of feeding experiences with a low-quality food (LQF) on sheep foraging behavior when the availability of a high-quality food (HQF) is variable. Twenty-four female 2-y-old Merino sheep were randomly split into two groups; one group consumed oat straw (OS, a LQF) for 20 min and immediately after a ration of soybean meal (CS+), whereas the other group consumed OS but the offer of the meal was delayed 5 h (CS-; i.e., control). After conditioning, pairs of sheep from the same treatment were arranged and their dietary preferences were evaluated (15-min tests) in a U-shaped corridor where they faced a choice at each end of the corridor of OS (ad libitum) and HQF (alfalfa pellets [AP, first trial] or corn grain [CG, second trial] in one of six levels of availability: 2, 4, 8, 12, 24, or 32 g/animal). Data from each level of HQF availability was analyzed separately using a mixed-effects model. During both trials OS intake was almost negligible at high levels of HQF and similar between groups (Table 0807). However, during high levels of restriction in HQF availability, OS intake increased abruptly (e.i., nonlinear relationship) and we observed greater intakes for sheep in CS+ than sheep in CS- (Table 0807). Increasing the quality of the HQF (AP to CG) reduced the likelihood of sheep accepting LQF at lower availabilities (e.g., 8 g of HQF; $P < 0.034$). To boost the benefits of a positive previous experience with LQF, restrictions should be placed on the accessibility and/or quality of the HQF (e.g., restricted foraging time, increased stock rate, etc.); otherwise, previous learning would remain silent or its effects over foraging behavior could be minimal.

Key Words: low-quality food, diet selection, sheep

Table 0807. Oat straw intake by pairs of sheep ($n = 6$) previously exposed to a preference conditioning protocol (CS+) or not (CS-) when tested in a U-shaped corridor with one of different levels of availability of a HQF

Type of HQF	Treatment	Availability of HQF, g					
		2	4	8	12	24	32
Alfalfa pellets	CS-	197.7	141.0	125.7	98.5	4.2	0.2
	CS+	278.2	279.5	239.7	78.6	44.7	4.0
SEM		32.9	23.9	36.6	74.1	20.7	1.7
P-value		0.045	< 0.001	0.027	0.849	0.166	0.104
Corn grain	CS-	267.3	168.7	42.5	30.3	15.3	4.0
	CS+	349.8	252.7	142.6	103.0	43.8	38.3
SEM		18.6	19.0	34.1	45.5	29.9	26.7
P-value		0.009	0.002	0.037	0.259	0.496	0.364

0808 (W007) Effects of bedding frequency on lying behavior of weaned calves. M. Terré*[1] and A. Bach[2], *[1]IRTA, Caldes de Montbui, Spain, [2]Dep. of Ruminant Production, IRTA, Caldes de Montbui, Spain.*

Twenty-eight Holstein male calves (BW: 79 ± 3.1 kg, age: 78 ± 2.5 d) were used to study whether lying behavior of weaned calves would be modified by bedding frequency. All animals were fed the same pellet concentrate and chopped straw, and they were bedded with sawdust, and kept in individual hutches. At the beginning of the study, 15-kg of sawdust were added to each hutch, and during the first 3 d of the study, 3 kg

of sawdust were added to each hutch (this was considered time 0 and used as covariate in the statistical analyis). Afterward, on Day 4, 6 kg of sawdust were added to all hutches, and thereafter half of the animals were bedded every other day (2B), and the other half every 4 d (4B) with 6 kg of sawdust. The study finished on Day 11 (3 d for the basal time plus 2 periods of 4 d each). Animals were weighed on d 1 and 11 of study, and concentrate intake was measured daily. Lying behavior was monitored by placing a data logger in the right hind leg to record movements at 1-min intervals, and bedding samples were obtained daily to determine the moisture content. Data were analyzed with a mixed-effects model with repeated measures considering lying time or concentrate intake of the basal time as a covariate, and calf and period as random effects. Linear correlations were determined between the moisture content of the bedding, lying time and concentrate intake. Moisture content of the bedding was greater ($P < 0.001$) the third and forth day of each experimental period in 4B than in 2B calves (50 vs. 31 ± 4.8% of moisture, respectively). However, neither lying time (1111 vs. 1105 ± 6.1 min for 2B and 4B, respectively) nor DM concentrate intake (2.72 vs. 2.76 ± 0.084 kg/d for 2B and 4B, respectively) or BW differed between both treatments. A slightly negative relationship was observed between moisture content of the bedding and lying time ($r = -0.23$, $P < 0.001$), and also a slightly negative correlation was found between lying time and DM concentrate intake ($r = -0.26$, $P < 0.001$). In conclusion, sawdust bedding at 50% moisture did not change lying behavior, DM concentrate intake, and performance of weaned calves in a short-period study.

Key Words: bedding, lying behavior, weaned calves

0809 (W008) Effect of oral meloxicam on indicators of pain following band castration in beef calves.

S. Marti[*1], M. J. Jelinski[2], L. C. Dorin[2], E. D. Janzen[3], M. E. Olson[4], B. J. Ralston[5], and K. S. Schwartzkopf-Genswein[1], *[1]Agriculture and Agri-Food Canada, Lethbridge, AB, [2]Veterinary Agri-Health Services, Airdrie, AB, Canada, [3]University of Calgary, AB, Canada, [4]Alberta Veterinary Laboratories, Calgary, Canada, [5]Alberta Agriculture and Rural Development, Calgary, Canada.*

The objective of this study was to evaluate if oral meloxicam could mitigate post-procedural indicators of pain associated with band castration in beef calves. One hundred intact Angus bull calves (BW 299 ± 3.3 kg) were randomly assigned to treatments according to a 2 × 2 factorial design assessing castration method (band castration (B) or sham castration (S)) and provision of a pain mitigating agent at the time of castration (1mg/kg of meloxicam oral suspension (15mg/ml) (M) or non-medicated (N) given an oral saline solution) to yield BM, BN, SM, SN treatments (25 calves/group). Behavioral and physiological indicators of pain were assessed over a 9-wk period post-castration. Animal BW (kg) was recorded weekly to calculate ADG and feed intake (kg/d; FI) daily for all animals over the experimental period. A subsample of 48 calves were randomly selected to obtain more detailed measurements on d 0 and weekly until the end of the study including salivary cortisol (ng/mL), blood cell count (CBC), and gait stride length (cm). In addition, 16 calves (4/treatment) were fitted with data loggers to monitor lying and standing duration (min/d) and number of steps (no./d) taken over a 4-d period post-castration. No differences ($P > 0.05$) were observed in lying and standing duration, stride length or number of steps between M and S calves from d 0 to 6. Similarly, M and S calves did not differ ($P > 0.05$) in BW, ADG, FI, or CBC values over the 63 d study. However, a castration × medication × day effect ($P = 0.03$) was observed for ADG with BM calves tending to have a higher ADG ($P = 0.07$) than BN calves on d 7. Salivary cortisol concentrations were greater ($P < 0.05$) in B than S calves from 60 to 120 min following castration but there was no difference ($P > 0.05$) between M and N calves. Overall, meloxicam administered orally at the time of band castration had little effect on indicators of pain post-castration. However, there was some evidence that ADG was improved in M calves on d 7. More study on the timing of drug administration is required to determine optimal circulating levels relative to the time of the procedure when it may have the greatest benefit.

Key Words: pain mitigation, band castration, meloxicam, beef calves

---

0810 (W009) Behavior of pigs infected with *Salmonella* and fed diets containing a probiotic or a physiological promoter.

V. F. Buttow Roll[1], E. Barba-Vidal[*2], L. Castillejos[3], X. Manteca[2], and S. Martín-Orúe[2], *[1]Dep. of Animal Science, Faculty of Agronomy Eliseu Maciel, Federal University of Pelotas, Brazil, [2]Animal Nutrition and Welfare Service Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [3]Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain.*

This trial evaluated the effects of a *Bacillus licheniformis* (10^9 CFU/kg of feed; PROPORC; NOREL S.A.) and a physiological promoter based on sodium butyrate (3 kg/t feed; GUSTOR BP70; NOREL S.A.) on the behavior of pigs challenged with *Salmonella* Typhimurium. A total of 72 piglets, weaned at 28 d, were housed in 24 pens and fed three diets: 1) Control diet (CTR), 2) CTR + probiotic (PRO), and 3) CTR + physiological promoter (PHP). After a 1-wk adaptation period, pigs were orally challenged with 10^8 CFU of *Salmonella* Thyphimurium. Behaviors were recorded in the morning and afternoon (0830 to 1030 and 1400 to 1600) for 5 d beginning 2 d before of the challenge (day -2 and -1) and 3 d after the challenge day (Day 2, 3, and 4 post infection, PI). Use of the space (feeder, light, drinker areas), active behaviors (exploration, feeding, drink-

ing, walking, and others) and inactive behaviors (lying ventrally or laterally, and in contact or not with a pen mate) were registered. A repeated measures procedure was used for statistical analysis. No effect of PHP was found. Effects of PRO were observed mostly during the morning. Active behaviors as well as inactive behaviors were higher and lower in pigs fed PRO ($P < 0.008$ and $P < 0.001$, respectively) compared with the other groups. These animals spent less time lying in contact with pen mates ($P = 0.012$), while total time exploring the pen, feeding and other active behaviors, were higher ($P = 0.05$, $P = 0.003$ and $P = 0.03$, respectively). In contrast, the total time lying laterally and ventrally with contact was significantly lower on pigs fed PRO ($P < 0.001$ and $P = 0.008$ compared to CTR and PHP, respectively). Pigs fed the PRO used more the feeding area ($P = 0.02$) and less the lying area ($P < 0.001$). In the afternoon pigs were more active before the challenge than on Day 4 PI ($P < 0.001$). Before inoculation there were significantly fewer pigs lying ventrally in comparison with the d 2 and 4 PI ($P = 0.01$). Positive contacts, exploration, and feeding behaviors were also less frequent on Day 4 PI in comparison with the day before challenge ($P < 0.05$). The use of feeder area decreased ($P = 0.001$) after the challenge. In conclusion the PRO has a positive effect on some behavioral measures, mainly those related to the exploring the pen, feeding and other active behaviors in the morning.

Key Words: probiotics, *Salmonella,* sodium butyrate

0811 (W010) Integrating animal science and human medicine: development of a novel porcine model for calcium oxalate stone formation. B. P. Trojan*[1], S. J. Trojan[2], A. Navetta[1], S. Filleur[1], and T. Nelius[1], *[1]Texas Tech University Health Sciences Center, Lubbock, [2]Texas Tech University, Dep. of Animal and Food Sciences, Lubbock.*

Increased collaboration between animal science Dep.s and medical schools has been highly encouraged in recent years to enhance research funding competiveness. Development of animal models for investigating human health problems has been pivotal for the discovery of treatments for many life-threatening human illnesses. A team of researchers from the Dep. of Animal and Food Sciences at Texas Tech University and the Texas Tech University Health Sciences Center collaborated to develop a porcine model for use in the study and treatment of human calcium oxalate stone formation. Porcine were chosen as the model as they are the most congruent mammal to humans, both anatomically and physiologically, for the study of kidney stone disease. Male, Large White-Chester crossbred pigs ($n = 16$; 19 kg initial BW) were assigned to one of the following seven treatments: 1) 0.8% ethylene glycol administered in drinking water (EG) and 2 µg/kg BW vitamin D dissolved in syrup (Vit. D); 2) EG + 100 mg/kg BW ammonium chloride dissolved in syrup (AC); 3) EG + 5 mg/kg BW gentamicin intramuscularly 3x/wk (GENT); 4) EG + 0.5 mg/kg BW Lasix dissolved in syrup; 5) EG + Vit. D + AC; 6) EG + Vit. D + GENT; and 7) control. Treatments were administered for 28 d; blood was collected and renal panels were obtained on d 0, 14, and 28. Urine was collected on d 0, 14, and 28 and analyzed for pH, Ca, citrate, oxalate, creatinine and P. Renal and bladder ultrasound was conducted intermittently throughout the 28-d period. Animals were euthanized at the end of the study for collection of renal tissue for gross and microscopic analysis of crystal stone formation and inflammation. No crystal deposition was observed in control animals; however, all other treatments developed calcium oxalate stones, confirmed by histopathological analysis of hematoxyin and eosin staining, fluorescent microscopy and stone analysis by infrared spectrum. All treatment combinations examined in this study successfully induced stone formation in pigs. Of the treatment combinations, EG + Vit. D provided the most straightforward model for inducing kidney stone formation and is one that can be employed to study kidney stone disease and mitigation in humans.

Key Words: animal model, animal science, human medicine

0812 (W011) Effects of group size and social rank on welfare and performance of gestating sows in a group-housing system with floor feeding. Y. Li* and L. Wang, *University of Minnesota, West Central Research and Outreach Center, Morris.*

This study was conducted to investigate the interactive effect of group size and social rank on welfare and performance of gestating sows group-housed in pens with floor feeding. Pregnant sows ($n = 152$, parity 1 to 6) were allocated to four large pens (26 sows/pen) and eight small pens (six sows/pen) at 35 d after mating. Both large and small pens provided the same floor space allowance (1.5 m^2/sow). Aggressive interactions among sows during the initial 2 h and during the first meal after mixing were recorded. Rank indices were calculated for each sow based on outcomes of fights, and sows were categorized as high, middle, and low ranking within each pen. Sows were scored for skin lesions at 24 h and 5 wks after mixing. Salivary samples for cortisol analysis were collected from high ranking and low ranking sows during the same periods as assessment of skin lesions. Body weights before mixing, before the subsequent farrowing, and at weaning, litter size and weight at birth and weaning were registered for each sow. Data were analyzed using the PROC MIXED and Glimmix of SAS. There was no interaction of group size and social rank for any variable. Low ranking sows fought less frequently (9.3 vs. 20.7 fights/sow/2h, SE = 3.17; $P < 0.001$) than high ranking sows at mixing, but had similar skin lesions ($P > 0.10$) at 24 h after mixing as high-ranking sows. Low ranking sows sustained more skin lesions ($P = 0.01$) than high-ranking sows at 5 wks after mixing. Low ranking sows and high ranking sows entered gestation pens with similar body weights, but low ranking sows gained less weight (33 vs. 50 kg, SE =

5.6; $P < 0.001$), and had lower weights (250 vs. 268 kg, SE = 5.9; $P < 0.001$) before farrowing than high-ranking sows. There was no difference in cortisol concentration between high- and low-ranking sows. Group size did not affect the number of fights per sow involved, but sows in large pens had more skin lesions ($P < 0.001$) at 24 h and at 5 wks ($P < 0.001$) after mixing than sows in small pens. Neither social rank of the sow nor group size affected litter size or litter weight at birth or at weaning. These results suggest that low ranking sows had poor welfare than high ranking sows in pens with the floor feeding system, as indicated by reduced weight gain and increased skin lesions.

Key Words: group size, social rank, sows

0813 (W012) Grazing and feedlot performance and carcass quality measurements of beef cattle surgically castrated at different stages of maturity with or without analgesia. E. A. Backes*[1], A. C. Brown[1], E. B. Kegley[1], J. T. Richeson[2], H. D. Hughes[2], M. L. Thomas[1], K. Anschutz[1], and J. G. Powell[1], *[1]Dep. of Animal Science, University of Arkansas Division of Agriculture, Fayetteville, [2]Dep. of Agricultural Sciences, West Texas A&M University, Canyon.*

Castration is a common and justifiable management practice used by beef cattle producers; however, it may expose calves to both stress and pain, which may negatively affect animal performance. The objective was to determine the effects of surgical castration at birth or weaning with or without oral analgesic ongrowth performance and carcass quality. This abstract summarizes grazing and feedlot performance, and carcass measurement. Bull calves ($n = 60$) from the University of Arkansas cow/calf unit were allocated randomly near birth to one of four castration methods, consisting of surgical castration near birth or at weaning with or without oral administration of meloicam (1 mg/kg BW). After a 56-d weaning period, calves were transported to West Texas A&M University (WTAMU) for the grazing and feedlot phases. Body weight was determined on arrival and at the end of the grazing phase (start of feedlot phase) and end of the feedlot phase. Calves were allocated to a heavy and low weight group within each treatment on arrival of the feedlot phase. During the 110-d grazing phase, steers were grazed a single group and had access to sorghum × sudan and native pastures consisting of buffalograss (*Buchloedactyloides*) and bluegrama grass (*Boutelouagracilis)*. Throughout the finishing period steers were fed a common feedlot ration. When steers were determined to have reached a suitable degree of finish (1.27 cm backfat), they were harvested at a commercial plant and carcass data were recorded by personnel from the WTAMU Beef Carcass Research Center. Performance and carcass measurements were analyzed using PROC MIXED of SAS, and quality grades were analyzed using Chi-square. Starting (270, 273, 276, and 270 kg, respectively) and ending BW (381, 378, 383, and 374 kg, respectively), ADG, and total gain during the grazing phase did not differ ($P \geq 0.42$) across the four castration treatments. Ending BW (619, 624, 630, and 618 kg, respectively), ADG, total gain during the feedlot phase, and d on feed did not differ ($P \geq 0.50$) between treatments. Carcass weight, fat thickness, color, ribeye area, internal fat, preliminary yield grade, yield grade, and quality grade did not differ ($P \geq 0.17$) across treatments. Therefore, surgical castration performed at either birth or weaning with or without oral analgesia did not affect calf performance during the grazing and feedlot phases and did not affect carcass quality measurements.

Key Words: castration timing, performance, carcass quality

0814 (W013) Evaluation of a disposition scoring system in pen-raised white-tailed deer. K. J. Stutts*, J. L. Lucia, M. J. Anderson, M. M. Beverly, and S. F. Kelley, *Sam Houston State University, Huntsville, TX.*

Pen-raised white-tailed does ($n = 63$) ranging in age from 1.5 yr to 6.5 yr were utilized to evaluate the accuracy of a subjective disposition scoring system for deer by assessing the physiological response to restraint through measurement of serum cortisol concentration. Does were administered annual vaccinations and dewormer while restrained in a drop-floor chute designed for whitetail deer. Following processing and before being released from the chute, blood samples were obtained via jugular venipuncture and serum was harvested to determine cortisol concentration by RIA analysis. Disposition scores ranging from 1 to 5 (1 = docile and 5 = aggressive) were also assigned by independent observers to evaluate deer behavior while restrained in the chute. Pearson correlation coefficients were used to determine the relationship between cortisol concentration and disposition scores, and a one-way ANOVA was utilized to determine if differences existed among mean cortisol concentration for each of the disposition scores. A moderately positive relationship ($r = 0.30$, $P < 0.02$) existed between disposition score and serum cortisol concentration; however, there was no difference in mean cortisol concentration for does receiving a score of 1, 2, 3, or 4 (56.0, 69.7, 69.3, and 54.0 ng/mL, respectively). Does that received a disposition score of 5, indicating the most aggressive behavior while restrained in the chute, had a greater ($P < 0.01$) mean serum cortisol concentration (118.8 ± 13.1 ng/mL) when compared to does receiving a lower numerical disposition score. These results indicate that the disposition scoring system accurately identified does undergoing the greatest physiological stress while restrained in a working chute, but the scoring system requires modification to accurately assess lower levels of stress associated with scores 1 through 4 of the system.

Key Words: deer, stress, disposition

0815 (W014) Objective movement of calf-fed Holstein steers fed in confinement. J. A. Reed[*1], N. May[1], T. McEvers[1], L. A. Walters[1], J. P. Hutcheson[2], and T. E. Lawrence[3], *[1]West Texas A&M University, Canyon, [2]Merck Animal Health, Summit, NJ, [3]West Texas A&M University, Canyon.*

The objective of this study was to determine the impact of zilpaterol hydrochloride (ZH) on movement behavior of calf-fed Holstein steers fed in confinement. The experimental design was a randomized complete block, with a 2 × 11 factorial treatment arrangement of ZH supplementation 0 or 20 d by 11 slaughter dates (254, 282, 310, 338, 366, 394, 422, 450, 478, 506, and 534 d on feed). Steers were fed in 28-d periods; d 1 to 4 included no ZH supplementation, d 5 to 24 included ZH (8.33 mg/kg dietary DM) supplementation, and d 25 to 28 allowed for withdrawal. Animal movement was monitored during each 28 d using IceQube pedometers (IceRobotics, Edinburgh, Scotland, UK), which recorded standing time (mm:ss), lying time (mm:ss), number of steps taken, and number of lying bouts continuously during the 28-d study period. Data collection began at 1200 h on d 1 to remove variation from movement caused by processing the animals at approximately 700 h; data collection ended on d 28 at 2400 h. Data were analyzed as repeated measures using a compound symmetry covariance structure via the GLIMMIX procedure of SAS. Treatment means were generated using the LSMEANS option and separated when significant with the PDIFF option that was adjusted with the Bonferroni correction to reduce the probability of a type-I error $\alpha = 0.05$. Treatment x days on feed interactions occurred ($P < 0.01$) for each outcome variable; they were likely the cause of small sample size per slaughter group and are not likely to be biologically repeatable. No difference ($P > 0.05$) was observed between ZH supplementation treatment groups in the quantity of minutes spent standing (0 d ZH = 565; 20 d ZH = 557), minutes spent lying (0 d ZH = 875; 20 d ZH = 883), or number of steps taken per 24-h day (0 d ZH = 1602; 20 d ZH = 1637). However, the number of lying bouts was different ($P < 0.01$) between treatment groups; cattle supplemented ZH exhibited 10.7 lying bouts, whereas those not supplemented ZH had 11.9 bouts. These results indicate similar objective movement between calf-fed Holstein steers supplemented ZH for 0 or 20 d.

Key Words: zilpaterol hydrochloride, movement, pedometers.

0816 (W015) A competitive and unpredictable feeding environment disrupts feeding and social behavior of pre-partum dairy cows. K. Proudfoot[*1], D. Weary[2], and N. von Keyserlingk[2], *[1]Ohio State University, Columbus, [2]University of British Columbia, Vancouver, Canada.*

Management during the pre-calving period can alter the behavior of dairy cows. The objective was to determine the effect of a competitive and unpredictable feeding environment on feeding and social behavior of pre-partum dairy cows. Sixty-four animals were randomly assigned to treatment ($n = 4$ animals × 8 groups) or control groups ($n = 4$ animals × 8 groups). Each group consisted of three multiparous cows and one primiparous heifer. During a 1-wk baseline period (5 wk before calving) all groups had free access to four Insentec feed bins. From 4 wk before calving until calving, control cows were given ad libitum access to six feed bins. For treatment groups, four non-experimental cows were added to the pen. After 2 wk, treatment groups were moved into a pen with four new cows. Throughout the treatment period morning feeding times were delayed at random 0, 1, or 2 h on alternate days. Cows were excluded if they calved with twins, aborted or calved > 2 wk early. Feeding behavior (intake, feeding time, rate of intake, visits to the feed bins, and intake per visit) and social behavior (total, initiated and received replacements at the feed bins) were collected electronically. Group was considered the experimental unit. Data were analyzed using a mixed model in SAS, including baseline data and parity as covariates, week as a repeated measure (wk 3, 2, and 1 before calving) treatment as the main effect, a week*treatment interaction and group as a random effect. Treatment did not affect feed intake, but decreased time spent feeding (3.9 vs. 4.2 ± 0.1 h/d; $P = 0.003$) and increased feeding rate (82 vs. 63 ± 2 g/min; $P < 0.001$). Treatment groups visited the feeder less often compared to controls (47 vs. 87 ± 3 visits/d; $P < 0.001$), and consumed more feed during each visit (0.39 vs. 0.19 ± 0.01 kgDM/visit; $P < 0.001$). Treatment groups were involved in more competitive replacements at the feeder (30 vs. 22 ± 1 no./d; $P < 0.001$), both initiated (15 vs. 10 ± 1 no./d; $P < 0.001$) and received (15 vs. 12 ± 1 no./d; $P < 0.001$) compared to control cows. In summary, a competitive and unpredictable feeding environment disrupts feeding and social behavior of dairy cows; these effects may be especially problematic for pre-partum cows that are particularly susceptible to disease.

Key Words: close-up, stress, parturition

0817 (W016) Effects of within dyad weight variation on competition, feed intake, and milk production of dairy cows sharing feeding gates. J. R. R. Dórea*[1], A. L. Stanton[2], C. M. Stoffel[2], and L. E. Armentano[2], [1]*University of São Paulo, Piracicaba, Brazil,* [2]*University of Wisconsin–Madison, Madison.*

The goal of this study was to identify the effect of weight variation in cow pairs on animal performance and ingestive behavior under competitive conditions. Twenty-four primiparous and 36 multiparous lactating cows were paired (within parity) to form 30 experimental units (feeding gates). Pairs were fed six diets in five 6 × 6 balanced Latin squares with 21-d periods, using data from the last 5 d. Each pair had access to one gate that allowed one animal to eat at a time, and cows that filched feeds in other gates were excluded during the statistical analysis. Each dyad was categorized based on the difference in weight within dyad. Differences above average (60 kg) were categorized as High. Below average differences in size were categorized as Low. Within cow pair, individual animals were classified by size as either the larger animal in the pair (Large) or the smaller animal in the pair (Small). The effect of size (large/small) and difference (high/low) were tested. For High and Low difference pairs the number of displacement (gate exchange < 1 min) per wk were 55.79 and 90.38 per wk, respectively ($P < 0.05$). An interaction between size and difference was significant for dry matter intake, feeding rate, displacements and milk yield, ($P < 0.05$). In High differences, small cows had greater DMI (% BW) compared to large cows ($P < 0.05$). In Low difference pairs, size did not impact DMI. Milk yield was 4.4 ± 1.1 kg/d lower for Small cows compared to Large cows ($P < 0.05$). For High difference pairs, size was not associated with milk yield ($P > 0.05$). These results suggest that in highly competitive situations, cows close in size have more aggression, poorer welfare, and milk production than animals with a greater difference in weight. This has implications for identifying animals with poor welfare in competitive environments.

Key Words: animal behavior, competition, performance

0818 (W017) Impact of feeding and housing strategy on calf performance and behavior. *S.* H. Ward*, K. Parker, and K. Hart, *Mississippi State University, Starkville.*

Forty-eight Holstein calves were fed either two or three times per day and housed either individually or in pairs (2XI, 2XP, 3XI and 3XP). Calves were randomly assigned to treatments at birth and remained on their treatment until 8 wk of age. At 8 wk of age, calves were moved to a grouped pen and body measures were taken until 10 wk of age. For calves that were on 2XP or 3XP, pairing occurred on d 3 ± 2 d. All calves were fed 3.8L of colostrum within 24 h of birth and then fed whole milk. Calf starter (Startena, Purina Mills, 22% CP) was offered from d 3 and increased by 0.45 kg when less than 0.45 kg was left. DMI and respiration and fecal scores were collected daily. Body weight (BW), hip and wither height, heart girth, and hip width were collected weekly. Play behavior, time spent lying, standing, eating, and drinking were also measured at wk 3, 5, and 7. At wk 8, latency to feed was observed when calves were released into groups. Data were analyzed using the PROC MIXED of SAS (Cary, NC). Separation of means was evaluated with the PDIFF procedure of SAS based on Fisher's F-protected least significant difference test. Significance was declared at $P < 0.05$. There was no effect of treatment on BW or measures or ADG. However, in weeks 6, 9, and 10 calves on 3XP had greater ADG than calves on 2XP (1.15, 1.49, 1.38 vs. 0.72, 0.84, 0.47 kg/d, respectively; $P < 0.05$) and 3XI (1.15, 1.49, 1.38 vs. 0.87, 0.79, 1.19 kg/d, respectively; $P < 0.05$). In wk 6 and 10, 3XP calves had greater ADG than 2XI calves (1.15kg, 1.38kg vs.89kg, 1.06kg respectively). There was no effect of feeding frequency on starter intake, however, calves housed in pairs tended to consume more starter than those housed individually (0.79 kg DM/d vs. 0.84 kg DM/d; $P < 0.07$). Analysis of behavior data indicates no impact of housing type on latency to feed, however, calves fed 3x/day consumed feed within 23.5 min and calves fed 2x/day consumed feed within 37.5 min. Currently, this data demonstrates that, while nutrient values were not different between treatments, both feeding frequency and housing type can impact calf growth and tended to impact intake and latency to feed.

Key Words: dairy calves, housing, feeding behavior

0819 (W018) Communicating farm animal welfare science: Wisconsin dairy producers' attitudes toward and interest in cow welfare. C. Skasa[1], S. Turner[2], and A. L. Stanton*[3], [1]*University of Wisconsin–Eau Claire, Eau Claire,* [2]*University of Wisconsin–Eau Claire, Eau Claire,* [3]*University of Wisconsin-Madison, Madison.*

Farm animal welfare research is gaining momentum in the United States, but few focused assessments of U.S. producer opinions and knowledge about welfare-friendly management practices exist in the literature. By soliciting producer opinions, gaps in producer knowledge and possible strategies to disseminate research-based best practices can be identified. This study of Wisconsin (WI) dairy producers targeted the following: producers' opinions about farm animal welfare and controversial on-farm management practices; their familiarity with farm animal welfare initiatives; and their interest in learning about dairy cattle welfare, including how they currently obtain that information. Surveys were mailed to a computer-generated random sample ($n = 1000$) of WI dairy producers with a response rate of 48.1%. Question topics included impact of management practices on cattle welfare, cattle's ability to experience affective states, familiarity with farm animal welfare initiatives, and accessibility of information about cattle

welfare. Associations between responses and farm size, age, education, and housing type were evaluated with chi-squares test in SAS. Results indicated that farm type, farm size, producer age, and producer education level impacted survey responses. Notably, tie stall farms, smaller farms (1 to 50 head), and producers who identified as university graduates were more likely to disagree with the statement that tail docking is necessary to maintain cow cleanliness ($P < 0.01$). Free stall farms were more likely to agree that milk production is the best indicator of a cow's welfare ($P = 0.05$), as were producers aged 65 and older ($P = 0.02$). Overall, farms that had both free stall and tie stall housing were most familiar with animal welfare initiatives, including extension-sponsored conferences ($P = 0.03$), a university-sponsored welfare-friendly cattle housing guide ($P = 0.01$), and the National Dairy FARM Program ($P < 0.01$). Study results could be used to target welfare education, such as benchmarking information on critical on-farm welfare issues, based on producers' current knowledge and preferred mode of information delivery.

Key Words: welfare, dairy, opinions

0820 (W019) Effect of transportation stress on cytokine gene expression, hematic biometry and blood chemistry in heifers. B. Avila*, J. Kawas, D. Zamora, and H. Fimbres, *Universidad Autónoma de Nuevo León, Escobedo, México.*

Transportation is probably the most stressful event cattle can experience affecting health, performance, meat quality and causing considerable economic losses. The objective of this study was to determine the effect of long-term transport stress on blood chemistry, hematological, and cytokine gene expression measurements. Blood samples from 16 *Bos taurus* x *Bos indicus* heifers from a feedlot located in northeastern México, were obtained by coccygeal venipuncture. Heifers weighed an average of 300 kg. Samples were obtained from eight heifers newly arrived from a 40-h road trip (0 DPA) as they were unloaded and restrained in a hydraulic chute to receive routine weighing and physical check-up, and the other eight heifers were in their 25th day post-arrival (25 DPA). Cytokine gene expression, hematic biometry, and blood chemistry were analyzed. For gene expression, blood samples were stabilized for RNA extraction, and RNA yielded was quantified and standardized. Specific primers were used for the amplification of cytokines TNF-α, IFN-γ, IL-2 and glyceraldehyde 3-phosphate dehydrogenase (GAPDH), the latter used as an internal control gene. Amplified products were analyzed by electrophoresis and quantitative values were calculated for each band using the myImageAnalysis software from Thermo Scientific. Blood chemistry results showed higher concentrations of albumin ($P = 0.013$), amylase ($P = 0.027$), alanine aminotransferase ($P = 0.003$), bilirubin ($P = 0.001$), and cholesterol ($P = 0.013$) in the 0 DPA group. Hematocrit ($P = 0.022$) and hemoglobin ($P = 0.001$) values were lower in heifers at 25 DPA. Cortisol concentration was higher ($P = 0.001$) in the 0 DPA group. On the quantitative gene expression analysis, we observed that the expression of TNF-α was greater ($P = 0.001$) in the 25 DPA group. At the TNF-α amplification two un-specific bands were found, only in the animals of the 0 DPA group. These bands were sequenced, and BLAST analysis suggests that they correspond to bovine lymphotoxin (LT). Literature shows that LT and TNF-α are coded in the same gene, even though, they have different promoters and polyadenylation sites. In conclusion, homeostatic impairment, high stress levels and immunological changes were apparent in recently transported heifers as evidenced by the blood chemistry and hematological measurements, the higher cortisol concentration, the reduction in cytokine TNF-α expression and LT co-expression. Further studies should look into the mechanism that promotes LT expression in animals exposed to transport stress, to probably be used as a biomarker for transport stress.

Key Words: stress, transport, heifers

0821 (W020) Flight speed as predictor of cattle ability to adapt to feedlots. D. R. Soares*[1], J. N. S. G. Cyrillo[2], A. C. Sant'anna[3], T. S. Valente[4], K. S. Schwartzkopf-Genswein[5], and M. J. R. Paranhos da Costa[6], *[1]Bolsista do CNPq– Brasil. Programa de Pós-Graduação em Zootecnia, Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal–SP, Brazil, [2]Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho-SP, Brazil, [3]Departamento de Zootecnia, Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal-SP, Brazil, [4]Programa de Pós-Graduação em Genética e Melhoramento Animal, Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal-SP, Brazil, [5]Agriculture and Agri-Food Canada, Lethbridge, AB, [6]Pesquisador CNPq–Departamento de Zootecnia, Faculdade de Ciências Agrárias e Veterinárias, UNESP, Jaboticabal-SP, Brazil.*

The aim of this study was to assess the efficacy of flight speed (FS) as a predictor of cattle ability to adapt to feedlots. Ninety-four animals were studied at the Instituto de Zootecnia research farm in Sertãozinho-SP, Brazil. Cattle were from three herds: 28 Nellore from a Control herd (not genetically selected for maximum post-weaning weights), 26 Nellore from a Selection herd, and 40 Guzerat (animals of both herds were selected based on a maximum differential in yearling weight) were assessed over a 173-d study. Cattle were housed according to their breed (Nellore and Guzerat) in two feedlot pens (68.59 and 105.60 m^2/animal, respectively). Flight speed (FS, m/s) was assessed 1 d after obtaining initial body weight. ADG (kg/d) and bunk attendance (BA, min/d) were used as confirmatory indicators of cattle adaptation to feedlot. ADG was calculated for the entire feeding period (ADGtot; d 1 to

d 169), and also for three feeding phases, defined as initial (ADGin, from d 1 to d 56), intermediate (ADGit, from d 57 to d 113) and the final (ADGfi, from d 114 to d 169). BA was recorded on Days 5, 13, 21, 35, 42, 50, 171, 172, and 173 of the study from 0700 to 1200 h by direct observation using a 10 min interval scan sampling technique. BA was also calculated for the entire feeding period (BAtot, from d 5 to d 173) and for three feeding phases defined as initial (BAin, from d 5 to d 21), intermediate (BAit, d 35 to d 50) and final (BAfin, d 171 to d 173). Regression analysis was used to assess the effect of FS on ADG and BA for the entire feeding period as well as each feeding phase using a model that included the fixed effects of herd and FS as a covariate (linear effect). Flight speed had significant effects on ADGit (ADGit = 0.78- 0.025*FS; R^2 = 0.31; $P < 0.05$), ADGfin (ADGfi = 0.80- 0.016*FS; R^2 = 0.34; $P = 0.08$) and ADGtot (ADGtot = 0.72- 0.015*FS; R^2 = 0.41; $P < 0.05$). No relationship ($P > 0.05$) was observed between FS and BA. The results of this study indicate that FS (assessed within the first d of arrival to the feedlot) has potential to be used as an indicator of cattle ability to adapt to the feedlot, however further studies are needed for a more thorough understanding of this relationship.

Key Words: adaptability, confinement, temperament

0822 (W021) Influence of pen-shade on respiratory rate and panting score in two breed types of growing bull-calves. *A*. Camacho[*1], B. J. Cervantes[2], L. R. Flores[1], J. J. Lomeli[1], J. A. Romo[1], and R. Barajas[1], *[1]FMVZ-Universidad Autónoma de Sinaloa, Culiacan, México, [2]Ganadera los Migueles, S.A. de C.V., Culiacan, México.*

Twenty growing bulls 233 ± 24.9 kg (75% Black Angus blood with remainder of Brahman and Brown Swiss in undetermined proportion, $n = 10$; and Brahman white coated bulls, $n = 10$) were used in an experiment to determine the influence of pen-shade on respiratory rate and panting score in two breed types of growing bull-calves. The experiment was performed during. Bull-calves were blocked by breed type (Angus cross AC type or Brahman BR type) and in groups of five assigned to two category of allotment (pens without shade NS or shaded-pens SH). During 28 alternated days (July and August, 2013), inside of pens air temperature (At), relative humidity (RH), air velocity (Av), and soil temperature (St) were recorded at 0100 and 1400 h, and THI calculated; with a similar schedule respiratory rate (RR) in breaths per min (bpm) and panting score (PS) were visually measured. Animals were fed at 1700 h to minimize the impact of digestive process on heat load during physiological measurements. Data were analyzed by ANOVA and best subset regression. Mean climatic conditions were air temperature 36.4°C (27.6–49.5°C), relative humidity 47.9 (24.7–82.5%), and THI 85.7 (79.1–96.4). RR was higher ($P < 0.01$) for AC than in BR cattle (73.7 vs. 48.7 bpm), and lower ($P < 0.01$) in SH than NS (52.6 vs. 69.8 bpm). Interaction breed x allotments was observed ($P < 0.01$), where BRNS cattle has similar RR than ACSH ($P > 0.10$), mean values were 85.3, 54.3, 62.0, and 43.1 bpm for ACNS, BRNS, ACSH, and BRSH, respectively. PS shown a similar behavior than RR, and its relationship was RR = 33.73 + (24.024 * PS); $r^2 = 0.84$, $P < 0.00001$. General equation for RR = 6.208 + (2.418 At) + (0.1672 St)- (5.043 Shade)- (24.68 Breed type); $r^2 = 0.69$, $P < 0.00001$. And for breed type was AC was RRAC = - 47.3917 + (3.164 At) + (0.2399 St)- (7.169 Shade); $r^2 = 0.72$; $P < 0.00001$; and RRBR = - 17.84 + (1.876 At)- (3.3758 Shade); $r^2 = 0.35$; $P < 0.00001$. Results suggest that panting score could be practical usable in different bred types of cattle, and the benefices of pen-shade helping cattle to cope heat load becomes important in cattle with lower genetic adaptation for confront hot environments.

Key Words: cattle, respiratory rate, pen-shade

0823 (W022) Association among residual feed intake, residual body weight gain, residual intake and body weight gain and temperament of Nellore cattle. C. L. Francisco[*1], A. M. Jorge[2], A. M. Castilhos[1], F. D. Resende[3], J. M. B. Benatti[4], M. B. Silva[1], and R. F. Cooke[5], *[1]Universidade Estadual Paulista–FMVZ, Botucatu, Brazil, [2]Faculdade de Medicina Veterinária e Zootecnia, Universidade Estadual Paulista, Botucatu–SP, Brazil, [3]Agência Paulista de Tecnologia dos Agronegócios–APTA, Colina, Brazil, [4]Universidade Estadual Paulista–FCAV, Jaboticabal, Brazil, [5]Oregon State University–EOARC Burns, Burns.*

A study was conducted to investigate association among residual feed intake (RFI), residual body weight gain (RG), residual intake and body weight gain (RIG) and temperament of Nellore (*Bos indicus*) young bulls ($n = 44$; 387 + 22 kg initial body weight; 22 + 1 mo of age). Animals were evaluated for temperament at feedlot entry (d 0). Individual temperament scores were calculated by averaging steer chute score (5-point scale: 1 = calm, no movement; 5 = violent and continuous efforts) and exit score (calculated by dividing exit velocity results into quintiles; 1 = slowest steers; 5 = fastest steers). Animals were also classified according to temperament type [adequate temperament (ADQ) or excitable temperament (EXC)]. Animals were maintained in individual drylot pens (8 m^2) and individual feed intake was measured during the trial period (d 0 to 109; finishing phase) to determine daily dry matter intake (DMI). Body weights (BW) were measured on d 0 and d 109 to determine the average daily gain (ADG). The DMI and ADG were used to determine the RFI. Residual body weight gain was calculated based on the regression of $BW^{0.75}$ and feed intake. Residual intake and body weight gain was determined from linear combination into RFI and RG. Data were analyzed using PROC MIXED in SAS with fixed effects of temperament; animal was experimental unit.

No differences ($P > 0.05$) were detected for RFI (-0.05 vs. 0.01, for ADQ and EXC steers, respectively; $SE = 0.18$) and RIG (0.04 vs. -0.05, for ADQ and EXC steers, respectively; $SE = 0.20$) between temperament types. However, ADQ steers had greater RG ($P = 0.02$) than EXC steers (0.05 vs. -0.10, for ADQ and EXC steers, respectively; $SE = 0.06$). In conclusion, residual gain is associated with temperament and it is independent of differences in feed intake in Nellore cattle. *Supported by FAPESP#2010/09516–1.*

Key Words: residual feed intake, residual body weight gain, residual intake and body weight gain, temperament.

0824 (W023) Association among peripartum health parameters, cud chewing, and activity.

D. N. Liboreiro[*1], K. S. Machado[1], P. Basso Silva[2], M. M. Filho[1], G. Franco[1], A. E. Barreto[1], M. I. Endres[2], and R. C. Chebel[1], *[1]Dep. Veterinary Population Medicine, University of Minnesota, St. Paul, [2]University of Minnesota, St. Paul.*

Objectives of the current experiment were to evaluate cud chewing and activity of cows with peripartum disorders. Holstein animals (nulliparous = 77, parous = 219) were fitted with cud chewing/activity monitors from −17 to 17 d relative to calving. Blood sampled weekly from 0 to 20 d relative to calving were used for determination of β-hydroxybutyrate (BHB) concentration and incidence of ketosis (BHB > 1400 mmol/L). Blood sampled on d 0, 1, and 2 relative to calving were used for determination of total Ca concentration and incidence of sub-clinical hypocalcemia (Ca < 8.5 mg/dl). Cows were examined for retained placenta (RP) and metritis by study personnel. Data regarding twin calving and stillbirth were recorded. Outcomes measured over time (e.g., rumination and activity) were analyzed by ANOVA for repeated measures using the PROC MIXED. Nulliparous animals spent less time cud chewing than parous animals ($P < 0.01$). There was a tendency for RP to be associated with cud chewing ($P = 0.08$) because from −4 to 10 d relative to calving animals with RP had reduced cud chewing time ($P < 0.01$). Even though there was no association between sub-clinical hypocalcemia and cud chewing time ($P = 0.19$), the interaction between sub-clinical hypocalcemia and days relative to calving was associated with cud chewing time ($P < 0.01$) because on days −16, −13, −11, and 0 relative to calving animals with sub-clinical hypocalcemia had reduced cud chewing time. Concentration of Ca was correlated with cud chewing time ($r = 0.15$; $P = 0.02$). Similarly, ketosis was not associated with cud chewing time ($P = 0.77$) but the interaction between ketosis and days relative to calving was associated with cud chewing time ($P < 0.01$). From 6 to 17 d relative to calving animals with ketosis had reduced cud-chewing time. Concentration of BHB was correlated with cud-chewing time ($r = 0.16$; $P < 0.01$). Nulliparous animals had ($P < 0.01$) greater activity than parous cows. There was a tendency ($P = 0.10$) for animals with stillbirth to have greater activity. There was ($P < 0.01$) an association between RP and activity because from 0 to 11 d relative to calving activity of RP animals was reduced. Although ketosis was not ($P = 0.91$) associated with activity, on d 0 and 1 relative to calving ketotic cows had greater activity and on d 10, 15, 16, and 17 relative to calving ketotic cows had reduced activity. Peripartum disorders are associated with altered cud chewing time and activity in the peripartum period.

Key Words: transition cow, cud chewing, activity

0825 (W024) Animal welfare policies in South Korea.

D. H. Kim[1], J. H. Jeon[2], S. H. Moon[3], M. J. Kim[4], D. M. Ha[1], H. S. Park[5], N. Whitley[5], and S. H. Oh[*5], *[1]Gyeongnam National University of Science and Technology, Jinju, South Korea, [2]National Institute of Animal Science, Suwon, South Korea, [3]Konkuk University, Chungju, South Korea, [4]Seongwoon Livestock Production, Geochang, South Korea, [5]North Carolina A&T State University, Greensboro.*

With the increased global interest in animal welfare, South Korea has implemented laws and policies related to animal production. The goal of this research is to review animal welfare trends in South Korea and introduce the farms that produce livestock with animal welfare in mind. The animal protection laws and policies implemented in South Korea include breeding management, transportation management, slaughter methods, animal welfare, prohibition of animal abuse, and farm regulations. By setting new standards, animal welfare will develop as a leading growth tool in the future livestock industry. In countries with leading livestock industries like the U.S., France, Denmark, and others, certification marks are given to animals produced under strict animal welfare policies to differentiate them from other livestock, and those produced within those certification programs are sold at a relatively higher price. European consumers willingly pay a higher price for products from animals raised under animal welfare certification program guidelines and feel pride in their belief that supporting those products contributes to the good of society. Following these trends, a certification system, which provides legal verification to those farms that comply with the government standard in animal welfare, was stipulated in South Korea. The system went into effect in 2012 with the chicken egg industry. Pigs were included in the system in 2013, and broilers were included in the certification system in 2014. Beginning in 2015, the system will expand annually to include native Korean cattle, beef cattle, dairy cattle, and others.

Key Words: South Korea, animal welfare, policy

0826 (W025) Influence of environmental conditions across day on respiratory rate and panting score of beef cattle in a hot and humidity weather.

A. Camacho*[1], B. J. Cervantes[2], E. X. Murillo[1], M. B. Corona[1], M. A. Osuna[1], and R. Barajas[1], *[1]FMVZ–Universidad Autónoma de Sinaloa, Culiacan, México, [2]Ganadera los Migueles, S.A. de C.V., Culiacan, México.*

Twenty growing bulls 278 ± 11.8 kg (75% Black Angus blood with remainder of Brahman and Brown Swiss in undetermined proportion, $n = 10$; and Brahman white coated bulls, $n = 10$) were used in an experiment to determine the influence of environmental conditions across day on respiratory rate and panting score of beef cattle in a hot and humidity weather. The experiment was performed during August 2013. In groups of five, bulls with same breed were placed in provided or no-shade ground pens (6 × 12 m). During 12 d from 0800 to 1600 h, inside of pens with 1-h intervals, air temperature (At), air relative humidity (RH), air velocity (Av), and soil temperature (St) were measured; one bull in each pen by time and day was randomly selected to respiratory rate (RR) in breaths per min (bpm) and panting score (PS) measurement by direct observation. Data of 12 d were pooled and analyzed by ANOVA. Across experiment, weather conditions were: At 36.30°C (range 25.2 to 53.0), RH 50.30% (range 21.5 to 82.6), Av 3.20 km/h (range 0 to 12), THI 85.93 (range 75 to 98), and St 35.47°C (range 15.7 to 73.9). Mean values of RR and PS were 65.95 ± 1.034 bpm and 1.18 ± 0.037, respectively. At 0800 h RR and PS were 44 bpm and 0.61 with 29.66°C At, 67.86% RH, and 80.35 THI. Mean maximum air temperature (40.65°C), soil temperature (41.10°C), and THI (89.08) were observed at 1300 h, while maximum respiratory rate (72.81 breaths/min) and panting score (1.57) delayed 1 h peaked at 1400 h. Means value of At and THI diminished ($P < 0.05$) at 1500 h; whereas RR, PS were coupled with soil temperature and delayed 2 h more (1700 h) to descend below of climax values ($P < 0.05$). It is concluded that respiratory rate and panting score delays proximately 1 h to reach the highest values after air temperature and THI arrive at its day peak values, and spend around 2 h to decline after air temperature and THI decreases; data suggest that descend of respiratory rate and panting score could be associated with soil temperature.

Key Words: air temperature, cattle, respiratory rate

ANIMAL HEALTH: **MODELS OF ANIMAL IMMUNE STATUS AND PERFORMANCE**

0827 (M016) Gastrointestinal and hepatic tissue fatty acid composition and interleukin-6 concentration in broiler chickens: Effect of maternal dietary n-3 fatty acids. C. J. Bullock, G. Bobe, and G. Cherian*, *Oregon State University, Corvallis.*

Early exposure to nutrients and fetal programming has gained increased attention because of its association with chick quality and viability. In chickens, the 21-d incubational period contributes to over 35% of a bird's life span. During this period, the egg provides polyunsaturated fatty acids (*P*UFA) to the chick embryo. We hypothesized that early exposure of n-3 and n-6 PUFA through egg lipids can alter tissue fatty acid (FA) composition and interleukin-6 (IL-6) production in the progeny chickens during growth. The objectives of the study were to determine: 1) the extent to which maternal (yolk) n-3 or n-6 FA are retained in the duodenum, jejunum, ileum, and liver tissue of the chicken, and, 2) the effect of maternal FA composition on IL-6 concentrations in serum and hepatic tissue in broiler chickens when fed a diet lacking in long chain (> 20-C) n-3 and n-6 FA during growth. Fertile eggs obtained from Lohman-Brown layer hens (n = 75) fed corn-soy diets supplemented with 3.5% yellow grease, sunflower oil or fish oil were incubated. These fat supplements were selected as sources of saturated, n-6 or n-3 FA. Chicks were raised up to d 14 on a commercial diet lacking long-chain n-6 and n-3 FA. Chick tissues (duodenum, jejunum, ileum, liver, and blood) were collected on Day 1, 7, and 14 and were subjected to FA and IL-6 analysis. The egg yolk arachidonic (20:4 n-6) and docosahexaenoic acid (DHA, 22:6 n-3) content was 3.1, 3.6, 1.0 and 1.6, 1.0, and 6.1 for eggs from hens fed yellow grease, sunflower or fish oil diets ($P < 0.001$). The DHA content in duodenum was highest up to d 14 of growth in chicks from fish oil-fed hens ($P < 0.001$). The long-chain n-6 to n-3 ratio was lowest in the duodenum, jejunum, ileum, and liver in chicks hatched from fish oil-fed hens ($P < 0.001$) up to d 14 post-hatch. A significant maternal diet by age interaction was observed for liver and serum IL-6 concentrations ($P < 0.001$). On the day of hatch, chicks from fish oil-fed hens had the lowest liver and serum IL-6 concentrations, whereas at d 14, chicks from fish oil-fed hens had higher liver and serum IL-6 concentrations than chicks from sunflower oil-fed hens ($P < 0.05$). In conclusion, our results indicate that inflammatory pathways and eicosanoid metabolism of broiler chicks can be altered by the maternal dietary ratio of long-chain n-6: n-3 FA.

Key Words: chicken, interleukin-6, n-3 fatty acids

0828 (M017) Sandwich enzyme-linked immunosorbent assay for detection of *Fasciola gigantica* excretory secretory in goats sera. H. R. Metawi*[1] and E. M. Oudah[2], [1]*Animal Production Research Institute, Agriculture Research Center, Cairo, Egypt,* [2]*Faculty of Agriculture, Mansoura University, Egypt.*

Fascioliasis is considerd a major animals health problem. Many immulogical techniques have been developed over years using the different *Fasciola* antigens for diagnosis of parasitic infection and to replace the parasitological techniques, which are time-consuming and usually proved to be inadequate and unreliable. Viable *F. gigantica* flukes were obtained from infected cows at a local abattoir and kept in suitable meduim inside CO_2 incubators to produce excretory/secretory (E/S) antigenes. The pure E/S was collected, and their protein contents were estimated. The bands of sizes 27, 30, 40, 60, and 60/62 were used to obtain suitable antibody probe to be used in isoloting target antigen of E/S origin from infected Egyptian Nubian goats sera. The 40-kilo Dalton immunogenic of E/S origin sandwich enzyme-linked immunsorbent assay is highly specific in detecting *F. gigantica* infection in Egyptan Nubian goats. It also offers a promissing diagnostic tool.

Key Words: Egyptian Nubian goats, *Fasciola gigantica*, sandwich

0829 (M018) Response of beef cows offered a chlortetracycline fortified mineral and either strip or continuous stocked to stockpiled fescue. M. S. Gadberry*[1], D. S. Hubbell, III[2], J. D. Tucker[2], T. Hess[2], P. A. Beck[3], J. Jennings[1], J. G. Powell[4], and E. A. Backes[4], [1]*Dep. of Animal Science, University of Arkansas, Little Rock,* [2]*University of Arkansas Livestock and Forestry Research Station, Batesville,* [3]*Dep. of Animal Science, University of Arkansas, Hope,* [4]*Dep. of Animal Science, University of Arkansas Division of Agriculture, Fayetteville.*

Food and Drug Administration proposed changes to the U.S. feed law addresses judicious use of medically important antimicrobials. Cattle producers grazing Kentucky 31 tall fescue (*Festuca arundinacea*) routinely feed mineral fortified with chlortetracycline (CTC). Available CTC fortified minerals often contain 3.08 g/kg CTC (350 mg CTC/113.4 g mineral consumed). Fescue management may include fall stockpiling for deferred grazing with forage being allocated using either continuous or strip stocking. This project evaluated the effect of CTC delivered in a free choice mineral supplement with either strip stocking (STRIP) or continuous stocking (CONT) on stockpiled fescue. The study design was a 2 × 2 factorial with three 2.4-ha pasture replications per treatment combination. The same mineral package was used for both the no CTC (CTC-) and CTC (CTC+) supplements. The CTC+ mineral contained 3.08 g/kg CTC. Ninety-six pregnant *Bos taurus* cows

were randomly allocated to the 12 pastures. STRIP pasture was allocated at 0.04 ha/d in 4 and 3 d strips. Grazing occurred from December 4 to January 29. The STRIP:CTC- had the least, per cow mineral intake (7.4 ± 0.43 g/d), differing ($P < 0.1$) only from CONT:CTC- and STRIP:CTC+. All other mineral intakes were similar (8.5 ± 0.43 g). Initial rising plate estimated forage allowance was 2513 ± 129.2 kg/ha. Forage utilization was not affected by either grazing method or CTC addition and averaged 47 ± 3.7%. The numerical difference in forage utilization was 44% (CONT) and 49% (STRIP). CTC+ resulted in a 22 kg greater BW change ($P < 0.05$) from the initial to interim weigh date but not interim to final (7 kg less than CTC-). Final BW and BCS were not affected by grazing management or CTC+. External body temperature and thermocirculatory index (TCI, based on rectal, skin, and ambient temperature) at the rump and ear differed between STRIP and CONT ($P < 0.05$) but was not affected by CTC+. CTC+ had a greater skin temperature between the dew claw ($P < 0.1$) at the interim but not final weigh date. CTC+ had no effect on TCI. In conclusion, grazing method did not significantly affect forage utilization, BW, or BCS but resulted in different skin temperature responses. Adding CTC to the mineral primarily resulted in an initial BW gain response without affecting final BW and BCS. Feeding CTC to cattle grazing stockpiled fescue did not result in a sustained benefit for performance or body temperature.

Key Words: chlortetracycline, fescue, strip grazing, strip stocking

---

0830 (M019) Regulation of gene expression and chemotactic and phagocytic function of bovine neutrophils incubated with citrus oil and lipopolysaccharides.

M. Garcia[*1], D. Biswas[1], T. H. Elsasser[2], and K. M. Moyes[1], [1]*Dep. of Animal and Avian Sciences, University of Maryland, College Park,* [2]*USDA/ARS Growth Biology Lab, Beltsville, MD.*

Antibiotic use is coming under increasing public scrutiny due to the possible development of resistant pathogens and risk of residues appearing in the milk. Therefore, new strategies to control or treat mastitis are warranted. Recent studies have shown that citrus derived oil (CO) inhibited growth of major mastitis-causing bacteria. However, the effect of CO on the function of bovine blood neutrophils (BBN) is currently unknown. The objective of this study was to identify the effect of CO and lipopolysaccharide (LPS) endotoxin on BBN by evaluating function and relative expression of genes in vitro. Jugular blood (~150 mL) was collected from 11 healthy Holstein cows in mid-lactation (> 100 DIM). BBN were isolated and incubated with or without 0.01% CO and 50 µg LPS/mL for 2 h at 37°C, 95% humidity, and 5% CO_2. After incubation, BBN chemotaxis and phagocytosis capabilities were determined in vitro, the cell pellet was recovered, and relative gene expression was analyzed via qPCR using the $2^{\wedge-\Delta\Delta Ct}$ method. Three pre-planned non-orthogonal contrasts were evaluated for gene expression. Non-LPS challenged BBN incubated with CO had a 47% increase ($P = 0.03$) in migration in response to IL-8 and a moderate increase in phagocytic capacity (15.9 vs. 14.2%, $P = 0.02$). This effect indicates that the CO was not impairing the function of BBN. However, the pattern of gene expression did not reflect the functional response, where BBN incubated with CO, regardless of LPS challenge, reduced expression ($P < 0.05$, fold-change (FC) $\leq$ -1.57) of several pro-inflammatory genes (IL1B, NFKB, SOD2, TNFA, and TLR2) with the exception of IL8, which tended to be up -regulated ($P < 0.06$, FC = 1.92) when compared to controls. For controls, expression of TLR4, critical for LPS recognition, was downregulated ($P = 0.03$, FC = -1.66) due to LPS although expression of *TNFA* was up-regulated ($P = 0.01$, FC = 2.62). In addition, the anti-inflammatory mechanism of CO at the gene-level does not appear to be mediated by IL10, where IL10 was downregulated ($P < 0.01$, FC = -3.78) in BBN incubated with CO when compared to controls. In conclusion, CO downregulated the expression of pro-inflammatory genes in BBN. However, CO does not appear to be inhibitory for overall BBN function in vitro. Future studies examining the effect of CO on BBN during mastitis in dairy cattle are warranted.

Key Words: neutrophil, citrus oil, genes

0831 (M020) Effect of *Penicillium* mycotoxins on bovine macrophage (BoMac) function.

S. Y. Oh[*1], H. J. Boermans[2], H. V. L. N. Swamy[3], T. K. Smith[1], and N. A. Karrow[1], [1]*Dep. of Animal and Poultry Science, University of Guelph, ON, Canada,* [2]*Dep. of Biomedical Sciences, University of Guelph, ON, Canada,* [3]*Haladi Consultancy Services, Bangalore, India.*

Penicillium mycotoxins (*P*M) are natural contaminants that are commonly found in improperly stored animal feeds. Although exposure to certain PMs has been reported to affect immune function, little data are available for ruminant species. Therefore, in this study bovine macrophages (BoMacs) were exposed to the following PM: citrinin (CIT), ochratoxin A (OTA), patulin (*P*AT), mycophenolic acid (MPA) and penicillic acid (*P*A), and macrophage function was assessed by measuring cytokine gene expression, the production of reactive oxygen species (ROS), and phagocytosis of *Mycobacterium avium* ssp. *paratuberculosis* (MAP), which is the causative agent of Johne's disease. Real-time PCR analysis of pro-inflammatory cytokines interleukin (IL)-1α and IL-6, anti-inflammatory cytokines IL-10 and transforming growth factor-β (TGF)-B, as well as neutrophil stimulating cytokines IL-12 and IL-23 was assessed following 6 and 24 h of PM exposure at concentrations that inhibited BoMac proliferation by 25% (IC25). The mycotoxin treatments altered the gene expression of cytokines at 24 h. Ochratoxin A induced IL-1α expression ($P < 0.05$), while IL-6 expression was suppressed ($P < 0.01$). Mycophenolic acid induced the IL-1α expression

($P < 0.05$) and reduced the expression of IL-12α ($P < 0.01$) and IL-10 ($P < 0.01$). Patulin suppressed the expression of IL-23 ($P < 0.01$), IL-10 ($P < 0.05$), and TGF-b ($P < 0.05$). Neither CIT nor PA affected the expression of these genes. The mycotoxins also affected BoMac intracellular ROS production and phagocytosis at the higher concentrations. Pretreatment with CIT at 300.0 μM increased pathogen associated molecule (*P*AM)-3-induced ROS production, which appeared to contribute to cell death. In contrast, PAT and PA significantly decreased the ROS production at concentrations ranging from 1.3 μM to 10.0 μM and from 31.3 μM to 125.0 μM, respectively; these two PMs simultaneously increased BoMac viability at 10.0 μM and 125.0 μM, respectively, even though they caused the cell death at higher concentrations. Although OTA did not affect the ROS production, an increasing trend in the phagocytosis of MAP was observed from 3.1 to 12.5 μM. In contrast, a decreasing trend in phagocytosis was observed for PAT concentrations from 2.5 to 10.0 μM. These findings suggest that exposure to sublethal concentrations of PM can alter immune function, which could affect innate antimicrobial resistance and immunoregulation.

Key Words: *Penicillium* mycotoxins, bovine macrophages, immunomodulation

---

0832 (M021) The Mycobacterial Diseases of Animals (MDA) Multistate Initiative— A cooperative effort addressing animal diseases. K. E. Olson[*1], V. Kapur[2], P. Coussens[3], and D. H. Lein[4], *[1]KEO Consulting, Schaumburg, IL, [2]Pennsylvania State University, State College, [3]Michigan State University, East Lansing, [4]Cornell University, Ithaca, NY*.

Johne's Disease Integrated Program (JDIP) efforts are well-known and documented. Primary funding was through USDA grants that allowed leveraging of additional public and private resources to expand the effort. The grants have come to an end, so a plan for the future was needed. JDIP addressed many knowledge gaps, but much work remains, so a range of options for the consortium was considered. Primary objectives were to maintain the networking, collaboration and basic infrastructure developed through JDIP, allowing participants to identify, obtain, and share resources needed to address Johne's and other mycobacterial diseases. To this end, a proposal was, developed and later, approved by USDA's National Institute for Food and Agriculture (NIFA) to begin operation as Multistate Initiative: NE1201, Mycobacterial Diseases of Animals (MDA). The multi-state initiative (MI) is focused on two mycobacterial disease complexes— paratuberculosis (Johne's disease; JD) and the tuberculosis complex of diseases (TBc; i.e bovine tuberculosis). The initiative includes five objectives: 1) increase understanding of the epidemiology and transmission of MDA, including predictive modeling; 2) develop and implement new generations of diagnostic tests for JD and TBc; 3) improving our understanding of the biology and pathogenesis of MDA, as well as the host response to infection; 4) develop programs to evaluate and develop new generations of vaccines for JD and TBc; and 5) develop and deliver JD and TBc education and outreach material in electronic and print form for use by producers and other stakeholders. Use trade media, producer organizations, and other outlets to aid in dissemination of information. Projects within each objective, with cross-cutting contributions, are designed to address major animal, human, and societal issues surrounding detection and control of mycobacterial infection, including how these organisms move and spread within cattle, small ruminant, and wildlife populations.

Key Words: mycobacterial disease, Johne's, tuberculosis

0833 (M022) Up-regulation of fetal cardiac genes following persistent and transient bovine viral diarrhea virus infection. *S*. W. Hahm[*], T. R. Hansen, and H. Han, *Colorado State University, Fort Collins.*

Transplacental infection by non-cytopathic (ncp) bovine viral diarrhea virus (BVDV) during early gestation results in persistently infected (PI) fetuses with lifelong viremia. Conversely, infection of ncp BVDV later in gestation (~day 150) or after birth leads to transient infection (TI). We hypothesized that ncp BVDV infection of the dam would alter gene expression related to development of fetal heart and vascular remodeling. Gene expression in the right ventricular heart (RV) of uninfected bovine fetuses was compared to PI and TI fetuses. Naïve pregnant heifers were challenged with 2 mL of ncp BVDV (4.4 log10 TCID50/mL) on d 75 (*P*I fetus; $n = 6$) or Day 175 (TI fetus, $n = 6$) or kept uninfected (Control fetus; $n = 6$). Maternal blood ncp BVDV RNA increased in concentration following PI and TI and then diminished. Fetuses were collected via caesarean section and necropsied on d 190 of pregnancy. To examine fetal cardiac gene expression, quantitative real-time PCR was completed. Data were analyzed using PROC GLM procedure of SAS. BVDV RNA concentration in the RV was greater in PI fetuses when compared to uninfected control and TI fetuses ($P < 0.05$). BVDV was not detected in TI fetal heart because of clearance of virus between d 175 and 190. Atrial natriuretic peptide (ANP) and B-type natriuretic peptide (BNP) act to reduce blood pressure. The mRNA concentrationsfor ANP and BNP were greater ($P < 0.05$) in RV of the TI fetuses, when compared with controls. Vascular endothelial growth factor (VEGF; angiogenic) and cyclin D1 (marker for left ventricular hypertrophy) mRNA concentrations were upregulated ($P < 0.05$) in TI fetuses. Fibroblast growth factor receptor1 (FGFR1; angiogenic) mRNA concentration was greater in RV of PI and TI fetuses ($P < 0.05$). Chemokine ligand 12 (CXCL12) and its receptor, chemokine receptor4 (CXCR4) facilitate fetal cardiac development and may assist in remodeling/repair following acute myocardial infarction. Concentrations of the mRNAs encod-

ing CXCL12 and CXCR4 tended to be upregulated in RV of TI fetuses ($P = 0.0860$, $P = 0.0951$; respectively). Maternal ncp BVDV infection may impaired fetal cardiac development via up-regulation of vascular regulatory, cardiac remodeling, and angiogenic genes regardless of TI or PI. *USDA NIFA AFRI 2008–35204–04652.*

Key Words: bovine viral diarrhea virus, fetus, heart

0834 (M023) OmniGen-AF supplementation inclusion rate independently promotes immune function in a rat model. J. A. Branson*[1,2], D. J. McLean[1], N. E. Forsberg[1], S. A. Armstrong[1], T. H. Schell[1], and G. Bobe[2], *[1]OmniGen Research, Prince Agri Products, Corvallis, OR, [2]Oregon State University, Corvallis.*

Feeding OmniGen-AF (OG; Prince Agri Products, Inc., Quincy, IL), a branded proprietary product, supports immune function in many domestic animals. Targeted profiling of immune-associated genes in whole blood is an established methodology to evaluate the efficacy of feed additives with immune-altering properties. We hypothesized that higher daily inclusion rate of OG than 0.5% may be required to optimize immune function. The objective of this study was to evaluate the effect of dietary OG inclusion rate (0.5% vs. 1.0%) on the expression profile of immune-associated genes. Male CD rats (5/treatment) weighing 180 to 200 g had ad libitum access to a diet with 0 (control), 0.5 (1×), or 1% (2×) of OmniGen-AF for 28 d. At the end of the feeding period, whole blood was collected. RNA was purified from whole blood samples and used to generate cDNA that acted as template in the Rat Innate and Adaptive Immune Responses RT^2 Profiler PCR array (SABiosciences). Using PROC GLM, we compared cDNA abundance of immune-associated genes between control and supplemented groups (0.5 or 1%) with a $P < 0.05$ cut-off value for significance. Of the 79 immune-associated genes that were expressed above the detection limit in all samples, 16 (seven up -regulated) and 13 genes (eight up-regulated) were altered by 0.5% and 1% OG supplementation, most of which (11 with six up-regulated) were altered at both OG inclusion rates. Genes that were up-regulated at both rates include IL13 (0.5%: +3.16, 1%: +3.70-fold-change), IL5 (0.5%: +2.64, 1%: +2.62), Irak1 (0.5%: +2.50, 1%: +1.98), Nod2 (0.5%: +1.83, 1%: +2.02), IFNa1 (0.5%: +1.81, 1%: +2.10), and Cd80 (0.5%: +1.77, 1%: +2.47). Genes that were downregulated at both inclusion rates include TLR3 (0.5%: -2.22, 1%: -2.39), CxCL10 (0.5%: -2.19, 1%: -2.26), STAT1 (0.5%: -2.07, 1%: -1.99), STAT3 (0.5%: -2.05, 1%: -1.92), and NFκb1 (0.5%: -1.84, 1%: -1.75). In conclusion, our results suggest that OG supplementation promotes immune function through various pathways including pathogen recognition, adaptive immune cell activation, and various transcription factors, independent of dietary inclusion rate.

Key Words: gene profiling, immunity, OmniGen-AF

0835 (M024) Effects of betaine on growth performance, carcass characteristics, and meat quality of broilers. J. Ma, W. Chang*, G. Liu, H. Cai, S. Zhang, and A. Zhen, *Feed Research Institute, Chinese Academy of Agricultural Sciences, Beijing.*

This study was to evaluate the effects of betaine on growth performance, carcass characteristics and meat quality of broilers. A total of 240 1-d-old healthy Arbor Acres male broilers were randomly allotted to four groups with six replicates per group and 10 birds per replicate by a single factor completely randomized design. The four diets included a basal diet and three experimental diets supplemented with 0.05, 0.10, and 0.20% betaine, respectively. Birds were slaughtered at 42 dold. The results showed that 0.20% betaine supplementation significantly increased ADG of broilers by 6.53% ($P < 0.05$) but did not significantly affect ADFI and F/G ($P > 0.05$), compared with the control group. Betaine supplementation at the 0.20% level improved breast muscle percentage 9.23% and decreased the values of drip loss 36.36% in breast muscle of broilers ($P < 0.05$). There was no significant difference in dressing percentage, eviscerated yield percentage and thigh muscle percentage between control group and experimental groups ($P > 0.05$). Supplementing betaine of 0.05, 0.10, and 0.20% in diets resulted in significant increase of IMP contents of 13.94, 17.94, and 12.10%, and increase of IMF content of 44.70, 42.92, and 53.14% in breast muscle of broilers, compared with the control group, respectively ($P < 0.05$). The IMF content of 0.20% betaine group was significantly higher than that in 0.05% and 0.10% betaine supplementation groups($P < 0.05$). The IMF content in thigh muscle of broilers in 0.05, 0.10, and 0.20% betaine supplementation group were improved 13.46, 28.53, and 13.75% than that in control group, respectively($P < 0.05$). The content of IMF of 0.10% betaine supplementation group was significantly higher than that in 0.05 and 0.20% betaine group($P < 0.05$). In conclusion, supplementing 0.20% betaine in diet could significantly improve ADG, carcass characteristics, and meat quality of broiler, with an exception of higher IMF content in thigh muscle in 0.10% betaine supplementation group.

Key Words: betaine, carcass characteristic, meat quality

Table 0835.

Treatment	control	0.05% betaine	0.10% betaine	0.20% betaine	*P*–value
ADFI(g/d)	104.26 ± 0.83	104.76 ± 5.85	103.31 ± 4.18	104.13 ± 2.44	0.335
ADG(g/d)	58.39 ± 1.63[a]	60.22 ± 1.47[ab]	57.73 ± 4.22[a]	62.47 ± 1.03[b]	0.029
F/G	1.84 ± 0.14	1.74 ± 0.11	1.79 ± 0.10	1.73 ± 0.02	0.224

0836 (M025) Effects of dietary polyphenols on inflammatory processes, nutrient digestibility, and microbiota in the intestine of piglets. A. Fiesel[1], D. K. Geßner[1], B. Eckel[*2], and K. Eder[1], *[1]Institute of Animal Nutrition and Nutrition Physiology, Universität Gießen, Gießen, Germany, [2]Dr. Eckel GmbH, Niederzissen, Germany.*

The weaning period of piglets is a stressful event characterized by an increased occurance of enteric infections and a pro-inflammatory intestinal condition with negative effects on feed consumption and animal growth. Recent studies have shown that polyphenolic compounds exert anti-inflammatory effects in the intestine. This study investigated the hypothesis that feeding the polyphenol-rich dietary supplements grape seed and grape marc meal extract (GSGME) or spent hops has the potential to suppress inflammatory processes in the intestine of piglets. Besides, the influence on nutrient digestibility and fecal microbiota composition should be investigated for the first time. A feeding trial with 48 5-wk-old piglets was performed. The control group received the basal diet mainly based on wheat, barley, and soybean meal; the GSGME group received the diet supplemented with 1% GSGME (AntaOx, Dr. Eckel GmbH, Niederzissen, Germany); and the hop group received the basal diet supplemented with 1% spent hops (AntaPhyt H, Dr. Eckel GmbH). Statistical analysis was done by one-way ANOVA. There were no differences in average daily gains, daily feed intake, and final body weights between the three groups. However, the gain:feed ratio was increased in the hop group ($P < 0.05$) and the GSGME group ($P = 0.15$). Moreover, both treatment groups had lower expression levels of pro-inflammatory genes (e.g., TNFα, IL-1β and IL-8) and nutrient transporters (SGLT1, GLUT2, GLUT5, PEPT1) in the mucosa of duodenum, ileum and colon ($P < 0.05$). In line with this, decreased digestibilities of crude protein and crude fiber have been observed in the hop group ($P < 0.05$). Supplementation of GSGME and hop revealed an increased fecal pH value, lower levels of volatile fatty acids (acetate, propionate, butyrate) together with changes in the fecal microbial composition with a lower amount of *Streptococcus* spp. and Clostridium cluster XIVa ($P < 0.05$). In conclusion, this study confirmed the anti-inflammatory effect of polyphenol-rich dietary supplements that can be a useful dietary strategy during weaning. It is suggested that the improved feed efficiency results from decreased inflammatory processes and might be also due to an interaction with the gut microbiota and their metabolites.

Key Words: grape seed and grape marc meal extract, hop, anti-inflammatory

0837 (M026) Effects of CO_2 and filter pore size on bovine neutrophil chemotaxis. A. M. Barnard*, R. Nebenhaus, S. Polukis, and T. F. Gressley, *University of Delaware, Newark.*

In vitro chemotaxis assays are an efficient and cost-effective way to assess neutrophil (PMN) function, but variations in the procedure may impact assay results. The aim of this study was to evaluate the effects of CO_2 and membrane pore size on chemotaxis of PMN from lactating cows ($n = 9$; 4–163 DIM). Neutrophils were isolated and adjusted to 2×10^6 cells/mL. Media consisted of HBSS supplemented with 5% FBS. The bottom wells of 48-well chemotaxis chambers (Neuro Probe Inc., Gaithersburg, MD) contained media supplemented with 50 ng/mL of complement component 5a (C5a) or 100 ng/mL of Interleukin 8 (IL-8). Polycarbonate membranes with 3, 5, or 8 μm pores separated the bottom and top wells. Neutrophil suspension (50 μL) was added to the top wells, and chambers were incubated at 37°C for 1 h in the presence or absence of 5% CO_2. Negative controls contained no chemoattractant in either well, and positive controls contained 50 ng/mL of C5a in both top and bottom wells. All combinations of cow PMN, CO_2, pore size, and chemoattractant were evaluated in triplicate wells over 6 different test dates. Raw adherence (RawAd) was determined by counting PMN adhered to the bottom of the membrane in five microscope fields per well. Relative adherence (RelAd) was calculated as (RawAd test well)/(RawAd negative control well) × 100%. Data were analyzed using the Glimmix procedure of SAS with the fixed effects of CO_2, pore size, chemoattractant, and all interactions and random effects of date and cow within date. Both RawAd and RelAd were affected by CO_2, pore size, chemoattractant, and CO_2 × pore size ($P < 0.001$), and RawAd was affected by CO_2 × chemoattractant ($P < 0.001$). Both RawAd and RelAd decreased in the presence of CO_2. RawAd increased and RelAd decreased with increasing pore size. For both RawAd and RelAd, chemotaxis to C5a and IL-8 did not differ but both were greater than chemotaxis to controls. The CO_2×pore interaction for both RawAd and RelAd was driven by a reduced increase in chemotaxis with increasing pore size when CO_2 was present. The CO_2 × chemoattractant interaction for RawAd was due to muted effects of C5a or IL-8 on chemotaxis in the presence of CO_2. Of the conditions evaluated, we propose that the use of a 3 μm membrane and incubation without CO_2 may be preferable because this combination resulted in the greatest increase in adherence relative to the negative control.

Key Words: neutrophils, chemotaxis, bovine

0838 (M027) Preliminary evaluation of the effect of a mushroom (*Coriolus versicolor*) probiotic on gene expression in goat blood. K. A. Ekwemalor*, *North Carolina Agricultuiral and Technical State University, Greensboro.*

Gastrointestinal parasites pose a serious threat to the global goat industry due to resistance of parasites to anthelmintic drugs. Oral administration of anthelimintics may activate genes in peripheral blood and impact goat health and production. *Coriolus versicolor* is a mushroom with immunostimulant properties used as a dietary supplement as an immunostimulant. CorPet biomass (Mycology Research Laboratories Ltd, UK) is a mushroom (*Coriolus versicolor*) based feed that is being used as a probiotic in horses and small animals as an immunostimualnt. White-rot fungi such as *Coriolus versicolor* are efficient lignin degraders and have been studied for their ability to ferment different crop residues to produce improved animal feed for ruminants such as goats. Although the impact of white rot fungi on animal feed has been studied the effect of their use as feed supplements on the animal needs further study. The objective of this study was to evaluate the effect of aqueous extracts of CorPet on gene activation in adult Boer goats infected with gastrointestinal parasites. Following initial screening for infection, goats were assigned to three groups of five ($n = 15$). Powdered CorPet was soaked in hot or cold water with stirring. Sterile filtered extracts were prepared. Goats were drenched daily with 10 mL of the hot (treatment I) or cold extract (treatment II) daily for a 4-wk period, and a control group of five age-matched goats received sterile water (treatment III). The groups were reversed for a further 4 wk. Body weight, PCV, fecal sample, and blood were collected in PAXgene tubes. Total RNA was isolated using the Zyomed kit. Haemonchus and coccidi were counted using a 3069 stereo microscope. There was no significant difference between the hot and cold treatment. There was an effect treatment on weight of the animals due to treatment ($P > 0.0041$). The Nanodrop spectrophotometer was used to evaluate RNA concentration and purity. The average concentration and purities of the different treatment groups for each week revealed some variation over time. Administration of Corpet as an oral drench may stimulate gene expression in peripheral blood and may impact rumen microorganisms. Further studies using more samples are needed to assess the impact on diversity and feed efficiency.

Key Words: anthelmintics, immunostimulant, CorPet

0839 (M028) Current colostrums management practices on Jersey farms in Vermont and New York State. K. M. Morrill*[1], M. M. Spring[2], and H. D. Tyler[2], [1]*Cornell University, Ithaca, NY,* [2]*Iowa State University, Ames.*

The objective of this study was to evaluate current colostrum management practices on Jersey farms in New York and Vermont. Colostrum management surveys consisting of seven general farm questions and 24 colostrum management questions were mailed to 75 dairy farms in New York and Vermont in June 2013. A total of 38 farms responded to the survey (50.66%). Of the 38 farms that responded, 10 provided calf serum for IgG analysis. Farms represented conventional (56%), organic (3%), and combinations of conventional and grazing (41%) operations. Farm size ranged from < 100 cows (67%), 100 to 199 (15%), 200 to 500 (10%), 501 to 1000 (5%), 1001 to 2000 cows (3% of respondents). Colostrum collection occurred within 1 h on 16% of farms and within 6 h on an additional 58% of farms. Fresh cows were milked most often in the same parlor as the rest of the herd (69%) and were frequently milked last (52%). Colostrum was transferred to an average of 2.32 containers (SD = 0.47) before feeding. Mean time to first colostrum feeding was 7.79 h (SD = 7.62); 24% of farms surveyed fed calves within 1 h, 33% within 2 h of birth, 35% within 6 h of birth and 8% of calves were fed within 12 h of birth. Mean colostrum consumption within the first 24 h was 3.00 L (SD = 1.11) with a range of < 1 (3% of farms) to > 4.5 L (13% of farms). Colostrum quality was a concern on 55% of the farms and was assessed on 78% of the farms. The most common methods of assessment were to evaluate color and consistency of colostrum; only one farm was using a refractometer to measure colostrum quality. The majority of farms surveyed (82%) would discard unacceptable colostrum. The following conditions led to discarding colostrum on greater than 20% of farms surveyed: mastitis, sick cow, positive for Johne's or Leucosis, watery appearance, or bloody appearance. Only one farm routinely monitored passive transfer in newborn calves. These data suggests that farms in this study are willing to discard colostrum from sick cows or visible altered (bloody); however, colostrum management practices on Jersey farms in New York and Vermont have room for improvement, primarily in timing of feeding, amount of quality colostrum fed within 24 h and assessment of passive transfer.

Key Words: colostrum, management, survey

0840 (M029) Effect of 2,4-thiazolidinedione treatment in milk production and leukocytes phagocytosis after sub-clinical mastitis induction in lactating dairy goats. *S. G. Richards*, L. Robertson, D. Dahl, L. Johnston, C. T. Estill, and M. Bionaz, Dep. of Animal and Rangeland Sciences, Oregon State University, Corvallis.*

Mastitis is one of the most costly diseases for the dairy industry. There is indirect evidence suggesting that peroxisome proliferator-activated receptor γ (PPARγ) regulates milk fat synthesis and may help to prevent mastitis. We postulate that continuous activation of PPARγ in the mammary gland can improve response to sub-clinical mastitis and increase milk fat synthesis. To test this, 25 lactating Saanen goats received either 8 mg/kg BW daily intravenous injections of the PPARγ

activator 2,4-thiazolidinedione (TZD) or saline. Following 1 wk of treatment, half of the TZD and half of the saline treated goats received intramammary infusion (IMI) of 1.7×10^8 CFU/mL of *Streptococcus uberis* (*S. uberis)* in both mammary halves (MTZD and MCTR), while the remaining goats in each group received IMI of saline (CTZD and CTRL). Animals were monitored for 12 d after IMI. Milk was collected daily during the trial to measure yield and composition, including somatic cell count (SCC). Bacteriological analysis of the milk was performed before infusion and 24 h after IMI. Rectal temperature (RT) was assessed daily after IMI. Blood was collected during the trial to assess leukocytes phagocytosis. Body weight and body condition score (BCS) were assessed weekly. Data were analyzed using GLIMMIX of SAS with TZD, IMI, time and all interactions as main effect and goat ID as random. Significance was determined with a Tukey-adjusted $P < 0.05$. Milk SCC increased significantly after IMI in goats infused with *S. uberis,* but the goats receiving TZD had an overall lower SCC. There was a significant decrease in milk yield in mastitis groups but no effect of TZD. There was a decrease in milk fat (mg/d) after IMI in MCTR, while the MTZD group maintained milk fat comparable to non-mastitis groups. The mastitis groups had a much higher percentage of milk protein than non-mastitis groups, but no TZD effect was observed. Compared to 2 d before, after IMI we observed a decrease in % blood neutrophils and increase in % lymphocytes, which was larger in goats infused with *S. uberis*. The phagocytic activity of monocytes increased more in groups infused with saline compared to *S. uberis*. No effect on body weight, BCS, and rectal temperature was observed. The results confirmed successful induction of sub-clinical mastitis, uncovered a positive effect of TZD on SCC and in preventing milk fat depression due to sub-clinical mastitis, but TZD treatment did not affect leukocytes.

Key Words: PPARγ, goat, subclinical mastitis

0841 (M030) Cross-talk between liver and mammary tissue after experimental *Escherichia coli* mastitis in Holstein dairy cows using RNaseq.

M. Bionaz*[1], K. M. Moyes[2], and P. Sørensen[3], [1]*Dep. of Animal and Rangeland Sciences, Oregon State University, Corvallis,* [2]*Dep. of Animal and Avian Sciences, University of Maryland, College Park,* [3]*Center for Quantitative Genetics and Genomics, Dep. of Molecular Biology and Genetics, Aarhus University, Tjele, Denmark.*

Using RNaseq combined with bioinformatics tools, our objective was to identify cross-talk between liver and mammary tissue and key pathways altered during intramammary (IMI) challenge with *Escherichia coli* (*E. coli*). Six cows were inoculated with ~20 to 40 CFU of live *E. coli* into one mammary quarter at ~4 to 6 wk in lactation. Biopsies were performed at -144 and 24 h relative to challenge in liver and at 24 h in both rear quarters (i.e., infected and non-infected) of the mammary gland. Each sample was sequenced using a 100 bp paired-end approach. Sequence reads were aligned to the Bovine genome and the number of reads that mapped to each of the 24,616 Ensembl genes was determined. A generalized linear model was fitted for the read count of each gene and differential expression was assessed using a likelihood ratio test statistic after adjustment for multiple testing (FDR). Ingenuity Pathway Analysis coupled with the Dynamic Impact Approach analysis of differentially expressed genes (overall time effect FDR $\leq$ 0.05, post-hoc $P \leq 0.05$) indicated that IMI induced a large biological response in the liver and mammary tissue with a strong inhibition of metabolism, especially related to lipid, glucose, and xenobiotic metabolism, in the former and induction of inflammatory response/immune cells activation in the latter. Analysis of upstream regulators indicated a prominent role of several cytokines, growth factors, and transcription regulators in the two tissues' transcriptomics adaptation to IMI, clearly lipid-related and inhibited in the liver and inflammatory-related and activated in mammary tissue. The analysis uncovered a substantial cross-talk between the two tissues during IMI with a communication almost unidirectional (i.e., from mammary to the liver) via the induction of the hepatic proliferation, regeneration, and inflammatory response due to a large number of cytokines with an increased expression in the mammary gland and able to interact with highly induced hepatic receptors. The analysis indicated that only three proteins (SPP1, EPO, and GRP) with an increased hepatic expression due to IMI could potentially interact with receptors involved in leukocytes differentiation/proliferation with an increased expression due to IMI in mammary tissue. The larger enrichment of immune cell-related functions in the data from the mammary tissue suggests increased recruitment of active immune-cells to the mammary tissue. The analysis uncovered a large communication from the mammary to the liver to coordinate the inflammatory response with very few factors potentially released by the liver to control mammary gland response.

Key Words: dynamic impact approach, liver, mastitis, RNaseq

0842 (M031) Identifying the major bacteria causing intramammary infections in individual milk samples of sheep and goats using traditional bacteria culturing and Real-time Polymerase Chain Reaction. M. Rovai[1], G. Caja[1], A. Salama[*1,2], A. Jubert[3], B. Lazaro[4], M. Lazaro[3], and G. Leitner[5], *[1]Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain, [2]Animal Production Research Institute, Dokki, Giza, Egypt, [3]Laboratori Interprofessional Lleter de Catalunya (ALLIC), Cabrils, Spain, [4]Vacunek, Ibaizabal Bidea 800, Parque Científico y Tecnológico de Bizkaia, Derio, Spain, [5]National Mastitis Reference Center, Kimron Veterinary Institute, Bet-Dagan, Israel.*

Milk provides the major source of income in dairy farms, while one of the main causes of milk production losses is intramammary infection (IMI). Depending on the bacteria type involved, some bacteria cause clinical infection, while the majority of the bacteria cause subclinical with no visible signs of infection. Consequently, to identify infected animals, as well as the bacteria, milk sampling and laboratory diagnosis are needed. Use of DNA based methods such as real-time PCR has increased sensitivity and shortened time for bacteria identification, compared to traditional bacteriology; however, results should be regarded with caution. One-hundred eight lactating dairy ewes (Manchega, 56; Lacaune, 52) and 24 Murciano-Granadina dairy goats were used for identifying the main bacteria causing IMI using traditional bacterial culturing and real-time PCR and their effects on milk performances. Milk samples were taken aseptically from each udder-half for bacterial culture and somatic cell count (SCC) three times throughout lactation. The IMI was assessed based on bacteria isolated in $\geq$ 2 samplings accompanied by increased SCC. Mammary gland infection was caused mainly by *S. aureus* and various CNS species, and resulted in lowering milk yield and decrease of its quality as indicated by coagulation. Prevalence of subclinical IMI was 42.9% in Manchega, 50.0% in Lacaune and 41.7% in goats, estimated milk yield loss being 13.1, 17.9, and 18.0%, respectively. According to bacteriology results, 87% of the identified single bacteria colonies or culture-negative growths were repeatable throughout samplings, and bacteriology and PCR had 100% agreement. Nevertheless, the study emphasized that one sampling may not be sufficient to determine IMI, and therefore, other inflammatory responses such as increased SCC should be monitored to identify true infections. Moreover, when PCR methodology is used, aseptic and precise milk sampling procedure is the key for avoiding false positive amplifications. In conclusion, both PCR and bacterial culture methods proved to have similar accuracy for identifying infective bacteria in sheep and goats. Final methods choice will depend on their diagnosis time and analysis cost according to the farm management strategy (treatment and/or prevention of new infection).

Key Words: intramammary infection prevalence; small ruminant; real-time polymerase chain reaction

0843 (M032) Antibiotic dry-off therapy for intramammary infections in dairy sheep and goats. *M*. Rovai[1], G. Caja[1], A. Salama[*1,2], C. L. Manuelian[1], X. Such[1], M. Cervino[3], and G. Leitner[4], *[1]Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain, [2]Animal Production Research Institute, Dokki, Giza, Egypt, [3]Boehringer-Ingelheim España S.A., Barcelona, Spain, [4]National Mastitis Reference Center, Kimron Veterinary Institute, Bet-Dagan, Israel.*

Mammary glands are susceptible to new infections especially at the end of lactation and before parturition and control of subclinical udder infections is still an issue in small ruminants. Intramammary infections (IMI) during the dry period are likely to remain from the previous lactation to the next or develop during this period, which can lead to reducing milk production in the ensuing lactation. Ninety-four lactating dairy ewes (Manchega, 47; Lacaune, 47) and 20 Murciano-Granadina dairy goats were used to evaluate the effectiveness in reducing the prevalence of IMI with a dry-off antibiotic therapy (one syringe/gland of Mamyzin containing 100 mg of penethamate hydriodide, 280 mg of benethamine penicillin, and 100 mg of framycetin sulphate; Boehringer-Ingelheim, Sant Cugat del Vallès, Spain). At drying-off animals were classified into three groups according to the gland bacteria status: 1) N0 (non-infected animals without treatment), T0 (non-infected animals with dry-off therapy), and T1 (infected animals with dry-off therapy). The goat herd was classified into T0 and T1 groups due to the number of available animals. Prevalence of bacterial isolation from milk was determined at the following lactation (15, 40, and 60 DIM in sheep; 20 and 60 DIM in goats). Coagulase negative staphylococci were the most common isolates at dry-off. Incidence of new IMI was determined taking udder halves, previous infection information and results from all samplings after parturition. Rate of new infection was 20 and 18% for N0 and T0 sheep group, respectively. Mammary gland healthy status did not differ between N0 and T0 groups, showing that in this study, dry-off therapy did not protect against new infections in early lactation. Cure rate for the ewes infected and treated at dry-off was 84% after parturition. For goats, the used of antibiotic cured 67% of T1 group while there was no infection found in T0 does. The use of Mamyzin at dry-off showed to be effective to treat infected glands of sheep and goats, reducing IMI prevalence in the subsequent lactation.

Key Words: dry-off therapy, intramammary infection, dairy ruminants

0844 (M033) Tissue protein nitration and peripheral blood endotoxin activity are indicative of the severity of systemic organ compromise in naturally occurring clinical cases of bacterial mastitis in Holstein dairy cows. S. Kahl*, T. H. Elsasser, and G. Sample, *USDA, Agricultural Research Service, Beltsville, MD.*

The objective of this survey study was to determine a relationship between the intensity of tissue protein tyrosine nitration measured in samples of mammary gland, liver, pancreas, and lung compared to endotoxin (LPS) activity estimated in blood. Blood was collected from nine multiparous Holstein cows on confirmation by the State Diagnostic Laboratory of Maryland of mastitis and the relevant causative pathogen. In addition, control blood was collected from 17 healthy animals (cows and steers). Blood LPS activity (BLA) was estimated using an autologous neutrophil chemiluminescence-based assay (EAA, Spectral Diagnostics, Inc., Toronto, Canada) and expressed as a ratio of chemiluminescence of blood samples without and with an added reference quantity of LPS. In accordance with an approved USDA Animal Care Committee protocol, mastitis animals were subsequently euthanized and tissue collected for immunohistochemical (IHC) quantification (pixel density from digital image analysis) of antigens representative of protein tyrosine nitration (PNT) and inducible nitric oxide synthase (iNOS). Resolved pixel densities for pNT and iNOS were compared to a standardized panel of similar tissues previously obtained from healthy animals. Estimated BLA was higher ($P < 0.01$) in cows diagnosed with clinical mastitis than in healthy cows (0.354 ± 0.068 vs. 0.058 ± 0.010). All mastitic cows presented IHC evidence of pNT and iNOS in the designated lobulo-alveolar mammary tissues from both infected and noninfected quarters and peripheral presence of pNT and iNOS in liver, pancreatic islets, and lung alveolae and bronchiolar epithelial cells ($P < 0.03$ vs. control). Across the spectrum of BLA levels, correlation assessments suggested that the greatest levels of tissue pNT were associated with the higher levels of BLA. Given the known relationship between the presence of pNT in pathologic tissues and organ dysfunction, the data here suggest that mastitis generates perturbations in peripheral organs essential to proper metabolic and pulmonary function.

Key Words: mastitis, endotoxin, protein tyrosine nitration

0845 (M034) Proinflammatory responses of a hTERT-transformed, immortalized line of cultured bovine mammary epithelial cells (BME). T. H. Elsasser*[1], S. Kahl[1], D. E. Kerr[2], E. Zudaire[3], and F. Cuttitta[3], *[1]USDA, Agricultural Research Service, Beltsville, MD, [2]University of Vermont, Burlington, [3]NIH-NCI, Bethesda, MD.*

Cell Characterization: Primary cultures of BME were generated from healthy mammary glands as described (Vet Immunol Immunopath 101(3–4):191–202, 2004). Towards immortalization, BME from four cows were pooled and transfected with pCI neo-hEST2-HA, a human telomerase segment containing a neomycin/Geneticin resistance selection cassette (Cell 90:785–95, 1997). Cells were grown in DMEM +10%FBS and Geneticin (800 μg/ml) and followed through the ensuing selection growth lag to full proliferation capacity. Following 50+ passages, cells were further subcloned to increase epithelial and decrease myoepithelial cell content; the resulting culture was called ELS-321-Clone2B. For function studies and to achieve hormone and cytokine receptor access by the apical-lumenal polarized cells, cultures experiments were conducted on porous (0.4 μm) hanging well inserts coated with laminin-111. At confluence, cells had the following characteristics: tight junctions (electron microscopic confirmation of desmosomes, EpCAM-1 and E-cadherin immunostaining), expression (immunohistochemical localization) of prolactin receptor PRLr, xanthine oxidase (XO), inducible nitric oxide synthase (iNOS), and cytokeratin-18 (< 10% cells displayed myoepithelial smooth muscle actin). Proinflammatory Modeling: Confluent cells were challenged with 20 ng/ml recombinant bovine TNF-α and 200 ng/ml IL-17a. Media was collected at 0, 1, 4, and 24 h relative to challenge with respective cells on inserts fixed in paraformaldehyde for immunofluorescence analysis of nitrated proteins (PNT) and PRLr. Media content of lactate dehydrogenase progressively accumulated past time 0. The first noticeable cell response to challenge was the redistribution of PRLr followed by a reduction in numbers to < 10% T0 values. Cell pNT content was increased at T4, and progressively increased through T24. The data suggest that ELS-321–2B are well-suited to serve as an in vitro model to characterize BME responses to proinflammatory conditions.

Key Words: mammary, cell, proinflammatory

0846 (M035) A snapshot of multi-toxin contamination in feed— Summary of 37+ Analysis results for 2012–13. A. Yiannikouris*, *Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech, Nicholasville, KY.*

The large number and structural diversity of mycotoxins has impeded rapid quantification using LC-MS/MS owing to varying extraction efficiencies and interferences from feed and food matrices. Alltech researchers have successfully tackled

these challenges by developing the 37+ Analysis. This novel method provides simultaneous and accurate quantification for more than 37 mycotoxins in feed in a cost-effective manner. This approach normalizes losses during extraction and matrix suppression/enhancement by using labeled mycotoxins as surrogates and internal standards. In this analytical setting, four isotopologues were used to normalize the MS signals of known concentrations of 10 mycotoxin groups. During 2012–13, 3322 feed samples were received from across the world and subjected to the 37+ Analysis. The mycotoxin population followed a Gaussian distribution with measurable concentrations of mycotoxins detected in 99.6% of the 3322 samples (average = eight different mycotoxins/sample), with only 14 samples containing no detectable mycotoxins. The number of mycotoxins per sample at measurable concentrations ranged from 2 to 20, with ~87% of samples contaminated with 3 to 11 mycotoxins. Fumonisins closely followed by trichothecene B were the most prevalent. Trichothecenes, ergot alkaloids and other toxins, such as *Aspergillus* and *Penicillium* toxins found in stored feed accounted for 30% of the balance. Interestingly, hot spots of contamination accounted for 10s to 100s of ppm for certain mycotoxins. For the first time, analysis of the distribution of *Penicillium* toxin as well as potential synergistic compounds such as fusaric acid has been made possible. Mycotoxin concentrations were further interpreted and normalized according to known species-specific sensitivities. The latter were evaluated using principles of toxic equivalent factors used to perform risk assessment for PCBs, dioxins and furans and adapted to mycotoxins. This approach allowed evaluating the toxicological risk associated with levels of mycotoxins found in samples and normalized according to the impact of the distribution of the toxin for mixed animal species. The data showed that trichothecenes B accounted for the highest risk to animal performance or health, followed by aflatoxins (despite only accounting for 2% of mycotoxins found), ochratoxin and *Penicillium* toxins. In conclusion, the 37+ Analysis shows that the spectrum of mycotoxins that naturally contaminates feed commodities is exceedingly broad. For the first time, we are proposing a holistic strategy for accounting and reporting multiple mycotoxin contamination trends that were often neglected using other analytical approaches that focused only on a small number of contaminants.

Key Words: mycotoxin, mass spectrometry, UPLC-MS/MS, feed, contamination

0847 (M036) Identification of immune response markers to OmniGen-AF supplementation in a rat model.

J. A. Branson[*1,2], D. J. McLean[1], N. E. Forsberg[1], S. A. Armstrong[1], T. H. Schell[1], and G. Bobe[2], *[1]OmniGen Research, Prince Agri Products, Corvallis, OR, [2]Oregon State University, Corvallis.*

OmniGen-AF (OG; Prince Agri Products, Inc., Quincy, IL) is a branded proprietary product shown to augment immune function in ruminants and other species. Targeted profiling of immune-associated genes in whole blood is an effective platform for identification of multiple immune response markers to feed additives. The objective of this study was to identify multiple immune response markers that are increased by dietary OG throughout a 28-d supplementation period. We hypothesized that several immune-associated genes in whole blood are consistently up-regulated in a 28-d supplementation period. Fourteen male CD rats weighing 180 to200 g had ad libitum access to a diet containing 0 (control; $n = 5$, only 28 d) or 0.5% OG for 7 ($n = 4$) or 28 d ($n = 5$). Whole blood was collected at the end of the feeding period. RNA was purified from whole blood samples and used to generate cDNA that acted as template in the Rat Innate and Adaptive Immune Responses RT^2 Profiler PCR array (SABiosciences). Using PROC GLM, we compared cDNA abundance of immune-associated genes between control and supplemented groups (7 or 28 d) with a $P < 0.05$ cut-off value for significance. Of the 77 immune-associated genes that were expressed above the detection limit in all samples, six genes were up-regulated after 7 d of OG supplementation with only four genes up-regulated after 28 d of OG supplementation. Of these genes, three were up-regulated on both d 7 (Cd80: +2.40; Irak1: +2.25; Nod2: +2.08-fold-change) and 28 (Cd80: +1.77; Irak1: +2.50; Nod2: +1.83-fold-change). In conclusion, our results suggest Cd80, Irak1, and Nod2 as immune response markers are increased by dietary OG throughout a 28-d supplementation period.

Key Words: biomarker, immunity, OmniGen-AF

0848 (M037) Effects of recombinant bovine somatotropin treatment during the transition period on serum growth hormone and insulin-like growth factor 1 concentrations and liver content of lipid, triglyceride, and glycogen.

P. Basso Silva[*1], D. S. Lobao[2], D. H. Keisler[3], and R. C. Chebel[4], *[1]University of Minnesota, St. Paul, [2]Dep. Animal Science, University of Minnesota, St Paul, [3]University of Missouri–Division of Animal Sciences, Columbia, [4]Dep. Veterinary Population Medicine, University of Minnesota, St. Paul.*

Objectives were to evaluate the effects of treatment of peripartum Holstein cows with recombinant bovine somatotropin (rbST) on serum growth hormone (GH) and insulin-like growth factor (IGF)-1 concentrations and liver total lipid

(TL), triglyceride (TG), and glycogen (GLY) contents. Cows were assigned to one of three treatments at 253 ± 1 d of gestation: CON (0 mg/d rbST, $n = 53$), rbST87.5 (87.5 mg of rbST every 7 d, $n = 53$), or rbST125 (125 mg of rbST every 7 d, $n = 53$). Treatments were given weekly from d −21 to 28 relative to calving. Milk production data was collected weekly until 150 d postpartum. Blood was sampled weekly from d −21 to 21 relative to calving for determination of GH and IGF-1 concentrations. Liver biopsies were performed in a sub-group of cows ($n = 10$/treatment) at −21, −7, and 7 d relative to calving for determination of liver contents of TL, TG, and GLY. Continuous data were analyzed by ANOVA using the PROC MIXED. Treatment did not ($P = 0.75$) affect milk production (CON = 45.9 ± 1.3, rbST87.5 = 45.8 ± 1.4, rbST125 = 47.1 ± 1.3 kg/d) but there was an interaction between treatment and day ($P < 0.01$). Treatment affected GH concentration (CON = 13.0 ± 0.9, rbST87.5 = 16.1 ± 0.9, rbST125 = 18.2 ± 0.9 ng/ml; $P < 0.01$). Concentration of GH of rbST125 cows tended to be higher than rbST87.5 cows ($P = 0.11$), and rbST87.5 ($P = 0.02$) and rbST125 ($P < 0.01$) cows had higher GH concentrations than CON cows. Treatment tended ($P = 0.06$) to affect IGF1 concentration (CON = 84.6 ± 3.5, rbST87.5 = 92.9 ± 3.5, rbST125 = 96.2 ± 3.5 ng/ml). IGF-1 concentration was not ($P = 0.50$) different between rbST87.5 and rbST125 cows, but rbST87.5 cows tended to ($P = 0.10$) and rbST125 cows had ($P = 0.02$) greater IGF1 concentration than CON cows. The interaction between treatment and day ($P = 0.01$) demonstrated that the rbST treatment effect on IGF-1 concentration was observed primarily before calving. There was no effect of treatment on TL ($P = 0.80$) and TG ($P = 0.24$) liver content. Although GLY liver content was not ($P = 0.19$) affected by treatment, rbST125 cows tended to have greater GLY liver content compared to rbST87.5 ($P = 0.10$) and CON ($P = 0.13$) cows at −7 and 7 d relative to calving. Peripartum treatment with rbST increased serum GH concentration during the peripartum period and serum IGF1 concentration prepartum. The increased GLY liver content in rbST treated cows may indicate a more efficient use of fatty acids and sparing of glycogen as a consequence of rbST treatment.

Key Words: transition cow, recombinant bovine somatotropin, metabolism

---

0849 (M038) Vitamin D signaling enhances expression of antibacterial β-defensin genes in bovine monocytes.

C. D. Nelson*[1], K. E. Merriman[1], and J. D. Lippolis[2], *[1]Dep. of Animal Sciences, University of Florida, Gainesville, [2]USDA, ARS, National Animal Disease Center, Ames*

Vitamin D contributes to immunity of cattle via an intracrine vitamin D pathway that is activated in macrophages in response to recognition of pathogens. The 1,25-dihydroxyvitamin D_3 ($1,25(OH)_2D_3$) that is produced in that pathway activates the vitamin D receptor and regulates the transcription of vitamin D-dependent genes. RNA sequence analysis of $1,25(OH)_2D_3$–treated monocytes compared to control-treated monocytes identified bovine β-defensin 3 (DEFB3) and β-defensin 6 (DEFB6) as potential targets of the activated vitamin D receptor. The DEFB3 and DEFB6 genes encode for small antibacterial peptides and are located on bovine chromosome 27 along with DEFB1, DEFB4A, DEFB5, DEFB7, DEFB10, enteric β-defensin (EBD), lingual antimicrobial peptide (LAP), and tracheal antimicrobial peptide (TAP). The objective of this study was to evaluate the effects of $1,25(OH)_2D_3$ on expression of the β-defensin genes in resting and stimulated monocytes. Peripheral blood monocytes from eight Holstein cows were treated with 0 or 100 ng/mL lipopolysaccharide (LPS) in combination with 0 or 10 nM $1,25(OH)_2D_3$ and cultured for 24h. The mRNA transcripts for each of the β-defensin genes were measured with real-time PCR and normalized to ribosomal protein S9 transcript abundance. The effects of $1,25(OH)_2D_3$ and LPS on expression of each of the β-defensin genes was analyzed with a general linear model that accounted for effects of cow and treatment. In the non-stimulated monocytes, the $1,25(OH)_2D_3$ treatment increased DEFB3, DEFB6, DEFB7, and DEFB10 gene expression ($P < 0.05$; 10 ± 3, 17 ± 8, 4 ± 1, and 5 ± twofold change ± SE, respectively). Similarly, the $1,25(OH)_2D_3$ treatment increased DEFB3, DEFB6, DEFB7, and DEFB10 gene expression in the LPS-stimulated monocytes ($P < 0.05$; 10 ± 3, 60 ± 28, 7 ± 2, and 20 ± sixfold change ± SE, respectively). DEFB1, DEFB4A, DEFB5, DEFB13, EBD, LAP, and TAP were not affected by $1,25(OH)_2D_3$ in either resting or LPS-stimulated monocytes. In addition, LPS treatment alone did not significantly increase any of the β-defensin genes evaluated in this study ($P > 0.05$). In conclusion, $1,25(OH)_2D_3$ induces expression of the DEFB3, DEFB6, DEFB7, and DEFB10 genes in bovine monocytes. Upregulation of these β-defensin antimicrobial genes in response to $1,25(OH)_2D_3$ suggests vitamin D is needed in cattle to support innate host defense mechanisms.

Key Words: vitamin D, innate immunity

0850 (M039) Effects of genotype and transportation stress on cytokine gene expression in steers.

M. A. Sales*[1], M. Ata[1], B. Williamson[1], K. P. Coffey[1], M. L. Looper[2], and C. F. Rosenkrans[1], *[1]University of Arkansas, Fayetteville, [2]USDA-ARS Dale Bumpers Small Farms Research Center, Booneville, AR*.

The objective of this study was to determine effects of transportation stress and single nucleotide polymorphisms (SNP) in the coding sequence of two stress indicators, cytochrome P450 and the prolactin promoter region (C994G and C1286T, respectively), on gene expression of the prolactin receptor (PRLR) and three cytokines: monocyte chemoattractant protein (MCP-1 or CCL2), interleukin-8, and tumor necrosis factor (TNF)-&α. Relative gene expression was quantified

by real-time reverse transcription PCR using custom-made TaqMan assays for each gene of interest (Applied Biosystems, LifeTechnologies, Carlsbad, CA) in peripheral blood mononuclear cells of Gelbvieh x Angus crossbred steers (n = 47; mean body weight = 303 ± 39 kg; mean age = 294 ± 19 d). Three time points relative to transport (T): 27 h before (T−27), and 6 and 20 h after transport (T+6 and T+20, respectively) from Booneville, AR to Stillwater, OK (386 km) were evaluated. Time relative to transport, genotype, and their interaction affected ($P < 0.05$) gene expression. A C1286T x time interaction affected ($P < 0.01$) CCL2 expression: lowest level was in CT steers at T+6. Time affected ($P < 0.01$) PRLR and TNF-&α; expression in both C994G and C1286T genotypes: highest level was at T+20, whereas expression at earlier time points was similar. Genotype affected CCL2 expression on both C994G and C1286T genotypes: expression levels were lowest ($P < 0.0001$) when steers were CT for the C1286T SNP, or CC ($P < 0.01$) for the C994G SNP. Genotype effects on PRLR and TNF-&α expression were evident only in C1286T genotypes: greatest ($P < 0.01$) expression of both genes was in CC steers. Our findings suggest that genotypes at C994G and C1286T SNP sites influence cytokine gene expression and may therefore be used as biomarkers for animal tolerance to shipping stress. Investigating effects of other stressors before and/or after transport on the expression of other stress response genes will help identify critical control points when developing practical and/or therapeutic measures to reduce transport stress.

Key Words: cytochrome P450, cytokine, prolactin

0851 (M040) prevalence and molecular identification of *Cryptosporidium* spp. in lambs on the Huasteca Alta region, State of Veracruz, México. S. S. Gonzalez[1] and I. Vitela-Mendoza*[2], [1]*Colegio de Postgraduados, Montecillo Estado de México,* [2]*Instituto Tecnologico El LLano, Aguascalientes, México.*

Cryptosporidium is a protozoan parasite that causes enteric infection in several mammalian species, including humans. This infection has a major impact in immunocompromised domestic mammals and public health because the parasite oocysts are resistant to environment and can contaminate food and water. In sheep, cryptosporidiosis is presented with mild to severe yellowish diarrhea, plus weight loss, depression, abdominal pain, and eventually the animal may die; usually, it is more common in lambs 1 to 30 d old. Therefore, the objective of this study was to determine the prevalence of *Cryptosporidium* spp., and identify the species of the oocysts in lambs maintained in extensive grazing systems at the Huasteca Alta region, Veracruz, México. From March to June 2012, 210 fecal samples were collected from Blackbelly x Pelibuey lambs 7 to 21 d old from 21 flocks located in seven locations at the Huasteca Alta region. The samples were processed by performing a fecal smear and then dyed by the Kinyoun acid-alcohol resistant staining, and then were observed with a microscope (LCD Digital Leica) at 100 X. A molecular diagnosis was performed using nested PCR to amplify the region of the 18S rRNA gene of the parasite (830 bp), and the positive samples were sequenced. The overall prevalence of *Cryptosporidium* spp. infection in lambs was 19.5%: 10.5% in 7 to 14 d old, and 9% in 15 to 21 d old. The prevalence in flocks ranged from 10 to 40%, and in 62% of them there was at least one infected lamb. In the seven locations positive lambs were detected, and the highest prevalence was observed in Tamiahua (36.67%). The sequenced samples had a homology between 96 and 100% with the 18S rRNA region of *C. parvum*. This is the first report of the presence of *C. parvum* in lambs in the Mexican tropic.

Key Words: *Cryptosporidium*, sheep, genotyping.

0852 (M041) Bacteriological culture and California Mastitis Test results of non-clinical quarters from cows with clinical mastitis. A. Lago[1] and N. Silva-del-Rio*[2], [1]*DairyExperts, Tulare, CA,* [2]*VMTRC, University of California, Tulare.*

The economic value of lactation therapy of subclinical mastitis with antibiotics is generally considered to be limited because of the cost of milk discarded during the withdrawal period. However, the treatment of quarters affected with subclinical mastitis when treating other quarters affected with clinical mastitis does not result in additional discarded milk. The objectives of this study were: a) describe bacteriological culture results of non-clinical quarters in cows affected with clinical mastitis; and, b) validate the California Mastitis Test (CMT) to identify subclinically infected quarters in these cows. A total of 109 cows with clinical mastitis from two dairy herds were identified with clinical mastitis at the general parlor and moved to a hospital pen, where they were milked at a hospital parlor. At the first milking at the hospital parlor, the CMT was performed and a milk sample was aseptically collected for culture from all quarters (clinical and non-clinical). Bacteria were isolated from 52% of the 110 quarters affected with clinical mastitis and from 35% of the other 319 non-clinical quarters. Coliforms (35%), non-agalactiae Streptococcus (25%), and coagulase-negative Staphylococcus (23%) were the bacteria most commonly isolated from clinical quarters. In non-clinical quarters coagulase-negative Staphylococcus (49%), *Bacillus* spp. (21%) and non-agalactiae Streptococcus (13%) were the bacteria most commonly isolated. Of all cows with clinical mastitis, 67% of them had bacteria isolated from at least one of the three non-clinical quarters. If also considering the quarter affected with clinical mastitis, 82% of the cows had at least one quarter infected. The CMT was evaluated for three diagnostic interpretations: identify bacterial growth, identify gram-positive bacterial growth, and identify non-agalactiae streptococci infections. The sensitivity of the CMT was 38, 43, and 29%, and the specificity 71, 70, and 68% for each one of the diagnostic interpretations, respectively. Therefore, the

CMT was not a sensitive enough tool for the identification of subclinically infected quarters in cows with clinical mastitis. The high proportion of infected non-clinical quarters in cows with clinical mastitis may warrant the need to evaluate the efficacy and cost-benefit of treating clinical and subclinical quarters simultaneously.

Key Words: clinical mastitis, subclinical mastitis, California Mastitis Test

---

0853 (M042) Effect of early feed restriction programs on IgY production of broiler chickens. M. L. Moraes*, F. M. Butzen, M. M. Vieira, C. M. M. Pimente, and A. M. L. Ribeiro, *Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil.*

It is known that feed restriction increases antibody production in poultry, but very little research exists exploring the after effects of feed restriction on the adaptive immune system. The objective of this experiment was to evaluate the effects of different programs of early feed restriction on IgY production in broiler chickens. A total of 384 Cobb 500 male broiler chicks were randomly assigned to 24 pens at d 1 of age. The study lasted 42 d. After a week adaptation period, four treatments were applied from d 8 to 16: T1– control group, standard diet (SD); T2– quantitative feed restriction (80% of ad libtum feed intake of the SD, according to the breeder management guide); T3– feed restriction by time (SD offered during 8 h/day); and T4– qualitative feed restriction (80% of the limiting nutrients; SD was diluted by the addition of 10% kaolin and 10% rice husk). At d 7 and 21, birds were injected with bovine serum albumin (BSA), and blood samples were collected weekly from d 7 to 42 for assessment of IgY anti-BSA production. There was no effect ($P > 0.05$) of the first BSA inoculation between treatments; however, at 28 d of age, birds in all the three early feed restriction programs had higher IgY anti-BSA than the control group ($P < 0.05$). At d 35, the quantitative and the by time feed restriction groups still showed residual effects of the BSA injection, but no difference ($P > 0.05$) was observed between the four treatments at 42 d. It is concluded that the three different programs of early feed restriction had beneficial effect on the humoral immune system after the restriction program had ended. Overall, the quantitative and the by time feed restriction programs promoted the longer lasting responses.

Key Words: chicken, feed restriction, IgY

0854 (T001) Immune status of dairy heifer calves in the northern plains of Costa Rica. Year III.

J. A. Elizondo-Salazar*[1], J. J. Arroyo-Arroyo[2], J. Sanchez-Salas[3], and J. Heinrichs[4], *[1]Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, [2]Universidad de Costa Rica, San José, [3]Cooperativa de Productores de Leche Dos Pinos R.L, San Jose, Costa Rica, [4]Pennsylvania State University, University Park.*

The objective of this study was to characterize the immune status of dairy calves in the northern plains of Costa Rica. The results correspond to total serum protein (TSP) measurements obtained from 657 female calves in 23 dairy farms during the period of August and November 2012. Dam breeds were classified into Holstein, Jersey, Holstein x Jersey crosses, and other. Blood samples were collected between d 1 and 7 of age into serum (red top) Vacutainer tubes, refrigerated overnight, centrifuged, and the serum separated from clot within 24 h of collection. A hand-held refractometer was used to measure STP. For the purpose of this study, failure of passive immunity was considered when TSP concentration was less than 5.5 g/dL. GLM procedure was used to establish differences between parity and breed of the dams. Descriptive statistics were generated to define percentage of failure of passive transfer by breed and parity of the dam. TSP concentration ranged from 2.4 to 10.0, with an overall mean of 5.7 g/dL. Of all the calves evaluated, 44.9% presented failure of passive transfer. Calves born to Jersey and Holstein x Jersey crosses had significantly higher TSP concentrations than calves born to Holstein and other breeds. When considering lactation number of the dam, offsprings born to third lactation cows showed the lowest percentage of calves with inadequate transfer of immunity. The findings of this study suggest that colostrum management practices should be placed to minimize the risk of failure of passive transfer in dairy herds in the northern plains of Costa Rica.

Key Words: total serum protein, immunoglobulins, passive immunity

0855 (T002) Passive transfer of immunity of dairy calves in the central northern region of Costa Rica.

J. A. Elizondo-Salazar*[1], O. A. Vargas-Villalobos[1], L. Noguera-Solera[2], and J. Heinrichs[3], *[1]Estación Experimental Alfredo Volio Mata, Facultad de Ciencias Agroalimentarias, Universidad de Costa Rica, [2]Cooperativa de Productores de Leche Dos Pinos R.L, Alajuela, Costa Rica, [3]Pennsylvania State University, University Park.*

The objective of this study was to characterize the immune status of dairy calves in the central northern region of Costa Rica. The data correspond to total serum protein (TSP) measurements obtained during the period of August and November 2012 in 47 dairy farms. Three hundred thirty-seven female and 127 male calves were sampled. Dam breeds were classified into Holstein, Jersey, Holstein x Jersey crosses, and other. For the purpose of this study, failure of passive immunity was considered when TSP concentration was less than 5.5 g/dL. TSP concentration ranged from 3.0 to 10.0, with an overall mean of 5.7 g/dL. Of all the animals evaluated, 40.5% had failure of passive transfer. When sex of the calves was considered, 39.2% of females and 44.1% of males failed to obtain adequate concentration of TSP, and there were no significant differences (5.8 vs. 5.7 g/dL, respectively) ($P > 0.05$). Calves born to Holstein cows had significantly lower TSP concentrations than calves born to other breeds ($P > 0.05$). When considering calving of the dam, there were no significant differences on TSP concentration of calves; however, offspring born to fourth lactation cows showed the highest percentage of animals with inadequate transfer of immunity. Calves that were allowed to suckle their dams showed a 48.8% failure of passive immunity against 34.1% of calves that were given colostrum by bottle. The findings of this study suggest that colostrum management practices should be placed to minimize the risk of failure of passive transfer in dairy herds in the central northern region of Costa Rica.

Key Words: total serum protein, immunity, passive immunity

0856 (T003) Effects of added spray-dried whole colostrum and spray-dried plasma on veal calf health and performance.

D. Wood, R. Blome, and J. Sowinski, Animix, Juneau, WI.*

The study objective was to evaluate the effects on calf health and performance from supplementing either whole spray-dried colostrum (SDC) or additional spray-dried plasma (SDP) on top of a spray-dried plasma-containing (5.2% plasma inclusion rate, otherwise all-milk) veal starter formula (fed d 1 to 57) and a spray-dried plasma-void veal finisher formula (fed d 58 to 140). Auction-sourced Holstein bull calves ($n = 128$; approximately 1 wk of age) were randomly placed in individual, raised stalls for 10 wk and were then reared as pairs loose-

housed. Treatment pairs were equally placed within each row, i.e., calves in stalls 1 and 2 were fed supplemental WPC/dry fat blend control (WPC), calves in stalls 3 and 4 were supplemented SDP/dry fat blend, and calves in stalls 5 and 6 were supplemented SDC. SDC contained 13% IgG and SDP/dry fat blend was formulated to also contain 13% IgG. Both SDC and WPC were 44.3% CP and 18.1% fat. To be formulated with 13% IgG and 18.1% fat, SDP had to contain 57.3% CP, resulting in SDP-fed calves receiving an additional 200 g of CP over the feeding period verses SDC or WPC. Calves experiencing FPT (< 5.5 g/dL serum total protein) were 70.4, 76.2, and 83.3% of all calves in WPC-, SDP- and SDC-fed groups, respectively. The calves were fed formula and supplemented 25 g/feeding (2x/day) of the respective supplement wk 1, 15 g/feeding wk 2, 10 g/feeding wk 3 through 5, 5 g/feeding wk 6 and 7, and 2.5 g/feeding wk 8 through 20, when slaughtered. Accounting for total solids intake, calves were started on a 25:18 (CP:Fat), increased to 871 g/day of a 21:18 by 21 d age (medicated to d 21) and 1742 g per day of a 20:18 by 53 d age. Calves received no dry feed. Data was analyzed using F-test for variances and student *t* test comparing two means. Calves fed additional SDP outgained ($P < 0.05$) WPC by +2.52 kg d 1 through 53 (SDC was intermediary). SDC tended ($P < 0.077$) to outgain WPC by +8.57 kg d 53 through 140 (SDP was intermediary). SDP and SDC reduced incidences of refusals ($P < 0.05$). SDC tended ($P < 0.082$) to reduce the number of calves treated verses SDP (WPC intermediary). SDC and SDP improved intake. SDP improved 53-d gains.

Key Words: calf, colostrum, plasma

0857 (T004) Holstein calves fed non-saleable milk that was pasteurized or raw had decreased incidence of abnormal feces and hematology measures than calves fed accelerated milk replacer.

L. E. Hulbert[*1], J. A. Noel[2], S. C. Trombetta[1], S. R. Montgomery[1], G. A. Hanzlicek[3], and B. J. Bradford[1], *[1]Dep. of Animal Sciences and Industry, Kansas State University, Manhattan, [2]Kansas State University, Manhattan, [3]Diagnostic Medicine Pathobiology, College of Veterinary Medicine, Kansas State University, Manhattan.*

The objectives were to determine the health and blood parameters before, during, and after weaning of 114 Holstein heifers fed either accelerated milk-replacer (Mrp; 28% CP, 18% fat) or non-saleable milk (3.59 ± 0.28% True-Protein; 4.12 ± 0.37% fat) that was either pasteurized (*P*st) or raw (Raw; refrigerated and fed < 24 h after collection). Calves were randomly assigned feeding treatments at age 0 d. Colostrum (1 L) was fed in less than 14 h after birth (Mrp and Pst = pasteurized colostrum; Raw = raw colostrum). All calves were bottle-fed 1.8 ± 0.20 SD L, 3x/day; all calves were provided fresh water and grain ad libitum throughout the experiment. Calves began step-down weaning at age 5 wk and completed weaning at age 6 wk. Blood samples were collected at ages 3, 5, and 7 wk and were analyzed for complete blood counts (CBC) using a Procyte Idexx Analyzer. In addition, whole blood was tested for bactericide capacity against live *E. coli* 51813 (%Bact). Fecal scores were observed twice daily, on a 1-to-3 scale (FS1 = normal, FS2 = loose, FS3 = scours). The Mrp-fed calves had more ($P < 0.01$) observations (% obs) with FS2 than the Pst- and Raw-fed calves (13.2 vs. 7.32 and 8.9 ± 0.69% obs, respectively), although there were few scouring (FS3; 0.36 ± 0.01% obs) incidences in this experiment. Likewise, Mrp-fed calves had greater hematocrit % compared to the other calves ($P < 0.01$), but Pst- and Raw-fed calves had similar hematocrit % (32.4 vs. 27.9 and 28.4 ± 0.55%, respectively). At age 3 wk, Mrp-fed calves had greater circulating monocytes ($P = 0.02$) compared to the other calves, but there were no differences between Pst- and Raw-fed calves (10.4 vs. 9.2 and 8.2 +0.40%, respectively). Although there were no differences among treatments for % Bact or other hematological measures ($P > 0.10$), all calves had lower neutrophil:lymphocyte, more circulating monocytes and greater % Bact at age 7 wk compared to ages 3 and 5 wk ($P < 0.05$), suggesting that the change in diet from milk or MR to grain influences innate immune and hematological measures. The increased incidence of abnormal fecal scores among Mrp-fed calves and higher hematocrit percentages needs further consideration, especially before age 3 wk. In addition, these findings suggest that raw milk may be adequate for maintaining healthy CBC and fecal score measures on a well-managed, low-disease incidence dairy.

Key Words: milk replacer, pasteurization, calves, hematology

0858 (T005) Effects of Celmanax supplementation to prepartum dairy cows on colostrum quality and the subsequent growth and health of their calves.

C. Campos-Granados[*1], A. Rojas-Bourrillon[1], and C. C. Elrod[2], *[1]University of Costa Rica, San Jose, [2]Vi-COR, Inc., Mason City, IA.*

The objective of this study was to assess the effects of supplementing prepartum dairy cows with a product derived from yeast culture and enzymatically hydrolyzed yeast cell wall (Celmanax (CEL), Vi-COR, Mason City, IA) on colostrum quality and the subsequent health and performance of their calves. Thirty prepartum multiparous Jersey cows were blocked by parity, body condition 21 d before expected calving date and productive and reproductive performance, and randomly assigned within block to one of two treatments ($n = 15$) from 21 d before expected calving date until calving. Rations were top-dressed with CEL at the rate of 0 or 40 g/d throughout the experiment. Calves were fed 3 L of colostrum from their dam within 2 h of birth and then 4 L of whole milk daily through wk 8. Total Ig in colostrum from each cow was evaluated at 25°C from the first milking with a Colostrometer, and a sample was taken for determination of IgG by ELISA.

Approximately 48 h after birth, a blood sample was drawn by venipuncture from each calf for the determination of serum protein by refractometer and IgG by ELISA. Daily feed intake, weekly weight and hip height, and the incidence of pneumonia and scours were recorded. Data were analyzed using mixed models with repeated measures over time. Total Ig in colostrum was significantly increased by CEL treatment ($P < 0.05$; 90.06 ± 23.74 vs. 105.94 ± 17.59 mg/mL for 0 and 40 g/d, respectively) but there was no effect on colostrum yield or IgG content ($P > 0.05$). There was no effect of treatment on birth weight, serum protein, or serum IgG ($P > 0.05$). Average daily gain (382.86 ± 61.20 vs. 410.94 ± 51.22 g/day for 0 and 40 g/day, respectively), hip height increase (1.45 ± 0.33 vs. 1.70 ± 0.31 cm/week for 0 and 40 g/d, respectively), and feed consumption (446.67 ± 9.92 vs. 439.01 ± 6.12 g/day for 0 and 40 g/d, respectively) were not affected by treatment ($P > 0.05$). Odds ratios were calculated and the odds of a calf presenting with scours or pneumonia were 3.5 and 5.0, respectively, times more likely in the calves whose dams did not consume CEL prepartum. CEL supplementation prepartum improved colostrum quality and calf health.

Key Words: immunity, transition cow, calf, health, yeast culture.

0859 (T006) Maternal energy status during mid-gestation affects the immune response in the resultant beef offspring. A. R. Taylor*[1], D. A. Mohrhauser[1], R. Neiger[1], E. J. Blom[1], K. R. Underwood[1], R. H. Pritchard[1], A. E. Wertz-Lutz[2], B. P. Holland[3], and A. D. Weaver[4], *[1]South Dakota State University, Brookings, [2]ADM Alliance Nutrition, Inc., Quincy, IL, [3]Merck, Volga, SD, [4]South Dakota State University, Rapid City.*

Fetal or developmental programming relates the effects of maternal stressors on the developing fetus and potential consequences later in life. Specifically, beef cattle may experience decreased forage availability and quality during gestation, potentially altering nutrient availability and ultimately fetal development. Immune function has major economic implications in the beef industry; however, the understanding of maternal environment on development of the immune system in beef offspring is limited. Therefore, the objective of this study was to determine the effects of maternal energy status during mid-gestation on humoral immune response and tissue morphology of immunologically relevant tissues in beef offspring during the feedlot phase. Beef cows were allotted to one of two treatments: 1) Positive Energy Status (PES; $n = 76$)-fed to maintain BCS 5.0–5.5; or 2) Negative Energy Status (NES; $n = 75$)-fed to lose 1 BCS over the ensuing 91-d mid-gestation period (84 ± 11 d). Following treatment, cows were commingled and managed as a common group through weaning. Calves were weaned, shipped, and allotted into feedlot pens according to gender, dam energy status, and stratified by weight. A subsample ($n = 30$) of calves were subcutaneously injected with 4 mg ovalbumin antigen at d 0 of antigen challenge and again on d 28 of antigen challenge, with blood collected every 7 d from d 0 through d 56 to measure antibody titers. An ELISA was used to determine serum antibody titers in response to the ovalbumin challenge. Additionally, a subsample of calves were harvested following the receiving ($n = 12$) and finishing period ($n = 12$) for histological examination with hematoxylin and eosin stain of lymph nodes, spleen tissue, and gut-associated lymphoid tissue. Ovalbumin data were analyzed as a repeated measures model using the PROC MIXED of SAS (SAS Inc., Cary, N.C.). No morphological differences were observed in tissues. There were no differences ($P > 0.05$) in gender main effects in response to a novel antigen. An anamnestic response was observed over time ($P < 0.05$), which was expected following second exposure to the antigen. There was a difference ($P < 0.05$) between treatments over the sampling period with calves from PES cows having a greater antibody titer of 13.44 compared to calves from NES cows with an antibody titer of 12.38. These results suggest cows in a NES during mid-gestation produce calves with a decreased ability to produce antibodies to a novel antigen and thus a decreased humoral immune response.

Key Words: cattle, fetal programming, immunology

0860 (T007) Comparison of ivermectin and extended-release eprinomectin deworming treatment on stocker and subsequent feedlot performance and carcass characteristics of fall-born Angus heifers. C. A. Clark*[1], B. J. Dedrickson[2], J. L. Sorensen[2], and P. J. Gunn[3], *[1]Armstrong Memorial Research and Demonstration Farm, Iowa State University, Lewis, [2]Merial, Duluth, GA, [3]Iowa State University, Ames.*

The objective of this study was to compare the effects of ivermectin and extended-release eprinomectin on stocker and feedlot performance as well as carcass characteristics. Sixty purebred, fall-born Angus heifers (277 ± 23 kg BW; 4.90 ± 0.34 BCS) were blocked by BCS and BW, and allotted to one of two injectable deworming treatments after 35 d of grazing summer pasture: 1) ivermectin (Ivomec; IVO), or 2) extended-release eprinomectin (LongRange; LR). Concurrent fecal samples were taken at treatment initiation. Heifers were placed back on the same pasture until the pasture was no longer suitable for grazing (total of 63 d). Interim BW was taken 27 d after treatment initiation, and fecal samples, BW, and BCS were taken at grazing termination. At grazing termination, heifers were transported to a feedlot where they remained commingled and fed a finishing ration for 150 d. Upon arrival, heifers were stratified by BW within grazing treatment and allotted to either receive (Ivomec; DWRM) or not receive a deworming treatment at processing (NO). Fecal samples were collected 4 d before transport for slaughter. Carcass data were collect by the Tri-County Steer Carcass Futurity. Binary

and continuous data were analyzed using the GLIMMIX and PROC MIXED of SAS, respectively. Heifer BW and BCS did not differ between treatments throughout the grazing period ($P \geq 0.67$). Although ADG did not differ during the first 27 d, LR heifers had greater overall ADG and increased BW change ($P = 0.01$) during the grazing period. Although fecal egg count (FEC) did not differ at treatment initiation, FEC was greater in IVO (5.138 eggs/g) than LR (0.073 eggs/g) heifers at grazing termination ($P < 0.01$). Final fecal egg counts were nearly undetectable before transport to slaughter and did not differ ($P \geq 0.16$). There were no differences in feedlot performance or carcass characteristics due to grazing period, feedlot period or the interaction between the two treatments ($P \geq 0.09$). Based on data presented in this study, in cattle that have been effectively managed to reduce or eliminate internal parasite infection during a grazing period, there may be no benefit to deworming at feedlot arrival. However, even at extremely low, subclinical levels of infection during the stocker phase, parasites can have a significant impact on performance. These data highlight the importance of parasite control during the stocker phase, even at subclinical infection levels.

Key Words: feedlot, parasite, stocker

0861 (T008) Effect of rumen and fecal inocula from calves fed either milk replacer or whole milk fed on intestinal cells and digestive tract microbiota.

M. Terré*[1], S. Genís[1], C. Yunta[1], A. Bach[2], and A. Arís[1], *[1]IRTA, Caldes de Montbui, Spain, [2]Dep. of Ruminant Production, IRTA, Caldes de Montbui, Spain.*

The objective of this study was to evaluate cell viability and inflammatory status of intestinal cells incubated with rumen and fecal inocula obtained from Holstein calves fed either a milk replacer or whole milk. Liquid rumen and fecal samples were obtained from 10 calves at 5 wk of age. Calves were either fed a milk replacer supplemented with *Enterococcus faecium* at the rate of $1.5x10^9$ cfu/kg (MR), or whole milk (WM). Samples from each group of animals (five animals per group) were pooled, centrifuged, and suspended with PBS at 3%. *Lactobacillus and Bifidobacteria* were quantified by qPCR from the rumen and fecal-pooled samples. The experiment was repeated twice with 10 other calves fed similarly. Jejunum tissue from 12-mo-old bulls was collected at a slaughterhouse to obtain jejunum primary cells and perform further in vitro experiments. Jejunum cells were cultured during 6 h with the fecal and ruminal inocula in 24-well plates at 37°C under a 5% CO_2 atmosphere. After the incubation, the supernatant was recovered to determine LDH activity as a cell damage marker. Cells were washed and lysed with TriZol (Invitrogen) to extract RNA and quantify, by qPCR, the expression of TNFα as an inflammation marker. Data were analyzed with a mixed-effects model considering sample and milk type as fixed effects, and period as random effect. *Bifidobacteria* and *Lactobacillus* contents were greater ($P < 0.05$) in feces (15.6 ± 1.04 and 14.1 ± 0.73 Ct, respectively) than in rumen (21.8 ± 1.04 and 21.8 ± 0.73 Ct, respectively) samples, and *Bifidobacteria* contents tended ($P = 0.10$) to be greater in samples from MR than in those from WM calves (17.1 vs. 20.2 ± 1.04 Ct, respectively). Viability of jejunum cells and the expression of TNFα were similar when cultured with rumen inoculum from MR and WM calves. However, LDH activity was greater ($P < 0.05$) in jejunum cells (less cell viability) when incubated with fecal inoculum from WM (0.50 ± 0.296 mU/mL) than from MR (0.14 ± 0.296 mU/mL) calves. The expression of TNFα was greater ($P < 0.05$) when cells were incubated with MR ($8.8x10^5 \pm 8.89x10^6$) than with WM ($3.2x10^5 \pm 8.89x10^6$) fecal inoculum. In conclusion, fecal inoculum from MR calves improve cell viability and trigger the inflammatory status of intestinal jejunum cells when compared with WM fecal inoculum. These effects might be mediated by the greatest amount of *Bifidobacteria* in the fecal samples from MR calves, which might be favored, by the presence of *Enterococcus faecium*in the milk replacer.

Key Words: jejunum primary cells, milk replacer, whole milk

0862 (T009) The effect of four antiseptic compounds on umbilical cord healing and infection rates in the first 24 h in dairy calves from a commercial herd.

A. L. Robinson*, L. L. Timms, K. Stalder, and H. D. Tyler, *Iowa State University, Ames.*

The objective of this study was to compare the effect of four umbilical dips on the healing rate and incidence of infection of umbilical cords in newborn calves ($n = 60$). Late gestation Jersey cows were monitored at a commercial farm (Sioux Jersey; Salix, IA) and newborn purebred ($n = 30$) and crossbred ($n = 30$) calves were obtained within 30 min after birth. Calves were alternately assigned by birth order to four treatment groups: 7% iodine, 1000 ppm chlorine created using a novel chlorine disinfectant technology (ECAlogix System– Zurex Pharmagra), chlorohexidine, and ZuraLac (Zurex Pharmagra). Before dipping (within 30 min of birth), diameter of the umbilical cords (as an indicator of cord drying and healing) were determined using digital calipers. In addition, as an indicator of umbilical infections, surface temperature of the umbilical stump (along with a reference point at the midpoint of the sternum) was determined using a dual laser infrared thermometer (model 42570, Extech Instruments Nashua, NH). These measurements were all repeated at 24 ± 1 h of age. All data were analyzed using mixed model methods (PROC MIXED, SAS version 9.2). All models included the fixed effects of breed (Jersey or Jersey cross), sex (bull or heifer) and treatment. Fixed effect interactions were not included in the statistical model due to the relatively small sample size. There were no treatment differences ($P > 0.05$) for healing rate of umbilical cords. Initially, mean umbilical cord diameter was 22.84 ± 3.89 mm, and they healed to a mean diameter of 7.64 ± 4.12

mm at 24 h of age. Similarly, there were no treatment effects ($P > 0.05$) on incidence of umbilical infections. Mean surface temperature of the umbilical stump was 33.1 ± 2.2° at birth (1.5 ± 1.6° higher than the sternal reference temperature) and at 24 ± 1 h of age the mean temperature of the umbilical stump was 33.0 ± 4.3° (0.5 ± 1.8° lower than the sternal reference temperature). These data suggest that these dips are equally effective for preventing infections and permitting healing of the umbilical cord when used within 30 min of birth.

Key Words: calves, umbilical cord, umbilical dip

0863 (T010) Relationship between birth weight and calving ease with passive transfer of immunoglobulins in neonatal beef calves.

J. J. Gaspers*[1], G. Stokka[2], B. W. Neville[3], and C. R. Dahlen[1], *[1]North Dakota State University, Fargo, [2]North Dakota State University, Cooperstown, [3]North Dakota State University, Streeter.*

The absorption of immunoglobulins (Ig) found in the colostrum is a passive transfer of immunity that neonatal calves will receive from their dams. Calves that do not receive adequate levels of Ig from their dams can experience increased morbidity and mortality. Primiparous commercial crossbred beef heifers ($n = 53$) were used to evaluate the relationship of Ig absorption from colostrum and passive transfer of immunity on various neonatal traits. Heifers calved in March and April. Females were kept in a dry lot and fed a total mixed ration meeting 100% of NRC requirements through parturition. Onset of the third stage of labor, time to birth, time to stand, and time of first nursing were recorded. Calving ease (CE; 1 = no assistance, 5 = caesarian section), calf vigor (CV), birth weight, and 24-h blood samples for serum Ig were taken from each calf via jugular venipuncture. Mothering score, colostrum samples for colostral Ig, weight, body condition score, udder suspension (1 = broken floor, 9 = very tight), and teat size (1 = very large, 9 = very small) were recorded from the dams. All statistical analyses were conducted using PROC Reg and PROC Corr in SAS. There was a negative correlation between serum IgG and CE ($P = 0.01$), positive correlations between birth weight and CE ($P < 0.001$), and udder suspension and teat size ($P = 0.001$). A tendency for a negative correlation was found between serum IgG and birth weight ($P = 0.11$) and a positive correlation between serum IgG and teat size ($P = 0.10$). After correlations were found, stepwise regression calculations were completed on all significant correlative variables. A linear regression was found between CE and serum IgG ($P = 0.01$), and quadratic regression between birth weight and serum IgG ($P = 0.04$). Difficulties during third stage labor increased as calf birth weight increased. The increases in CE scores were associated with decreased serum IgG found in the calf after 24 h. This depression of serum IgG due to calving difficulty may impair the ability of calves to adequately defend against pathogen exposure and may influence subsequent growth and performance.

Key Words: beef, immunoglobulins, neonate

ANIMAL HEALTH: COW AND HEIFER HEALTH

0864 (W026) Identification of serum innate immunity reactants in transition dairy cows before clinical signs of laminitis. G. Zhang*, D. M. Hailemariam, E. Dervishi, Q. Deng, S. A. Goldansaz, S. M. Dunn, and B. N. Ametaj, *Dep. of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Laminitis (LAM) is prevalent in dairy cows and early diagnosis and timely treatment of the disease can lower animal suffering, improve recovery rate, increase longevity, and minimize cow loss. However, there are no indications of disease until it appears clinically, and presently the only approach to deal with the sick cow is intensive treatment or culling. The objective of this study was to identify potential predictive biomarkers of LAM in transition dairy cows. Blood samples were collected from the coccygeal vein once per week before morning feeding from 100 multiparous Holstein dairy cows during −8, −4, disease diagnosis, and +4 wks relative to parturition. Six healthy cows (CTR) and six cows that showed clinical signs of disease (i.e., LAM) were selected for intensive serum analyses. Concentrations of 3 cytokines interleukin-1 (IL-1), interleukin-6 (IL-6), and tumor necrosis factor-α (TNF-α); 3 acute phase proteins (APPs) haptoglobin (Hp), serum amyloid A (SAA), and lipopolysaccharide binding protein (LBP), as well as 3 metabolites lactate, non-esterified fatty acids (NEFA), and β-hydroxybutyrate (BHBA), were measured in serum by ELISA or colorimetric methods. Health status, feed intake, rectal temperature, and milk yield was monitored for each cow during the whole experimental period. Data were processed statistically by PROC MIXED of SAS 9.2. Results showed that cows affected by LAM had greater concentrations of lactate, IL-6, SAA, and LBP in the serum vs. CTR. Most interestingly, enhanced serum concentrations of lactate, IL-6, SAA, and LBP at −8 and −4 wk before parturition were significantly different in cows with LAM as compared with the CTR ones. The disease also lowered the overall milk production and feed intake as well as milk fat and fat:protein ratio. In conclusion, LAM affected serum concentrations of the several parameters related to innate immunity and carbohydrate metabolism that might be serve to monitor health status of transition dairy cows. At this point we are not certain whether these are typical LAM biomarkers or indicators of general disease state. More research is warranted to validate these data.

Key Words: dairy cows, innate immunity, laminitis

0865 (W027) Milk yield and reproductive performance of Holstein cows seropositive for tuberculosis. D. S. Resendiz*, *Universidad Autónoma Agraría Antonio Narro, Torreon, México.*

Bovine tuberculosis is a critical, debilitating and chronic disease of dairy cattle in intensive systems. Studies done in the past have not completely characterized the impact of this disease on productivity of cows. Therefore, the objective of this study was to find out if seropositivity for tuberculosis impairs reproductive performance and milk yield in high milk-yielding Holstein cows. For this purpose 1044 healthy cows and 105 Holstein cows seropositive for tuberculosis were used. Cows tested positive for bovine tuberculosis were from various large commercial dairy operations from the same region. Cows that reacted to an intradermal injection of tuberculin were transferred from their barns to an isolated new dairy facility. Cows free from this disease were placed in the same barn as the seropositive cows, but in an isolated division and served as control animals. The GENMOD, npar1way, and LIFETEST procedures of SAS (SAS Inst., Inc., Cary, NC, USA) were used to assess the significance of treatment on reproductive variables. The reproductive performance of positive reactors was impaired; overall pregnancy per artificial insemination differed ($P < 0.05$) between seropositive and healthy cows (16.9 vs. 20.7). Seropositive animals required 4.52 ± 2.94 services per pregnancy compared with 4.34 ± 2.72 for control cows. The intervals between calving and conception were similar between seropositive (154 ± 78 d) and seronegative animals (150 ± 77 d). Control cows tended ($P = 0.08$) to produce more milk than seropositive cows over a 305-d lactation (10,684 ± 1720 vs. 10,345 ± 1736; three milkings per day, mean ± SD). It was concluded that cows tested positive for bovine tuberculosis exert a mild but significant negative effect on both reproductive performance and milk yield.

Key Words: tuberculosis, bovine, milk

0866 (W028) Behavior of lactating dairy cows under mild and severe heat stress with free access or not to shadow. V. Fischer*[1], E. Forgiarini Vizzotto[1], A. Susenbach de Abreu[1], A. Thaler Neto[2], M. Tempel Stumpf[1], D. Werncke[1], and F. André Schmidt[2], *[1]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil, [2]Universidade Estadual de Lages, Brazil.*

In the tropics, during several months of the year, air temperatures are well above the upper critical temperature for lactating dairy cattle. Despite this fact, many dairy farmers still do not provide shade. The objective of this trial was to study the behavior of dairy cows with or without access to shadow under mild (afternoon THI = 74.7) and severe heat stress (afternoon THI = 81.2). Twenty-eight Holstein cows in mid-lactation producing 21 ± 3 L per day were used. Cows were

Table 0866.

Attribute	P > F (interaction)			Heat stress					
				Mild			Severe		
	Heat stress severity	Access to shadow	Heat stress x access to shadow	with shadow	without shadow	P > F	with shadow	without shadow	P > F
Walking (min)	0.0140	0.0001	0.0001	19.6	31.1	0.0323	12.1	52.0	0.0001
Ruminating (min)	0.0001	0.3382	0.0001	175.4	142.3	0.0021	13.1	61.0	0.0001
Grazing (min)	0.3308	0.0001	0.0001	219.0	232.0	ns	257.9	169.2	0.0001
Idling (min)	0.0001	0.1926	0.0436	192.3	201.8	ns	271.0	230.1	0.0243
Lying (min)	0.0054	0.0001	0.0001	158.6	151.8	ns	186.7	50.0	0.0001
Body temperature (°C)	0.0072	0.0001	0.0112	39.6	40.0	0.0298	39.64	40.68	0.0001

split into four groups according to heat stress intensity (mild and severe) and access to shadow (with and without). Behavior of all cows was visually observed from 0600 h to 0900 h for 4 d, and time spent grazing, ruminating, idling, walking, lying, and number of water ingestion bouts were recorded. Body temperature and respiratory rate were recorded at 1800 h. Data was submitted to analysis of variance according to a completely randomized design considering main effects of heat stress severity ($n = 2$), access to shade ($n = 2$) and their interaction. Respiratory rate was greater under severe compared with mild heat stress (100.8 × 72.8, $P < 0.001$) and when no shadow was provided compared with free access to shadow (98.9 × 74.7, $P < 0.001$). Significant interactions were detected for time spent ruminating, grazing, walking, idling, lying, and for body temperature. Shadow was beneficial even under mild heat stress, as cows spent less time walking and spent more time ruminating, but provision of shadow did not improve time spent grazing, idling or lying. Under severe heat stress, provision of shadow helped cows in reducing walking time and allow acceptable values for time spent grazing, idling, and lying besides body temperature, but it was unable to keep ruminating time. Dairy cattle should have free access to shadow independently of severity of heat stress.

Key Words: behavior, heat stress, shadow

0867 (W029) Risk factors for hypocalcemia incidence and their effect on milk yield and reproduction in a grazing Jersey, Guernsey, and Holstein herd in Costa Rica.

A. Saborío-Montero*, and J. M. Sánchez, *Centro de Investigaciones en Nutrición Animal y Escuela de Zootecnia, Universidad de Costa Rica, San José.*

The aim of this study was to determine risk factors for hypocalcemia (blood Ca concentration under 8.0 mg/dl) and its effect on milk yield and reproduction in three breeds of dairy cows under the same feeding, management and environmental conditions. The study was conducted on a dairy farm located in Cartago, Costa Rica, and comprised a total of 152 cows (62 Jersey, 41 Guernsey, and 49 Holstein). Average lactation number for the three breeds was 2.73 ± 1.59. During the close-up period cows grazed kikuyu grass (*Kikuyuocloa clandestina*) (14.8% DM, 23.4% CP, 54% NDF, 0.35% Ca, 0.31% Mg and 3.50% K) and were supplemented with 4 kg/animal/d of a concentrate mixture low in Ca (14% CP, 31% NDF, 0.2% Ca, 0.42% Mg and 1.38% K) and 1 kg of hay (82.3% DM, 5.1% CP, 61.4% NDF, 0.4% Ca, 0.35% Mg and 1.8% K)/d. Cows were fed 1 kg of concentrate (18.6% CP, 0.90% Ca, 0.42% Mg and 1.38% K)/2.5 to 3.0 kg of milk during lactation. Blood samples of cows within 24h from calving were taken from the coccygeal vessels and analyzed for Ca, using atomic absorption spectrophotometry, to establish relationships with productive, reproductive and inherent variables. Results are shown in Table 0867. Milk yield in the previous lactation in Guernsey, BCS at calving in Jersey and calving number in Jersey and Holstein cows were risk factors ($P < 0.05$) for suffering hypocalcemia at peripartum. Likewise, Ca concentration was related ($P < 0.05$) to actual milk yield in the succeeding lactation in Guernsey, and to calving interval in Holstein. These results suggest that Ca concentration at parturition in Guernsey cows could be driven by productive variables and in Jersey and Holstein cows seems to be related to inherent factors. These variables should be studied in a wider population for a better understanding of the causes of hypocalcemia incidence in dairy cattle.

Key Words: dairy cows, hypocalcemia, risk factors

Table 0867. Variables associated with blood Ca concentration in peripartum (calving ± 1d) according to breed

Variable	Ca concentration as association variable				Breed
	Pearson correlation		Linear regression		
	Rho	P	R^2	P	
Previous milk yield **	-0.516	0.012	0.266	0.012	Guernsey
Actual milk yield*	-0.371	0.043	0.138	0.043	Guernsey
BCS at calving**	-0.312	0.024	0.097	0.024	Jersey
Calving number**	-0.335	0.008	0.112	0.008	Jersey
Calving number**	-0.323	0.024	0.085	0.024	Holstein
Calving interval*	-0.403	0.027	0.163	0.027	Holstein

* Ca dependent variable.

** Risk factor for hypocalcemia.

0868 (W030) Activation of innate immunity in transition dairy cows before clinical appearance of milk fever. G. Zhang*, D. M. Hailemariam, E. Dervishi, Q. Deng, S. A. Goldansaz, S. M. Dunn, and B. N. Ametaj, *Dep. of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Milk fever (MF) is a metabolic disease of transition dairy cows associated with calcium imbalance at the onset of lactation. Its pathogenesis and etiology still remain unclear. The objective of this study was to identify alterations in innate immunity reactants and carbohydrate and lipid metabolites in the blood of transition dairy cows with or without MF. One hundred multiparous Holstein dairy cows were involved in the study and the experimental period lasted 16 wk from −8 wk before until +8 wk postpartum. Health status, feed intake, rectal temperature, and milk yield was monitored for each cow during the whole experimental period. Blood samples were collected from the coccygeal vain once per week before the morning feeding and stored until analyses at −80°C. Six healthy cows (CTR) and six cows that showed clinical signs of MF were selected for intensive blood analyses. Serum concentrations of lactate, non-esterified fatty acids (NEFA), β-hydroxybutyrate (BHBA), interleukin-1 (IL-1), interleukin-6 (IL-6), tumor necrosis factor-α (TNF-α), haptoglobin (Hp), serum amyloid A (SAA), and lipopolysaccharide binding protein (LBP) were determined. Feed intake, milk production and composition also were collected. Data were processed using the PROC MIXED of SAS 9.2. Results indicated that concentrations of serum lactate, IL-6, TNF-α, SAA, Hp, and LBP were significantly greater in cows with MF than CTR. Most interestingly, serum lactate, TNF-α, SAA, LBP, and Hp in cows with MF were different from CTR cows starting at ~ 4 to 8 wk before diagnosis of disease. Overall feed intake and milk production was lower in MF-affected cows. Interestingly overall milk fat was greater in MF cows vs. CTRs. In conclusion cows affected by MF showed alterations of innate immunity reactants and metabolites related to carbohydrate metabolism weeks before clinical appearance of MF. Since innate immunity is a general non-specific host response to sickness these metabolites might be used to indicate general health status of the transition dairy cows ahead of clinical disease event. More research is warranted to validate these data and better understand etiopathogenesis of MF in transition dairy cows.

Key Words: dairy cow, Innate immunity reactants, milk fever

0869 (W031) Transition dairy cows show blood alterations in innate immunity ahead of occurrence of retained placenta. G. Zhang*, D. M. Hailemariam, E. Dervishi, Q. Deng, S. A. Goldansaz, S. M. Dunn, and B. N. Ametaj, *Dep. of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Retained placenta (RP) is defined as failure to expel the fetal membranes from the uterus within 24 h after calving. The incidence of RP in a dairy farm, under normal conditions, averages 7 to 10%. RP results in increased days open, calving to first heat interval, services per conception, and days from calving to first service. The etiopathology of RP is not known and it is of interest to search for contributing factors that induce the disease. The objective of this investigation was to evaluate whether there are alterations in blood variables related to innate immunity and carbohydrate and lipid metabolism in transition dairy cows with placental retention. One hundred multiparous Holstein dairy cows were involved in the study. Seventeen blood samples were collected from the coccygeal vein during the −8 to +8 wk around parturition, once per week before the morning feeding. Six healthy control cows (CTR) and six cows with RP were selected and serum samples collected at −8, −4, time of diagnosis of disease, and +4 wk relative to parturition were analyzed for lactate, non-esterified fatty acids (NEFA), β-hydroxybutiric acid (BHBA), interleukin-1 (IL-1), interleukin-6 (IL-6) and tumor necrosis factor-α (TNF-a), haptoglobin (Hp), serum amyloid A (SAA) and lipopolysaccharide binding protein (LBP). In addition, health status, feed intake, rectal temperature, and milk yield data were monitored for each cow during the whole experimental period. Results revealed that cows with RP had greater concentrations of serum lactate, IL-1, TNF-a, SAA, and LBP in comparison with CTR. Intriguingly, elevated concentrations of all five variables were observed at −8 and −4 wks before the occurrence of RP compared to CTR cows. Cows with RP also had lower feed intake and milk production vs. control animals. However milk composition was not affected by RP. Overall results suggest that serum lactate, IL-1, TNF-a, SAA, and LBP can be used, in the future, to indicate cows that might have health issues during the transition period. More research is warranted to better understand the agent(s) that contribute(s) to RP in transition dairy cows.

Key Words: transition dairy cows, retained placenta, innate immunity

0870 (W032) Hypocalcemia and hypomagnesemia prevalence in a grazing Jersey, Guernsey, and Holstein herd in Costa Rica. J. M. Sánchez* and A. Saborío-Montero, *Centro de Investigaciones en Nutrición Animal y Escuela de Zootecnia, Universidad de Costa Rica, San José.*

The aim of this study was to determine the prevalence of hypocalcemia and hypomagnesemia in Jersey, Guernsey, and Holstein cows at parturition under the same feeding, management and environmental conditions. The study was conducted on a dairy farm located in Cartago, Costa Rica, during a 9-mo period and comprised a total of 152 cows (62 Jersey, 41 Guernsey, and 49 Holstein). During the close-up period cows grazed intensively managed kikuyu grass (*Kikuyuocloa clandestina*) (14.8% DM, 23.4% CP, 54% NDF, 0.35% Ca, 0.31% Mg and 3.50% K) and were supplemented with 4 kg/animal/d of a concentrate mixture low in Ca (14% CP, 31% NDF, 0.2% Ca, 0.42% Mg and 1.38% K) and 1 kg of hay (82.3% DM, 5.1% CP, 61.4% NDF, 0.4% Ca, 0.35% Mg and 1.8% K)/d. Cows were fed 1 kg of concentrate (18.6% CP, 0.90% Ca, 0.42% Mg and 1.38% K)/2.5 to 3.0 kg of milk during lactation. Blood samples were taken from the coccygeal vessels at peripartum (calving ± 1d) and were analyzed for Ca and Mg. The blood thresholds to classify cows as clinically or sub clinically hypocalcemic were less than 5.5 and 5.5 to 8.0 mg/dl of Ca, respectively. A value of 1.8 mg/dl of Mg or lower was set as criterion to classify cows as hypomagnesemic. Results are shown in Table 0870. Jersey cows were more prone to develop clinical hypocalcemia during peripartum than Holstein cows in this herd (OR = 3.48, 95% CI: 0.76–15.9), and Guernsey cows were more likely to suffer hypomagnesemia than Jersey cows during the same period (OR = 8.47, 95% CI: 1.30–55.2). These results suggest that Jersey grazing cows are more susceptible to clinical hypocalcemia and Guernsey to hypomagnesemia. High prevalence of subclinical hypocalcemia found in this study in Jersey, Guernsey, and Holstein cows could comprise cow health and productivity, and more research should be done to better understand Ca metabolism during the transition period in grazing cows.

Key Words: grazing dairy cows, hypocalcemia, hypomagnesemia

Table 0870. Blood calcium and magnesium concentration and prevalence of clinical and subclinical hypocalcemia and hypomagnesemia according to breed

	Ca (mg/dl)		Mg (mg/dl)		Hypocal.(%)		Hypomag.
Breed	Mean	95% CI	Mean	95% CI	Clin.	Subcl.	(%)
Jersey	7,49	7,11–7,87	2,78[a]	2,64–2,92	13	50	2
Guernsey	8,09	7,63–8,56	2,35[b]	2,18–2,52	0	44	12
Holstein	7,85	7,42–8,28	2,37[b]	2,22–2,53	4	55	0

[a,b] Means in the same column not sharing a common superscript are different ($P < 0.05$).

0871 (W033) Milk and blood selenium concentrations in dairy cattle differ depending on the source of selenium supplementation (sodium selenite, selenium-yeast or l-selenomethionine). L. Vandaele[1], B. Ampe[1], S. Wittocx[2], L. Segers[2], M. Rovers[*2], A. van der Aa[3], G. du Laing[4], and S. De Campeneere[1], *[1]Institute for Agricultural and Fischeries Research (ILVO), Melle, Belgium, [2]Orffa Additives BV, Werkendam, Netherlands, [3]Excentials BV, Werkendam, Netherlands, [4]Ghent University, Belgium.*

Adequate selenium (Se) levels are beneficial for dairy cattle health and fertility. Since many regions in the world have soils with low Se content, supplementation of this trace element is very often warranted. The aim of the present study was to evaluate three different Se sources: sodium selenite (NaSe), selenium-yeast (SeYeast) and L-selenomethionine (SeMet) in their potential to achieve adequate blood and milk Se levels. A feeding trial was set-up with 26 high-producing Holstein Friesian cows. After a 2-wk pre-treatment period without Se supplementation, cows divided in four homogenous groups receiving either no supplementation (Ctrl) or 0.3 mg per kg dry matter (DM) of either NaSe, SeYeast or SeMet for the next 7 wk. Cows were given maize and prewilted grass silage ad libitum, a protein source and a balanced concentrate. Milk and blood serum samples were taken during the pre-treatment period (wk 0) and at wk 3 and 7 after the start of supplementation. Blood serum Se concentrations were analysed by atomic absorption spectrometry. Milk Se concentration was determined by inductively coupled plasma mass spectrometry. Data within each week have been analyzed using ANOVA with treatment as fixed effect. DMI was constant during the trial. Milk production was 29.9kg in Ctrl, 31.6kg in NaSe, 28.3kg in SeYeast and 27.8kg in SeMet cows. Milk composition showed small differences between treatments. The mean blood serum Se and milk Se concentrations during the pre-treatment period were not different between groups (Table 0871). The increase in milk Se concentration between wk 0 and 3 was significantly more pronounced for SeMet in comparison with SeYeast and NaSe, which indicates a better transfer from feed to milk after SeMet supplementation. After 7 wk supplementation Se levels in blood and milk were equally high for SeYeast and SeMet and lower for Ctrl and NaSe. Increase in milk Se content after supplementation is clearly affected by type of Se source.

Key Words: dairy, selenium, transfer

Table 0871. Blood and milk Se in Ctrl, NaSe, SeYeast and SeMet at wk 0, 3, and 7

	Wk	Ctrl	NaSe	SeYeast	SeMet
Blood Se (µg/L)	0	34 ± 10	25 ± 4	35 ± 13	31 ± 10
	3	39 ± 12[a]	63 ± 14[b]	71 ± 13[b]	68 ± 11[b]
	7	23 ± 5[a]	57 ± 12[b]	71 ± 13[c]	69 ± 10[c]
Milk Se (µg/kg)	0	16 ± 2	15 ± 1	14 ± 2	16 ± 2
	3	18 ± 3[a]	26 ± 2[b]	45 ± 6[c]	61 ± 4[d]
	7	21 ± 9[a]	46 ± 15[b]	63 ± 12[c]	75 ± 14[c]

[a,b,c,d] Values with different superscript differ significantly between groups within the same week (row).

0872 (W034) Dynamic of intramammary infections in 3/4 Holstein x Zebu dairy cows from a herd of Minas Gerais State, Brazil. C. V. Ladeira[1], F. N. Souza[1], D. R. Freitas[1], L. G. Ladeira[2], D. S. Rodrigues[2], M. O. Leite[1], L. M. Fonseca[1], C. M. Penna[1], M. A. P. Brito[3], and M. P. Cerqueira[*4], *[1]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, [2]EPAMIG, Belo Horizonte, Brazil, [3]Embrapa, Juiz de Fora, Brazil, [4]Universidade Federal de Minas Gerais* (*School of Veterinary Medicine), Belo Horizonte, Brazil.*

The aim of the present study was to assess the occurrence of subclinical bovine intramammary infections (IMIs) in 3/4 Holstein x Zebu cattle in a dairy herd from Empresa de Pesquisa Agropecuaria de Minas Gerais (EPAMIG). Thus, composite milk samples (n = 132) from 44 cows were collected in April, July, and September (dry period) for bacteriological examination and somatic cell count (SCC). Bacterial analysis was conducted by culturing 0.01 mL of each sample on 5% ovine blood agar plates and MacConkey agar. The plates were incubated for 48 h at 35°C, which was followed by gram staining, observation of colony morphology and biochemical testing. The cow was regarded as uninfected when the milk SCC was < 200,000 cells/mL and bacteriologically negative. A new IMI was determined when a cow was bacteriologically negative and had SCC < 200,000 cells/mL, and in the next sampling the milk sample was bacteriologically positive and/or have SCC > 200,000 cells/mL, or a different pathogen was isolated. If the same pathogen was isolated in all milk samples, the cow was regarded as chronically infected for that pathogen. A cure occurred when a cow that was regarded as infected became uninfected at the end of experiment (bacteriologically negative and SCC < 200,000 cells/mL). From the 44 cows, 22 (50%) were chronically infected by *S. aureus* (77.27%, n = 17), *Streptococcus* sp. (9.09%, n = 2), coagulase negative staphylococci (CNS; 9.09%, n = 2) and *Corynebacterium* sp. (4.55%, n = 1). Six cows (13.64%) were initially regarded as healthy, and from these cows, four cows (75%) have become infected. Furthermore, three cows (6.82%) have been cured from IMI (two by *S. aureus* and one by CNS) at the end of experiment. Finally, 13 cows (29.55%) have become infected by a different pathogen from that established at the beginning of the experiment (four by *S. aureus* and CNS, two by *Klebsiella* sp., two by *Corynebacterium* sp. and one by *S. aureus* and *Corynebacterium* sp.). From those, five cows (38.46%) have been cured and then, established a new infection by a different pathogen. The percentage of spontaneous cure of *S. aureus* IMI was 18.18%. Thus, this study demonstrated the dynamic of IMIs in a herd that needs a continuous assessment of mastitis pathogens for a comprehensive control of IMIs.

Key Words: mastitis, milk, dairy cattle

0873 (W035) In vitro efficacy of teat disinfectants against *Staphylococcus aureus* strains isolated from bovine mastitis in Brazil. R. P. Santos[1], F. N. Souza[1], C. C. Vasconcelos[2], A. Cortez[2], D. O. Lapinha[1], A. B. Jardim[1], A. F. Cunha[1], M. O. Leite[3], M. R. Souza[3], A. Q. Lana[1], M. B. Heinemann[1], and M. P. Cerqueira[*3], *[1]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, [2]Laboratorio Veterinario Vidavet, Botucatu, Brazil, [3]Universidade Federal de Minas Gerais* (*School of Veterinary Medicine), Belo Horizonte, Brazil.*

The present study sought to explore the in vitro efficacy of four antiseptics against *Staphylococcus aureus* isolated from milk of dairy cows with mastitis. The efficacy of chlorhexidine (2.0%), chlorine (2.5%), quaternary ammonium (4%), lactic acid (2.0%) and iodine (0.6%) was accessed in concentrations conventionally used as commercial antiseptics before and after teat dipping. We used 50 *S. aureus* strains isolated from milk of 50 different dairy herds located at Minas Gerais, Sao Paulo, Parana, and Rio Grande do Sul States, Brazil. The efficacy of antiseptics were evaluated by incubation of *S. aureus* with the disinfectant at four different times (15, 30, 60, and 300 min). We used 0.8 mL of each antiseptic, 0.2 of sterile milk, and 1.2 mL of a bacteria solution (MacFarland scale 1) for all treatments and testing times. The activity of the antiseptics was accessed by bacteria growth in brain-heart infusion broth and 5% sheep blood agar plates. If there was no bacteria growth in brain-heart infusion broth and blood agar plates, the antiseptic was regarded as efficient. Statistical analysis was performed using Cochran's Q test. We found higher activity of quaternary ammonium (98% at all testing times) and chlorhexidine (84% at 15 min, 90% at 30 min, 94% at 60 min, and 96% at 300 min) against *S. aureus* at all testing times (P = 0.001), followed by iodine (46% at 15 min, 56% at 30 min, 66% at 60 min, and 78% at 300 min) and chlorine (30% at 15 min, 40% at 30 min, 48% at 60 min, and 64% at 300 min). Lactic acid showed the worst results (4% at 15 min, 4% at 30 min, 8% at 60 min, and 14% at 300 min) at all testing times and its use should not be recommended. Due to variation in sensitivity and resistance of *S. aureus* to antiseptics, the appropriateness of a given intervention should be based on efficacy in the specific application.

Key Words: dairy cow, intramammary infection, milking, teat dip

0874 (W036) Profile of clinical and subclinical mastitis pathogens isolated from cows housed on compost bedding. F. V. R. Portilho, S. Favero, G. G. Wanderley, H. Langoni, and J. C. F. Pantoja*, *Sao Paulo State University, Botucatu, Brazil.*

Compost bedding has been increasingly used worldwide. The organic nature of the bedding calls for investigations regarding the role and diversity of pathogens causing intramammary infections in cows housed in this system. The objective of this longitudinal study was to describe the distribution of mastitis pathogens isolated from cows housed on compost bedding. Three farms were visited monthly between May 2013 and January 2014. Farms A, B, and C had 33, 53, and 145 lactating cows and used peanut shell, sawdust, and wood shavings as bedding, respectively. Bedding was cultivated twice a day with new material added to the barn twice a month. Quarter milk samples were collected monthly from a sample of high SCC cows (> 200,000 cells/mL) in each heard and from all cases of clinical mastitis. Pathogens were grouped as environmental streptococci (*Streptococcus uberis*, *Streptococcus dysgalactiae* and *Enterococcus* spp.), CNS (coagulase-negative staphylococci), coliforms (*Escherichia coli*, *Klebsiella* spp. and *Enterobacter* spp.) and others (*Serratia* spp., *Pseudomonas* spp. and *Bacillus* spp.). The average monthly prevalence of subclinical mastitis (based on SCC) per farm was 39.6, 44.0, and 43.5% for farms A, B, and C, respectively. The distribution of culture results for subclinical mastitis (N = 469 quarters) was: negative: 39.4%; *Corynebacterium bovis*: 19.0%; CNS: 10.2%; environmental streptococci: 9.4%; *Staphylococcus aureus*: 6.2%, *Streptococcus agalactiae*: 6.0%; contaminated: 4.9%; coliforms: 3.2%; other: 1.3%, yeast: 0.2%, and *Prototheca* spp.: 0.2%. Culture results for clinical mastitis (N = 128 quarters) were: negative: 34.3%; coliforms: 16.4%; *C. bovis*: 9.4%; *Strep. agalactiae*: 9.4%; contaminated: 8.6%; CNS: 7.8%; environmental streptococci: 7.0%; other: 3.9%, and *Staph. aureus*: 3.1%. The most prevalent coliforms causing clinical and subclinical mastitis were *E. coli* (67% of 21) and *Klebsiella* spp. (74% of 15 cases), respectively. Preliminary results suggest that the distribution of pathogens was similar to those previously reported in Brazil for farms that used other bedding materials such as sand or pasture. *Prototheca* spp.was isolated from one cow on Farm C. *Nocardia* spp. infections were not found and the prevalence of other pathogens of concern such as *Serratia* spp. and *Pseudomonas* spp. was low.

Key Words: milk quality, mastitis, compost bedding

0875 (W037) Risk factors for repeated cases of clinical mastitis during the same lactation. B. dos Santos, G. G. Wanderley, H. Langoni, and J. C. F. Pantoja*, *Sao Paulo State University, Botucatu, Brazil.*

The objective of this nested case-control study was to identify factors associated with the occurrence of repeated clinical mastitis (CM) cases during the same lactation. Between July 2013 and January 2014, a 400-cow herd of Holstein cows was visited monthly for data collection. Quarter milk samples were collected from all CM cases. A repeated case was defined when a cow experienced the second case of CM (regardless of the quarter) within the same lactation. For each repeated case that occurred, three control cows matched by days in milk (DIM) were randomly selected. On the visit day, teat and udder measurements were performed on cases and controls, such as position of the udder floor in relation to the hock, udder depth, teat length and diameter, teat end hyperqueratosis score, ease of milking score, and presence of udder abnormalities (lesions or unbalance). Milk production, parity and the occurrence of further cases of CM were also recorded. The odds of a repeated clinical case were estimated as a function of the variables studied. Data from 68 repeated cases and 171 controls were available. The median time to the first case of mastitis and interval between the first and second cases were 136 DIM and 58 d, respectively. Of the 68 case-cows, 24% had the same pathogen isolated from both the first and second cases, and 57% experienced CM in the same quarter. Parity was associated with the occurrence of a repeated case only in the univariate analysis and was forced into the final model. Cows of first parity were 2.5 more likely to experience a repeated case when compared to cows of parity > 2 (P = 0.04). Ease of milking and udder position in relation to the hock remained in the final model. Cows whose udder was below the hock and cows easy to milk were 6.5 (P < 0.01) and 6.8 (P < 0.01) times more likely to experience a second case of CM when compared to those whose udder was above the hock or difficult to milk, respectively. Results of this study suggest that ease of milking is an important risk factor for repeated CM that should be carefully considered in genetic improvement programs.

Key Words: milk quality, epidemiology, clinical mastitis

0876 (W038) Incidence of retained placenta and the consequences on milk production and reproductive wC. C. Campos, and R. M. Santos*, *FAMEV–UFU, Uberlândia, Brazil.*

Retained placenta (RP) promotes delay in uterine involution and resumption of ovarian activity, besides increasing risk of uterine infections, being the major reason for low fertility of dairy cows. This study aimed to evaluate the effects of parity and calving season in RP incidence, in milk production and in calving to conception interval (CCI), as well as RP effects on these variables. Data were collected at a farm located in Rio Paranaíba city, Minas Gerais state, Brazil during 2012. The herd was composed of 700 Holstein dairy cows producing 32 kg of milk production per day. Calving of 291 cows was registered during the experiment period. To diagnose RP occurrence, cows were observed during calving, and immediately after calving, and those cows that had not eliminated

all of placenta until 12 h after fetal expulsion was considered with RP. The effects of parity and calving season on RP incidence were analyzed by logistic regression, and the effects of parity, calving season and RP occurrence on milk production and on CCI duration were evaluated by analysis of variance, both using SAS program. The incidence of RP in this herd was 13.75% (40/291). The RP incidence was not affected by parity and calving season, however there was a tendency (P = 0.066) of lowest incidence of RP for calving that had occurred during winter. The effects of parity, calving season and RP occurrence on milk production adjusted to 305 d of lactation were not verified (P > 0.05). CCI duration was influenced (P = 0.007) by parity, cows with three or more lactations had higher interval from parturition to conception. The effects of calving season (P = 0.001) and RP occurrence (P = 0.043) were also detected on CCI duration. Calving that had occurred during summer resulted in significant increase on CCI (263.00 ± 107.70) compare to winter (121.02 ± 60.64). Cows that developed RP had an interval from parturition to conception longer than cows without RP (139.64 ± 73.83 vs. 166.30 ± 95.90). The efficacy of RP treatment implemented by the farm could justify the absence of detectable effects of RP occurrence on milk production; however it was not enough to overcome the negative effects of RP on Holstein cows fertility.

Key Words: placenta, postpartum, bovine

0877 (W039) Associations between severity and etiology of clinical mastitis and pregnancy outcomes to first-service in dairy cows. M. J. Fuenzalida*[1], P. D. Carvalho[2], M. C. Wiltbank[2], P. M. Fricke[1], and P. L. Ruegg[1], *[1]Dep. of Dairy Science, University of Wisconsin–Madison, Madison, [2]University of Wisconsin, Madison.*

The objective of this study was to describe associations between the occurrence and severity of clinical and subclinical mastitis with pregnancies per artificial insemination (P/AI) after artificial insemination (AI) at first service. A total of 3164 cows from four commercial dairy farms were enrolled in a prospective cohort study between May 2011 and December 2013. Cows were submitted for first AI, and pregnancy outcomes were determined by using pregnancy-specific protein B (> 0.3ng/mL) and transrectal ultrasonography 32 to 39 d after AI. Clinical mastitis events were categorized as mild (abnormal milk) or moderate/severe (udder affected to animal depression or fever). Subclinical mastitis was defined when SCC exceeded 150,000 cells/mL. Udder health was categorized based on mastitis events occurring within the period from 3 d before to 32 d after first AI as: 1) subclinical mastitis only (SM); 2) clinical mastitis only (CM); 3) subclinical and clinical mastitis (SCM); or 4) no mastitis events. Chi-square tests were used to determine associations between udder health categories and P/AI at first AI. Occurrence of mastitis was associated with reduced P/AI (P < 0.001). As compared to P/AI of healthy cows (48%), cows that experienced SM (41.8%), CM (40.7%) or SCM (30.5%) had fewer P/AI. As compared to healthy cows, the odds of P/AI were 0.8 times as likely in cows that experienced SM (P = 0.005) or CM (P = 0.04) or 0.6 times as likely in cows that experienced SCM (P < 0.001). Among cows that experienced CM, P/AI did not vary based on severity (P = 0.69) or etiology (P = 0.26). As compared to P/AI of healthy cows (48%), cows with CM caused by Gram-negative bacteria (27.8%), Gram-positive bacteria (40.5%) and cases from cows that resulted in no growth (39.8%) had fewer (P = 0.006) P/AI. We conclude that both clinical and subclinical mastitis influenced P/AI and differences in P/AI were observed among etiologies and clinical presentation. *Supported by AFRI Competitive Grant no. 2010–85122–20612.*

Key Words: fertility, severity, pathogen

0878 (W040) Application of probiotics in the vaginal tract modulated bacterial composition in transition dairy cows. B. N. Ametaj*, *Dep. of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Uterine infections are highly associated with infertility, which is the main reason for culling of dairy cows. The objective of this study was to test whether intravaginal infusion of probiotics could modify the bacterial composition of the vaginal tract of transition dairy cows. One hundred pregnant Holstein cows were randomly (based on parity, body condition score, and milk yield) assigned to three groups 2 wk before the expected day of parturition (wk 0) as following: 1) a dose of probiotics on wk -2 and -1 and a dose of carrier (sterile skim milk) on wk +1 (TRT1); 2) a dose of probiotics on wk -2, -1, and +1 (TRT2), and 3) a dose of carrier on wk -2, -1, and +1 (CTR). Probiotics were a culture mixture of 3 lactic acid bacteria (LAB) composed of *Lactobacillus sakei* FUA3089, *Pediococcus acidilactici* FUA3138, and FUA3140, which were infused at 10^8–10^9 cfu per dose. Vaginal mucus was collected once a week on wk -2, -1, 0, +1, +2, +3 and +8. Vaginal pH was monitored once a week from wk -2 to +3; vaginal microbiota were monitored by quantitative PCR. At wk +3, compared with the control group, TRT1 increased the gene copy number of *Lactobacillus* group by 3 log (P < 0.01), *L. sakei* by 1.5 log (P < 0.05), and *Enterococcus* spp. by 2.5 log (P < 0.01). Meanwhile, TRT2 increased the number of *L. sakei* by 2.5 log relative to the control group (P < 0.05). No difference was observed among treatment groups in terms of gene copy numbers of total bacteria, *Bacteroides* group, *Bacillus* spp., *Staphylococcus* spp., *Enterobacteriaceae*, *E. coli* and pediocin structural gene pedA. The canonical score plot demonstrated that the gene copy numbers of *Lactobacillus* group discriminated best for TRT1, whereas those of *L. sakei* and *Bacillus* spp. discriminated best for TRT2. The bacterial composition of CTR was not discriminated by any of the bacterial populations determined. No differences were

observed among treatment groups regarding the vaginal pH of periparturient dairy cows. In conclusion, vaginal infusion of probiotics around calving modulated the vaginal microbiota of dairy cows as indicated by alterations in the number of *Lactobacillus* group, *L. sakei*, and *Enterococcus* spp.

Key Words: bacterial composition, dairy cow, probiotics, vaginal tract

---

0879 (W041) Intravaginal administration of probiotics modulated serum metabolites and milk composition of transition dairy cows. B. N. Ametaj*, *Dep. of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

Transition dairy cows experience great metabolic fluctuations due to dietary changes and calving-induced stress, which also influence milk composition. Therefore, the objective of this study was to evaluate metabolic responses of periparturient dairy cows administered intravaginally with probiotics around calving. One hundred pregnant Holstein cows were randomly (based on parity, BCS, and milk yield) assigned to three groups 2 wk before the expected day of parturition as following: 1) one dose of probiotic culture on wk -2 and -1 and one dose of carrier on wk +1 (TRT1); 2) one dose of probiotics on wk -2, -1, and +1 (TRT2), and 3) one dose of carrier on wk -2, -1, and +1 (CTR). Probiotics were a mixture of 3 lactic acid bacteria (LAB) composed of *Lactobacillus sakei* FUA3089, *Pediococcus acidilactici* FUA3138, and FUA3140, which were infused at 10^8–10^9 cfu per dose. Blood samples were collected from wk -2 to +3, and milk samples from wk +1 to +5 on a weekly basis. The concentration of serum metabolites and milk components were determined by spectrophotometry, and data were analyzed with SAS 9.2 software. Concentrations of cholesterol in the serum were 108 ± 4, 116 ± 4, and 95 ± 4 mg/dL ($P < 0.01$) in TRT1, TRT2, and CTR, respectively. Concentrations of lactate in the serum were 5.88 ± 0.50, 4.85 ± 0.39, and 3.52 ± 0.35 mmol/L ($P < 0.05$) in TRT1, TRT2, and CTR, respectively. Cows in TRT2 had lower serum NEFA than CTR (452 ± 64 vs. 631 ± 59 μmol/L, $P = 0.05$) but greater BHBA (736 ± 43 vs. 595 ± 43 μmol/L, $P < 0.05$). Treatments had no effect on concentrations of glucose or insulin in the serum. In addition, TRT2 had the highest content of milk lactose (4.39 ± 0.02%, 4.53 ± 0.03%, and 4.44 ± 0.03% in TRT1, TRT2, and CTR, respectively, $P < 0.01$), whereas TRT1 had the greatest content of milk protein (2.99 ± 0.04, 2.93 ± 0.05, and 2.82 ± 0.05% in TRT1, TRT2, and CTR, respectively, $P < 0.05$). No differences were detected in the content of milk fat, total solid content, or SCC. In conclusion, data indicated that administration of probiotics in the vaginal tract of periparturient dairy cows modulated serum concentrations of selected metabolites related to carbohydrate and lipid metabolism as well as milk composition. More research is warranted to understand how intravaginally infused probiotics affect blood metabolites and milk composition.

Key Words: probiotics, serum metabolites, milk composition

0880 (W042) Association among peripartum body condition score and metabolic parameters of Jersey cows and cure of sub-clinical mastitis in the dry period and incidence of sub-clinical and clinical mastitis postpartum. D. N. Liboreiro*, and R. C. Chebel, *Dep. Veterinary Population Medicine, University of Minnesota, St. Paul.*

Objectives were to evaluate the associations among peripartum metabolic parameters and cure of sub-clinical mastitis in the dry period and incidence of clinical and sub-clinical mastitis postpartum in Jersey cows. Cows ($n = 167$) having sub-clinical mastitis within 30 d before drying-off [linear somatic cell count (LSCC) > 4] were considered to be cured if LSCC < 4 within 34 d postpartum. Animals (multiparous = 745, nulliparous = 230) having LSCC > 4 within 34 d postpartum were considered to have sub-clinical mastitis. Clinical mastitis was characterized by change in milk and/or udder swelling (multiparous = 937, nulliparous = 320). Animals received body condition (BCS) and locomotion (LS) scores at -21 and 3 d relative to calving. Blood sampled from -21 to 7 d relative to calving was analyzed for non-esterified fatty acid (NEFA) and blood sampled from 0 to 7 d relative to calving was analyzed for β-hydroxybutyrate (BHB). Binary data was analyzed by logistic regression. Likelihood of cure of sub-clinical mastitis in the dry period had a quadratic association with BCS -21 d relative to calving ($P = 0.03$) and a negative linear association with NEFA concentration from -21 to 7 d relative to calving ($P = 0.07$). Likelihood of incidence of sub-clinical mastitis within 34 d postpartum had a quadratic association with BCS -21 d relative to calving ($P < 0.01$), a negative linear association with BCS loss in the last 21 d of gestation ($P < 0.01$), and a negative linear association with NEFA concentration from -21 to 7 d relative to calving ($P = 0.08$). Likelihood of clinical mastitis in the first 7 d postpartum had a negative linear association with BCS -21 d relative to calving ($P = 0.02$). Similarly, likelihood of clinical mastitis in the first 21 d had a negative linear association with BCS -21 d relative to calving ($P = 0.08$). We conclude from this experiment that BCS -21 d relative to calving, BCS change during the prepartum period, and NEFA concentration in the peripartum period are associated with udder health during the transition period, which is likely a consequence of the association between energy status and immune function.

Key Words: mastitis, transition cow, energy status

881 (W043) Evaluation of the ketone bodies concentration and clinical parameters in dairy cows supplemented with rumen-protected choline during the transition period. R. C. D. Souza[*1], R. C. Souza[1], R. F. Cota[1], J. M. Leão[2], I. B. Fortes[1], and L. S. D. Andrade[1], *[1]PUC Minas, Betim, Brazil, [2]UFMG, Belo Horizonte, Brazil.*

The use of rumen-protected choline (RPC) is a strategy to improve fat metabolism in the liver and reduce the prejudicial effects of negative energy balance in dairy cows during the peripartum. The objective of this study was to evaluate serum levels of ketone bodies and clinical parameters of dairy cows and heifers supplemented with RPC during the transition period (from 21 d pre-partum until 21 d post-partum). Thirty-two lactating F1 Holstein x Gir cows (16 multiparous and 16 primiparous) were blocked by parity and randomly assigned to one of two dietary treatments: addition of 60 g of RPC (AC) as Toplac Transition (Nutrifarma, Maripá, PR, Brazil) and no addition of RPC (NC). Diets contained 60% forage as corn silage and were isoproteic and isoenergetic according to the NRC (2001) model. Supplementation of RPC was done 21 d before expected parturition until 21 d post-partum. Blood samples, of coccygeal vein or artery, were collected 2 h after feeding on the d −21,−14, and −7 pre-partum and on the d 7, 14, 21 post-partum to obtain ketone bodies concentration by the portable electronic method Optium Xceed ™. The clinical parameters were evaluated using the methodology described by Rosenberg (1983). The experimental design used was completely randomized blocks with split plots. Ketone bodies concentration means were compared using Tukey test ($P < 0.05$) and clinical parameters (retained placenta) were evaluated by Chi-square test using the PROC MIXED for SAS. No effect of the use of RPC was observed on the ketone bodies concentration ($P = 0.4262$). However, at times evaluated, the lowest ketone bodies concentration in heifers were at parturition, 0.28 and 0.32 µmol/dl, respectively for animals AC and NC ($P = 0.0001$). No effect of time was observed on the concentration of ketone bodies in multiparous. On partum day, the ketone bodies concentration of AC group was lower in heifers (0.28 µmol/dl) than multiparous (0.57 µmol/dl; $P = 0.0062$). On clinical examination it was observed in the post-partum 16.66% of the AC group with retained placenta and 66% of the NC animals with retained placenta ($P = 0.0360$). Rumen protected choline supplementation to F1 Holstein x Gir multiparous cows reduced the incidence of retained placenta showing that this supplement can improve immunity in cattle. However, no effect was observed of rumen protected choline supplementation on the ketone bodies concentration.

Key Words: rumen-protected choline, ketone bodies concentration, clinical parameters.

0882 (W044) Switching lactating Jersey cows from a high neutral detergent fiber diet to an isoenergetic high soluble carbohydrate diet induces mild inflammation. G. Taasoli[1,2], C. R. Nightingale[*1], F. Kafilzadeh[2], D. Ghadimi[3], J. A. Carroll[4], and M. A. Ballou[1], *[1]Texas Tech University, Dep. of Animal and Food Sciences, Lubbock, [2]Razi University, Dep. of Animal Science, Kermanshah, Iran, [3]MRI, Institute of Physiology and Biochemistry, Karlsruhe, Germany, [4]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX.*

The objective was to investigate whether switching to a high soluble carbohydrate diet induced a systemic inflammatory response in peak lactating Jersey cows. Seven multiparous Jersey cows were selected from a commercial dairy farm. Cows were 71 ± 3 DIM and had an average BW of 407 ± 17.9 kg (mean ± SD). Each cow was individually housed in a 4-by-10-m soil surface pen. All cows received the high neutral detergent fiber (NDF; 33.8% DM)/low non-fiber carbohydrate (NFC; 34.3% DM) diet for 2 wk and then switched to an isonitrogenous/isocaloric reduced NDF (30.2% DM)/high NFC (40.7% DM) diet for 1 wk. The NFC content of the diet was increased by replacing corn distillers products and whole cottonseed with steam flaked barley and canola meal. Feed intake was collected from −7 to 7 d relative to the diet change. Milk yield, milk composition, and peripheral blood samples were collected immediately before switching the diets and 2, 4, and 7 d after the diet change. Blood hematology and plasma haptoglobin, zinc, interleukin-6, and tumor necrosis factor-α concentrations were analyzed. The switch in diet caused a decrease in DMI (19.6 vs. 17.0 ± 0.46 kg/d; $P < 0.0001$). Milk production decreased on d 2 (27.9 vs. 25.5 ± 1.17 kg/d for d 0 and 2 relative to the diet switch, respectively; $P = 0.042$), but had returned to baseline yields by d 7. No differences ($P > 0.473$) were observed in blood hematology, except that hemoglobin concentrations were increased after the diet switch (9.9 vs. 10.9 ± 0.35 g/dL; $P = 0.02$). Plasma haptoglobin concentrations tended to be elevated on d 7 relative to d 0 (62.4 vs. 142.3 ± 23.5 µg/mL; $P = 0.095$). In addition, plasma zinc concentrations were reduced on d 7 relative to d 0 (1.82 vs. 1.42 ± 0.138, mg/L; $P = 0.048$). There were no differences ($P > 0.324$) in the plasma concentrations of either interleukin-6 or tumor necrosis factor-α in plasma after the diet change. These data indicate that switching from a lower NFC diet to an isoenergetic high NFC diet suppressed DMI and caused mild inflammation among peak lactating Jersey cows as evident by the greater plasma concentrations of the positive acute phase protein, haptoglobin, and reduced concentrations of plasma zinc, a negative acute phase metabolite.

Key Words: inflammation, neutral detergent fiber, soluble carbohydrate

0883 (W045) Effects of oral calcium supplementation on body temperature, incidence of uterine diseases, and milk yield in dairy cows. N. Martinez*[1], L. D. P. Sinedino[1], R. S. Bisinotto[1], R. Daetz[1], G. C. Gomes[1], L. F. Greco[1], W. W. Thatcher[1], C. A. Risco[2], and J. E. P. Santos[1], *[1]Dep. of Animal Sciences, University of Florida, Gainesville, [2]Dep. of Large Animal Clinical Sciences, University of Florida, Gainesville.*

Objectives were to determine the effects of oral Ca supplementation (CaS) on the incidence of uterine diseases in dairy cows considered at low (LRM; normal calving) or high risk (HRM; dystocia, twins, stillbirth, retained placenta and/or vulvo-vaginal laceration > 3 cm) of developing metritis. The hypotheses were that oral CaS with boluses containing $CaCl_2$ and $CaSO_4^-$ (each containing 43 g of Ca) during the first 4 DIM maintain blood ionized Ca (Ca^{2+}) concentrations $\geq$ 1.0 mM and reduce the incidence of uterine diseases regardless of risk of metritis. In this randomized complete block design, HRM cows (n = 225) were matched with LRM (n = 225) on the day of calving based on parity. Each pair of matched cows was randomized to one of three treatments: CaS0, no Ca supplementation; CaS2, 2 boluses at 0 and 1 DIM; CaS4, 2 boluses at 0 and 1 DIM followed by 1 bolus at 2, 3, and 4 DIM. Blood Ca^{2+} was measured in a subset of cows (n = 60) before the first bolus administration and 35 min after each dose for the first 4 DIM using a Vetscan Istat handheld analyzer (Abaxis). Rectal temperature and vaginal discharge were monitored in the first 10 DIM. Metritis was defined as fetid, watery vaginal discharge, and puerperal metritis (PuMet) was defined as metritis with rectal temperature $\geq$ 39.5°C. Endometritis was considered as mucopurulent vaginal discharge. Milk yield was evaluated weekly during the first 30 DIM. Cows with at least one corpus luteum in two ultrasounds performed 2 wk apart beginning on 38 DIM were considered cyclic. Data were analyzed using PROC GLIMMIX and PROC GENMOD of SAS. Oral supplementation with Ca during early postpartum increased blood Ca^{2+}concentrations; however, the two regimens of Ca supplementation failed to reduce the incidence of metritis in either HRM or LRM groups.

Key Words: dairy cows, Ca supplementation, metritis

0884 (W046) Blood calcium dynamics after prophylactic treatment of subclinical hypocalcemia with oral or intravenous calcium. C. D. Blanc*[1], M. Van der List[2], S. S. Aly[3], H. A. Rossow[3], and N. Silva-del-Rio[3], *[1]Pacific Rim Dairy, Corcoran, CA, [2]Boehringer Ingelheim, St Joseph, CA, [3]VMTRC, University of California, Tulare.*

Total serum Ca dynamics and urine pH levels were evaluated after prophylactic treatment of subclinical hypocalcemia after parturition in 33 multiparous Jersey/Holstein crossbreed cows. Cows were blocked according to their calcemic status at the time of treatment (Vetscan 200–1000R, Abaxis) [normocalcemic (8.0- 9.9 mg/dl; n = 15), or hypocalcemic (5.0–7.9 mg/dL; n = 18)] and randomly assigned to one of three treatments: Control [no Ca supplementation (n = 11)]; intravenous Ca [Ca-IV (n = 11), 500 mL of 23% Ca Gluconate (10.7 g Ca, Durvet, Blue Springs, MO)]; and oral Ca [Ca-Oral (n = 11), one oral bolus (Bovikalc bolus, Boehringer Ingelheim, St. Joseph, MO) containing $CaCl_2$ and $CaSO_4$ [43 g Ca] two times 12 h apart]. Total serum Ca levels were evaluated at 0, 1, 2, 4, 8, 12, 16, 20, 24, 36, and 48 h after treatment application (Enzymatic Rate/Automated Chemistry Analyzer method, Marshfield lab, WI) and urine pH at 0, 1, 12, 24, 36, and 48 h (on-farm with Oakton pH Testr 20). Overall, total serum Ca levels did not differ with treatment. But Ca-IV cows experienced a sharp increase in serum Ca levels after treatment (Peak = 11.4 mg/dL at 1 h), followed by a steep decline (nadir = 6.4 mg/dL at 24 h). Total serum Ca levels were higher for Ca-IV than control and Ca-Oral at 1, 2, and 4 h after treatment, but lower than Ca-Oral at 20, 24, and 36 h and control at 36 and 48 h. Treatment, time and treatment by time interaction were significant for urine pH. Mean urine pH was lower for Ca-Oral cows (6.69) than for control (7.52) and Ca-IV (7.19) cows. Urine pH levels at 1 h after treatment

Table 0883.

	Treatment							
	CaS0		CaS2		CaS4			
	HRM	LRM	HRM	LRM	HRM	LRM	*SE*	*P*
Ca^{2+}, mM	1.08[a]	1.09[a]	1.15[b]	1.17[b]	1.21[c]	1.20[c]	0.02	< 0.01
Temperature, °C	38.87	38.76	38.91	38.77	38.90	38.74	0.03	0.60
Milk, Kg/d	29.4	32.9	29.4	30.7	27.7	32.1	1.1	0.35
Uterine Diseases	%(n/n)							
Metritis	56.0(42/75) [a]	10.7(8/75) [a]	64.0(48/75) [b]	21.3(16/75) [b]	55.4(41/74) [a]	21.3(16/75) [a]		< 0.01
PuMet	14.7(11/75)	1.33(1/75)	18.7(14/75)	5.33(4/75)	18.9(14/74)	6.7(5/75)		0.30
Endometritis	39.1(27/69)	23.2(17/73)	33.3(24/72)	21.6(16/74)	32.4(23/71)	19.2(14/73)		0.59
Cyclicity 52 d	71.0(49/69)	73.3(55/75)	75.3(55/73)	81.3(61/75)	69.4(50/72)	78.1(57/73)		0.42

[a,b,c] different superscripts indicate differences among treatments (P < 0.05).

were lower for Ca-IV compared to both Control and Ca-Oral. At 12, 24, and 36 h, urine pH levels were lower for Ca-Oral compared to both Control and Ca-IV. This was expected as the oral Ca supplementation used (Bovikalc) is designed as an acidifying agent. Wide fluctuations in blood Ca are observed after prophylactic intravenous Ca supplementation in normo- and subclinical hypocalcemic cows. The implications of these transient changes in serum Ca have still to be determined.

Key Words: hypocalcemia, hypercalcemia, dairy cattle

ASAS UNDERGRADUATE STUDENT POSTER COMPETITION

0885 (T011) Effects of supplementing Holstein heifers with dietary melatonin during late gestation on serum antioxidant capacity and anti-Müllerian hormone of offspring. B. O. Fleming*, K. E. Brockus, C. G. Hart, and C. O. Lemley, *Mississippi State University, Starkville.*

Previously, our laboratory observed an increase in maternal serum antioxidant capacity during late gestation dietary melatonin supplementation. Therefore, the objective was to examine the effects of supplementing melatonin to dams during late gestation on offspring serum antioxidant capacity and anti-Müllerian hormone concentrations. On d 190 of gestation, heifers (n = 20) were blocked by BW and then randomly assigned to one of two dietary treatments: 1). 20 mg of dietary melatonin per day (MEL) or 2). no melatonin supplementation (CON). Dietary treatments were terminated on d 262 of gestation. MEL heifers received 2 mL of 10 mg/mL melatonin in ethanol while CON heifers received 2 mL of ethanol alone. At birth, calves were separated from their dams and given 3.8L of colostrum. Calves were fed 5.7L of whole milk daily and offered 0.9 kg/d of starter grain. Starter was increased by 0.9 kg/d when orts were 0 kg. Calf (n = 18) total antioxidant capacity was determined in serum on wk 0, 1, 2, 3, and 4 of age. Concentrations of anti-Müllerian hormone were determined in female offspring (n = 15) on wk 4 of age. Data were analyzed using the PROC MIXED of SAS. For repeated measures the model statement contained treatment, age, and their respective interaction. Total antioxidant capacity was not different (P = 0.14) between calves from MEL treated dams vs. calves from CON treated. A main effect of age (P < 0.001) was observed for total antioxidant capacity, which was increased at wk 1 of age vs. 0, 2, 3, and 4. Concentrations of anti-Müllerian hormone tended to be increased (P < 0.10) in heifer calves from MEL treated dams (0.82 ± 0.19 ng/mL) vs. calves from CON treated dams (0.35 ± 0.19 ng/mL). In conclusion, the increase in maternal antioxidant capacity following dietary melatonin supplementation did not affect calf antioxidant capacity of serum during early postnatal development. Interestingly, the tendency for increased heifer calf anti-Müllerian hormone concentrations deserves further investigation into offspring ovarian reserves.

Key Words: anti-Müllerian hormone, antioxidant, melatonin

0886 (T012) Effects of electrostatic particle ionization on hog barn air quality, emissions, and pig growth performance. K. N. Card*[1], J. A. De Jong[1], J. M. DeRouchey[1], P. J. Tomlinson[1], M. J. Baumgartner[2], and Z. Liu[1], *[1]Kansas State University, Manhattan, [2]BEI Ag Solutions, Olivia, MN.*

Electrostatic particle ionization (EPI) systems emit negative ions, which in turn create polarized air particles. These polarized air particles attach to conductive or grounded surfaces in the barn. An experiment was conducted to determine the effects of EPI on hog barn air quality, emissions, and nursery pig growth performance. To make the comparison, the EPI system was installed in two identical nursery barns (200 pigs/barn) at the same location. During five 6-wk periods (6 to 23 kg BW) the EPI system was utilized in a single barn for one complete turn and then rotated to the opposite barn to ensure no barn effects would be present (five replications per treatment). Each barn was equipped with three external exhaust fans, and 12 internal attic air inlets. Pigs were allotted randomly between barns at the beginning of each period and measurements were taken every week for the 6-wk period. Dust particles were collected weekly inside the barn and in exhaust air for determination of particle size and average quantity for the turn. Additional measurements included in-barn air hydrogen sulfide and ammonia as well as ADG and final BW. Overall, there were fewer (P < 0.02) in-barn 0.3, 2.5 and 10.0 µ dust particles when the EPI system was active. The EPI system also reduced (P < 0.03) 0.3, 2.5 and 10.0 µ dust particles/m^3 in exhaust fan air. There were no differences for in-barn air ammonia and hydrogen sulfide concentrations. The EPI system tended to improve (P = 0.09) ADG and final BW. In conclusion, EPI was able to reduce airborne dust concentrations in-barn and in exhaust air and tended to improve growth performance.

Key Words: electrostatic particle ionization, emissions, nursery pig

Table 0886.

Treatment:	Control	EPI	SEM	Probability P <
ADG, g	414	442	12.5	0.09
Final BW, kg	22.60	23.27	2.25	0.06
Inside dust, particles/min				
0.3 µ	687,345	417,797	98,698	0.02
2.5 µ	173,363	77,759	27,236	0.01
10.0 µ	166,980	72,998	30,189	0.01
Exhaust dust, particles/m^3				
0.3 µ	104.37	54.70	16.84	0.03
2.5 µ	18.51	7.52	4.35	0.02
10.0 µ	7.03	2.51	1.57	0.03
Ammonia, ppm	4.02	4.21	1.39	0.86
H2S, ppm	0.81	0.82	0.31	0.89

0887 (T013) Effects of different cooling interventions on stationary livestock trailers at a commercial packing plant.

M. Heiller*[1], L. Edwards-Callaway[2], R. Bailey[3], N. Pudenz[4], M. Klassen[4], M. J. Ritter[5], A. Dezeeuw[4], and P. J. Rincker[6], *[1]Iowa State Univeristy, Ames, [2]JBS, Greely, CO, [3]JBS, Marshalltown, IA, [4]Elanco, Greenfield, IN, [5]Elanco Animal Health, Bondurant, IA, [6]Elanco Animal Health, Dahinda, IL.*

The objective was to determine effects of different cooling interventions on trailer temperature (T), relative humidity (RH), and transport losses over 20 min before unloading. Three treatments included: 1) Control (no water or fans), 2) Fan (20 min in front of a bank of fans), and 3) Shower+Fan (5 min of showering using the internal trailer system followed by 20 min in front of a bank of fans). Data was collected using HOBO data loggers placed inside the trailer on arrival at the packing plant on 150 trailers in blocks where all three treatments were represented with 60 min of each other. Data was summarized at time points 0, 5, 10, 15, and 20 min and was analyzed with PROC MIXED in SAS using block as a random effect. Results on trailer T (Table 0887a) indicate that the Control treatment increased numerically over time, the Fan treatment prevented a rise in T, and the Shower+Fan treatment was the coolest ($P < 0.05$) at all time points. RH inside the trailers was similar ($P > 0.05$) in the Control and Fan treatment, but higher ($P < 0.05$) in the Shower+Fan treatment at all time points (Table 0887b). No differences were determined on the incidence of dead on arrivals ($P = 0.87$) or fatigued animals ($P = .077$). Further investigation of the data revealed an interaction ($P = 0.02$) between treatment and environmental temperature where the temperature differences between treatments become greater at higher environmental temperatures.

Key Words: swine, trailer, cooling, fans

Table 0887a. LSMeans of the difference between trailer and environmental temperatures (°C) during the 20 Min before unloading by treatment

Time Interval	Control	Fan	Shower+ Fan	SEM	*P*-value
0	0.30[a]	0.82[a]	-0.78[b]	0.28	< 0.0001
5	1.04[a]	0.65[a]	-0.86[b]	0.23	< 0.0001
10	1.52[a]	0.43[b]	-0.61[c]	0.20	< 0.0001
15	1.77[a]	0.38[b]	-0.43[c]	0.20	< 0.0001
20	2.11[a]	0.52[b]	-0.25[c]	0.21	< 0.0001

[1]Average environmental placement temperature was 27.53°C
[a,b,c] means within a row lacking common superscripts are different ($P < 0.05$).

Table 0887b. LSMeans of relative humidity (%) by treatment

Time Interval	Control	Fan	Shower+ Fan	SEM	*P*-value
0	56.51[a]	56.27[a]	69.52[b]	2.43	< 0.0001
5	59.15[a]	56.46[a]	64.76[b]	2.58	< 0.0001
10	57.93[a]	57.32[a]	63.23[b]	2.59	0.0006
15	57.63[a]	57.50[a]	62.07[b]	2.65	0.0044
20	57.58[a]	57.43[a]	60.60[b]	2.67	0.0319

[a,b,c] means within a row lacking common superscripts are different ($P < 0.05$).

0888 (T014) Effects of poor maternal nutrition during gestation on gene expression in liver of offspring.

K. K. McFadden*, M. L. Hoffman, K. N. Peck, S. A. Reed, S. A. Zinn, and K. E. Govoni, *Dep. of Animal Science, University of Connecticut, Storrs.*

Poor maternal nutrition during gestation can reduce growth and circulating growth factors secreted by the liver, as well as alter lipid metabolism. However, the mechanisms that lead to these alterations are not well understood. We hypothesized that poor maternal nutrition during gestation would alter expression of key genes involved in lipid metabolism and the somatotropic axis in the liver of offspring. Thirty-six multiparous ewes were individually housed and fed 100, 60, or 140% of NRC requirements beginning at d 31 ± 1.3 of gestation. Lambs were euthanized within 24 h of birth (1 d; $n = 18$) or 3 mo of age ($n = 15$). Lambs from ewes fed 100, 60, or 140% will be referred to as CON, RES, and OVER, respectively. At euthanasia, whole livers were harvested, weighed and tissue samples collected. Total RNA was extracted and gene expression determined by real-time reverse transcriptase (RT)-PCR. Data were analyzed using PROC GLM with significance considered at $P \leq 0.05$ and a tendency at $0.05 < P \leq 0.10$. As previously reported, BW were 13% greater in OVER vs. CON ($P \leq 0.05$). Liver weight was 43% greater in OVER vs. CON ($P = 0.08$) at 1 d when adjusted for BW, but no difference was observed at 3 mo ($P = 0.6$). At 1 d, relative to CON, the expression of sterol-regulatory element binding protein-I (SREBP-I), a regulator of hepatic lipogenesis, was reduced 2.6 ± 0.1 and 3.7 ± 0.1-fold in RES and OVER, respectively ($P < 0.01$). The expression of IGF-I receptor (IGF-IR) was reduced 1.7 ± 0.1 and 2.0 ± 0.2-fold in RES ($P = 0.03$) and OVER ($P = 0.09$), respectively at 1 d relative to CON. Expression of IGFBP-4 was reduced 2.6 ± 0.1 and 1.7 ± 0.1-fold in RES ($P = 0.01$) and OVER ($P = 0.07$), respectively at 1 d relative to CON. Expression of SREBP-I, IGF-IR, and IGFBP-4 were not altered at 3 mo ($P \geq 0.3$). Relative to CON, expression of IGFBP-3 increased 1.7 ± 0.2-fold in OVER ($P = 0.04$) at 3 mo, but was unaltered at d 1 ($P \geq 0.8$). Maternal diet did not affect IGF-I at either time point ($P \geq 0.3$). In conclusion, poor maternal nutrition alters genes involved in lipid metabolism and IGF action, which may contribute to altered growth and increased fat deposition in offspring.

Key Words: liver, sheep, somatotropic axis

0889 (T015) Interleukin-1 β decreases myoblast fusion in vitro. B. E. Sullivan[*1] and S. A. Reed[2], *[1]University of Connecticut, Storr, [2]Dep. of Animal Science, University of Connecticut, Storrs.*

During times of stress, systemic pro-inflammatory cytokine levels are increased, which may prevent optimal growth and development of muscle and/or induce muscle atrophy. Pro-inflammatory cytokines can induce negative responses in muscle by altering the balance of protein synthesis and degradation in established myofibers, or by influencing the proliferation and differentiation of myoblasts. Interleukin-1 β (IL-1β) is a pro-inflammatory cytokine involved in stress and disease responses, but little is known about how IL-1β affects myoblast function. We hypothesized that IL-1β would decrease myoblast proliferation and/or differentiation. To test this hypothesis, C2C12 mouse myoblasts were treated with 0.1 ng/mL or 1.0 ng/mL of IL-1β, or carrier only (control). To determine proliferation rate, myoblasts were plated at $2.6x10^3$ cells/cm^2 and cultured for 48 h in the presence or absence of IL-1β. Cells were pulsed with bromodeoxyuridine (BrdU), fixed, and immunostained. The number of BrdU positive cells was quantified as a percent of total nuclei (identified by Hoescht 33342). To determine if IL-1β affected fusion, myoblasts were plated at $2.0x10^4$ cells/cm^2 in growth media for 48 h, at which time media was changed into differentiation media supplemented with 0.1 ng/mL or 1.0 ng/mL of IL-1β, or carrier only. Cells were immunostained with myosin heavy chain (MyHC) and Hoescht 33342. Fusion index was determined by quantifying the number of nuclei within multinucleated myotubes divided by total nuclei. Finally, to determine the effect of IL-1β on myotube size, myoblasts were cultured for 48 h in growth media and 48 h in differentiation media. Cells were cultured for an additional 48 h in the presence or absence of IL-1β, fixed and immunostained for MyHC. Myotube diameter and fusion index were quantified. All data was analyzed using ANOVA in GraphPad Prism followed by Tukey's test for multiple comparisons. There were no significant effects of IL-1β on proliferation or fiber diameter ($P \geq 0.05$). However, fusion was decreased 13.5% in myoblasts treated with 1.0 ng/mL of IL-1β ($P \leq 0.05$). In conclusion, IL-1β decreases myoblast fusion, but does not affect proliferation or fiber diameter. These results suggest that IL-1β may contribute to poor muscle growth by decreasing fusion of myoblasts into existing myofibers, preventing optimal hypertrophy.

Key Words: cytokine, fusion, IL-1β, myoblasts

0890 (T016) Sperm maturation (capacitation) but not progesterone reduces the abundance of a receptor for oviduct glycans. R. A. Winters[*1], E. Silva[1], and D. J. Miller[2], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]University of Illinois, Urbana.*

As sperm travel through the female reproductive tract they bind to glycan motifs on cells lining the oviduct lumen, forming a sperm reservoir. Near the time of ovulation, sperm are released and travel to the site of fertilization. Our lab has found that a boar sperm protein called lactadherin binds to an oviduct trisaccharide, Lewis^x, to mediate sperm binding to oviduct cells. It has been suggested that sperm release from the oviduct reservoir is partially mediated by an increase in progesterone concentration in the oviductal fluid that would affect sperm capacitation and promote release from oviduct Lewis^x, perhaps by releasing sperm lactadherin. We tested this hypothesis in experiments to define the effect of sperm capacitation and progesterone exposure on sperm lactadherin abundance. Sperm from fertile boars were washed using a Percoll cushion. Treatments consisted of: 1) sperm capacitation for 4 h using mTALP medium containing BSA and sodium bicarbonate, and 2) sperm treatment with increasing concentrations of progesterone (0, 80, 800nM) for 30 min in mTALP. After treatment, sperm protein was extracted using a 0.1% Nonidet P-40 lysis buffer, and samples were submitted to western blot analysis. Experiments were repeated at least twice. Based on western blotting with a lactadherin antibody, two protein bands migrating at 35 kDa and 47 kDa were identified. The greater signal was present at 47 kDa and, based on its migration, it is recognized as lactadherin. The 47 kDa signal (lactadherin) was higher in sperm before capacitation than after capacitation. Based on western blot results, lactadherin concentration was not affected by progesterone treatment; the abundance of the 47 kDa band did not change. In conclusion, two bands were detected by the lactadherin antibody, suggesting the presence of two protein isoforms. Lactadherin abundance on the sperm surface was reduced after sperm capacitation but progesterone did not affect the abundance of lactadherin. The reduction in lactadherin during capacitation may contribute to sperm release from the oviduct. *This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–67015–20099 from the USDA National Institute of Food and Agriculture.*

Key Words: sperm, capacitation, oviduct

0891 (T017) Variations in the expression of triglyceride synthesis genes in pigs provided *Enterobacter cloacae*. S. J. White*[1], J. A. Carroll[2], J. A. Thornton[1], P. R. Broadway[3], J. G. Wilson[1], and J. R. Donaldson[1], *[1]Mississippi State University, Starkville, [2]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [3]Texas Tech University, Wolfforth.*

Enteric infections are leading causes of morbidity and mortality among livestock. Weanling pigs are particularly susceptible to infections, primarily due to reduced amounts of adipose tissue. Limited stores of adipose tissue can lead to an insufficient supply of energy during times of nutritional restriction that would be available to mount an effective immune response. Previously, two novel probiotics (*Enterobacter cloacae* JD6301 and JD8715, a genetically altered form that produces extracellular lipids) were found to increase circulating triglycerides in pigs. In this current study, 36 weanling pigs were supplemented with *Enterobacter cloacae* JD6301 or JD8715 for 7 d prior and 3 d afterward relative to an orally inoculated *Salmonella typhimurium* ($1x10^9$ CFU) challenge. To determine if either probiotic altered the production of triglycerides in response to the infection, adipose tissues were collected from four pigs every 24 h in relation to the challenge to evaluate potential differences in lipogenesis. Total RNA was isolated post challenge and analyzed for variations in the expression of genes involved in triglyceride synthesis and compared to control pigs only provided phosphate buffered saline. The data indicate that pigs provided JD8715 had an increase in lipoprotein lipase ($P = 0.027$), and a decrease in the insulin-induced gene 1 ($P = 0.02$), apolipoprotein A1 ($P = 0.04$), and DGAT2 ($P = 0.009$) 1 d post-challenge in comparison to controls. A 16-fold increase ($P = 0.001$) in the insulin-induced gene 1 was also observed on d 3 in pigs provided JD8715 compared to control pigs. Together, these data suggest that providing *Enterobacter cloacae* JD8715 increased the amount of triglycerides available to the pigs, thus potentially improving the availability of energy. Further research is needed to determine how this increase modulates the immune response.

Key Words: pigs, lipids, adipose tissue

0892 (T018) Gene set enrichment analysis of residual feed intake in Hereford cattle. L. D. Kidder*[1], A. Wojtowicz[1], J. F. Taylor[2], C. M. Seabury[3], K. A. Johnson[1], and H. L. Neibergs[1], *[1]Washington State University, Pullman, [2]University of Missouri, Columbia, [3]Texas A&M University, College Station.*

Feed comprises 66 and 77% of the total cost of calf and yearling finishing systems, respectively. Heritabilities for feed intake and feed efficiency (FE, estimated as residual feed intake, or RFI) have ranged from 0.08 to 0.46 in previous studies, highlighting the potential for selection to bring about significant gains in feed efficiency and profitability within the beef industry. The objective of this study was to identify gene pathways significant for FE as measured by RFI through the use of gene set enrichment analysis (GSEA) using single nucleotide polymorphisms (SNPs) as proxies for bovine genes. A population of 847 Hereford cattle (181 purebreds and 666 high-percentage Hereford crossbred animals consisting of 23 females and 824 males ranging in age from 210 to 496 d) from a single ranch were evaluated for a period ranging from 70 to 140 d on feed (DOF). Only 31 animals were fed over 72 d. Average daily gain (ADG), dry matter intake (DMI), initial weight (IW), mid-test metabolic weight (MMWT), and DOF were recorded across the feeding period for each individual. Covariates for the genome wide association study (GWAS) consisted of age, sex, DOF and % Hereford. GWAS was followed by GSEA of SNP data with *Bos taurus* gene sets sourced from GO, KEGG, Panther, Reactome, and Metacyc. Gene sets containing fewer than 10 or greater than 200 SNPs were excluded from the analysis. A total of 19,598 bovine genes were mapped within gene sets, and proxy SNPs were mapped to genes located within 20 kilobase pairs. The null distribution of the GSEA test statistic was approximated using 10,000 random permutations. Genotypes were obtained from the Illumina BovineSNP50 ($N = 361$) and BovineHD ($N = 486$) BeadChips and imputed to 778,000 SNPs using Beagle. The GO pathway GO:0044706 multi-multicellular organism process with 90 genes was significant for RFI with a false discovery rate of 0.061 and a normalized enrichment score of 3.978. There were a total of 51 leading edge genes in GO:0044706. The top 10 genes were: PGR, CORIN, STAT5B, TIMP1, PCSK5, THRB, NR2F2, MMP2, FKBP4, and JUNB. Heritability for RFI was estimated to be 0.49. These results suggest that genetic selection for RFI has potential to dramatically affect the efficiency and, therefore, profitability of beef cattle production.

Key Words: genetics, RFI beef

0893 (T019) pH fluctuations in the hindgut of horses relative to meal feeding. K. M. DeLano*[1], T. L. Douthit[1], A. Reeg[1], N. M. Bello[1], M. E. Gordon[2], and K. Williamson[2], *[1]Kansas State University, Manhattan, [2]Purina Animal Nutrition, LLC, Gray Summit, MO.*

This study assessed changes of pH over time in the equine hindgut relative to meal feeding. Nine quarter horses with cecal cannulae surgically inserted 4 yr before the experiment were utilized. The group was comprised of five geldings and four mares, with ages ranging from 8 to 10 yr old, and body weight between 455 and 590 kg. Horses were housed in heated individual stalls, with ad libitum access to water and white salt blocks. The horses' diet consisted of 1.5% BW prairie grass hay and 0.5% BW concentrate (Omolene 200, Purina Animal Nutrition, LLC, St. Louis, MO), with the concentrate fed in the morning only (0700) and the hay divided into two daily feedings (0700 and 1930). Horses were maintained on this

regimen for three separate 21-d periods. During the last 3 d of each period (d 19 to 21), pH was measured in cecal and fecal samples collected at -1, +1, +4, +8, +12, +16, +20, and +24 h relative to feeding of the concentrate meal. Cecal and fecal pH fluctuations over time were jointly modeled using a general linear mixed model. Hindgut pH dynamics relative to feeding differed between the cecum and the feces ($P < 0.0001$). In the cecum, a decline in pH (approx. 0.363 ± 0.03; lsmean ± SEM) was observed as soon as 4 h after feeding ($P < 0.0001$). Minimum pH values in the cecum were recorded 8 h after feeding, and a return to baseline cecal pH was apparent at 20 to 24 h after feeding. In the feces, a smaller decline was observed (approx. 0.144 ± 0.044) but it did not become apparent until 8 h after feeding ($P = 0.035$). The minimum fecal pH was reached at 12 h after feeding ($P = 0.0055$); by 16 h after feeding, there was no evidence for differences from baseline pH ($P = 1.00$). These results suggest a maximum time lag in pH fluctuations of approximately 4 h between the cecum and the feces. It is necessary to note that more precise lag times could not be quantified with this study design, as measurements were taken every 4 h. Further research is needed to fine-tune predictive ability of fecal pH on cecal pH over time.

Key Words: cecal pH, equine, fecal pH

0894 (T020) Oral supplementation with vitamin E and fertility in young bulls raised in Brazilian midlewest. R. D. Almeida*, L. K. Hatamoto-Zervoudakis, W. A. D. S. Marinho, B. H. Tsuneda, F. A. D. P. D. B. Arguello, J. T. Zervoudakis, M. F. Duarte Junior, P. P. Tsuneda, and T. B. Castaldeli, *Federal University of Mato Grosso, Cuiaba, Brazil.*

The sperm cells are highly susceptible to peroxidative damage, such damage in their sperm membrane occurs due to oxidative stress that is responsible for the reduction in the fertility of sperm. One of the causes of the increase in oxidative stress is increased environmental heat stress and consequent increase in temperature testicular promoting the increase in NADPH oxidase activity and increased availability of transition metals. Dietary deficiencies may also be associated with the decrease in the antioxidant defense mechanisms. Vitamin E is a fat-soluble antioxidant and has the ability to prevent the spread of chain reactions induced by ROS in biological membranes, representing an important defense against oxidative damage caused to the sperm membrane. The objective of this study was to evaluate whether oral supplementation with vitamin E alters bulls fertility and performance of bulls raised in pastures in tropical conditions. We used 16 bulls/Brangus, with a mean of 24 mo and 462.2 kg were randomly divided into two groups: GC = Control group (concentrated supplementation without adding vitamin E), vitamin E group GE = (400UI/animal/day supplemented with vitamin E). The animals were maintained on pasture, and supplemented (4,5 kg/animal) with concentrated feed once a day. During the supplementation period, four samples (days: D0, D30, D60 and D75) were made by electrostimulation. In each collection were evaluated: weight (BW), Diameter (TPER) and Testicular Consistency (TC), Volume (VOL) and Concentration (CONC) of the ejaculate, Motility (MOT) and Vigor (VIG) sperm, Percentage of primary defects (*P*D), Secondary (SD) and Total (TD), Sperm viability (EOS), the Integrity of sperm membrane (HYPO) and Crossomal (POPE). The experiment was conducted in a completely randomized design. Data were analyzed using ANOVA 5%. It was found BW treatment effect ($P = 0.0472$), TPER ($P = 0.0015$), TC ($P = 0.0367$), EVIG ($P = 0.0183$) and a trend effect for SD ($P = 0.0617$). The results obtained in the experimental conditions of this study, it is concluded that oral supplementation with vitamin E, 400UI/day does not altered semen quality, however detracted and testicular characteristics of bulls raised on pasture in tropical conditions.

Key Words: reactive oxygen species, oxidative stress, lipid peroxidation.

0895 (T021) Polymelia in Holstein cattle. K. D. Moss*[1], F. Avila[2], B. M. Marron[3], T. Raudsepp[2], J. Beever[3], M. Neupane[1], S. Parish[1], J. Kiser[1], B. Cantrell[1], and H. L. Neibergs[1], *[1]Washington State University, Pulllman, [2]Texas A&M University, College Station, [3]University of Illinois, Urbana.*

Polymelia is a congenital condition where an animal has more than the normal number of limbs. Previous reports have suggested that polymelia is due to abnormal chromosomal breaks or alternatively due to a mutation found to segregate in Angus cattle. A male Holstein calf was presented to the WSU Veterinary Hospital with scoliosis, a deviated tail, and two additional front legs originating from each scapula. The objective of this study was to determine if polymelia in this Holstein calf was due to the mutation identified in Angus cattle, a gross chromosomal abnormality or potentially another genetic cause. A 10-mL blood sample was taken via the jugular vein for genetic analyses. Five mL of blood was used to prepare a karyotype of the calf to identify chromosomal abnormalities. From the remaining 5 mL of blood, DNA was extracted for genotyping. Genotyping of this Holstein calf for the specific mutation present in Angus cattle was performed using a PCR-RFLP technique. Genotypes were also obtained from the Holstein calf using the Illumina bovine HD BeadChip. A genome wide association study (GWAS) was conducted with the polymelia calf compared with 2800 control Holstein calf samples. The statistical approach used for the GWAS was EMMAX (Efficient Mixed-Model Association expedited) within the SNP & Variation Suite 7 software package (Golden Helix, Bozeman, MT). GWAS data underwent quality control filtering for minor allele frequency (< 1%), SNP call rate (< 95%), and animal call rate (removal of animals with less than 95% of SNPs called). Population stratification was tested

for ($lambda_{GC}$) before GWAS analysis. Loci associated with polymelia were found to be associated when $P < 1x10^{-50}$. The karyotype results showed no evidence of increased levels of chromosomal breaks in the Holstein calf. The PCR-RFLP genotype of the Holstein calf was consistent with a homozygous normal Angus animal. Furthermore, sequencing of the entire coding sequence of the gene mutated in Angus cattle, revealed no additional polymorphisms that might cause the polymelia phenotype. No population stratification was identified ($lambda_{GC}$ = 1.04) in the Holsteins genotyped by the Bovine HD SNP assay. The GWAS association analysis identified three loci associated with polymelia: one locus on BTA13 ($P < 1x10^{-281}$), BTA10 ($P < 2x10^{-110}$) and BTA20 ($P < 2x10^{-52}$). These preliminary results suggest that polymelia may be due to more than one locus and mutations that may cause polymelia are not shared across all breeds.

Key Words: polymelia, genetics, Holstein

0896 (T022) Effect of supplementation of the middle and freezing with vitamin E about the feasibility and quality of frozen bovine semen. R. D. Almeida*, L. K. Hatamoto-Zervoudakis, M. F. C. Filho, J. T. Zervoudakis, P. P. Tsuneda, and T. B. Castaldeli, *Federal University of Mato Grosso, Cuiaba, Brazil.*

The conditions of storing semen induce the formation of free radicals from the oxidation of fatty acids components of the plasma membrane. Those effects are related with the aggression on the plasma membrane and other cellular organelles, caused by oxidative stress, heat shock and formation of intracellular ice crystals. The interception of reactive oxygen species is based in breaking the chain reaction that occurs with free radicals to form oxidation products. This breakdown promoted by certain antioxidants, for example, α-tocopherol (vitamin E), radicals must not result in final products that is, without electrostatic despareado. This work had as purpose to appraise the quality and the feasibility of frozen semen in medium supplemented with vitamin E. Semen collections of 16 bulls Brangus race of reproductive age with proven fertility and healthy were performed. The semen was collected by eletroejaculation method, isolated shock heat, light and previously heated. Immediately after collection each ejaculate obtained was divided into two fractions where each fraction was diluted in one of two treatments being: T1-control (medium without supplementation), T2-medium supplemented with 2.0 mmol/L of vitamin "E". The basic medium used for freezing was tris-yolk sodium citrate, and the methodology used was described by Beconi et al. (1991). The semen was stored in straws of 0.25 and maintained in nitrogen until the time of analysis. For evaluation of sperm viability it was used the method for staining with eosin associated negrosina in thawed semen, cells with membrane lesions present in the nucleus stained by eosin, remaining reddish, the living cells, colorless microscopic reading. In force and motility parameters did not differ between treatments. On sperm viability (eosin/negrosina) had a significant difference between treatments ($P = 0.0031$), where treatment control was superior to treatment with vitamin E, indicating that the inclusion of 2.0 mmol/L was deleterious to sperm viability. More studies should be conducted to find an optimal concentration to ensure a better sperm viability after thawing semen.

Key Words: anti-oxidant, frozen semen

0897 (T023) The effects of cutting height and plant maturity on yield and nutritional value of brome forage. M. A. Woolsoncroft*, S. R. Duncan, A. J. Sexten, and A. K. Sexten, *Kansas State University, Manhattan.*

It is well-known that quality of forage decreases as plants matures. Although some forage quality must be sacrificed to achieve sustainable yields, the purpose of this study is to determine the combination of cutting height and stage of plant maturity that optimizes both quality and forage yield. A brome pasture was divided into 27 plots (3.05 m × 4.57 m) in a completely randomized block design with a 3 × 3 factorial treatment arrangement to determine the effect of cutting height (2.54 cm, 7.62 cm, or 12.7 cm) and plant maturity (boot, bloom, seed) on brome yield and nutritional value. A strip of forage (0.91 m × 3.05 m) was harvested from each plot. One grab sample from each strip was weighed in the field, oven-dried (49°C for 24 to 48 h), reweighed to determine percent dry matter and then calculate plot yield ($kg \cdot ha^{-1}$). A second grab sample from each harvested strip was collected and analyzed for DM, Ash, N, NDF, and ADF. Forage yield was greater ($P < 0.0002$) when brome was cut at 2.54 cm compared to 7.62 cm and 12.7 cm cutting heights. Brome cut at 7.62 cm and 12.7 cm produced similar yields. Cutting height had no effect on any of the nutritional parameters measured. Forage yield was greatest ($P < 0.0001$) for brome that was in the seed stage of maturity, followed by bloom then boot, which produced the lowest forage yield. Dry matter content was greatest ($P = 0.0001$) in the seed stage brome, but lower and similar between bloom and boot stage brome. Ash content was also similar between boot and bloom stage brome with both having a greater ($P = 0.002$) ash content than seed stage brome. Both NDF and ADF increased with plant maturity, with seed and bloom stage brome having a greater ($P = 0.0001$) fiber content than boot stage brome. Crude protein, estimated from N content, was greatest ($P = 0.0001$) in boot, followed by bloom, then seed stage brome, which contained the lowest CP content. Reducing cutting height produced a greater forage yield without negatively impacting nutritional value. More mature brome produced greater yields; however, nutritional value was decreased with increasing maturity. Cutting brome at a reduced cutting height in a younger stage of maturity can lead to better yields without sacrificing nutritional value.

Key Words: brome, plant maturity, cutting height

0898 (T024) Cattle requiring multiple treatments for bovine respiratory disease exhibit decreased capacity to protect against histone cytotoxicity.
J. Matera*, B. K. Wilson, J. Hernandez Gifford, C. R. Krehbiel, and C. A. Gifford, *Oklahoma State University, Stillwater.*

Bovine respiratory disease (BRD) is the leading cause of morbidity and mortality in feedlot cattle. Pneumonia associated with BRD causes significant inflammation and lesions in lung tissue of infected cattle. During acute inflammatory responses, circulating histones increase and contribute to mortality in rodents and humans, yet serum proteins provide protection against histone cytotoxicity in some cases. We hypothesized that cattle experiencing fatal cases of BRD have reduced ability to protect against histone cytotoxicity. Bovine kidney cells (MDBK) were exposed to 0, 50 μg/mL, and 100 μg/mL of histones from calf thymus for 18 h without serum. To assess cell viability, Resazurin was added (0.5%) and cells were incubated for an additional 6 h followed by fluorescent quantification. Because both doses exhibited cytotoxic effects, and work in humans suggests that serum histone levels rise to 50 μg/mL during sepsis, 50 μg/mL was chosen for subsequent studies. At feedlot arrival, serum samples were collected from 37 bull calves, followed by castration and normal feedlot processing procedures. Animals were retrospectively assigned to either Controls (never treated for BRD; CONT; $n = 12$), Recovery (treated once for BRD and recovered; RECOV; $n = 9$), Dead (treated once for BRD and subsequently died; DEAD; $n = 8$), or Chronic (treated four times for BRD; CHRON; $n = 8$). Duplicate wells containing MDBK cells were cultured in 96-well plates as described above except were supplemented with 1% serum from individual animals plus 50 μg/mL histones and duplicate wells with 1% serum alone. Fluorescent values from serum alone were subtracted from values obtained for histone treatment for each animal and analyzed using the GLM procedure of SAS. Results showed that histone treatment reduced cell viability in all groups and treatment group affected serum protective capacity ($P = 0.05$). Serum from CONT, RECOV, and DEAD calves all exhibited a similar ($P > 0.50$) response to histone treatment with values of −591.8 ± 549.9, -1086.9 ± 634.9, and -1193.8 ± 634.9, respectively. However, CHRON calves demonstrated an impaired capacity to protect against histones (-3054.4 ± 673.4) and were reduced ($P < 0.05$) when compared to each of the other groups. Results suggest that calves that require multiple treatments for BRD have reduced ability to protect against cytotoxicity of histones. Understanding the underlying mechanism responsible for protecting against histone cytotoxicity could lead to better identification of animals susceptible to severe cases of BRD.

Key Words: BRD, histones, feedlot, health

0899 (T025) Development of a non-invasive system for monitoring dairy cattle sleep.
J. M. Klefot*, J. L. Murphy, K. D. Donohue, B. F. O'Hara, M. E. Lhamon, and J. M. Bewley*, University of Kentucky, Lexington.*

Lack of sleep in dairy cattle may indicate shortcomings in housing, environment, or increased physiological disturbances. Little research has been conducted to assess sleep in production livestock, primarily because of limitations with monitoring abilities. Consequently, biological understanding of the production circumstances and facility options that affect sleep is limited. The objective of this study was to test a non-invasive system using a three-axis accelerometer monitor to measure head position of the cow to classify sleep, and wake behaviors. The duration of the study consisted of two 24-hour periods of observing four Holstein dairy cows in September 2013 at the University of Kentucky Coldstream Dairy. The three-axis accelerometers were attached to a harness on the side of each cow's neck to determine head and body movement. Human observation of the animals noted the times of active behaviors and very low activity, or sleep behaviors. Wake behaviors were classified as standing and alert. Sleep was classified with the behaviors of lying with no movement and eyes closed with head rested on the ground or flank. The radial signal was extracted from the xyz components of the accelerometer to obtain a motion signal independent of direction. Radial signal features were examined for maximizing the performance of detecting sleep behavior using a Fishers linear discriminant analysis (LDA) classifier. This study included a total of 652 min of high activity behaviors and 107 min of sleep behavior recorded from two cows with usable data. Results from a bootstrapping analysis show an agreement between human observation and the LDA classifier of 93.7 ± 0.7% for wake behavior and 92.2 ± 0.8% for sleep behavior, with a 95% confidence interval. This monitor may be used to help understand options for monitoring sleep in research and production settings.

Key Words: behavior, sleep, accelerometer

0900 (T026) Associative effects of feeding varying levels of soyhulls to lambs consuming grass hay.
K. M. Ulmer*, D. D. Harmon, S. J. Neil, A. K. Revercomb, J. G. Young, L. A. Engel, and M. A. McCann, *Virginia Polytechnic Institute and State University, Blacksburg.*

Soyhulls are routinely utilized as a supplement to forage based diets in ruminants. Previous studies have focused on low and moderate supplementation rates where soyhulls have generally been effective and economical. Recent grain prices have increased pressure on livestock producers to potentially expand their use of soyhulls in situations where higher levels of performance are desired. The objective of this study was to compare the effect of various levels of soyhull supplementation on nutrient digestibility in lambs fed a basal diet of chopped grass hay. Eight St. Croix

cross wether lambs (39 ± 4 kg) were randomly assigned to four diets using a 4 × 4 replicated Latin square design. All lambs were offered a chopped grass hay free choice and supplemented at 0, 1, 2, or 3% of body weight in soyhulls (DM basis). Each period consisted of a 9-d adjustment period followed by a 5-d collection period. Lambs were housed individually and fitted with total fecal collection bags during the adjustment period of each diet. At the conclusion of each collection period and before proceeding to the next adjustment period, lambs were weighed to adjust supplementation levels. During collection periods, daily feed, refusals and feces weights were recorded and samples retained for analysis. Samples were dried, ground, and analyzed for dry matter (DM), crude protein (CP), ash, neutral detergent fiber (NDF) and acid detergent fiber (ADF). Data were analyzed in SAS using the PROC GLIMMIX procedure with a model including diet and period. Linear, quadratic and cubic treatment effects were evaluated using preplanned contrasts. Daily DM intake increased linearly ($P < .01$) with increasing soyhull supplementation. Dry matter digestibility increased quadratically ($P < .01$) as soyhull supplementation increased (56.6, 63.0, 65.4, and 66.4, respectively). Similarly, both NDF and ADF digestibility exhibited a quadratic response ($P < .01$) as dietary soyhull level increased. However, contrary to DM digestibility, NDF and ADF displayed peak digestibility at the 2% supplementation level. Results would suggest that supplementation of soyhulls above 2% of body weight would provide diminishing benefits as compared to lower levels of supplementation. Depression of NDF and ADF digestibilities at the 3% supplementation level contributed to the reduced DM digestibility improvement. Further research is needed to determine if reduced fiber digestibility was the result of increased rate of passage and reduced ruminal digestion.

Key Words: soyhulls, associative effects, lambs

0901 (T027) Adding post-extraction algal residue (PEAR) to cattle finishing diets reduces the quantity of fecal volatile chemicals often associated with feedlot malodors.

H. R. Voegele*[1], C. R. Kerth[1], T. A. Wickersham[2], J. C. Hoffman[1], and T. J. Luckemeyer[1], *[1]Texas A&M University Animal Science Dept., College Station, [2]Texas A&M University, College Station.*

Efficiencies of finishing cattle in feedlots have resulted in lower production costs and less expensive beef for consumers. But an increase in the size of feedlots, and resulting waste malodors, along with urban sprawl have brought the public and feedlots closer together and given urgency to finding methods to reduce feedlot malodors. Our objective was to feed post-extraction algal residue (PEAR) to steers to reduce the incidence of fecal malodor chemical compounds. Six steers were fed PEAR (1.25 kg/d, as-fed) along with a 90% concentrate and 10% forage diet for 35 d before harvest. One wk prior and 1 wk after the addition of PEAR to the feed, fecal samples were collected from each steer to produce fecal samples with and without PEAR within the same animal. Fecal samples were stored in an enclosed plastic bag immediately after collection (−80°C) until analyses. Each sample was placed in a 760 mL glass jar submerged in a 60°C water bath, and thawed to 25°C. A 75 µm carboxen/polydimethylsiloxane solid phase microextraction (SPME) fiber was then inserted into the jar and collected for 120 min. The SPME was desorbed in a multi-dimensional GC/MS with dual olfactory ports. All eluted chemicals were quantified as total ion counts (TIC) under the curve of each elution peak corresponding to each chemical identified by the MS library. Simple ANOVA was conducted to determine the effect of adding PEAR to the diet of steers on the relative quantity of fecal aroma chemical compounds. The general classification of amine/amide compounds tended ($P = 0.071$) to be reduced when PEAR was added to the feed. The addition of PEAR reduced the quantity of indole (manure/stench), the butyl ester of acetic acid (acid/burnt aroma), and carbon disulfide (rotten eggs) in fecal samples by 92.5, 80.5, and 97.1%, respectively ($P < 0.02$). Additionally, the quantity of the volatile chemicals dimethyl disulfide (garlic/burnt rubber), ethyl vinyl sulfide (sulfurous), and butyric acid (vomit) in the feces were reduced ($P < 0.05$) to undetectable levels with the addition of PEAR in the feed. The addition of PEAR to cattle finishing diets reduced the quantity of volatile chemicals often associated feedlot malodors.

Key Words: algae, beef, odor

0902 (T028) Treatment response to bovine respiratory disease in beef stocker calves was not positively affected when using isoflupredone acetate as ancillary therapy.

C. E. Crews*[1], J. G. Powell[2], E. B. Kegley[2], J. L. Reynolds[2], and J. A. Hornsby[2], *[1]University of Arkansas, Fayetteville, [2]Dep. of Animal Science, University of Arkansas Division of Agriculture, Fayetteville.*

The objective of this study was to evaluate the use of isoflupredone acetate as ancillary therapy in the treatment of bovine respiratory disease in high-risk stocker calves. Crossbred male beef calves ($n = 192$; BW = 221 ± 3.9 kg) were acquired in two blocks from regional auction markets and were transported to the University of Arkansas Stocker and Receiving Cattle Unit. Calves were observed daily for signs of respiratory illness, and antibiotic treatment was administered if calves displayed signs of illness and rectal temperature was ≥ 40°C. Calves ($n = 72$) requiring antibiotic treatment for respiratory illness were assigned randomly to either treatment 1 (injection of florfenicol) or treatment 2 (injection of florfenicol with isoflupredone acetate). Treatments occurred between d 2 and d 14 of the study. Both treatment groups were rechecked 48 h post treatment to determine treatment efficacy. Blood was collected twice (at treatment and recheck) via jugular venipuncture to evaluate complete blood cell count. Body weights were recorded at d 0, 14, 28, and 46 (block 1) or 42 (block 2). No difference was evident between treatment groups for medical treatment cost ($P = 0.54$) or number of calves requiring a second or third antibiotic treatment ($P \geq 0.61$). Upon

recheck, neutrophils were higher and lymphocytes were lower in calves that received isoflupredone acetate ($P \leq 0.04$) compared to calves that received only antibiotic therapy. Consequently, the neutrophil to lymphocyte ratio was greater ($P < 0.01$) in calves that received isoflupredone acetate compared to those that only received antibiotic therapy. No difference existed in overall white blood cell count at recheck ($P = 0.67$) or body temperature at recheck ($P = 0.43$). Calves that received isoflupredone acetate tended to exhibit greater ($P = 0.09$) ADG between d 14 and 28 compared to calves that were treated with only antibiotic therapy, 1.04 kg and 0.77 kg, respectively. Overall ADG for the entire receiving study was similar ($P = 0.88$) for both treatments. Results indicate that treatment of bovine respiratory disease with isoflupredone acetate as ancillary therapy to an antibiotic regimen does not have a positive effect on overall ADG, and it does not reduce medical treatment cost or the number of repeat treatments.

Key Words: bovine respiratory disease, ancillary therapy, isoflupredone acetate

---

0903 (T029) The effects of stage of production and implant exposure on feedlot performance, carcass characteristics, and relative mRNA gene expression. K. E. Larrabee*, B. C. Bernhard, C. L. Maxwell, B. K. Wilson, S. Roberts, and C. R. Krehbiel, *Oklahoma State University, Stillwater.*

Black-hided heifers ($n = 187$; 362 kg) were used in a 122-d finishing study to determine the effects of a trenbolone acetate-estradiol implant [Revalor 200 (200 mg of trenbolone acetate and 20 mg of estradiol)] on feedlot performance, carcass characteristics, and relative mRNA gene expression when administered at specific stages of production. Treatments included 1) no implant (CON), 2) implantation on d 0 (EARLY), or 3) implantation on d 56 (LATE). A subset of heifers from each treatment were harvested at d 28 and 84 to collect LM samples that were utilized to measure relative gene expression involving myogenesis and intracellular signaling mechanisms. After d 55, ADG (1.68 vs. 1.31 kg) and G:F (0.172 vs. 0.134) were improved for EARLY vs. non-implanted heifers ($P < 0.05$). From d 56 to 122, ADG improved with implantation and was greatest for LATE ($P < 0.05$), while G:F was only improved by LATE ($P < 0.01$). Overall, implantation improved ADG (1.24 vs. 1.04 kg) and G:F (0.136 vs. 0.114) compared to CON heifers ($P < 0.01$), regardless of timing. Dry matter intake was not affected ($P = 0.41$) by implantation protocol. Implantation increased HCW (340 vs. 320 kg), dressing percentage (65.9 vs. 65%), and LM area (92.3 vs. 85.8 cm^2) vs. non-implanted cattle ($P < 0.05$), regardless of timing. Back-fat, marbling score, and REA/HCW ratio were unaffected by treatment ($P > 0.18$), as well as quality and yield grade distributions ($P > 0.21$). The mRNA expression of myostatin and insulin-like growth factor-1 were not affected by treatment at d 28 ($P > 0.18$). At d 84, myostatin was significantly reduced in heifers that had been implanted compared to CON (5.01 vs. 8.06; $P = 0.02$), regardless of timing. Insulin-like growth factor-1 was not affected by treatment ($P > 0.18$), but mRNA expression levels were decreased at d 84 compared to d 28 (31.8 vs. 50.2; $P < 0.05$). The expression of paired box 7 was increased in EARLY cattle compared to CON cattle at d 28 (0.682 vs. 0.467; $P = 0.05$). Paired box 7 mRNA gene expression of EARLY heifers at d 28 was greater than LATE heifers at d 84 (0.682 vs. 0.371; $P < 0.05$). The results of this study suggest that anabolic growth promotants improve cattle performance and production efficiency without altering carcass quality, independent of exposure time. This study also indicates that stage of production has the greatest effect on relative mRNA gene expression.

Key Words: feedlot and carcass performance, gene expression, implantation

---

0904 (T030) The effects of corn silage diets on intestinal morphology in dairy calves. T. J. Pogreba*[1], S. I. Kehoe[1], K. Dill-McFarland[2], and G. Suen[2], *[1]University of Wisconsin–River Falls, River Falls, [2]University of Wisconsin-Madison, Madison.*

A calf's diet in the first few weeks of life is critical for gastrointestinal tract development. Current feed prices are causing producers to experiment with less expensive alternatives. These different feeds may affect the development of the gastrointestinal tract, which can further affect feed efficiency and calf performance. Therefore, evaluating intestinal morphology is an indicator of how well the animal is absorbing nutrients. The objective of the study was to determine the post-weaning effects of calf starter and corn silage fed to pre-weaned dairy calves on jejunal morphology. A total of 45 calves ($n = 15$/trmt) were fed a diet of whole milk with one of the following treatments: 100% calf starter (C), 60% calf starter and 40% corn silage (CC), or 100% corn silage (CS). Nine calves were sacrificed 8 wk after birth. Jejunal samples were collected to compare between the three treatment groups. Samples were preserved in formalin and later phosphate buffered saline until further analysis. Using a cryo-microtome, slices of tissue were made into nine slides per calf and stained with methylene blue. Pictures were taken with a compound light microscope and measured using the ImageJ computer program (NIH, Bethesda, MD). Measurements were recorded including villi length, crypt depth, and villi width. Measurements were averaged per section block and were statistically analyzed using the PROC MIXED in SAS 9.2. Significance was determined at $P < 0.05$ and trends at $P < 0.15$. Least squares means of villi lengths were 97.65, 105.61, and 89.57 µm for treatments C, CC, and CS, respectively ($P = 0.12$). Least squares means of crypt depths were 46.10, 48.58, and 38.69 µm for treatments C, CC, and CS, respectively ($P = 0.03$) and villi diameters were 14.51, 15.38, and 17.17 µm for treatments C, CC, and CS, respectively ($P = 0.69$). Results from the study indicated that the calves fed CS had significantly shorter crypt depths and tended to have shorter villi lengths compared with the other treatments. This may indicate better intestinal development in calves fed either 100% calf starter or a mix of 60% calf starter and 40% corn silage.

Key Words: calves, corn silage, intestine

BEEF SPECIES:
FEEDLOT AND STOCKER

0905 (T031) The effect of good or poor residual feed intake sires on feedlot heifer performance and carcass characteristics. K. M. Retallick*[1], D. B. Faulkner[2], and D. W. Shike[3], *[1]CalPoly, San Luis Obispo, CA, [2]University of Arizona, Oro Valley, [3]University of Illinois, Urbana.*

Performance and intake data were collected for 90 d on Angus yearling bulls (n = 8) to calculate residual feed intake (RFI) on these potential sires. These bulls were than used as herd sires during the fall breeding season. The Angus x Simmental heifer (n = 84) progeny of these sires were randomly allotted to pens, managed similarly, and fed a common diet. Heifers had intake data collected for 70 d and were weighed every 2 wk for calculation of RFI during this period. Thirty-seven heifers were sired by poor RFI (RFI = 0.64 to 1.35) sires, and 47 heifers were sired by good RFI (RFI = -0.08 to -0.86) sires. The objective of this study was to observe performance and carcass characteristics of feedlot heifers sired by good or poor RFI sires and determine phenotypic feed efficiency correlations between sire and heifer progeny. Data were analyzed using PROC MIXED of SAS with sire RFI classification (poor or good) as a fixed effect and pen a random effect. Individual animal was the experimental unit. Phenotypic correlations were analyzed with the PROC CORR procedure of SAS. Heifer performance did not differ for initial weight, final weight, or ADG. Heifers sired by good (low value RFI) sires had a 0.65 kg/d lower DMI ($P < 0.05$) than heifers by poor (high value RFI) sires. As a result, heifers by good RFI sires had a 0.51 kg/d lower RFI than heifers by poor RFI sires. Heifers by good RFI sires also had a desirable 4.4% increase ($P = 0.21$) in G:F. Hot carcass weight, rib eye area, backfat, and yield grade did not differ. A 28-unit marbling advantage ($P = 0.18$) was given to poor RFI sired heifers. Heifer RFI was correlated to DMI at 0.78 ($P < 0.05$). Heifer RFI and heifer G:F were correlated at -0.27 ($P < 0.05$); however, sire RFI was not significantly correlated to heifer G:F. Sire RFI was correlated to heifer DMI at 0.33 ($P < 0.05$). Sire RFI was correlated at 0.47 ($P < 0.05$) to heifer RFI. The significant correlation of sire RFI to heifer RFI as well as desirable effects on performance and carcass traits assists in the quantification of the advantages of selecting for RFI.

Key Words: sire residual feed intake, heifer performance, feed efficiency

0906 (T032) Feed efficiency and carcass traits for Nellore young bulls fed processed soybean grains. M. C. L. Alves, M. M. Ladeira*, D. R. Casagrande, J. R. R. Carvalho, P. D. Teixeira, L. A. Silveira, A. C. Rodrigues, and L. R. Santos, *Universidade Federal de Lavras, Brazil.*

Use of lipid sources in beef cattle diet is recommended to increase diet energy density, and reduce acetate:propionate ratio and methane production, which may benefit ruminal fermentation and improve feed efficiency. The objective of this study was to evaluate the feed efficiency and carcass quality of Nellore young bulls fed ground soybean or extruded soybean. Sixty animals (average body weight of 320.33 ± 8.12 kg) were used in a completely randomized design. Corn silage was fed as the forage source along with three different types of concentrates, representing the following treatments: no soybean, ground soybean (GSB) and extruded soybean (ESB). Dietary crude protein averaged 13.9%, while soybean diets contained 6.1% ether extract. Animals were allocated to 12 pens based on dietary treatment (four pens/treatment). Animals were weighed at the beginning, after 26 d of adaptation to experimental diets, and at the end of the feedlot to calculate average daily gain after fasting cattle for 16 h. After 88 d on feed, cattle were slaughtered using cerebral concussion and exsanguination followed by recording hot carcass weights. After 24 h of chilling at 1°C, cold carcass weights were recorded, along with measuring subcutaneous fat thickness and longissimus muscle area between the 12th and 13th ribs. The statistical model included the effects of diet with data analyzed using PROC GLM (SAS 9.3). There were no effects of diet on performance and carcass characteristics (Table 0906). The feeding of processed soybeans did not affect feed efficiency and carcass traits for young Nellore bulls. *Funded by Fapemig, CNPq, Capes, and INCT-CA.*

Key Words: extruded, feedlot, lipids, oilseeds

Table 0906. Dry matter intake (DMI), average daily gain (ADG), feed efficiency (G:F), final body weight (FBW), hot carcass weight (HCW), cold carcass weight (CCW), longissimus dorsi muscle area (LMA), longissimus dorsi muscle area per 100 kg of carcass (LMA/100kg), backfat thickness (BF), dressing percentage (DP) for young bulls fed processed soybean

Item	NSB[1]	GSB[2]	ESB[3]	SEM	*P*–Value
DMI (kg/d)	10.2	9.85	9.96	0.298	0.73
ADG (kg/d)	1.50	1.44	1.53	0.059	0.55
G:F	0.14	0.14	0.15	0.004	0.46
FBW (kg)	440	438	451	10.029	0.56
HCW (kg)	250	249	259	4.633	0.26
CCW (kg)	246	244	255	4.410	0.24
LMA (cm^2)	66.1	66.6	68.2	2.252	0.86
LMA (cm^2/100kg)	27.8	27.3	26.8	1.089	0.83
BF (mm)	3.03	2.73	2.88	0.237	0.68
DP (%)	56.0	56.1	56.8	0.347	0.25

[1] Diet with no soybean

[2] Diet with ground soybean

[3] Diet with extruded soybean.

0907 (T033) Supplementing beef cattle finishing diets containing wheat distillers grain with feed enzymes to decrease the ratio of n-6/n-3 fatty acids in meat. Z. He*[1,2], M. He[1], Y. Zhao[1,3], N. D. Walker[4], K. A. Beauchemin[1], T. A. McAllister[5], and W. Yang[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, [2]Key Laboratory for Agro-Ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, The Chinese Academy of Sciences, Changsha, [3]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China, [4]AB Vista Feed Ingredients, Marlborough, UK, [5]Agriculture and Agri-Food Canada, Lethbridge, AB.*

The objective of this study was to determine the effects of dietary feed enzyme (FE) supplementation on fatty acids (FA, % of total FA) profiles of the pars costalis diaphragmatis (PCD) muscle of beef cattle fed finishing diets with or without inclusion of wheat dried distillers grain with solubles (DDGS). One hundred sixty crossbred yearling steers (initial BW 495 ± 37.9 kg) were blocked by BW and randomized into 16 pens (10 steers/pen). The pens were randomly assigned to one of four treatments: 1) control (CON; 10% barley silage and 90% barley grain-based concentrate), 2) WDG (CON diet substituting 30% wheat DDGS for barley grain), 3) WDGL (WDG diet supplementing with low FE; 1 mL FE/kg diet DM), and 4) WDGH (WDG diet supplementing with high FE; 2 mL FE/kg diet DM). The PCD samples were collected from cattle at slaughter at the end of the finishing period (120 d) with a targeted live weight of 650 kg. Data were analyzed using the PROC MIXED of the SAS (SAS Institute Inc.), considering treatment (diet) as fixed effect. Contrasts were generated to compare the CON and WDG diet. Linear and quadratic orthogonal contrasts were generated to exam the effect of increasing FE in the diet containing wheat DDGS. Concentration of total polyunsaturated fatty acids (*P*UFA) in muscle was greater ($P < 0.01$; 4.52 vs. 3.41), whereas total monounsaturated FA tended ($P = 0.08$; 45.0 vs. 47.1) to be less for steers fed WDG than steers fed CON. In addition, inclusion of wheat DDGS into the diet vs. diet containing no DDGS increased ($P < 0.01$) concentration of conjugated linoleic acids and vaccenic acid (CLA+VA; 1.22 vs. 0.78) and decreased ($P = 0.03$) total trans FA (excluding CLA and VA; 0.98 vs. 1.27), consequently resulted in higher ($P < 0.01$) ratio of n-6/n-3 PUFA (10.95 vs. 7.72). Increasing FE application in wheat DDGS diets linearly decreased ($P = 0.02$) the ratio n-6/n-3 FA (10.95 to 9.23) in muscle without affecting amount of individual or total FA. These results suggest that application of FE in finishing diets containing wheat DDGS may improve FA profiles of beef which could benefit human health.

Key Words: beef, fatty acid, feed enzyme

0908 (T034) Effects of fat level in distillers grain on finishing feedlot performance and carcass traits. V. L. Anderson*[1] and C. L. Engel[2], *[1]North Dakota State University, Carrington, [2]Carrington Research Extension Center, North Dakota State University, Carrington.*

The objective of this study was to evaluate the effects of different corn oil levels in distillers grains (DG) on beef cattle performance during finishing and the effects on carcass traits. Angus sired steers ($n = 182$, 461.97 ± 4.38 kg) were blocked by weight (fall calves and yearlings) and allocated to one of four treatments based on corn oil level in DG: 1) control (CON) no DG, 2) low corn oil (LOW, 5.47%), 3) medium corn oil (MED, 8.05%), and 4) high corn oil (HIGH, 12.96%). Eleven or 12 steers were assigned to each of 16 pens with four replicates per treatment. Steers were fed a corn-based diet (136 Mcal/kg) to appetite formulated to meet or exceed NRC requirements. Steers were weighed after 28 d on feed and at the end of the finishing period which was an additional 41 d for the light blocks and 77 d for the heavy blocks. Steers were marketed in two drafts at Tyson Fresh Meats, Dakota City, NE, with carcass traits evaluated by the same trained grader. Fat level in the ration for the respective treatments was 3.58, 4.02, 4.52, and 5.48, for CON, LOW, MED, and HIGH. DG was included in the finishing diet at 19.4% (DM basis) with sunflower meal (2.44% oil) used in the CON ration. DMI tended to increase linearly with corn oil during the first 28 d on feed ($P < 0.07$) with 12.54, 12.78, 13.11 kg/hd/d consumed by LOW, MED, and HIGH, respectively. Feed intake was affected quadratically during the final finishing period ($P < 0.03$) and over the entire feeding period ($P < 0.05$). There is some suggestion ($P < 0.13$) of linearly improving gain with increasing corn oil during the first 28 d on feed; however, overall ADG was not affected by treatment ($P > 0.27$). Gain efficiency was not affected ($P > 0.26$) by treatment. Marbling score increased linearly ($P < 0.02$) with increasing corn oil. Yield Grade tended to increase linearly ($P < 0.07$) from 2.98 to 3.27 for CON and HIGH, respectively, and REA tended to decrease ($P < 0.07$) with increasing corn oil but other carcass traits were not affected ($P > 0.27$). These data indicate that higher corn oil in DG has some positive effect on feed intake and marbling but does not affect gain or gain efficiency.

Key Words: beef, distillers grain, corn oil

0909 (T035) Effects of zilpaterol hydrochloride feeding time on Nellore bulls performance and carcass characteristics. A. C. R. Dos Santos*[1], M. Caetano[1,2], R. S. Goulart[1,3], S. B. Pflanzer[4], S. Luz e Silva[5], and D. P. D. Lanna[1], *[1]University of Sao Paulo/ESALQ, Piracicaba, Brazil, [2]University of Adelaide, Roseworthy, Australia, [3]MSD Saúde Animal, Sao Paulo, Brazil, [4]University of Campinas/FEA, Campinas, Brazil, [5]University of Sao Paulo/FZEA, Pirassununga, Brazil.*

Nellore bulls (n = 96; initial BW = 377 ± 21.4 kg) were used in a randomized complete block design arranged in a 4 × 2 factorial to evaluate effects of zilpaterol hydrochloride (ZH; 8.33 mg/kg of diet DM basis) on performance and carcass traits. Total days on feed (DOF) were 90 and 117, and there were four periods of ZH feeding (0, 20, 30, or 40 d before slaughter) plus a 3-d ZH withdrawal period for all animals. No interactions between ZH and DOF were detected for the performance or carcass characteristics (P > 0.10). There was a linear increase for G:F (β = 0.0005; P < 0.01), HCW (β = 0.4304; P = 0.03), dressing percentage (β = 0.0541; P < 0.01), and LM area (β = 0.1318; P = 0.01) with length of ZH feeding. Additionally, there was a linear decrease for kidney, pelvic and inguinal fat (β = -0.0384; P = 0.04) when ZH feeding period was increased; however, no difference was noted for 12th-rib fat. In conclusion, Nellore bulls fed ZH had improvements in feed efficiency and carcass traits over controls, and these were independent of DOF. The effects of increasing the length of ZH treatment to 30 or 40 d were relatively small, and this data can be used to find the best economic option based on feed, cattle, and ZH costs.

Key Words: β-agonist, beef cattle, feedlot

Table 0909. Effect of ZH feeding period on Nellore performance and carcass traits

	ZH feeding period					
	0	20	30	40	SEM	*P*-value
Final BW, kg	561	572	566	571	10.60	0.68
ADG, kg/d	1.75	1.87	1.81	1.91	0.06	0.28
DMI, kg/d	10.22	10.12	9.96	9.83	0.27	0.60
G:F	0.171	0.185	0.182	0.194	0.006	< 0.01**
HCW, kg	306	320	319	324	7.06	0.03*
Dressing percentage, %	54.6	55.9	56.3	56.7	0.30	< 0.01**
Kidney, pelvic and inguinal fat, kg	13.4	11.6	11.9	11.9	0.55	0.04*
12th-rib fat, mm	5.38	4.63	4.72	5.17	0.27	0.17
LM area, cm^2	76.3	79.2	81.7	81.1	1.87	0.02*

* Linear effect (P < 0.05).

** Linear effect (P < 0.01).

0910 (T036) Influence of calcium depletion and repletion on beef tenderness of steers fed zilpaterol hydrochloride. J. O. Carothers*, D. N. Burton, K. R. Underwood, and R. H. Pritchard, *South Dakota State University, Brookings.*

The objective of this study was to evaluate the influence of manipulating dietary Ca to influence tenderness via the calpain system in steers fed zilpaterol HCl (ZIL). Steers (n = 120; BW 478 ± 18 kg) were blocked by BW, and randomly assigned to one of three treatments 50 d before initiating dietary treatments. Dietary treatments included: 1) Control, conventional finishing diet (sans ZIL); 2) Control diet plus ZIL (6.78 g/T) fed for 20 d; and 3) depleted dietary Ca while feeding ZIL. Cattle on treatments 2 and 3 were changed to diet 1 for 3 d before harvest, which restored dietary Ca for cattle on treatment 3 and accommodated ZIL withdrawal requirements. A subsample of steers were taken to quantify serum Ca levels, and shear force values for strip loins and sirloin butts. Blood was collected from the subsample 24 h before harvest (48 h after cattle treatment 2 and 3 switched to diet 1). Muscles were cut into steaks and aged 14 d. Orthogonal contrasts were used to compare control vs. ZIL (treatment 1 vs. 2 and 3) and Ca manipulations (treatment 2 vs. 3). Feeding ZIL caused increased (P < 0.05) BW (610 vs. 620 kg), ADG (1.32 vs. 1.66 kg), and G:F (116 vs. 152 g/kg) compared to control. Zilpaterol increased (P < 0.05) HCW (373 vs. 392 kg), dressing percentage (63.08 vs. 65.10%) and LMA (82.26 vs. 91.52 cm^2) but did not affect (P > 0.05) marbling score (Small73 vs. Small55) when compared with control. Calcium manipulation did not affect (P > 0.05) live or carcass variables or serum Ca levels (10.6 vs. 11.0 mg/dl). Zilpaterol increased WBSF values (P < 0.05) for 14 d aged strip steaks (5.28 vs. 6.99 kg), while having no effect (> 0.05) on shear force values for sirloin butts (6.24 vs. 6.83 kg). Dietary Ca manipulations did not affect (P > 0.05) shear force values. Manipulating dietary Ca did not adversely affect live performance or carcass traits. Prolonged repletion (3 d) may have been too long to allow for influences on the calpain system to affect tenderness.

Key Words: beef, zilpaterol, tenderness

0911 (T037) Using early ultrasound measurements to predict beef carcass quality grade. J. K. Smith*, M. D. Hanigan, S. P. Greiner, and M. A. McCann*, Virginia Polytechnic Institute and State University, Blacksburg.*

Although many cattle producers have focused selection efforts toward enhancing carcass marbling, a number of pre- and post-weaning management factors often limit the ability of finished cattle to achieve their marbling potential. Enhancing the ability of a feeder to predict finished quality grade (QG) before entry into a finishing program would allow for more strategic utilization of management practices that impact QG,

particularly for cattle with lower likelihood of achieving QG-based retail brand acceptance. The objective of this experiment was to evaluate the ability of early ultrasound measurements collected before finishing to predict finished carcass marbling score (MS) and QG. Serial early ultrasound measurements of ribeye area (REA), 12th-rib subcutaneous fat thickness (SFT) and percent intramuscular fat (IMF) were collected from early- and conventionally-weaned Angus-sired steers ($N = 60$) from three separate calving seasons within a single herd. Ultrasound measurements were collected at the time of early-weaning (EW; 105 ± 18 d of age), conventional-weaning (CW; 210 ± 18 d of age), and again on conclusion of backgrounding (360 ± 60 d of age) immediately before feedlot arrival. Cattle were adapted to a concentrate and corn silage-based ration and finished for 131 ± 34 d at one of two feedlots before being harvested on reaching a common ultrasound predicted SFT of 1 cm. Carcasses were evaluated by a panel of trained analysts to determine MS and QG. Initial screening for factor effects of weaning treatment, sire, and ultrasound predicted REA, SFT and IMF measurements for each of the three time points via the screening procedure of JMP Pro (version 10.0.2; SAS Institute, Cary, NC) indicated that IMF and REA measurements collected at CW and immediately before feedlot arrival explained a significant ($P < 0.05$) portion of the variation in carcass MS. Full four-way factorial regression models were then generated to predict carcass MS ($R^2 = 0.83$; $P < 0.05$) and the probability of achieving a specific QG ($R^2 = 0.95$; $X^2 = 129$; $P < 0.0001$) using the Fit Model procedure of JMP Pro. These results provide evidence that early carcass measurements for REA and IMF can be effectively utilized to explain a major portion of the variation in finished carcass MS and QG. Such information could be utilized to produce models that allow feeders to predict carcass QG at receiving.

Key Words: beef, quality, marbling

0912 (T038) Influence of breed on the sensory meat quality and consumer acceptability in extensively reared beef.

M. E. A. Canozzi[1], L. Sphor[1], C. M. Pimentel[2], J. O. Barcellos[3], C. H. E. C. Poli[1], R. D. Sainz[4], and L. Kindlein[*1], *[1]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil, [2]Universidade de Brasília, Brazil, [3]Universidade Federal Do Rio Grande Do Sul, Porto Alegre, Brazil, [4]University of California–Davis, Davis.*

We evaluated the sensory characteristics of meat from different animal types, including cattle (Angus and Brangus) and buffalo raised on pasture, and collected information on socio-demographic determinants of consumer preference. Samples were roasted rib eye, sliced and served in a disordered and monadic manner to 188 untrained tasters. A nine-point hedonic scale was used to assess odor, color, tenderness, succulence and overall appearance. Analysis of variance was conducted using the GLM procedure, considering animal type and socio-demographic characteristics as fixed effects and using the LSMEANS procedure for multiple mean comparisons. Differences ($P < 0.001$) between animal types were observed only for tenderness, with Brangus (7.02) and buffalo (6.82) meat being superior to Angus (6.25). Regardless of the meat origin, age, income, smoking and place of purchase affected the perceived attributes ($P < 0.05$). People aged over 50 yr gave higher mean scores for odor and color ($P < 0.05$), indicative of greater satisfaction and less demanding tastes when compared to other age categories. Most meat was purchased from supermarkets and butchers (82%). The majority (84%) of the panelists reported acquiring chilled rather than frozen meat, which may account for the high juiciness, flavor intensity, flavor, and overall acceptability reported. Despite the variability in the intrinsic characteristics of the meat products, differentiation by the consumer is not easy to determine, with little impact of socio-demographic characteristics on organoleptic perception. The different types of animals did not affect the general visual appearance of the meat as perceived by the consumer. Meat from Brangus cattle and buffaloes raised on pasture was considered more tender by an untrained taste panel than that from Angus cattle raised under the same conditions.

Key Words: beef, quality, palatability

0913 (T039) Evaluation of growth and performance characteristics before entering the feedlot as an indicator for contracting bovine respiratory disease.

S. Miller[*1], M. D. Garcia[2], R. Walker[3], T. Page[1], and K. W. Harborth[1], *[1]Louisiana State University, Baton Rouge, [2]Louisiana State University, Baton Rouge, [3]Louisiana State University AgCenter, Homer.*

The objective of the current study was to evaluate growth and performance traits before entering the feedlot as potential indicator of bovine respiratory disease (BRD) susceptibility. A population of 560 spring-born crossbred steers (2009–11) from the Central Research Station and the Hill Farm Research Station in Louisiana were evaluated for growth and performance before being shipped (2010–12) to a commercial feedlot in Guymon, OK. The growth and performance traits evaluated consisted of birth weight, weaning weight, and hip height. Bovine respiratory disease status was recorded by the feedlot and consisted of animals treated for BRD or animals that subsequently perished due to BRD infection. A total of 24 steers over the 2-yr evaluation period contracted BRD and were subsequently treated or perished in the feedlot. The PROC MIXED model of SAS was utilized to determine if associations between growth and performance traits and BRD status in the feedlot were linked. Fixed variables in the model included year of entrance into the feedlot, farm of origin and BRD status while in the feedlot. Growth and performance traits were fit in the model as random variables. Analyses revealed that no one trait had a significant effect ($P < 0.05$) on BRD status in the feedlot. However, birth

weight did exhibit a genetic trend ($P < 0.09$) in which animals with larger average birth weights (39.84 kg) had a higher degree of BRD incidence in the feedlot than animals with smaller birth weights (37.63 kg) in the utilized population. While no one growth and performance trait was statistically significant ($P < 0.05$), the fixed variable of year was highly significant ($P < 0.0001$) in the statistical model, thus necessitating further evaluation of other environmental and management variables that could be influencing susceptibility of contracting BRD during the feedlot stage of production.

Key Words: bovine respiratory disease, feedlot, growth and performance

---

0914 (T040) Maximizing profit in a feedlot enterprise using systems analysis thinking and linear programming. K. J. Retallick*[1], T. E. Adcock[1], T. R. Schultz[1], J. M. Bormann[1], R. L. Weaber[1], D. W. Moser[1], and M. D. MacNeil[2], *[1]Kansas State University, Manhattan, [2]Delta G, Miles City, MT.*

Systems' thinking is a management discipline that concerns understanding a complex entity studying the components and interactions between them that form the entirety of that entity. In this case, a system analysis approach was applied to a stereotypical situation of a farmer/feeder. Feedlot enterprises were evaluated using linear programming to maximize profitability from excess feedlot capacity. The hypothetical feedlot analyzed was based on data recorded by Iowa State University Extension. Four alternative beef cattle enterprises: weanlings, yearlings, performance-tested bulls, and beef replacement heifers, were investigated as alternative uses for the excess capacity. An earthen feedlot facility with shelter was modeled. Capacity was constrained by 60,000 linear inches of bunk and a weekly feed holding capacity of 5000 bushels of whole corn. The objective function summed the products of per head profit and numbers of each class of cattle. Results from three alternative scenarios have been presented here. Linear programming models were solved using Microsoft Excel. Simulation 1 involved only the two initial constraints on capacity and maximum profit resulted when 4630 yearlings and 159 performance-tested bulls filled the feedlot. This system assumed both yearlings and performance-tested bulls were turned over twice a year with consistent availability of cattle. In Simulation 2, it was assumed the owner-operator owned 1500 weaned calves, and these were forced into the solution. In this scenario, profit margins were maximized when 3439 yearlings, 26 performance-tested bulls, and the 1500 weaned calves filled the feedlot. Simulation 3 included 200 owned replacement females. This constraint pushed the system to fill the feedlot with 3200 yearlings, 1500 owned weanlings, and 200 owned replacement females. This simulation exercise represents the value of applying both systems thinking and linear programming in real management situations to determine maximum profits with resources available.

Key Words: cattle, feedlot, profit

BEEF SPECIES: COW-CALF AND BULL

0915 (W047) Pregnant beef heifers categorized by residual feed intake measured in adolescence exhibit differential intake and feeding behaviors when fed a restricted diet. C. Fitzsimmons[*1,2], G. Muhire[1,2], F. Paradis[1,2], L. McKeown[1,3], C. Straathof[1], H. Block[4], M. G. Colazo[3], C. Li[1,2], *B. Yaremcio[5], J. A. Basarab[6], and H. Bruce[1], [1]University of Alberta, Edmonton, Canada, [2]Agriculture and Agri-Food Canada, Edmonton, AB, Canada, [3]Alberta Agriculture and Rural Development, Edmonton, Canada, [4]Agriculture and Agri-Food Canada, Lacombe, AB, Canada, [5]Alberta Agriculture and Rural Development, StettlerCanada, [6]Alberta Agriculture and Rural Development, Lacombe, AB, Canada.*

Selection for residual feed intake (RFI) in cattle will bring about changes in metabolism and physiology that are not explicitly known. We appraised feed intake and feeding behavior in heifers, characterized by a range of RFI, when fed two different planes of nutrition from d 30 to 150 of pregnancy. Sixty-nine purebred Angus heifers, with RFIf (RFI corrected for fat, ave = 0.047, SD = 0.7678) measured in adolescence, entered a GrowSafe automated feed intake recording system after confirmation of pregnancy at 30 d post artificial insemination (AI). Heifers were divided randomly yet equally in terms of RFIf, weight at start of test (SOT), and SOT rib and rump fat, into two diet-groups. Heifers received a ration formulated to allow gain of either 0.5 kg/d (L-diet) or 0.7 kg/d (H-diet). Rations were fed until 150 d of pregnancy and were adjusted periodically to account for heifer and fetal growth plus decreasing fall temperatures. Heifer weight, as well as rib and rump fat were measured approximately once every 4 wk, and individual feed intake and feeding behavior was continuously measured by GrowSafe. All weight and fat measurements, feed intake and behavior were analyzed using PROC GLM in SAS 9.0, with RFIf, diet (H- or L-diet), RFIf*diet, and AI (first or second) included in the model. There were no significant differences due to RFIf, diet, or their interaction on SOT weight, or SOT rib and rump fat. By end of test (EOT), significant diet effects were seen on EOT weight, both EOT rib and rump fat, and ADG during the feed trial ($P < 0.01$), with heifers consuming H-diet displaying higher weights and fat measurements, but no effect of RFIf was detected. However, significant diet and RFIf effects were detected in average daily intake, feeding duration and head-down time ($P < 0.05$), where heifers with lower RFIf ate less, had a lower average daily feeding duration and head-down time, than those with higher RFIf. Therefore, regardless of diet consumed and under limiting nutritional conditions, low RFIf pregnant heifers ate less, yet maintained the same growth and body condition when compared to high RFIf pregnant heifers. This result is important as RFIf is typically measured on virgin animals and under ad-libitum conditions. If selection for RFI is to become mainstream in the cattle industry, investigating the performance of high and low RFI animals in different nutritional environments and physiological conditions is important.

Key Words: behavior, cattle, residual feed intake

0916 (W048) Physiological stress response of heifers divergently ranked for residual feed intake following a bovine corticotrophin releasing hormone challenge. A. K. Kelly[*1], A. G. Fahey[2], B. Earley[3], M. McGee[3], and D. A. Kenny[4], *[1]School of Agriculture and Food Science, University College Dublin, Ireland, [2]School of Agriculture and Food Science, University College Dublin, Ireland, [3]Teagasc Grange, Dunsany County Meath, Ireland, [4]Teagasc Grange, Meath, Ireland.*

The objective of this study was to determine whether beef heifers previously ranked on the basis of phenotypic RFI differed in their physiological stress response to an exogenous corticotrophin-releasing hormone (CRH) challenge. Yearling Limousin × Friesian heifers ($n = 86$) were ranked on phenotypic RFI. The 15 highest [mean 0.47 kg/d; high RFI] and 15 lowest [mean -0.53 kg/d; Low RFI] ranking animals were used for this study. To facilitate intensive blood collection heifers were fitted aseptically with indwelling jugular catheters on d -1. To examine the response of the adrenal cortex, a standardised dose of bovine CRH (bCRH;0.3 µg/kg BW) was administered (Day 0). Before heifers undergoing bCRH challenge dexamethasone (20 µg/kg BW) was administered intramuscularly on day -1. Baseline blood samples were collected into tubes containing lithium heparin as an anti-coagulant at −60 and 0 min before the administration of dexamethasone. On Day 0, serial heparinised blood samples were collected at −40, -20, 0, 20, 40, 60, 80, 100, 120, 150, 180, 210, 240, 270, 330, and 390 min relative to the time of CRH administration (0 min) for plasma cortisol and DHEA concentrations. Data were analyzed using a repeated measures mixed models ANOVA (PROC MIXED) in SAS incorporating terms for RFI group, sample time and their interaction, as appropriate. Residual feed intake ranged from -1.27 to 1.87 kg DM/d. (SD = 0.93) representing a mean daily difference of 3.14 kg DM in feed consumed between the most and least efficient animals. Low RFI animals consumed 18% less feed than animals with high-RFI. Least square means for RFI and F:G were higher ($P < 0.05$) for high RFI than for low RFI animals. Neither a RFI × sampling time interaction nor a direct effect of RFI was detected for DHEA, cortisol or cortisol:DHEA concentrations in response to the exogenous bCRH challenge. No difference ($P > 0.10$) in median plasma area under the curve (AUC) for cortisol, DHEA or cortisol:DHEA was observed between the two

RFI groups. The maximum concentration and change in cortisol and DHEA concentrations owing to CRH were not different between the high and low RFI phenotypes. Furthermore, across animals, AUC, maximum concentration or change in cortisol or DHEA concentrations were not associated ($P > 0.10$) with DMI, F:G or RFI co-efficients. These data suggest that the responsiveness of the hypothalamic-pituitary-adrenal axis is unlikely to contribute to appreciable variation in the efficiency feed utilisation of cattle.

Key Words: feed efficiency, stress, cortisol

0917 (W049) Relationship of metabolic hormones, urea, and body composition with feed efficiency in Angus heifers carrying different genetic markers under grazing condition. A. I. Trujillo*[1], A. Casal[1], M. Carriquiry[1], and P. Chilibroste[2], [1]*Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay,* [2]*Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay.*

The objective of this research was to explore potential physiological indicators of residual feed intake (RFI) in two beef cattle groups carrying simultaneously different genetic markers (GM) associated with low and high RFI (V and C groups, respectively) under grazing conditions. Twelve Angus heifers of each group (aged 369 ± 28 d, 294 ± 37.4 kg of body weight (BW), at the beginning of the experiment) ranked by BW and RFI in a previous feedlot experiment were randomly assigned to four paddocks of an unrestricted high-quality temperate pasture during 57 d. Concentrations of serum IGF-1, leptin, and urea at d 1, 21, and 53, ultrasound subcutaneous fat thickness at d 1 and 56, (SFT), subcutaneous 12/13th rib fat depth, intramuscular fat percentage and eye muscle area at d 40 (SBF, IMF and EMA, respectively) as well as estimation of body composition by the urea dilution technique at d 56 (whole body fat content–BF% and whole body protein content– BCP%) were obtained. Data were assessed using a mixed model. Concentrations of IGF-1 did not differ between GM but tended ($P < 0.078$) to be affected by the interaction between GM and sampling date, being lower in V than in C group at d 1 (274.3 vs. 321.5 ± 22.6 mm/L). Leptin concentrations tended ($P = 0.09$) to be greater for V than C group (2.80 vs. 2.33 ± 0.24mm/L, respectively) and were neither affected by sampling date nor by their interaction. Serum urea concentrations were not affected by GM nor by its interaction with sampling date. The EMA, SFT, SBF, IMF and % BCP did not differ between GM, however estimated BF % and BF:BCP ratio were greater ($P = 0.035$, $P = 0.038$, respectively) in V than in C group (23.7 vs. 20.6 ± 1.29%, 1.64 vs. 1.39 ± 0.12). Leptin concentration and BF % were both negatively correlated ($r = -0.43$ $p = 0.037$ and $r = -0.38$, $p = 0.071$, respectively) with RFI. Our data suggest that leptin concentration and BF % could be used to screen for more efficient females under grazing conditions. Other experiments should be designed to uncover additional indicators underlying variation in RFI under grazing conditions.

Key Words: residual feed intake, beef cattle, pasture

0918 (W050) Effects of maternal plane of nutrition during mid- or late gestation on beef cow performance and progeny performance through weaning. T. B. Wilson* and D. W. Shike, *University of Illinois, Urbana.*

Objectives were to investigate the effects of maternal plane of nutrition during mid- or late gestation on cow BW, BCS, and lactation as well as calf growth through weaning. Spring-calving, multiparous cows ($n = 68$; BW = 631 ± 80 kg) were utilized in a 3 × 2 factorial design that included three planes of nutrition formulated to provide (limit-fed diet = 52% corn silage, 24% soy hulls, and 24% alfalfa haylage): 100% NRC energy and protein requirement (REQ), 70% NRC requirement (70%REQ), or 130% NRC requirement (130%REQ) applied during two stages of gestation: mid-gestation (MID, 196 ± 14 to 113 ± 14 d prepartum) or late gestation (LATE, 92 ± 6 to 9 ± 6 d prepartum). After treatment period, cows were fed a common diet formulated to meet NRC requirements. Treatment period ADG and BCS changes were greater ($P \leq 0.01$) for cows fed 130%REQ than 70%REQ, with REQ being intermediate. There was an interaction ($P = 0.04$) between plane of nutrition and stage of gestation in which treatment was applied for calf birth BW. When treatments were applied during mid-gestation, birth BW was greater ($P \leq 0.04$) for calves born to cows fed 70%REQ compared to calves from cows fed REQ or 130%REQ; however, there were no differences ($P \geq 0.65$) during late gestation. Milk production, at 101 ± 11 d postpartum and weaning (198 ± 11 d postpartum), was not affected ($P \geq 0.19$) by plane of nutrition. Calf weaning BW was not affected ($P \geq 0.17$) by plane of nutrition or stage of gestation in which treatments were applied. Ultrasound backfat at 101 ± 11 d of age was greater ($P \leq 0.04$) for calves born to REQ vs. 70%REQ or 130%REQ cows, yet was not different ($P = 0.12$) at weaning. Ultrasound marbling score was not affected ($P \geq 0.35$) by plane of nutrition, but; was greater ($P \leq 0.01$) for calves born to MID cows at 101 ± 11 d of age. Placing cows on diverging nutritional planes either during mid- or late gestation had profound effects on cow ADG and BCS change and may lead to altered calf body composition through weaning but did not affect calf weaning weight or pre-weaning ADG. There were no effects of an interaction between maternal plane of nutrition and stage of gestation in which treatments were applied, except for increased birth BW of calves born to cows that were nutrient restricted during mid-gestation.

Key Words: beef cow, gestational nutrition, fetal programming

0919 (W051) Effects of prepartum plane of nutrition during mid- or late gestation on beef cow BW, BCS, and preimplantation embryo recovery.

W. C. Meteer*[1], T. B. Wilson[2], P. Cardoso[2], and D. W. Shike[2], [1]*University of Illinois, Champaign,* [2]*University of Illinois, Urbana.*

Objectives were to evaluate potential effects of prepartum plane of nutrition during mid- or late-gestation on BW, BCS, and preimplantation embryo recovery. Spring-calving, multiparous beef cows (n = 60; BW = 657 ± 70 kg) were utilized in a 3 × 2 factorial arrangement that included three planes of nutrition formulated to provide (limit-fed diet = 52% corn silage, 24% soybean hulls, and 24% alfalfa haylage): 100% NRC energy and protein requirement (REQ), 70% NRC requirement (70%REQ) or 130% NRC requirement (130%REQ) fed during two stages of gestation: mid-gestation (Mid, 195 ± 5 to 112 ± 5 d prepartum) or late-gestation (Late, 91 ± 4 to 8 ± 4 d prepartum). After treatment period, cows were fed a common diet formulated to meet NRC requirements. All cows had their estrous cycles pre-synchronized with two injections (14 d apart) of PGF2α beginning 43 ± 4 d postpartum. A 7 d cosync protocol was used to synchronize cows. A 4-regimen of Folltropin (FSH) was administered to induce superovulation and GnRH was given 12 h and 24 h before breeding. Cattle were flushed 84 ± 4 d postpartum, and 7-d embryos were harvested. Cyclicity was accessed by P_4 analysis at 43 ± 4 and 57 ± 4 d postpartum. Statistical analysis was performed using the MIXED and GLIMMIX procedures in SAS. Nutritional plane did not affect (P = 0.61) percentage of cows cycling by 57 ± 4 d postpartum (70%REQ, 15.8%; REQ, 27.3%; 130%REQ, 21.1%). The Logistic model revealed that cows fed nutritional treatments during late-gestation had lower odds for cyclicity than cows fed nutritional treatments in mid-gestation [odds ratio (OR) = 0.18; P = 0.02]. Cows fed 130%REQ had greater ($P \leq 0.03$) BW than REQ and 70%REQ cows, and cows fed 130%REQ and REQ had greater ($P \leq 0.04$) BCS than cows fed 70%REQ at time of breeding. There was a plane of nutrition by stage of gestation interaction ($P < 0.01$) for total embryos recovered. When nutritional treatments were applied during mid-gestation, a greater number of total embryos were recovered from cows fed 70%REQ than from cows fed REQ and cows fed 130%REQ were intermediate; however, when nutritional treatments were applied during late-gestation, a greater number of total embryos were recovered from cows fed 70%REQ and REQ than cows fed 130%REQ. In conclusion, prepartum plane of nutrition during mid- or late-gestation affects cow BW, BCS, and total embryos recovered, but did not affect cyclicity in cows before breeding.

Key Words: embryo, gestational nutrition, reproduction

0920 (W052) Effects of breed, sex, parity, birth year, and birth season on body weight traits for five local cattle breeds and crossbreds in arid region of Punjab, Pakistan.

G. Bilal*[1], M. Moaeen-ud-Din[1], M. Aqeel[1], A. Ijaz[1], M. S. Khan[2], M. Y. Gondal[3], K. M. Khan[3], M. Mukhtar[3], and M. N. Manzoor[3], [1]*PMAS-Arid Agriculture University, Rawalpindi, Pakistan,* [2]*University of Agriculture, Faisalabad, Pakistan,* [3]*Barani Livestock Production Research Institute, Attock, Pakistan.*

The objectives of the present study were to study the effects of breed, sex, parity, year of birth, and season of birth on birth weight, weaning weight, and yearling weight recorded on 796 calves born between 1996 and 2008. This included offspring from five local cattle breeds (Dhanni, Lohani, Dajal, Red Sindhi, Cholistani) and crossbreds (Holstein or Jersey crosses) maintained at Barani Livestock Production Research Institute (BLPRI, Attock, Punjab, Pakistan). The data were analyzed using a mixed linear model with PROC MIXED (SAS). Overall means ± SD (obtained using PROC MEANS) of birth, weaning, and yearling weights were 18.59 ± 2.54 kg, 73.85 ± 19.04 kg and 113.65 ± 30.33 kg, respectively. All three growth traits varied with breed, sex, parity of dam and season of birth and year of birth. However, the birth weight did not vary among seasons (P = 0.16), and weaning weight did not vary between dam parity (P = 0.29). The calves of Lohani cattle (a short stature breed) had the lightest birth weights (16.6 kg) as compared to other breeds and crossbreds (> 18 kg). The heaviest weaning weights (93.0 kg) were found in calves from the Dajal breed, followed by weaning weights for Dhanni (79.9 kg), Cholistani (74.0 kg), Red Sindhi (71.9 kg), and Lohani (66.1 kg). The heaviest yearling weights were found in Dajal calves (147.4 kg), while the lowest yearling weights were found in Lohani calves (98.0 kg). Yearling weights for all other breeds ranged from 111 to 118 kg. Overall, birth, weaning and yearling weights were greater in male vs. female calves. The calves born to first parity cows had lighter birth and yearling weights, and similar weaning weights as compared to calves from later parity cows. Spring born calves had heavier weaning weights (79.2 kg) than summer born calves (71.7 kg). Summer born calves had lighter yearling weight (109.3 kg) than calves born in other seasons (118–120 kg). Additionally, when data were analyzed using a model considering all factors as random, breed explained the most variation for all three body weight traits. The observed between breed variation for growth indicates an untapped potential for beef production. Moreover, results from the present study have useful implications for breed improvement and management decisions for cattle breeds being raised under arid conditions.

Key Words: body weights, cattle breeds, arid region

0921 (W053) Effect of rumen protected carbohydrate supplementation on performance and plasma glucose concentrations in growing heifers. *J.* P. Russi*[1], P. Davies[2], N. DiLorenzo[3], and A. E. Relling[4], *[1]Facultad de Cs Veterinarias, UNLP, La Plata, Buenos Aires, Argentina, [2]INTA Gral. Villegas, General Villegas, Argentina, [3]University of Florida, Marianna, [4]Facultad de Ciencias Veterinarias UNLP, La Plata, Buenos Aires, Argentina.*

The objective of this study was to evaluate the inclusion of a ruminally protected carbohydrate (RUPCA) on performance and blood metabolites in growing heifers. One hundred thirty-five cross-bred heifers (136 ± 14kg) were used in an 84-d experiment. Heifers were blocked according to initial BW and placed (nine per pen) into 15 dirt floor pens (12 × 50 m). Heifers within blocks were randomly assigned to one of three treatments: T0) Control (100% basal supplement), T1) 50% RUPCA and 50% basal supplement, and T2) 100% RUPCA. Diets were (DM basis): 38.8% corn silage, 41.5% dry corn (finely ground), 2% minerals and vitamins mix, and 17.7% supplement (58.1% soybean meal, 39.9% carbohydrates, 2% urea, and 1% minerals). RUPCA and the basal supplement consisted of the same ingredients, differing on the processing of the carbohydrate (i.e., protected or not from ruminal degradation). Heifers had ad libitum access to feed and water during the study. Body weights were measured on d 0, 21, 42, 63, and 84. Dry matter intakes were measured every 7 d from d 21 when the adaptation to the diets finished. Blood samples were taken every 21 d and analyzed for glucose concentration. Back fat on the 12th Rib (BF) was measured on d 1 and 84. Data was analyzed as a randomized complete block design with repeated measures using a mixed model in SAS. There were no significant differences ($P > 0.10$) amongst treatments on initial BW, final BW, or ADG; however, cattle fed T1 had the lowest DMI ($P < 0.01$) and the greatest G:F ratio ($P < 0.02$). There were no differences in glucose concentrations ($P > 0.96$) or BF on d 84 ($P > 0.72$). In conclusion, including RUPCA at a rate of 8.87% of the diet DM improved G:F ratio by reducing DMI and not affecting ADG.

Key Words: carbohydrates, ruminally protected

Table 0921.

	Treatments				
	T0	T1	T2	SEM	*P*–Value
Initial BW, kg	136.5	136.3	136.3	0.5	0.95
Final BW, kg	236.1	232.8	237.0	2.25	0.37
DMI, kg/d	6.73[a]	5.79[b]	6.73[a]	0.087	< 0.001
ADG, kg	1.185	1.145	1.196	0.092	0.72
G:F	0.175[a]	0.212[b]	0.189[a]	0.009	0.02
Glucose, mg/dL	95.9	97.2	96.8	31.03	0.96
84 d Back fat measurement, mm	5.55	5.63	5.53	0.09	0.72

[a, b] Means without common superscript differ ($P < 0.05$). Final del formulario.

0922 (W054) Evaluation of forage soybean, with and without pearl millet, as an alternative forage for developing beef replacement heifers. E. Taylor*[1], P. J. Gunn[2], L. A. Horstman[3], R. L. Atkinson[4], K. D. Johnson[3], and R. P. Lemenager[3], *[1]Purdue University, Lafayette, IN, [2]Iowa State University, Ames, [3]Purdue University, West Lafayette, IN, [4]Southern Illinois University–Carbondale, Carbondale.*

Angus-Simmental beef replacement heifers (n = 90; BW = 366 kg ± 25; BCS = 5.53 ± 0.35) were used to evaluate the effects of feeding forage soybean-based silages on heifer BW, BCS, follicular growth and fertility. At 65 d before timed-artificial insemination (TAI), heifers were allotted by breed, BCS and BW into three replications per treatment to receive one of three diets; 1) alfalfa haylage (CON), 2) soybean silage (SB) or 3) soybean and pearl millet silage (SBPM). All diets were formulated to meet or exceed nutrient requirements (NRC, 2000) of replacement beef heifers with a targeted gain of 0.79 kg/d. Estrous cyclicity status of heifers was determined by two samples of blood taken 10 d apart before initiation of estrous synchronization and analyzed for circulating progesterone concentrations. Heifers were synchronized for ovulation using a 5-d Co-Synch + CIDR protocol and were observed for estrus on 12-h intervals between CIDR removal and TAI. Diameter of the largest antral follicle was determined at time of AI via ultrasonography. Bulls were placed with heifers 10 d after TAI for remainder of the breeding season. Pregnancy diagnosis was accomplished via ultrasonography 35 and 66 d post-TAI, respectively, for TAI and overall breeding season pregnancy. Data were analyzed with the GLIMMIX and PROC MIXEDs of SAS for categorical and continuous variables, respectively. Final BW (avg. 414 kg; $P \geq .10$) and BCS (avg. 5.28; $P \geq .07$) for the heifers were similar among treatments. The proportion of heifers showing estrus before TAI (51%) and interval to estrous in those females that exhibited estrus (55 h) did not differ among treatments ($P \geq .11$). Ovulatory follicle diameter (avg. 11.7 mm) was not different ($P > .31$) among treatments. No differences were noted in pregnancy rate to TAI (avg. = 48%; $P > .19$) or overall breeding season (avg. = 93%; $P > .99$) pregnancy rates. In summary, forage soybean-based silages, with and without pearl millet, are acceptable alternative forages for developing replacement beef heifers.

Key Words: forage, beef, heifer

0923 (W055) Plasma glucose concentration, subcutaneous fat thickness, and puberty attainment in Nellore heifers treated with recombinant bovine somatotropin. G. Nogueira*[1], D. Giraldo-Arana[1], J. S. Souza[1], M. A. Maioli[1], M. C. V. Miguel[1], R. S. Cipriano[2], T. Sayuri Aguiar[3], D. M. Pinheiro[1], and R. F. Cooke[4], *[1]UNESP, Araçatuba, Brazil, [2]UniSalesiano, Araçatuba, Brazil, [3]UNESP, Araçatuba, Brazil, [4]Oregon State University–EOARC Burns, Burns.*

In previous research, we observed that Nellore heifers that attained precocious puberty had greater plasma IGF-I but similar plasma leptin concentrations compared with cohorts that attained puberty later. Hence, this experiment evaluated the effects of bovine ST treatment as an alternative to increase plasma IGF-I concentrations on plasma glucose concentrations, body fat accretion, and puberty attainment of Nellore heifers. Thirty-one heifers were distributed in groups Treated (n = 16; 348 ± 52 d of age; 259 ± 49 kg of initial BW) or Control (n = 15; 356 ± 40 d of age; 260 ± 38 kg of BW). For 10 mo, Treated heifers received 250 mg of sometribove zinc every 14 d, whereas Control heifers concurrently received 2.5 mL of saline. All heifers were maintained on a single pasture and exposed to a teaser bull with a neck-marker device to identify mounted heifers. Ovarian ultrasonography was conducted every 14 d to determine corpus luteum presence. Every 2 mo, rump and back fat thickness were also estimated via carcass ultrasonography whereas blood samples were collected. Heifers were considered pubertal when teaser bull activity was observed and a corpus luteum was detected. Age at puberty and fat thickness were analyzed by unpaired t test, whereas plasma glucose concentrations were analyzed by the Mann Whitney test of GraphPad PRISM. No treatment effects were detected ($P \geq 0.30$) for puberty attainment, nor heifer age and BW at puberty. More specifically, seven Treated heifers (593 d of age and 394 kg of BW at puberty) and seven Control heifers (599 d of age and 411 kg of BW at puberty) reached puberty during the experiment. Back fat thickness was greater ($P = 0.03$) in Control compared with Treated heifers at 22 mo of age (5.0 vs. 4.0 mm, respectively). Rump fat thickness was also greater ($P \leq 0.05$) in Control compared with Treated heifers at 16 mo (5.0 vs. 4.4 mm), 18 mo (5.0 vs. 4.4 mm), 20 mo (5.5 vs. 4.8 mm), and 22 mo of age (5.8 vs. 4.6 mm). No treatment differences were detected ($P = 0.46$) for plasma glucose concentration (90 vs. 89 mg/dL for Treated and Control heifers, respectively). In summary, Nellore heifers administered bovine ST at the experimental conditions utilized herein had decreased subcutaneous fat accretion, but similar plasma glucose concentrations as well as BW and age at puberty compared with cohorts receiving saline.

Key Words: bovine ST, heifers, Nellore, puberty

0924 (W056) Effect of dried distillers grains with solubles and dried citrus pulp supplementation on metabolic and reproductive parameters of Charolais beef cows grazing buffelgrass in Northeastern México. E. Garza Brenner*[1], H. Bernal Barragán[1,2], E. Gutiérrez Ornelas[1,2], F. Sánchez Dávila[1], A. S. Juárez Reyes[2,3], and E. Olivares Sáenz[1], *[1]Universidad Autónoma de Nuevo León, San Nicolás de los Garza, México, [2]Red Internacional de Nutrición y Alimentación en Rumiantes, Durango, México, [3]Universidad Juárez del Estado de Durango, México.*

The objective of this study was to evaluate body weight, body condition and reproductive performance of Charolais beef cows (n = 32) grazing buffelgrass (Cenchrus ciliaris L., 7.0% crude protein (CP) and 56.6% NDF) supplemented with two isocaloric agroindustrial byproducts. Cows were blocked by age, parity, body condition score (initial BCS was 4.75) and body weight, and randomly assigned to individually receive 1 kg/d of either dried distillers grains with solubles (DDGS; 30.3% CP, 2.65 Mcal ME/kg DM), or a 50:50 mixture of DDGS and dried citrus pulp (DDGS:DCP; 17.45% CP, 2.82 Mcal ME/kg DM) during a 30-d breeding period, applying the standard 9-d synchronization protocol utilizing a controlled internal drug-release (CIDR) device and an additional 8-d CIDR resynchronization beginning on the fifth day after artificial insemination. Body weight (BW), and body condition score (BCS) were registered, and blood samples were collected via coccygeal venipuncture on d 0, 9, 16, 24, and 30, and analyzed to determine Urea Nitrogen (BUN, colorimetrically), and plasma Progesterone (ELISA) using commercial kits. Estrus appearance was registered by visual observation, and pregnancy diagnosis was confirmed using transrectal ultrasonography. Data were analyzed using two-way ANOVA (for BW, BCS, BUN and progesterone), and Chi-square test (for reproductive traits). Cows receiving DDGS:DCP were heavier on d 16 (487 vs. 464 kg) and d 24 (500 vs. 485 kg, $P < 0.05$) than those supplemented with DDGS, whereas BCS (mean = 5.0) was not different between treatments ($P > 0.05$). Cows supplemented with DDGS had increased ($P = 0.01$) BUN values on d 9 and 24 (12.8 vs. 8.3 and 11.3 vs. 9.4 mg/dL), compared to cows supplemented with DDGS:DCP. No differences were found between treatments in plasma progesterone concentrations ($P > 0.05$). Cows receiving DDGS:DCP presented 20 estrus, whereas cows receiving DDGS showed 13 estrus ($P < 0.05$). Differences in pregnancy rate (56.2% for DDGS:DCP; 68.7% for DDGS) were not significant ($P > 0.05$) between treatments. In summary, supplementing DDGS:DCP to Charolais beef cows grazing buffelgrass increased body weight and estrus appearance, but not BCS and pregnancy rate compared with DDGS supplementation.

Key Words: beef cows, dried citrus pulp, dried distillers grains with solubles

0925 (W057) Evaluation of anthelmintic resistance of intestinal parasitic nematodes in heifers in south central Nebraska. S. A. Jones[1], C. C. Chase*[1], R. Cortinas[2], D. Griffin[3], L. A. Kuehn[1], K. Shuck[3], K. Whitman[3], R. G. Tait, Jr.[1], and J. W. Keele[4], *[1]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [2]University of Nebraska Lincoln, Lincoln, NE, [3]Great Plains Veterinary Educational Center, Clay Center, NE, [4]USDA-ARS, Clay Center, NE*

Internal parasitic nematodes impact the livestock industry through losses in reproductive efficiency, rate of gain, carcass quality, milk production, or immune response. The frequent use of anthelmintics with drug formulations in which chemical activity persists for long periods selects for worm resistance and has contributed to parasite resistance to multiple classes of dewormers. We evaluated the effectiveness of two classes of anthelmintics, avermectin and fenbendazole, on fecal parasite load in yearling heifers grazing on irrigated pastures in south central Nebraska. Both of these anthelmintics have been used historically at U.S. MARC. Hence, a reduction in efficacy for these two historically used anthelmintic classes would be indicative of resistance. Spring-born heifers (n = 1015, average BW = 295 kg) were grazed on irrigated, mixed legume and cool season grass irrigated paddocks starting April 15, 2013. Heifers were managed in four pastures and fecal egg counts (FEC) 10% of each grazing group (25 hd minimum) were monitored weekly using a modified Wisconsin fecal floatation technique. When average FEC numbers for the sample reached > 25 eggs per 2 g, heifers in the group were weighed, fecal sampled for FEC (pre-treatment), and randomly assigned to one of three treatment groups (no dewormer; Avermax injectable (avermectin) at 1 mL/50kg BW subcutaneously; or Safeguard 10% Suspension (fenbendazole) at 2.3 mL/45.5 kg BW orally) by age and breed stratification. Treatments occurred July 16, 17, 26, and 27, 2013. Animals were sampled and FEC counts were obtained 2 wk later (post-treatment). The percentage of zeros for FEC was 4.5 for pre-treatment and 39.0 for post-treatment. Because of the high proportion of zero valued FEC, pre-treatment and post-treatment FEC were analyzed assuming a zero inflated negative binomial distribution. The zero inflated negative binomial model fit better than the standard negative binomial for post-treatment FEC (P = 0.0026) but not for pre-treatment FEC (P = 0.363). The effects of pasture (or breed) and treatment interacted ($P = 1.13 \times 10^{-17}$) with treatment having larger effect in pastures with higher FEC pre-treatment. Considering main effects, pasture affected FEC both pre- ($P = 4.44 \times 10^{-17}$) and post-treatment ($P = 9.41 \times 10^{-12}$). Treating animals with either Avermax or Safeguard reduced FEC ($P = 1.25 \times 10^{-94}$), and Safeguard's effect was greater than Avermax ($P = 9.73 \times 10^{-13}$). Treatment with anthelmintics is efficacious and has greater impact when parasitic load is greater. High efficacy of treatment indicates that little or no resistance has accumulated in parasitic nematode populations at USMARC.

Key Words: parasitic intestinal nematodes, cattle, fecal egg counts, resistance, althelmintics

0926 (W058) Effect of an injectable trace mineral on pregnancy rate of virgin heifers when synchronized using the 5-d Co-Synch plus CIDR or 14-d CIDR-PG protocol. C. J. Brasche*[1], J. B. Hall[2], and M. E. Drewnoski[1], *[1]University of Idaho, Moscow, [2]University of Idaho, Carmen.*

This study examined the effect of using a commercially available injectable trace mineral (TMI) on the reproductive performance of virgin heifers. Angus-crossbred heifers (n = 109, BW = 358 ± 3.7 kg) were blocked by weight and randomly assigned to treatment in a 2 × 2 factorial of either TMI containing copper, manganese, selenium, and zinc or no injection (CON) and one of two synchronization protocols, either a 14-d CIDR-PG protocol or a 5-d Co-Synch plus CIDR protocol. The objective of this study was to determine the effects of TMI before fixed time artificial insemination (AI) on conception to AI as well as the effects on overall pregnancy rate after exposure to bulls. Thirty-3 d before AI, heifers receiving TMI were given Multimin90 (0.57 mL/45.5 kg of BW). For the 14-d CIDR-PG protocol, a controlled internal drug release device (CIDR) was inserted 33 d before insemination and removed 14 d later. Prostaglandin (*P*G) was injected 16 d after CIDR removal and heifers were artificially inseminated 73 h later. For the 5-d protocol, a CIDR was inserted 7 d before AI and an injection of gonadotropin-releasing-hormone (GnRH) was given. Five d later the CIDR was removed, and a PG injection was given. A second PG injection was given 5.6 h later, and heifers were artificial inseminated 55 h after the last PG injection. All heifers received an injection of GnRH concurrently with AI and exposed to bulls 9 d post AI. Conception was determined using ultrasonography at 55 and 105 d post-AI. At 105 d post-AI, there was a synchronization protocol by TMI interaction for rate of heifers conceiving to AI (P = 0.04). However, conception to AI within the 5-d Co-Synch plus CIDR protocol (CON 66.0% vs. TMI 52.0%) and within the 14-d CIDR-PG protocol (CON 55.0% vs. TMI 75.0%) did not differ ($P \geq 0.13$) between the CON and TMI. There was no interaction (P = 0.18) between synchronization protocol and TMI for overall pregnancy rate after timed-AI and natural service. However there was significant effect of TMI (P = 0.02) on overall pregnancy rate with heifers receiving TMI (93.0%) having a greater (P = 0.02) pregnancy rate than the CON (83.0%) after AI and exposure to bulls. This data suggests that use of a TMI 30 d before the breeding season may improve reproductive performance of virgin heifers.

Key Words: heifer, injectable trace mineral, reproduction

0927 (W059) Oral suplementation with selenium for young Brangus bulls raised in pasture: seminal quality in fresh and frozen semen. T. B. Castaldeli*, L. K. Hatamoto-Zervoudakis, B. H. Tsuneda, J. T. Zervoudakis, W. A. D. S. Marinho, F. A. D. P. D. B. Arguello, M. F. Duarte Junior, P. P. Tsuneda, and R. D. Almeida, *Federal University of Mato Grosso, Cuiaba, Brazil.*

Cryopreservation stimulates production of free radicals and oxidative stress. The selenium (cofactor of enzyme glutathione peroxidase) acts as antioxidant protecting sperm membrane of lipid peroxidation and against consequent loss of function. The aim of this study was to evaluate oral selenium supplementation on semen quality of fresh and cryopreserved semen from young Brangus bulls raised in pastures in central Brazil. Sixteen Brangus bulls (5/8 Angus, 3/8 Zebu) with 24 mo and 472 kg of body weight on continuous grazing with daily concentrate supplementation by 75 d were used. The treatments were: GC- control (no added selenium in concentrated supplementation), GS- selenium (concentrated with addition of 0.1 mg Se/kg of dry matter intake (DMI)). After collection were evaluated sperm motility (MOT), sperm vigor (VIG), sperm viability (SVIAB), spermatic membrane integrity (SMI) and acrosomal membrane integrity (AMI) and triple stain (TS). Then semen was diluted and cryopreserved in TRIS-egg yolk citrate extender with 4% of glycerol. Thawing was performed in water bath at 37°C for 30 s. After thawing the samples, aliquots to evaluation of MOT, VIG, SVIAB, SMI, AMI, and TS were removed. Experiment was conducted in a completely randomized design. Data were analyzed by ANOVA with significance level of 5%. Supplementation with selenium improved SMI ($P = 0.0480$) in fresh semen (CG 26.71 ± 2.89 vs. 37.45 ± 4.14 GS) and frozen semen (GC 8.75 ± 1.42 vs. GS 9.90 ± 1.59). Selenium supplementation did not alter other parameters evaluated ($P > 0.05$). Studies on selenium supplementation with qualitative and quantitative parameters of bovine semen are rare. Thus, further research should be done to better understand effect of selenium on reproductive function. Oral supplementation with selenium concentration of 0.1 mg/kg DMI for young Brangus bulls raised on pasture does not alter seminal parameters traditionally evaluated in fresh and cryopreserved semen, but improves integrity of sperm plasmatic membrane.

Key Words: antioxidant, cryopreservation, sperm membrane.

0928 (W060) use of vitamin c combined to pentoxifylline and fertility in cattle after cryopreservation. R. D. Almeida*, L. K. Hatamoto-Zervoudakis, M. F. Duarte Junior, J. T. Zervoudakis, P. P. Tsuneda, A. L. C. Rezende Fraga, F. A. D. P. D. B. Arguello, T. B. Castaldeli, and F. M. Wingert, *Federal University of Mato Grosso, Cuiaba, Brazil.*

The process of frozen of the sperm provides a resting state of the cell, reducing energetic expenditures and the production of catabolites, preserving the cell structure and the fertilizing capacity of sperm. In contrast to a loss of quality (40 to 50%) occurs if compared to fresh semen, resulting from cooling processes freezing and thawing. These losses occur due to decreased sperm viability or damage to the functional capacity of the surviving sperm. Vitamin C is considered an antioxidant extracellular fluid, acting by preventing the formation of lipid hydroperoxide in plasma lipoproteins, and protecting the lipids in cell membranes while maintaining their structural integrity and viability during the cryopreservation process. Pentoxifylline is a methylxanthine derivative compound, the same class as caffeine and has the characteristic of inhibiting adenosine cyclic monophosphate (AMP) phosphodiesterase, causing an increase in the intracellular concentration of cyclic adenosine monophosphate (cAMP), activating the adenylyl cyclase which causes the activation of protein kinase-dependent and phosphorylation of sperm proteins, which are essential in initiation and maintenance of sperm movement. The objective of the experiment was to evaluate the use of vitamin C combined with pentoxifylline in the middle of cryopreservation of bovine semen that reduces the damage caused by oxidative stress and preserves sperm quality after thawing. We used 10 Nellore bulls with age/weight average of 31 mo and 632 kg, subjected to a semi-intensive system, raised on pasture *Brachiaria brizanth* cv., kept in sexual rest. One ejaculate was collected by electrical stimulation, which was analyzed after diluted in extender TRIS-citrate-yolk-glycerol (4%), divided into two parts: a part of the control (without additives), and the other supplemented with vitamin C (0.45 mg/mL) + pentoxifylline (1 mg/mL). Afterward, the samples were cooled and frozen and stored until the time of analysis. After thawing, the samples were evaluated for motility and movement characteristics, plasma membrane integrity and acrosome, mitochondrial activity and level of lipid peroxidation (TBARS). The supplementation of cryopreservation did not alter ($P > 0.05$) the mitochondrial activity, acrosomal integrity, and concentration of spontaneous and induced TBARS. Based on the results, it is concluded that the addition of vitamin C + pentoxifylline was not effective in reducing the damage caused by oxidative stress and cryopreservation of bovine semen samples.

Key Words: antioxidant, fertility, oxidative stress

BREEDING AND GENETICS: APPLICATIONS AND METHODS IN ANIMAL BREEDING— BEEF

0929 (M043) Effects of functional polymorphisms on beef carcass merit. W. M. Snelling*, L. A. Kuehn, R. M. Thallman, G. L. Bennett, and E. J. Pollak, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

To develop a resource to identify polymorphisms present in common beef cattle breeds, and relate those polymorphisms to phenotypic differences, low-coverage genomic sequence was obtained on 186 purebred bulls from 15 predominant breeds in the United States and 84 crossbred sons of these bulls. These bulls were influential in the USMARC Germplasm evaluation population (GPE), enabling sequence-derived genotypes to be imputed throughout the population of individuals genotyped with the BovineHD (HD; n = 1027) and BovineSNP50 (n = 8697) platforms. Variants detected from these sequences were classified according to predicted effect on gene function, with 4699 predicted to cause a loss of gene function (LOF); 66,484 non-synonymous (NS) SNP causing an amino acid change in the protein produced by a gene, and 59,092 that may have a role in gene regulation (REG), occurring in annotated non-coding RNA or regions immediately surrounding a gene. Imputed genotypes of 685 purebred genotyped grandsires in the GPE population (18 to 74 bulls per breed) were used to represent each breed to assess diversity and determine breed effects on carcass merit. Relative genetic distances between breeds were consistent regardless of the set of genotypes considered. Brahman was furthest from any other breed, and Hereford the most distant from any other taurine breed. Similar distances were obtained using HD and ND SNP. The mean between-breed distance estimated with REG variants was about 10% higher than HD or NS, and distances using LOF variants were about 30% lower. Heritability estimates from GBLUP considering records of 5990 genotyped carcasses and treating breeds as genetic groups, ranged from 0.49 for ribeye area to 0.59 for marbling score when using only HD genotypes. Similar estimates were obtained in independent analyses using NS and REG, but the LOF estimates were lower, between 0.29 and 0.32. In four-component analyses with different genomic relationship matrices for HD, NS, REG, and LOF, 68% to 76% of additive variance was attributed to HD, and 2% or less to LOF. Contributions of both NS and REG were between 10 and 16% for carcass weight, marbling, and fat thickness. For ribeye area, the REG component was 31% of additive variance, and NS was nil. The GBLUP breed solutions were consistent with breed differences estimated in previous analyses. USDA is an equal opportunity employer and provider.

Key Words: beef cattle, genomic prediction, functional polymorphisms

0930 (M044) Steers' carcass characteristics with different genetic predominance fed with diets containing substitution levels of grain corn by millet grain. R. M. D. Silva*[1,2,3], J. T. Pádua[2], J. J. R. Fernandes[2], R. Z. Taveira[1], R. L. Missio[4], P. S. Pacheco[5], D. A. Fausto[6], and J. Restle[2], *[1]Universidade Estadual de Goiás, São Luis de Montes Belos, Brazil, [2]Universidade Federal de Goiás, Goiânia, Brazil, [3]FAPEG, Goiânia, Goiás, Brazil, [4]Universidade Tecnológica Federal do Paraná, Pato Branco, Brazil, [5]Universidade Federal de Santa Maria, Rio Grande do Sul, Brazil, [6]ESALQ/USP, Piracicaba, São Paulo, Brazil.*

This study aimed to evaluate the crossbred steers' carcass and meat characteristics with European or Zebu genotypic predominance. Considering that commercial animals were used, these animals were divided by genotypic predominance by visual evaluation. Feedlot finished with high diets concentrated percentage (80%), containing different levels of grounded millet grain as replacement for grounded corn grain (0, 33, 66, and 100%). Forty-five steers with European predominance and 44 steers with Zebu predominance, with initial average weight of 317.8 and 320.7 kg, respectively, and average age of 21 mo, were allocated in 16 collective pens. In the total, 89 animals were used from the beginning to the end of the feedlot. For the slaughter evaluation, 6 steers were used from each treatment for carcass evaluation. The animals from each genetic predominance were randomly chosen within of each level of corn substitution by millet grain. The experimental design was completely randomized with factorial arrangement 4 (diets) × 2 (genetic groups– predominance) × 6 (animals). The corn grain replacement by millet grain did not influence significantly slaughter weight (480.4 kg) ($P > 0.05$), hot carcass weight (259.5 kg) ($P > 0.05$), carcass yield (54.1%) ($P > 0.05$), or subcutaneous fat thickness (3.95 mm) ($P > 0.05$). Steers of predominantly European genotype showed significant higher values for slaughter weight (507.6 vs. 453.3 kg) ($P < 0.001$), hot carcass weight (269.6 vs. 249.3 kg ($P < 0.001$), and *Longissimus dorsi* area (65.34 vs. 56.83 cm2) ($P < 0.001$); however, they were lower in carcass yield (53.2 vs. 55.0%) ($P < 0.001$). Millet grain can be used in corn grain substitution for finishing steers since it does not change carcass traits of economic interest. Steers with European predominance are heavier at slaughter, presenting heavier and better carcass conformation.

Key Words: carcass weight, subcutaneous fat, zebu.

0931 (M045) Genome-wide association analysis for beef traits in Marchigiana cattle breed. S. Sorbolini[*1], C. Gruber[2], C. Dimauro[1], G. Gaspa[1], M. Cellesi[1], A. Valentini[2], and N. P. P. Macciotta[1], *[1]Università di Sassari, Italy, [2]Dipartimento per l'Innovazione dei Sistemi Biologici, Agroalimentari e Forestali, Viterbo, Italy.*

Genome-wide association studies (GWAs) are procedures that enable to correlate huge amounts of genetic and phenotypic data to find genomic regions that affect traits of economic importance. Several studies have been conducted for dairy cattle while few reports are available for beef cattle. In this study a GWA was performed on Marchigiana breed cattle, one of the most important beef breeds farmed in Italy. Phenotypes were body weight (BW), average daily gain (ADG), carcass weight (CW), dressing percentage (DP), pH at slaughtering (*P*H), shank circumference (SC) and head weight (HW) measured on 408 Marchigiana young bulls slaughtered between 16 and 24 mo of age. Animals were genotyped with the Illumina 54K bead-chip. Edits were on the call rate (> 0.99), number of missing (> 2, 5%), MAF (> 0.01). Data were analyzed with a mixed linear model that included the fixed effects of herd, date of slaughtering, fixed covariables of age at slaughtering, SNP genotype (coded as 0, 1, 2), and the random effect of the sire to account for population stratification. A permutation test with 10,000 replications for each marker was performed to account for multiple testing. Significant markers (Permutation corrected $P < 0.05$) were 12 for BW, 124 for ADG, 36 for CW, 28 for DP, 9 for pH, 19 for SC, and 41 for HW, respectively. Annotated genes in genomic regions corresponding to significant SNP were derived from the UCSC Genome Browser Gateway (http://genome.ucsc.edu/) using intervals of 500 Kbp (0, 25 Mbp upstream and downstream of the significant region). Among identified genes, some were related to bone metabolism, as the OSTN (Osteocrin), SPARC (secreted protein acid cystein rich), muscle physiology as MEF2C (myocyte enhancer factor 2) and CA3 (carbonic anhydrase III, muscle specific) feeding behavior as HCRTR2 (hypocretin (orexin) receptor 2) and fatty acid biosynthesis as ACACB (acetyl-CoA carboxylase β) and ACAD8 (Acyl-CoA dehydrogenase family, member 8), respectively. Of interest were also some genes that could be related to meat quality as FPGS (folylpolyglutammate synthase) on BTA11, TTPA (tocopherol (α) transfer protein) on BTA 14 and GGPS1 (geranylgeranyl diphosphate synthase 1) on BTA28. These genes are involved in the metabolism of antioxidants such as vitamins A, E and folate that are effective molecules in preventing oxidative stress.

Key Words: GWA, beef traits, Marchigiana cattle

0932 (M046) Estimation of genetic parameters for reproductive traits in a multibreed population of beef cattle. S. O. Peters[*1], K. Kizilkaya[2], D. J. Garrick[3], R. L. Fernando[3], E. J. Pollak[4], M. Enns[5], and I. G. Imumorin[6], *[1]Berry College, Mount Berry, GA, [2]Adnan Menderes University, |Aydin, Turkey, [3]Iowa State University, Ames, [4]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE, [5]Colorado State University, Fort Collins, [6]Cornell University, Ithaca, NY.*

Reproductive traits are very important economically relevant traits in beef cattle production, and estimation of genetic parameters for these traits is necessary to optimize selection response and improve profitability of beef production. The objective of this research was to determine genetic parameters for the reproductive traits of heifer pregnancy (HPG), stayability (ST), rebreeding rate (RR) and calving ease (CE) in a multi-breed cattle population. We analyzed a dataset of 10,245 HPG and ST records, 8740 RR records and 11,779 CE records from a large commercial operation in Nebraska that included pedigree information, contemporary groups and sire breed. Hierarchical threshold mixed models based on a probit link specification were used for the bivariate analysis of HPG and ST records and for the univariate analysis of RR and CE with maternal records. The posterior means and 95% posterior probability intervals of additive variance were estimated to be 0.227 ± 0.103 [0.104, 0.418] for HPG and 0.123 ± 0.043 [0.049, 0.215] for ST, and 0.211 ± 0.101 [0.074, 0.449] for RR and 0.216 ± 0.147 [0.04, 0.549] for CE, respectively. Also, the posterior mean and 95% posterior probability interval (*P*PI) of direct maternal variance were estimated to be 0.702 ± 0.229 [0.355, 1.230] for CE. Posterior mean inferences on direct heritability were found to be 0.056 ± 0.019 [0.025, 0.099] for HPG and 0.065 ± 0.021 [0.028, 0.111] for ST, 0.138 ± 0.053 [0.056, 0.254] for RR and 0.08 ± 0.05 for CE, respectively. Posterior mean inferences on maternal heritability were found to be 0.263 ± 0.07 [0.145, 0.417] for CE. The posterior mean of genetic correlation between HPG and ST was low and negative (-0.174 ± 0.289) and insignificant with [-0.665, 0.353] of 95% PPI. The posterior mean and 95% PPI of direct maternal genetic correlation was -0.235 ± 0.132 [-0.509, 0.024] for CE. The low heritability values observed in this study are similar to literature values and the low and negative correlation between HPG and ST indicate that genetic improvement geared towards improving HPG may have antagonistic effect on ST, but this effect is not statistically significant.

Key Words: reproductive traits, genetic parameters, threshold model

0933 (M047) Copy number variation in the genome of Nellore cattle. M. V. A. Lemos[1], M. P. Berton[2], C. Aboujaoude[3], F. Feitosa[4], G. C. Venturini[5], R. L. Tonussi[5], R. Espigolan[5], H. N. Oliveira[2], L. G. Albuquerque[6], and F. Baldi[*7], *[1]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil, [2]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, São Paulo, Brazil, Jaboticabal, Brazil, Jaboticabal, Brazil, [3]FCAV–UNESP, Jaboticabal, Brazil, [4]UNESP, Jaboticabal, Brazil, [5]Sao Paulo State University (UNESP), Jaboticabal, Brazil, [6]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, [7]Universidade Estadual Paulista "Júlio de Mesquita Filho"–UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil.*

The aim of this work was to study the distribution of CNVRs (regions of copy number variation) in the genome of Nellore cattle. A total of 3022 animals (females and males) finished in feedlot conditions were used. For genotyping, a panel with more than 777,000 SNP markers (High-density Bovine BeadChip) was used. Samples with Call rate lower than 90% were excluded. The PennCNV algorithm (Wang et al., 2007) was used for CNVs detection. To maintain the quality of the samples, samples with LRR (Log R ratio) standard deviation above 0.30, BAF (frequency of allele B) higher than 0.05 and waviness factor higher than 0.01, were excluded from the analyses (Liu et al., 2013), reducing the number of animals to 1561. The regions of CNVs (CNVRs) were generated by overlapping 73,073 CNVs identified by the CNVRuler program (Kim et al., 2012). Initially, different CNVs length were considered with a minimum size of 10kb, 50kb and all sizes, which resulted in 4459, 1365, and 6399 CNVRs, respectively. When all CNV sizes were considered, the average CNVRs length was 36.4 kb, ranging from 0.65 to 1310 kb. There was a higher incidence of CNVRs at BTA1 (483), BTA6 (381), and BTA2 (380). The chromosomes that showed lower incidence of CNV regions were BTA25 (85), BTA27 (104), and BTA28 (117). Considering the CNVs of all sizes, 35.7, 41.0, and 23.3% of the CNVRs were copy gain, copy loss and both (gain and loss in the same region), respectively. The 6399 CNV regions estimated in the present study coverage approximately 8.80% of the bovine genome (UMD_3.1, 2649,685,063 bp). This study confirms the existence of large structural variations in the genome of Nellore cattle and it would support the genetic improvement of this breed and elucidate the genetic mechanisms involved in the expression of productive traits.

Key Words: CNV, CNVR, Nellore

0934 (M048) Seasonality and fresh semen quality from Pantaneira and Nellore bulls raised in Brazilian Pantanal. L. E. S. Silva[1], L. K. Hatamoto-Zervoudakis[*1], A. F. Ramos[2], P. P. Tsuneda[1], F. M. Wingert[1], M. F. Duarte Junior[1], T. B. Castaldeli[1], R. D. Almeida[1], and J. D. O. Moraes[1], *Federal University of Mato Grosso, Cuiaba, Brazil, [2]EMBRAPA–CENARGEN, Brasilia, Brazil.*

Taurine cattle (*Bos taurus*) when subjected to tropical conditions have reduced fertility compared to zebu cattle (*Bos indicus*). The Pantaneira breed (*Bos taurus*) was recently recognized as a Brazilian native breed adapted into climatic conditions of Brazilian Pantanal. However, the seminal parameters of this breed are unknown. Thus, the aim of this work were knowing the seminal parameters Pantaneira breed and evaluate what breed (Pantaneira or Nellore breed) raised on pasture in the southern Brazilian Pantanal region is more adapted to regional climatic conditions. Seven Pantaneiro bulls and three Nellore bulls were used. Semen was collected by electroejaculation. Immediately after collection were evaluated: sperm motility (MOT), vigor (VIG), primary defects (PRIMDEF), secondary defects (SECDEF) and total defects (TOTDEF) semen concentration (CONC), sperm viability (SVIAB) and integrity of acrosomal membrane (ICM). The experiment was conducted in a 2 × 2 factorial arrangement (two breed and two seasons) and data were analyzed by ANOVA and Tukey test, with $\alpha = 5\%$. Seminal parameters in Pantaneira bull are within recommended standards for bovine. SVIAB was lower in winter in both breeds (95.76 ± 1.77% vs. 87.07 ± 4.78%, $P = 0.03$). Nellore bulls showed a higher amount of sperm with SECDEF in summer (2.16 ± 1.09% vs. 0.57 ± 0.31%; $P = 0.02$), and higher percentage of PRIMDEF (61.91 ± 5.92 vs. 26 ± 3.83%, $P = 0.01$) and TOTDEF (62.58 ± 5.63% vs. 27.33 ± 3.91%, $P = 0.03$) in winter. Were not found effects of breed, season, or interaction ($P > 0.05$) in other parameters evaluated. Although Pantaneira breed to be considered a taurine breed (*Bos taurus*), it passed a natural selection process by about 300 yr, adapting to high temperatures in central Brazil and probably has become more resistant to testicular degeneration process. In contrast, Nellore bulls appear to be more sensitive to heat stress by cold. Therefore, it is concluded that Pantaneira breed is most suitable breed to edaphoclimatic conditions in the Brazilian southern Pantanal.

Key Words: sperm morphology, heat stress, fertility

0935 (M049) Sliding window methods to detection of regions under selection in Nellore cattle.

D. F. Cardoso*[1,2], G. C. Venturini[3], D. J. A. Santos[4], R. R. Aspilcueta Borquis[1], A. A. Stella[1], F. Baldi[5], L. G. Albuquerque[1], M. E. Z. Mercadante[6], and H. Tonhati[1], *[1]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, [2]Bolsista–Fundação de Amparo à Pesquisa do Estado de São Paulo (FAPESP), São Paulo, Brazil, [3]Sao Paulo State University (UNESP), Jaboticabal, Brazil, [4]Universidade Estadual Paulista, Jaboticabal, Brazil, [5]Universidade Estadual Paulista "Júlio de Mesquita Filho", Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, [6]Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho–SP, Brazil.*

The directional selection in bovines lead to genetic differences between breeds or herds because the frequency of alleles range in function of trait selected. A frequency of alleles favorable to selected traits increasing and together also increases the frequency of alleles in adjacent loci. Therefore, mutations under selection are characterized as regions where the allelic frequencies are different from expected under chance or absence of selection. The objective in this study was identify regions under selection in Nellore cattle through of calculate of the difference in allelic frequencies between herds under divergent selection. To this end, we used three experimental herds belongs to Estação experimental de Zootecnia de Sertãozinho-SP, Brazil, two herd selected for higher yearling weight (NeS and NeT) and one herd control (NeC) selected since 1968 to weight near the average. We used 67 animals from NeC, 153 from NeS and 421 from NeT genotyped by the Illumina High Density Bovine SNP BeadChip (777K). After quality control were left 456,816 SNPs. We calculated the frequency of allele B for each SNP in each herd and the allelic difference in this frequency between each pair of herds. Then we adopted the method of comparison between populations described by Hayes et al. (2008) termed sliding window average. This one corresponded with the average of the absolute values of differences to each set of 10 adjacent SNPs, where values that exceeding 0.43 are considered significantly higher than expected in no selection. Although the amount of SNPs used in this study is much higher than that used to determine the empirical significance thresholds, the distribution of differences values here calculated show concordance with its patterns. As expected, a difference above 0.43 was not observed in the sliding window average from NeS-NeT if both herds were selected under same criterion, and intensity would not make sense; the difference between them exceeds the threshold established to predict selection effect on the frequencies. In the NeC-NeS and NeC-NeT sliding window averages there were significant values, 74 and 93, respectively, in chromosomes 3, 4, 6, 7, 12, 16, 18, 20, and 24. The correlation between differences from NeC-NeS and NeT-NeS was high ($r = 0.62$) and the region with max difference between herds contained the PPARGC1A gene, (Bta6). Further, we will analyze the role of genes around the regions considered under selection and also match these results with putative signature selections detected with other methods.

Key Words: divergent selection, SNPs

0936 (M050) Association between copy number variation regions in the Nellore cattle genome and meat tenderness.

M. P. Berton[1], M. V. A. Lemos[2], C. Aboujaoude[2], G. M. de Camargo[3], F. Feitosa[1], G. C. Venturini[4], R. L. Tonussi[4], R. Espigolan[4], D. M. Gordo[1], A. S. C. Pereira[5], H. N. Oliveira[1], L. G. Albuquerque[3], and F. Baldi*[2], *[1]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, [2]Universidade Estadual Paulista "Júlio de Mesquita Filho", Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, [3]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, [4]Sao Paulo State University (UNESP), Jaboticabal, Brazil, [5]State University of São Paulo, Jaboticabal, Brazil.*

The present study aimed to analyze the association between the copy number variation regions (CNVR) with meat tenderness of 737 Nellore bulls. The animals were finished in feedlot and slaughtered at approximately 2 yr of age. Samples from the *Longissimus dorsi* muscle with 2.5 cm (thickness) were collected to obtain the meat tenderness using a Warner-Bratzler shear force device. A panel with 777,962 SNPs markers (High-Density Bovine BeadChip) was used to genotype the animals. Samples with call rate below 90% were excluded. The parameters used to estimate the CNVs were: Log R Ratio (LRR) and B Allele Frequency (BAF). For quality control, samples with standard deviation values for LRR < 0.30, BAF < 0.05 and waving factor < 0.01 were eliminated. The CNVR were appointed as the CNVs overlaps in the samples, that were located by the CNVRuler software. The shear force data were adjusted for the effects of farm and year of birth, and management groups at birth, weaning and yearling. The model included the state of CNV as a fixed effect and the age of animal at slaughter as a covariate. The average shear force obtained was 5.51 kgf. A total of 4504 CNVRs with an average size of 36.59 kb were detected. There were 10 CNVRs with MAF greater than 0.05, and among them only two significant ($P < 0.05$) associated with meat tenderness (CNVR_1491, CNVR_1130). The CNVR_1491, located on chromosome 7, is in an intergenic region, possibly serving as an indirect marker. This CNVR is between two regions, the first is not characterized, and the second is a pseudogene of transcription factors for heat shock proteins; therefore, the significant *P*-value for this region is an indication that these genes may be influencing this trait. All these LOC regions are "like" regions, areas that have partial or total similarity to genes in other genome regions. The

CNVR_1130, located on chromosome 5, is in theory a intergenic region. There were four regions within this CNVR, two are not characterized and the other two are "like" sequences of the gene associated with butyrophilin protein subfamily 1 member A1, which participates in the formation of fat droplets in milk cattle. Theoretically, this gene may influence the subcutaneous fat thickness and therefore affect meat tenderness. The meat tenderness should be improved in Zebu cattle, and the CNVRs are a tool that can be used to genetic improve this trait.

Key Words: chromosomal region, CNVR, shear force

0937 (M051) An evaluation of 6 years of carcass and feedlot performance in Brahman and Brahman-influenced steers tested by the American Brahman Breeders Association (ABBA) National Carcass Evaluation Program.

A. Royer[*1] and M. D. Garcia[2], [1]*Louisiana State University, Baton Rouge,* [2]*Louisiana State University, Baton Rouge.*

The American Brahman Association has made concerted efforts to improve the carcass quality and composition of Brahman and Brahman-influenced cattle. Thus, the objective of the current study was to evaluate genetic trends for Brahman steer calves that have comprised 6 yr (2004–2010) of the American Brahman Breeders Association (ABBA) National Carcass Evaluation Program. A total of 418 steers were evaluated for growth traits, carcass quality, and composition traits. Steers were fed in Gonzalez, TX, until a desirable harvest weight was achieved. Steers were then transported to a commercial harvest facility where carcass quality and composition traits were collected. Growth and performance traits collected in the feedlot that were evaluated in the current study consisted of entrance weight into the feedlot (INWT), harvest weight (HRVWT) and average daily gain (ADG). Carcass quality and composition traits that were evaluated included hot carcass weight (HCW), ribeye area (REA), marbling score (MARSC), yield grade (YG), dressing percent, and Warner-Bratzler shear force (WBS) analysis for meat tenderness evaluation. The PROC REG procedure of SAS was utilized to determine the average increase or decrease of performance for each trait over the six year evaluation period. Entrance weights into the feedlot in 2004 averaged 239.47 kg and HRVWT averaged 494.35 kg. Entrance weights and HRVWT in 2010 had increased to 292.11 kg and 579.26 kg, respectively. Subsequently, all growth traits evaluated in the current study exhibited a linear increase over the six year evaluation period with INWT increasing 5.5 kg/year, HRVWT increasing 11.1 kg/year and average daily gain increasing 0.17 kg/year. When evaluating carcass quality and composition traits, it was revealed that all traits with the exception of MARSC exhibited a linear increase. Marbling score was the only trait observed not to increase over the six year testing period, decreasing at a rate of 3.7 marbling score units per year, respectively. The carcass traits that exhibited a linear increase over the six year evaluation period included HCW (7.2 kg/year), REA (0.55 cm/year), YG (0.04 units/year), WBS (0.41 kg/year) and dressing percentage (0.10/year).

Key Words: *Bos indicus*, genetic trends, carcass traits

0938 (M052) Relationship of physical characteristics and reproductive status in crossbred Angus replacement heifers.

J. E. Thames[*1], C. M. Turner[1], A. H. Brown, Jr.[2], C. F. Rosenkrans[1], K. Anschutz[2], and J. G. Powell[2], [1]*University of Arkansas, Fayetteville,* [2]*Dep. of Animal Science, University of Arkansas Division of Agriculture, Fayetteville.*

The objective for this study was to measure physical characteristics of developing replacement heifers and to determine if these traits were related to reproductive status at breeding. Contemporary Angus based replacement heifers (n = 89) were managed on pastures containing endophyte infected tall fescue at the University of Arkansas Beef Cattle Research Center near Fayetteville, AK. Measurements that were recorded for each heifer at weaning, yearling, and prebreeding included body weight, pelvic area, hip height, hip width, reproductive tract score, rump fat, back fat, rib eye area, and coat shedding score. A group of heifers (n = 26) were determined to be unsatisfactory for exposure to breeding (NE). Pregnancy status was determined for the remaining heifers (n = 63) following AI and pasture exposure to fertile bulls in a 60-d breeding period. No physical differences were found among the heifers that were exposed and did conceive (EC) (n = 32) compared to heifers exposed that did not conceive (EDC) (n = 31). Mean pelvic height was greater for EC heifers (38.68 ± 4.00) when compared to the NE (35.51 ± 4.00) and EDC (38.00 ± 4.00) heifers (P = 0.056). The NE group had a significantly greater mean coat shedding score than either EDC (P < 0.01) or EC heifers (P < 0.01), with EC heifers having the lowest mean coat shedding score (3.05, 2.62, vs. 2.52 ± 0.91, respectively). The physical characteristics including body weight, hip height, and rump fat that were measured for the NE group displayed an inverse trend to that of coat shedding score. The NE group exhibited lower (P < 0.05) values across all physical measurements compared to EC and EDC heifers. Coat shedding score was further analyzed by dividing the heifers data into two groups, with group one (g1) having coat scores 3 or less and group two (g2) having coat scores 4 or 5. Group one heifers were 10.38 ± 7.23, 21.48 ± 7.78, and 30.18 ± 7.96 kg greater in mean BW when compared to group 2 heifers at weaning, yearling, and prebreeding, respectfully (P = 0.14, P = 0.08, P < 0.01, respectfully). In conclusion, these data indicate that coat shedding score was inversely correlated to physical and ultrasound measurements taken at weaning, yearling and prebreeding. Producers selecting replacement heifers may be able to utilize coat shedding score as another characteristics to assess desirable replacement heifers.

Key Words: replacement heifer, beef cattle, coat shedding

GENOMIC METHODOLOGY

0939 (M053) Signature of selection reveals large difference in selection traits. X. Zhang*[1], I. Misztal[1], M. Heidaritabar[2], J. W. M. Bastiaansen[3], R. Hawken[4], R. Okimoto[4], R. L. Sapp[4], H. H. Cheng[5], D. A. L. Lourenco[1], and W. M. Muir[6], *[1]University of Georgia, Athens, [2]Wageningen University, Netherlands, [3]Animal Breeding and Genomics Centre, Wageningen University, Netherlands, [4]Cobb-Vantress Inc., Siloam Springs, AR, [5]USDA, ARS, ADOL, East Lansing, MI, [6]Purdue University, West Lafayette, IN.*

Selection on animals changes the population-wide frequency spectrum of genes related to the traits under selection. With the aid of single-nucleotide polymorphism (SNP) methods, it is possible to inspect for changes in allelic frequencies directly. To reveal the impact of recent selection on genetic variation, we compared the allele frequencies before and after three generations of selection on an index of three traits in two lines (F and M) sampled from commercial broiler chicken. Line M animals are from a sire line that was selected mainly for growth traits, and line F animals are from a dam line that was selected mainly for reproductive traits. Selection was performed by applying single-step Genomic Best Linear Unbiased Prediction (ssGBLUP). Genotypes were used in this study for allele frequency analysis. The M and F lines consisted of 4922 and 4904 genotyped animals, respectively. After quality control, genotypes included information on 52,742 and 52,639 SNPs in line M and F, respectively. Selection was for an index consisting of body weight at 6 wk, ultrasound measurement of breast meat, and leg score. The average allele frequency change for both lines on autosomes was 0.049. Threshold value for detecting selected regions, where allele frequency changes exceeded expectations under drift were 0.140 and 0.136 for line M and F, respectively. There were 25 and 17 selection regions detected on line M and F, respectively, without any overlap of regions between the lines. Average 4heterozygosity change in line F was greater compared to line M (0.008 vs. 0.003, $P < 0.01$). The putative selected regions between line M and F are different. The results we present indicate that in newly selected populations, the genotype frequencies across chromosomes change differently according to the selection lines even if animals are selected for same traits.

Key Words: SNP, allele frequency change, genomic selection

0940 (M054) Weighted single-step genomic BLUP: an iterative approach for accurate calculation of breeding values and SNP effects. X. Zhang*, D. A. L. Lourenco, and I. Misztal*, University of Georgia, Athens.*

The purpose of this study was to explore options for genome wide association analysis (GWAS) with single-step GBLUP (ssGBLUP). In GWAS by ssGBLUP, GEBV are converted to marker (SNP) effects. Unequal variances for markers are then derived from SNP solutions and subsequently incorporated into a weighted genomic relationship matrix. Improvements on the SNP weights can be obtained iteratively either by recomputing the SNP effects only or by also recomputing the GEBV. Four options were used to calculate the weights: 1) proportional to $2p_i(1-p_i)u_i^2$, where p_i and u_i are frequency and effect of the i-th SNP; 2) proportional to $2p_i(1-p_i)u_i^2$+ constant; 3) weights as in 1, but updating only the top 25 SNP; 4) updating only the top 5 SNP. A simulated data set was used that included 15,600 animals in five generations, of which 1540 were genotyped for 50k SNP. The simulation involved phenotypes for a trait with heritability of 0.5 potentially affected by 5 QTL. Accuracy between TBV and GEBV for genotyped animals in generation 5 was used for evaluation. Comparisons also involved BayesC with deregressed proofs and $\pi = 0.9999$. In single-step, SNP effects were tracked along 10 iterations and weights were equal to 1.0 in the first iteration. Results showed option 3 as the best in identifying simulated QTL without background noise and with precision in most of the regions, as well as BayesC; after two iterations, the accuracy of GEBV reached a plateau and was 0.91 as opposed to 0.88 for BayesC. Testing also included a commercial data set with 200k animals and 15K genotypes for 39k SNP. For one of the traits, Manhattan plots with option 3 and BayesC looked identical showing six large peaks and very small background noise. However, the realized accuracy was 0.16 in the first round and 0.14 in the subsequent rounds, as opposed to 0.19 for BayesC. For the other traits, the accuracy by BayesC was lower and Manhattan plots did not have clear peaks. The option to compute weights for SNP in ssGBLUP with the top 25 SNP gives a good identification of top segments. However, further work is required to compute weights to maximize accuracy for a variety of cases. In addition, a choice for GWAS in single-step approach is based on simplicity and flexibility in case of complex models.

Key Words: weighted SNP, ssGBLUP, BayesC

0941 (M055) Derivation of Bayes and Minimax decision rules for allelic frequencies estimation in biallelic loci. C. A. Martinez*[1,2], K. Khare[2], and M. A. Elzo[1], *[1]Dept of Animal Sciences, University of Florida, Gainesville, [2]Dep. of Statistics, University of Florida, Gainesville.*

In population genetics, allelic frequencies are typically estimated via maximum likelihood (MLE). Under this setting, allele frequencies are treated as unknown fixed parameters. However, population genetics theory indicates that allele frequencies vary at random, thus they should be treated as random variables. The aim of this study was to derive Bayes and Minimax estimators (ME) of allele frequencies for biallelic loci using decision theory. Because an optimal decision rule with uniformly smallest risk rarely exists, an approach is to establish principles that allow ordering of decision rules according to their risk function. Two general methods were used to obtain average risk optimality: the Bayes and the Minimax principles. Briefly, given a loss function and a prior distribution, the Bayes principle looks for an estimator minimizing the posterior risk, while the Minimax principle consists of finding decision rules that minimize the supremum (over the parameter space) of the risk function (the worst scenario). For an arbitrary locus, the sampling model was a trinomial distribution for numbers of individuals for each genotype and the prior was a Beta distribution, chosen because of mathematical convenience, flexibility and genetic interpretation of its parameters. Three types of loss functions were considered: square error (SEL), Kullback-Leibler (KLL), and a quadratic error loss (QEL). The SEL and KLL yielded the same estimator, which was a convex combination of the prior mean and the MLE. Using the Bayes estimator from QEL, a ME was derived by applying a theorem that states that a Bayes estimator with constant risk is also Minimax. The constant risk was obtained by finding appropriate hyperparameter values. This estimator was shown to be equivalent to MLE. The prior associated with this ME was uniform [0, 1]. One consequence of using the previous theorem on the derivation of ME is that the uniform distribution is a least favorable prior, that is, it causes the greatest average loss. Extension to several loci under linkage equilibrium and independent priors was discussed. The estimators derived here have the appealing property of allowing variation in allelic frequencies, which is more congruent with the reality of finite populations exposed to evolutionary forces. In addition, from a Bayesian perspective they permit modeling uncertainty and incorporation of previous genotypic information from the population.

Key Words: allele frequencies, average risk optimality, decision theory

0942 (M056) Adjusting genomic relationship matrices in single-step genomic BLUP for crossbred evaluations. D. Lourenco, and I. Misztal, *University of Georgia, Athens.*

Different breed-specific genomic relationship matrices (GB) were compared to the standard across-breed genomic relationship matrix (G) used in single-step genomic evaluations. Datasets were simulated that resembled a terminal-cross population. Two purebred lines were separated by 50 generations. Three scenarios considered selection based on high EBV, high phenotypes, and no selection. The datasets used for evaluations contained phenotypes and pedigrees for the last 15 generations and genotypes for the last eight generations of purebreds. Data on F1 animals were from a single generation. Number of purebred parents genotyped varied from 3100 to 3300 depending on the scenario, and number of genotyped F1 was 1200. The heritability for the simulated trait was 0.30. Testing involved four genomic matrices: GB1 considered specific allele frequencies (AF) for each pure and crossbred; GB2 used AF for crossbred calculated based on AF from the two purebreds; GB3 and GB4 had AF as in GB2 and GB1, respectively; however, each element was scaled by breed-specific scaling factors. Across-breed and breed-specific correction factors for G and all GB were also used to account for the non-random genotyping caused by selection. The validation was done in F1 animals and parameters of the regression of TBV on GEBV were used to assess the accuracy of evaluations. For G and all GB, coefficients of determination (R^2) and regression were higher when no artificial selection was applied. When no correction factor was used, R^2 for G, GB1, GB2, GB3, and GB4 for EBV selection were 0.33, 0.03, 0.37, 0.37, and 0.03, respectively; for mass selection were 0.23, 0.33, 0.37, 0.38, and 0.33, respectively; for no selection were 0.47 for G and 0.46 for all GB. However, after using breed-specific correction factors, the difference between G and GB was reduced and GB1 and GB4 gave similar results to G (R^2 = 0.40 under EBV and mass selection; R^2 = 0.47 under no selection), while GB2 and GB3 had slightly worse performance. Most unbiased predictions were with G and the correction factor applied, which regressions were close to 1.0 for the purebreds and from 0.65 to 1.0 for the crossbreds; the highest inflation was with the EBV selection and no phenotypes on crossbreds. Breed-specific genomic matrices provide little benefits for genomic evaluations in a terminal cross model. The best performance is with standard G corrected for an average selection across breed types.

Key Words: ssGBLUP, breed-specific, allele frequency

BREEDING AND GENETICS: APPLICATIONS AND METHODS IN ANIMAL BREEDING—DAIRY II

0943 (T041) Genome-wide association study on dairy cow mortality in three U.S. regions. S. Tsuruta[*1], I. Misztal[1], and T. J. Lawlor[2], *[1]University of Georgia, Athens, [2]Holstein Association USA Inc., Brattleboro, VT.*

Cow mortality, from DHI reports, is farmer provided information. The termination code = "dead" is the primary reason given for a cow leaving a herd, particularly late in lactation. This trait can be difficult to interpret because its definition and recording method may differ across farms. Our objective was to do a genome-wide association study (GWAS) on cow mortality and 305-d milk yield for three lactations and determine if there were differences in the genetic architecture associated with these traits in three different regions of the United States. Genomic EBV of cow mortality and 305-d milk yield were estimated with a single-step GBLUP using a threshold-linear model. The SNP file contained 42,503 usable SNP markers for 34,506 bulls obtained from USDA-AIPL. Data consisted of the entire U.S. DHI data for three lactations (10,748,430 animals; 6233,306 records) for cows calving from 1999 to 2008. Three U.S. regions— SE: Southeast (648,991 animals; 293,494 records), SW: Southwest (541,777 animals; 272,934 records), and NE: Northeast (1690,481 animals; 883,887 records)— were selected for regional comparison. Heritability estimate for 305-d milk first lactation yield was 29%. Heritability for mortality within the first lactation was 0.04, 0.06, 0.06, and 0.04 for SE, SW, NE, and U.S., respectively. Genetic correlations between first lactation mortality and 305-d milk yield were 0.14, -0.01, 0.02, and 0.25 for SE, SW, NE, and U.S., respectively. The genome was divided into equal segments of 20 sequential SNPs. As expected, a segment on chromosome 14 was significantly associated with milk production in all regions. The proportion of the total genetic variance for 305-d milk yield, explained by this segment, was 1%, 1%, 3% and 4% for SE, SW, NE region, and total U.S., respectively. Chromosome 14 showed a strong association with first parity mortality for the entire U.S., with the NE showing a strong association for all three parities. Milk components (higher or lower %fat) could be a possible explanation. Within the SE and SW regions, chromosome 14 did not show a significant association for any of the three parities. These results suggest that this farmer-recorded trait on mortality is being interpreted differently and/or there are different traits (genomic segments) responsible for cow mortality in different regions of the country.

Key Words: GWAS, cow mortality, region

0944 (T042) Multiple-breed genomic evaluations by using a reduced pool of SNP-markers. M. Cellesi[*1], N. P. P. Macciotta[1], P. Ajmone-Marsan[2], A. Rossoni[3], G. Marras[1], G. Gaspa[1], and C. Dimauro[1], *[1]Università di Sassari, Italy, [2]Università Cattolica del Sacro Cuore, Piacenza, Italy, [3]Associazione Nazionale Allevatori Razza Bruna, Bussolengo, Italy.*

Large reference populations (RP) of genotyped and phenotyped individuals are required to obtain reliable predictions in genomic selection programs. For small breeds, however, assembling such RPs could result particularly challenging. In this study, a multibreed approach was used to enhance the size of the RP. Data were genotypes of 2054 Italian Holstein and 634 Brown Swiss bulls, respectively, genotyped with the Illumina's 50K BeadChip. Phenotypes were deregressed proofs (DRP) for milk, fat and protein yield. An empirical technique, named Maximum Difference Analysis (MDA), was used to select a restricted pool of SNP-markers significantly associated with the considered trait (T). In each breed, animals were ranked according to a T. The best (B) 10% and the worst (W) 10% individuals were selected and the genotypic frequencies were evaluated. For each SNP, the maximum genotypic frequency in B and, in correspondence, the frequency for the same genotype in W were recorded and the difference between the two frequencies was calculated. A bootstrap procedure was then implemented to derive a posterior probability distribution that was used to declare a SNP positively associated with T. Markers negatively associated with T were detected through the same procedure with the only difference that, for each SNP, the maximum genotypic frequency was recorded in W. A BLUP model was used to estimate marker effects that were then used to calculate genomic breeding values of Brown Swiss younger bulls (50animals). Three datasets were used: all original SNPs, only the MDA selected markers (MDA_SNP) and the MDA_SNP for Brown Swiss plus MDA_SNP obtained for Holstein. MDA selected, for both breeds, around 1500 markers for each trait. Accuracies of genomic predictions (Table 0944) evaluated by using MDA_SNPs in the multi-breed scenario were greater than values obtained with all markers and in the single-breed scenario. Results suggested that the MDA applied to a small genotyped bovine population increases accuracies of genomic predictions of about 10%. A further improvement can be obtained in a multibreed scenario.

Key Words: SNP reduction, multiple breeds, genomic selection

Table 0944. Accuracies of genomic predictions for Brown Swiss

Scenarios	Milk	Fat	Protein
Brown Swiss all SNP	0.21	0.35	0.21
Brown Swiss MDA_SNP	0.31	0.43	0.30
Holstein + Brown Swiss MDA_SNP	0.36	0.43	0.34

0945 (T043) Determination of single nucleotide polymorphisms associated with subclinical ketosis in Jersey cattle. R. T. Fugate*[1], L. H. Dauten[2], G. R. Wiggans[3], and H. M. White[4], *[1]University of WI, Madison, [2]University of Connecticut, Storrs, [3]Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD, [4]Dep. of Dairy Science University of Wisconsin, Madison.*

Subclinical ketosis is a fresh cow disorder that is costly in terms of lost milk production and treatment cost. Although treatment and prevention strategies are available, prevention requires targeting animals that are likely to develop the disease. Whole-herd genotyping is becoming more common with commercial dairies, and identification of markers for ketosis predisposition would provide a valuable tool to producers. The objective of this study was to identify single nucleotide polymorphisms (SNP) that are associated with subclinical ketosis in Jersey cattle. Ketotic cows were identified by cowside test using the Precision Xtra meter. Blood and hair samples were collected from 54 Jerseys (ketotic and healthy herdmates on the same day) with < 30 d in milk on New England dairy farms. Mean parity of cows was 2.8, with no difference ($P >$ 0.05) between healthy and ketotic cows; no difference ($P >$ 0.05) also was found for milk yield, 305-d mature-equivalent milk yield (ME_{305}), or ME_{305} from the previous parity. Blood serum was analyzed for concentration of nonesterified fatty acid (NEFA) and β-hydroxybutyrate (BHBA). Hair samples were submitted to the American Jersey Cattle Association for genotyping with the BovineSNP50 BeadChip. Concentrations of NEFA and BHBA were analyzed using the SAS 9.2 PROC MIXED; differences in SNP frequency by ketosis status (healthy or ketotic) was analyzed using the $\chi 2$ test from the SAS 9.2 FREQ procedure. As expected, BHBA concentrations were greater ($P \leq 0.05$) for ketotic cows compared with healthy herdmates (1.63 vs. 0.91 ± 0.17 mmol/L). For NEFA, concentrations tended to be greater ($P \leq 0.01$) in ketotic cows compared with healthy cows (0.45 vs. 0.33 ± 0.05 mmol/L). Of the 54,609 SNP analyzed for each genotype, 1685 were different ($P \leq 0.05$) and 1862 tended to differ ($0.05 < P \leq 0.1$) between ketotic and healthy cows. These data suggest that genotypes from the BovineSNP50 BeadChip could be useful in predicting predisposition for ketosis in Jerseys, but examination of a larger data set is necessary to validate the predictive ability of the identified SNP.

Key Words: ketosis, Jersey, SNP

0946 (T044) Multi-trait, multi-breed conception rate evaluations. P. M. VanRaden[1], J. R. Wright*[1], C. Sun[2], J. L. Hutchison[1], and M. E. Tooker[1], *[1]Animal Improvement Programs Laboratory, USDA-ARS, Beltsville, MD, [2]National Association of Animal Breeders, Columbia, MO.*

Heifer and cow conception rates (HCR and CCR) were evaluated with multi-trait, multi-breed models including crossbred cows instead of the previous single-trait, single-breed models. Fertility traits benefit from multi-trait processing because of high genetic correlations and many missing observations, with 4 million HCR and 14 million CCR lactation records stored since 2003 vs. 66 million daughter pregnancy rate (DPR) records since 1960. Conception rates were previously modeled using multiple binary success records per parity (such as no, no, yes) that are now pre-adjusted for environmental effects and combined into lactation records for simpler multi-trait analysis with the continuous trait DPR. Genetic correlation estimates were 0.45 for HCR with CCR, 0.86 for CCR with DPR, and 0.36 for HCR with DPR. Inbreeding depression per 1% inbreeding was -0.21 for HCR, -0.10 for CCR, and -0.13 for DPR. Heterosis was 1.3 for HCR, 3.2 for CCR, and 1.4 for DPR. Crossbred cows get the combined effects of heterosis and no inbreeding compared to purebreds that may average 6%. Genetic differences among breeds were fairly consistent with phenotypic differences. Holsteins had the highest phenotypic and genetic averages for HCR, while Jerseys were highest for CCR. Evaluations from the new and previous models were correlated by > 0.95 for both HCR and CCR for recent Holstein bulls with > 50% reliability, but were less correlated in other breeds because of additional crossbred daughters and contemporaries. For Holstein sires with > 90% reliability, correlations between single-breed and multi-breed evaluations were 0.986 for HCR and 0.992 for CCR, indicating little change in rank when adding the other breeds. Genetic trend for CCR was more negative with multi-trait processing because of the correlation with DPR. Genetic trends were validated using Interbull tests 1 and 3. The genetic correlations with other countries estimated by Interbull changed little for Holsteins, averaging 0.02 higher for HCR and 0.02 lower for CCR, but were more variable for other breeds. The new model implemented in December 2013 combines data from all breeds and uses DPR as a correlated trait to improve HCR and CCR evaluations.

Key Words: conception, evaluation, multi-trait

0947 (T045) Genome-wide genotyping-by-sequencing (GBS) and association analysis of saturated and monounsaturated fatty acids in bovine milk identifies novel markers in Canadian Holstein cows. E. M. Ibeagha-Awemu[*1], S. O. Peters[2], I. G. Imumorin[3], and X. Zhao[4], *[1]Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada, [2]Berry College, Mount Berry, GA, [3]Cornell University, Ithaca, NY, [4]McGill University, Ste. Ann De Bell, PQ, Canada.*

The effect of bovine milk fatty acids (FA) on human development and heath has fueled concerted efforts towards exploitation of existing heritable variation for genetic improvement. Consequently, genomic regions as well as single markers associated with milk fat traits have been identified in many cattle breeds around the world. Since information on population specific markers of milk FA traits in Canadian Holstein cows is limited, we used the high throughput genotyping-by-sequencing (GBS) SNP mining method and association analysis to determine population specific markers associated with milk saturated FAs (SFAs) and monounsaturated FAs (MUFAs). Fatty acid profiles of 1200 cows from seven herds in Quebec were determined by gas chromatography and SNPs were genotyped by GBS method. Genome wide association analysis (GWAS) with 99,814 SNPs (> 70% call rates, accuracy of imputation score > 50% and MAF > 0.01) out of 515,820 SNPS was accomplished with the single-locus mixed linear model procedure (EMMA) implemented in Golden Helix SNP and Variation Suite v8.0 software (www.goldenhelix.com). Genome wide significance (BH *P*-value < 0.05, range 3.86E-05 to 0.049) was detected between 7 SFAs (C4:0, C6:0, C8:0, C13:0, C14:0, C23:0, and C24:0) and several SNPs located in intergenic, coding, splicing and 3' untranslated (UTR) regions. In particular, 15 significant associations for C13:0 are coding variants located in 15 genes, and 10 for C24:0 are also coding variants with many non-synonymous SNPs. One 3'UTR variant within CHFR (E3 ubiquitin-protein ligase) gene significantly associated with C6:0 and C8:0. Furthermore, genome wide significant (BH *P*-value < 0.05) associations were recorded between several SNPs and two individual MUFAs (oleic acid [C18:1n9c] and trans vaccenic acid [C18:1n11t]), total MUFAs and total SFAs. In particular, a synonymous variant (S25_37873086) within ACHE (acetylcholinesterase) gene significantly influenced both total MUFAs and total SFAs. Minor allele frequencies for all reported significant associations are $\geq$ 0.02. Since most of these associations are being reported for FAs for the first time with only six of the genes known to play a role in lipogenesis, our study has uncovered potential novel SNPs and genes that can be used in improvement of milk SFA and MUFA contents through breeding to ensure quality products for human consumption. Moreover, our results also further confirm the use of the GBS technique for identification of population-based unique SNPs for GWAS and for improvement breeding in dairy cattle.

Key Words: genome wide genotyping-by-sequencing, genome wide association study, saturated and monounsaturated fatty acids

0948 (T046) Peroxisome proliferator-activated receptor γ isoforms alter lipogenic gene networks in goat mammary epithelial cells. H. Shi[1], J. Luo[*2], D. Yao[1], and J. Zhu[1], *[1]Northwest A&F University, Yangling, China, [2]Northwest A & F University, Yangling, China.*

Lactation is a highly demanding lipid synthesis and transport process that is crucial for the development of newborn mammals. Peroxisome proliferator-activated receptor-γ (*P*PARG) was reported to promote adipogenesis and lipogenesis in adipose tissue, its role in the lactating mammary gland is less clear. PPARG is present in two isoforms generated by alternative splicing, PPARG1 and PPARG2. Their roles in ruminant lactation mammary gland have been poorly distinguished. To determine which of these isoforms is more closely associated with the regulation of the lipogenic pathways, their distributions were analyzed and key genes in the mammary lipid network were detected by quantitative PCR (qPCR) after overexpression of the two isoforms in goat mammary epithelial cells (GMEC). Various tissues of goats were collected to assay mRNA expression of PPARG isoforms. The adenovirus pAd-PPARG1 and pAd-PPARG2 were generated. The adenovirus (Ad-GFP) was used as a positive control. GMEC at about 80% conñuence were transfected with adenovirus at the same MOI and cultured in the DMEM/F-12, at 37°C in 5% CO_2. Transfected GMEC were cultured with ROSI or DMSO at 50 μM after 24 h of the initial culture and then harvested at 48 h (24 h later) for RNA extraction. Distribution analysis indicated that expression of PPARG2 was markedly greater in adipose than mammary gland and PPARG1 is the mainly isoform in goat mammary tissue. Both PPARG isoforms could significantly upregulate the mRNA expression of NR1H3, INSIG1, PLIN2, CD36, SCD, AGPAT6, DGAT1 under the treatment with rosiglitazone (ROSI). They had no significant effect on SCAP, PNPLA2 and PLIN3 in absence of ROSI. PPARG1 increased the SREBF1, FASN and ACACA while PPARG2 downregulated these genes expression. In conclusion, the data suggest that both PPARG1 and PPARG2 could largely affect fatty acid metabolism when stimulated. However, de novo lipogenesis in mammary cells appear more closely related to PPARG1 activation, with this nuclear receptor acting through its control of SREBF1 and to some extent NR1H3.

Key Words: PPARG, lipogenesis, mammary gland epithelial cells, goat

0949 (T047) Association between polymorphisms in the IGF-I, GHR and STAT5A genes and the interval from calving to conception and milk production in Holstein cows. L. Hax*, A. Schneider, C. Bespalhok Jacometo, P. Mattei, T. da Silva, G. Farina, and M. Nunes Corrêa, *Federal University of Pelotas, Pelotas, Brazil.*

The aim of this study was to investigate the association of polymorphisms in the insulin-like growth factor 1 (IGF-I), growth hormone receptor (GHR) and signal transducer and activator of transcription 5A (STAT5A) genes with the calving to conception interval (CCI) and milk production of Holstein cows. In this study 308 Holstein cows from a commercial herd in southern Brazil were used. The study evaluated cows between the first and sixth lactation with a CCI no longer than 250 d. The animals were reared in a semi-extensive system being milked twice a day. The CCI and milk production data were obtained from the farm management software. Blood samples were collected for DNA extraction. Genotypes were verified by polymerase chain reaction (*P*CR) using the following primers: IGF-I (TTAAATAATTGGGTTGGAAGACTGC and ACCTTACCCGTATGAAAGGAATATACGT); GHR (TGCGTGCACAGCAGCTCAACC and AGCAACCCCACTGCTGGGCAT); STAT5A (GAGAAGTTGGCGGAGATTATC and CCGTGTGTCCTCATCACCTG). The amplified fragments of IGF-I, GHR and STAT5A were digested with 3U of *Sna*BI, *Alu*I and *Bst*EII at 37°C for 3 h, respectively. The resulting fragments were subjected to agarose gel electrophoresis for subsequent UV visualization. Statistical analyzes were performed using the GLM procedure. A value of $P < 0.05$ was considered significant. The average milk production adjusted to 305 d of lactation and CCI were 5652 ± 1170L and 117 ± 57.8 d, respectively. There was no association between milk production and CCI with the genotypes identified for each gene. The presence of none, one or two alleles had no linear or quadratic association with the evaluated traits for IGF-I, GHR and STAT5A. There was no interaction between the genotypes of each studied gene for milk production and CCI. The low level of milk production suggests that these animals were not subjected to a major metabolic challenge. The somatotropic axis acts regulating metabolism and the reproductive system, and its balance is a result of the metabolic condition of the animal. Thus, it is likely that the function of the studied genes was not impaired in this low challenge condition, therefore without any major changes in the GH/IGF-I axis or folliculogenesis. Under such conditions, the effect of the polymorphisms studied were not observed, as previously shown in studies using high-producing dairy cows. In conclusion, the GHR *Alu*I, IGF-I *Sna*BI and *Bst*EII STAT5A polymorphisms are not good molecular markers for selection of dairy cows for milk production and CCI in semi-extensive production systems.

Key Words: genetic selection, molecular markers, reproduction

0950 (T048) A polymorphism within the prolactin gene is associated with milk production in Holstein dairy cows managed under summer heat stress conditions in northwest México. P. Luna*, *Instituto Tecnologico de Sonora, Ciudad Obregon, México.*

Holstein dairy cows managed in northwest México are exposed during summer to extreme ambient temperature and humidity that lead to heat stress. The physiological response from cows exposed to such weather conditions results from the perturbation of a gene network related to heat stress homeostasis. The prolactin signaling pathway has been proposed as an important mediator of this response in cattle. The objective of this study was to assess the association between a SNP polymorphism (rs110494133-A/G within intron 1) in the prolactin gene (PRL) and performance traits such as average and total milk production in Holstein cattle. The SNP allele frequency was 70% for A and 30% for G. No deviations from Hardy-Weinberg equilibrium ($X^2 = 1.00$, $P > 0.38$) were observed in the cow population. DNA was extracted from blood spotted on FTA cards from 118 cows, and genotyped using the sequenom mass array platform. Genotype to phenotype association analyses were conducted using a mixed effects model that included phenotype as the response variable, genotype as a fixed term, sire as a random term, and days in milk as a covariate. Mean values for milk production, serum prolactin, and rectal temperature were 22.1 ± 0.5 kg/d, 32.2 ± 1.2 ng/mL, and 38.3 ± 0.1°C, respectively. In a previous study, we reported that reduced serum levels of prolactin and increased rectal temperature were associated with lower milk performance, which was remedied by spray cooling the cows. In this study, the genotype term was as a significant ($P < 0.05$) source of variation in predicting milk production. Least square means among genotypes AA, AG, and GG were 24.6 ± 1.3, 21.2 ± 1.5, and 21.2 ± 1.7 kg/d for average milk production, and 7403 ± 13.8, 7397 ± 10.5, and 6241 ± 61.8 kg for total milk production, respectively. The A allele from the SNP in the PRL gene was the most favorable ($P < 0.05$) and increased average milk production (1.2 ± 0.3 kg/d) and total milk production (325 ± 63.5 kg). When the mixed model included serum prolactin or rectal temperature as the response variable instead of milk traits, the genotype term also resulted as a significant predictor ($P < 0.05$). We conclude that a SNP within the prolactin gene appears to be a predictor of lactation performance in Holstein dairy cows managed under summer heat stress conditions common to northwest México.

Key Words: heat-stress, prolactin, polymorphism.

BREEDING AND GENETICS: APPLICATIONS AND METHODS IN ANIMAL BREEDING—POULTRY

0951 (T049) Regulation of microRNAs in necrotic enteritis infected two genetically disparate chicken lines. Y. H. Hong*, *Chung-Ang University, Anseong-si, South Korea.*

Necrotic enteritis (NE) is an acute clostridial disease causing weight depression, loss of appetite, and sudden death. MicroRNAs (miRNA) play a critical role in post-transcriptional regulation by influencing the 3′-UTR of target genes. Using two inbred White Leghorn chicken lines, line 6.3 and line 7.2 showing Marek's disease-resistant and-susceptible phenotypes, respectively, we used small RNA high-throughput sequencing to investigate whether miRNAs are differently expressed in these two chicken lines after inducing necrotic enteritis (NE). The 12 miRNAs, selected from the most downregulated or up-regulated miRNAs following NE induction, were confirmed by their expressions in real-time PCR. Among these miRNAs, miR-215, miR-217, miR-194, miR-200a, miR-200b, miR-216a, miR-216b, and miR-429 were highly expressed in the intestine derived from line 7.2, whereas, miR-1782 and miR-499 were downregulated ($P < 0.05$). In spleen, miR-34b and miR-1684 were the most up-regulated miRNAs in line 6.3 ($P < 0.05$). Notably, five out of six target genes, CXCR5, BCL2, GJA1, TCF12, and TAB3 were differentially expressed between line 6.3 and line 7.2 ($P < 0.05$), and showed suppression in the MD-susceptible chicken line. Their expression levels were conversely correlated with those of miRNA obtained from both HTS and quantitative real-time PCR.

These results suggest that some miRNAs are differentially altered in response to NE, and they modulate the expression of their target genes in the two inbred lines. Collectively, high-throughput analysis of intestinal miRNAs from NE-afflicted inbred chickens showing different disease phenotypes led to the identification of host immunity genes regulated by miRNA. Future studies of the function of these miRNAs and their target genes in the host will lead to enhanced understanding of molecular mechanisms controlling host-pathogen interaction in NE.

Key Words: necrotic enteritis, miRNA, chicken

0952 (T050) Changes in variance of top SNP windows over generations under selection for three traits in broiler chicken. B. D. Fragomeni*[1], I. Misztal[1], D. Lourenco[1], I. Aguilar[2], and R. Hawken[3], *[1]University of Georgia, Athens, [2]Instituto Nacional de Investigación Agropecuaria, Las Brujas, Uruguay, [3]Cobb-Vantress Inc., Siloam Springs, AR.*

The purpose of this study was to determine whether the top SNP windows that explain the most variance are stable over multiple generations of selection in a GWAS analysis using single-step GBLUP. Phenotypes were available for five generations of a pure line of broiler chicken for body weight, breast meat, and leg score. Pedigrees included 297,017 animals, of which 294,632 had phenotypic records over five generations. Genotypes of 57,635 SNP were available for 4922 animals. After quality checks, 41,036 SNP and 4866 animals remained in the genomic file. SNP effects were calculated by a GWAS type analysis using single-step GBLUP approach. In each run, the generations were grouped from 1–3, 2–4, 3–5, and 1–5. The evaluation model included sex and contemporary group as fixed effects, animal additive and maternal permanent environmental as random. In GWAS by single-step GBLUP, genomic breeding values (GEBV) are converted to SNP effects. Variances of SNP effects were derived iteratively in three iterations without re-estimation of GEBV. As individual SNP explained very small portion of the total genetic variation, variances were then calculated for windows of 20 SNP and interpreted as the percentage of the total genetic variance. Ten windows for each trait were identified that explained the largest fraction of the variance in any combination of generations. All the top 10 windows explained at least 0.5% (but less than 2%) of the total genetic variance in all the traits. The variance explained by each window varied greatly among the combinations of generations. In several cases, a window identified as top for one combination of generations explained less than 0.1% variance in the remaining combinations. Top windows of SNP variance in the broiler population are unstable and unsuitable for direct selection. Results in this study could be influenced by many generations of intensive selection in broiler chicken and by a small number of genotypes.

Key Words: genomic selection, genome-wide association study, ssGBLUP

0953 (T051) Relationship between laying frequency and egg sizes in quail. O. T. Abanikannda*, O. N. Ottun, and A. O. Leigh, *Lagos State University, Ojo-Lagos, Nigeria.*

The number of eggs laid by hens during a laying cycle is one of the desirable traits in commercial egg production, and the size of eggs produced by hens determine the quality, grade, marketability, and acceptability of eggs by the consumers. Several factors such as breed, age, weight, and management

Table 0953. Mean ± SE of measured variables

Laying Group	N	HenWt (g)	FeedWt (g)	EggWt (g)	EggLt (mm)	EggWd (mm)	EggSSA (mm^2)	EggVol (mm^3)	EggDens
Low	4	166.40 ± 1.51	30.13 ± 0.84^{ab}	10.08 ± 0.11^{a}	30.39 ± 0.19	24.36 ± 0.14	22.40 ± 0.24	10.19 ± 0.16	1.0525 ± 0.0006^{a}
Medium	3	168.99 ± 0.92	27.30 ± 0.72^{b}	9.64 ± 0.11^{b}	29.92 ± 0.16	24.09 ± 0.14	21.81 ± 0.18	9.79 ± 0.12	1.0522 ± 0.0006^{b}
High	10	169.06 ± 0.78	32.64 ± 0.49^{a}	9.96 ± 0.04^{a}	30.01 ± 0.12	24.19 ± 0.10	22.01 ± 0.14	9.95 ± 0.09	1.0524 ± 0.0005^{a}

practices have been reported to influence quantity and quality of eggs produced by quail hens. This study investigates the relationship between quantity and quality of eggs as depicted by the frequency of lay and measurements taken on eggs. After an initial stabilization period, a total of 435 eggs were collected from 17 quail hens over a continuous laying period of 34 d. The hens were classified into three nominal groups as Low (17 to 21), medium (22 to 26) and High (26 to 31) depending on the number of days of lay during the study period. Majority (58.82%) of the hens were in the High laying group, while the Medium and Low laying groups accounted for 17.65 and 23.53%, respectively. Consequently, about two-thirds (66.44%) of the eggs studied were from hens in the High laying group. Parameters studied include Hen Weight (HenWt), Feed Consumed (FeedWt), Egg Weight (EggWt), Egg Length (EggLt), Egg Width (EggWd), Shape Index (ShpInd), Egg Surface Area (EggSSA), Egg Volume (EggVol), Egg Density (EggDens), and Surface Area to Volume Ratio (SSAVol). All statistical analyses (Descriptive, Correlation, Regression, and ANOVA where $Y_{ij} = \mu+\alpha_i+e_{ij}$) were done using Minitab 16 software. A one way analysis of variance (ANOVA) on each of the parameter revealed that only three of the parameters (EggWt, FeedWt and EggDens) were significantly ($P < 0.05$) affected by laying group (Table 0953). There was a significantly ($P < 0.001$) moderate correlation ($r = 0.5$) between ChickWt, FeedWt and EggWt and a highly significant ($P < 0.001$) correlation ($r = 0.99$) between EggWt and EggDens. Hens with lower frequency of lay consumed less feed and had higher egg weight, whereas hens in the middle laying group consumed least and had the least egg weight. Small-sized quail hens consumed moderately, laid least eggs laid but had the heaviest eggs.

Key Words: laying frequency, quail, egg weight

0954 (T052) Phenetic classification of six bird species based on the proximate and mineral composition of their eggs.

O. T. Abanikannda*, O. N. Ottun, and A. O. Leigh, *Lagos State University, Ojo-Lagos, Nigeria.*

Classification is a systematic grouping of organisms into categories on the basis of evolutionary or structural relationships between them, based on their biological similarities and differences. Phenetic classification is the quantification and statistical assessment of characters based on overall or observable similarities rather than on phylogenetic or evolutionary relationships, with an orderly arrangement of organisms in hierarchical series. A total of 240 eggs comprising 40 eggs from each of six species species (chicken, duck, guinea fowl, pigeon, quail, and turkey) were sampled. Proximate composition (moisture content, dry matter, total ash, crude protein, crude fat, and carbohydrate) of the eggs along with mineral analyses (calcium, magnesium, manganese, iron, zinc, and cobalt) were conducted using standard laboratory procedures for proximate and mineral assay. All statistical analyses which included descriptive, analysis of variance and multivariate cluster analyses were done with Minitab Statistical software. Specie was a highly significant ($P < 0.001$) source of variation in all variables measured except for crude fat, Mg and Zn, which were not affected ($P > 0.05$) by specie. The complete linkage method, with squared Euclidean distance and three clusters specified as final partition was used on the standardized variables. Three main clusters were identified with duck, turkey, and quail forming a cluster and joining with chicken and guinea fowl as a second cluster, while pigeon was in the third cluster. This clustering is close to the phylogenetic classification in traditional taxonomy of the three classes (anseriforms, galliforms and columbiforms), and provides a good basis for comparative classification of the six different species of birds.

Key Words: taxonomy, phenetic classification, cluster analysis

Table 0954. Clustering of the six species based on proximate and mineral composition analyses

Step	Number of Clusters	Similarity Level	Distance Level	Clusters Joined	New Cluster	Number of Observation in New Cluster
1	5	97.5304	1.5258	4	3	2
2	4	96.1613	2.3717	2	1	2
3	3	82.2077	10.9930	5	1	3
4	2	63.7853	22.3753	3	1	5
5	1	0.0000	61.7852	6	1	6

0955 (T053) Effect of shell thickness on quail chick pip-out at hatching.

O. T. Abanikannda*, A. O. Leigh, and O. N. Ottun, *Lagos State University, Ojo-Lagos, Nigeria.*

Economic losses incurred by farmers when chicks could not pip out at hatching is a major consideration in commercial hatchery operations. The inability of chicks to come out of an egg shell unassisted has its attendant consequences on the survival and livability of quail chicks. Aside from genetic effect, age and nutritional status of the hen, egg shell thickness is also a major factor. This study was conducted to determine

the effect of egg shell thickness on the on the ability of quail chicks to pip out of the shell at hatching. A total of 593 fertile eggs collected from a farm located in Jos, Plateau State, in the Savannah region of Nigeria, were incubated and hatched. The eggs were weighed and linear measures were taken using digital weighing scale and caliper. The measured variables include, egg weight, egg length, egg width, shell thickness, vertical and horizontal circumference, while shape index, egg density, egg volume, egg surface area, and surface area to volume ratio were computed. All statistical analyses were done using JMP statistical software for the descriptive statistics, correlation, model fitting, and logistic regression. After incubation, 570 eggs hatched, and eggs that were not hatched ($n = 23$) were opened up to determine if the chicks fully developed but could not pip out unassisted. The result revealed that there was no statistical difference ($P > 0.05$) in the mean of all variables studied. A binary logistic regression of the shell thickness on hatching status was not statistically significant ($P > 0.05$), indicating that despite the slight numerical difference in shell thickness of the two groups (Hatched, Not Hatched), it was not enough to invoke a statistical significance probably due to unequal subclass numbers in the two groups.

Key Words: hatchability, quail, egg shell

0956 (T054) Weight changes in quail eggs during incubation. O. T. Abanikannda*, O. N. Ottun, and A. O. Leigh, *Lagos State University, Ojo-Lagos, Nigeria.*

Commercially, quails are mostly raised for their meat and eggs. The eggs are tastier, low in calories and are good sources of essential vitamins, minerals and amino acid, thereby making it a preferred egg compared to other poultry eggs. Chick weight at hatch positively impacted on subsequent productivity indices of quails thereby making it a primary index for the future performance traits of the bird. Differences in chick weight at hatch have been largely influenced by the pre-hatch egg weight and weight loss associated with incubation. Chick weight is primarily determined by initial egg weight and is secondarily determined by weight loss during incubation, shell and residue weight, strain, incubation time and conditions, breeder age and chick sex. This study aims at investigating some egg measures and its influence on chick weight at hatch with a view to statistically predict its chick weight. The eggs used in this study were sourced from a semi-intensively managed poultry farm in Jos, Plateau State in the Savannah region of Nigeria. A total of 987 hatching quail eggs were collected and appropriately labeled for identification purposes and set for incubation. Out of the total eggs set, 606 eggs were hatched and were used for the analyses. Egg weight and egg shell weight were measured with a sensitive (0.00 g) digital scale, while egg length and width were measured with a sensitive (0.00 mm) digital Vernier caliper. Other measures included both the vertical and horizontal circumference of the eggs using a flex graduated tape, 14th day incubation weight of egg and chick weight at hatch. Indices such as shape index, egg density, egg surface area, egg volume, and incubation weight difference were computed. With the exception of shell thickness and shape index, all other variables were highly significantly ($P < 0.01$) impacted on chick weight and were used to model. The statistical model for predicting chick weight at hatch using the 11 variables that significantly influenced chick weight at hatch is given by: $Y = \beta_0 + \beta_1X_1 + \beta_2X_2 + \beta_3X_3 + \beta_4X_4 + \beta_5X_5 + \beta_6X_6 + \beta_7X_7 + \beta_8X_8 + \beta_9X_9 + \beta_{10}X_{10} + \beta_{11}X_{11}$. The model accounted for 31% of the variability in chick weight. The study revealed that egg weight, density, volume, and incubation weight loss were the largest influences on chick weight.

Key Words: quail eggs, incubation, chick weight

BREEDING AND GENETICS: APPLICATIONS AND METHODS IN ANIMAL BREEDING—LIVESTOCK I

0957 (W061) Whole genome association analysis for detecting QTLs related to fat and protein production in buffaloes. H. Tonhati*[1], D. F. Cardoso[1], R. R. Aspilcueta Borquis[1], N. A. Hurtado Lugo[2], G. M. de Camargo[1], L. G. Albuquerque[1], D. J. A. Santos[3], D. C. Scalez[1], and M. C. Nakagawa[4], *[1]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil, [2]Universidade Estadual Paulista "Júlio de Mesquista Filho", Jaboticabal, Brazil, [3]Universidade Estadual Paulista, Jaboticabal, Brazil, [4]State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil.*

Whole genome association studies are important for the livestock industry because they allow incorporation of the QTL detected in genetic evaluations, thus enabling greater selection accuracy and faster genetic progress. Therefore, this study aims at identifying loci associated with fat and protein production in river buffaloes. A total of 452 animals (57 males and 395 females) were genotyped using the 90K panel Axiom Buffalo Genotyping (Affymetrix). For sample quality control, we established the threshold values for: call rate 0.95 and heterozygosity ± 3 standard deviations. For the marker, we adopted call rate > 0.98, MAF > 0.05, HWE up to 10^{-6}, correlation between markers up to 0.998, plus the elimination of coinciding SNPs and with possible errors of physical positioning in relation to the reference map. The number of SNPs left after quality control was 56,716. Statistical analyses were performed using R scripts and the GenABEL software (Aulchenko et al., 2007). The information used in this studied were the de-regressed breeding values to traits production of fat (FY) and protein (PY), according to Garrick et al. (2009). These data were corrected for population substructure using the principal components obtained by multidimensional scaling of genomic similarity matrix, with residuals weighted by $c+(1-r^2)/r^2$. The significance level of 0.05 was corrected for Bonferroni. The five SNPs with the highest P-value (candidate SNPs) were selected for each trait, and through their genomic coordinates (BTAU_4.0 assembly), the annotation of the closest genes was taken out using the NCBI database (http://www.ncbi.nlm.nih.gov). After population structure corrections, the inflation factors (lambda) were estimated as 1.0014 and 1.0078 for FY and protein PY; within the acceptable range. At the significance level corrected by Bonferroni, only two SNPs were deemed significant for FY and PY. The significant SNPs for both traits were present on chromosome 10. Deiodinase type 2 (DIO2) was the closest gene (~150 Kb). This is the main enzyme that converts Thyroxine (T4) to the active Triiodothyronine (T3) (active form). From the prior knowledge that thyroid hormones directly influence lactation, this gene may explain the greater buffalo hardiness during this phase, adapted to feeding conditions poor in protein.

Key Words: milk quality, buffalo, markers

0958 (W062) Evaluation of single nucleotide polymorphism markers on four pig chromosomes for potential associations with halothane sensitivity phenotypes in a population of Yorkshire-Landrace pigs. K. R. Perry*, C. W. Ernst, J. P. Steibel, and R. O. Bates*, Michigan State University, East Lansing.*

We have previously reported that a proportion of pigs homozygous normal for the RYR1 g. 1843 C > T polymorphism were halothane sensitive and had lower post-mortem *Longissimus dorsi* pH. Pigs from this project (n = 363), which were progeny of Landrace sires and Yorkshire-Landrace F1 dams, were subsequently genotyped for 67 SNPs across four chromosomes (SSC6, SSC10, SSC12, and SSC14). These SNPs were located in or near genes responsible for malignant hyperthermia or myopathies in humans (CACNA1S, CPT2, SCN4 and RYR2) that may influence the stress response in pigs, including multiple SNPs within RYR1. The objective of this study was to determine the association of these SNPs with the halothane sensitivity phenotypes recorded in this population. Pigs were evaluated for limb rigidity (RIGID), limb tremors (TREM), and abdominal discoloration (AD) observed after halothane challenge. Halothane sensitivity was assessed after 60 sec exposure to 5% halothane gas in a closed system delivered at 2 L/min. Pigs were considered to be either sensitive (1) to halothane or not sensitive (0) for each trait. Assays were multiplexed and SNP genotypes collected using Sequenom MassArray. Twelve SNPs were discarded from analysis due to low genotyping call rate (< 90%). Twenty-nine of the remaining 55 SNPs were not in Hardy-Weinberg equilibrium ($P < 0.05$). The three halothane response variables were fit to a generalized linear model that included the fixed effects of sex and SNP, and the random effects of replication and litter. False discovery rate (FDR) was used to determine significance. For the 55 SNPs tested for each halothane sensitivity variable, generally there were few SNPs with P-values less than 0.05. Three SNPs for TREMOR, 1 for RIGID and 1 for AD had P-values less than 0.05. The FDR for all SNPs was greater than 0.25 and therefore it was determined that no SNP significantly associated with any of the three halothane response variables. These results indicate that halothane sensitivity in this population is not controlled by variation in these regions of the swine genome, and other genomic

regions should be investigated to determine the genetic control of halothane sensitivity.

Key Words: pig, halothane sensitivity, SNP

0959 (W063) Growth rate of purebred Berkshire pigs housed in hoop buildings in North Carolina.

S. H. Oh*, N. Whitley, F. McElveen, and H. S. Park, *North Carolina A&T State University, Greensboro.*

This study was designed to estimate growth curves of antibiotic free Berkshire purebred breeding stock reared in hoop buildings at the North Carolina Agricultural and Technical State University Farm. The location features a humid subtropical climate with subtropical summer temperatures and mild winters, and an average annual precipitation of approximately 110 cm. Litters were weaned at 4 wk old, and reared within deep-bedded outdoor hoop houses. Six boars and 21 sows were included in the population. Body weights of a total 124 pigs were collected every 4 wk from birth to 20 wk of age, resulting in 1206 total records. Gompertz growth curves were used to estimate parameters, resulting in 3.681 ± 0.369 as W_0, 0.029 ± 0.002 as m, and 0.006 ± 0.001 as D. Overall average daily gain at 20 wk of age was 0.39 ± 0.11 kg and ranged from 0.16 to 0.64 kg. Average daily gains were 0.38 ± 0.11 kg in boars and 0.40 ± 0.12 kg in gilts. These results were lower than the results reported by others, which may be due to different climates in the test populations and/or due to the closed population used in the present study.

Key Words: Berkshire, growth rate, hoop, outdoor

0960 (W064) Use of the canonical discriminant analysis for selecting a panel of informative markers in 21 Italian sheep breeds.

C. Dimauro*[1], M. Cellesi[1], L. Nicoloso[2], P. Crepaldi[2], N. P. P. Macciotta[1], G. Pulina[3], and F. Pilla[4], *[1]Università di Sassari, Italy, [2]Università di Milano, Italy, [3]Dipartimento di Agraria, University of Sassari, Italy, [4]Università del Molise, Campobasso, Italy.*

SNP markers can be useful to assign individuals to their breed. In the present research, a high density SNP chip was exploited to select a panel of markers useful to verify the origin of 462 individuals belonging to 21 Italian sheep breeds. Animals were genotyped using the Illumina's OvineSNP50 BeadChip and were divided into two groups: the training population (TP) of 420 sheep, 20 for each breed, and the validation population (VP) of 42 animals, two for each breed. SNPs with MAF < 0.20 were discarded and, after data editing, 40,856 markers were used, including 4937 monomorphic SNPs for at least one breed. The canonical discriminant analysis (CDA) was exploited to discriminate among breeds. CDA was first applied at chromosome level and markers with canonical coefficients higher than a fixed threshold were retained. The threshold was obtained through a recursive procedure: the CDA was repeatedly applied by increasing, at each run, the value at which a canonical coefficient is discarded. The procedure stopped when the remaining markers were a pool of linearly independent variables. A genome-wide CDA was then developed with only the selected SNPs, and the effective distance among groups was tested by using the Mahalanobis' distance and the corresponding Hotelling's T-square test. The discriminant analysis (DA) technique was then used to assign the VP to the breed of origin. Finally, the minimum number of significantly discriminant markers was obtained. With a canonical coefficient threshold value of 0.31, 155 linearly independent highly discriminant SNPs were retained. These selected markers provided at Hotelling's T-square test significant separation among all breeds ($P < 0.0000$) and the DA correctly assigned 40 out of 42 VP animals. Among the 155 markers, 46 were monomorphic for at least one breed. The selected markers could be used to develop an assay to routinely track monobreed products. Finally the minimum number of markers able to significantly discriminate all breeds was 48. However, by using this small panel of SNPs, the DA was able to correctly assign only 30 out of 42 VP animals.

Key Words: assignment test, SNP selection

0961 (W065) Genomic differences between Rambouillet sheep selected for high and low reproductive rate.

J. M. Thomson* and J. G. Berardinelli, *Montana State University, Bozeman.*

The Rambouillet sheep selection program at Montana State University began in 1968 with the establishment of the high (HL) and low (LL) reproductive rate lines. Sheep within these lines were selected based on the index of "I" = total number of lambs born in a lifetime/(age of ewe– 1). The lines have significantly differentiated phenotypically for, number of lambs born, number of lambs born per ewe exposed and per ewe lambing, and total kg of lamb weaned ($P < 0.01$) Furthermore, systemic progesterone concentrations during the luteal phase of the estrous cycle differ for HL and LL ewes ($P < 0.05$). Previous research in these flocks has shown differences between the lines for lambing rate, litter size and ovulation rate. Objectives of the present study were to: 1) evaluate if there are genomic differences between lines, and, 2) identify quantitative trait loci associated with each line and candidate genes within these loci. A sample set of 50 and 46 HL and LL sheep, respectively, were genotyped using the Ovine 60K SNP chip. The data for the genotypes were analyzed using the Golden Helix commercial software package. Principal component analysis indicated distinct clusters for the two lines of sheep when the first two eigenvectors were plotted, demonstrating that these lines

are, in fact, genetically different. Using an additive correlation association model and a Bonferroni correction, there were 14 markers that differed ($P < 0.01$). These markers are on chromosomes 1, 3, 9, and 24. The candidate genes that appear to differ include CHP2, ACOT11, NOS1AP, and EGFR. Further analyses and additional samples from each line are needed to better map the differences between the lines. In conclusion it appears that long-term selection for reproductive, a trait known to have low heritability, can be successful in generating animals, at least in sheep that are phenotypically and genetically different.

Key Words: genetic selection, genomics, physiology, reproduction

BREEDING AND GENETICS: MOLECULAR BIOLOGY AND GENOMICS

0962 (W066) Associations of the NCAPG I442M and GDF8 Q204X loci on feed efficiency at the onset of puberty in a beef x dairy cattle resource population. C. Kühn*, P. Widmann, R. Weikard, and E. Albrecht, *Leibniz Institute for Farm Animal Biology, Dummerstorf, Germany.*

Recent studies highlighted the NCAPG/LCORL region, as well as the GDF8 gene encoding myostatin, being associated with genetic modulation of growth in several mammalian species. Specifically, the NCAPG I442M locus had been associated with pre- and postnatal growth in cattle. Furthermore, it had been demonstrated that the highest effect of this genetic variant is expressed at the onset of puberty, which is suggested as the inflection point of the growth curve. Feed costs account for a large proportion of total costs for production in livestock. Thus, including information about feed efficiency in selection decisions would improve the profitability of livestock production. The aim of our study was to evaluate, if the NCAPG I442M or GDF8 Q204X loci had an effect on feed intake and/or feed efficiency at the onset of puberty in cattle. Our study included 176 F_2 bulls from a Charolais x German Holstein resource population generated by multiple ovulation and embryo transfer to virgin heifers that were kept under standardized environmental conditions. After an initial period of 4 mo on a milk replacer diet, the animals were fed ad libitum with concentrate (11.3 MJ ME/kg dry matter, comprising a mixture of barley, molasses chips, soybean extraction meal, molasses, minerals and a vitamin premix) and hay (9.0 MJ ME/kg dry matter). Feed intake was measured daily and body weight was recorded in monthly intervals. For this study, daily dry matter intake, feed conversion ratio and residual feed intake were investigated between d 183 and d 283 of age. Residual feed intake was calculated from daily dry matter intake, metabolic mid weight, and average daily gain. The alleles at the loci NCAPG I442M and GDF8 Q204X were tested for association with daily dry matter intake, feed conversion ratio and residual feed intake. The model fitted year of birth and season as fixed effects, the additive effect of the NCAPG 442M or GDF8 204X allele, and an infinitesimal polygenic animal effect. The analysis revealed that the NCAPG I442M locus was significantly associated with daily feed intake ($P = 0.03$), feed conversion ratio ($P = 0.00012$) and residual feed intake ($P = 0.00001$). In contrast, the GDF8Q204X locus showed only significant effects on feed conversion ratio ($P = 0.04$) and residual feed intake ($P = 0.0005$). Our data indicated that NCAPG I442M is associated with genetic modulation of growth as well as feed efficiency in cattle

Key Words: feed efficiency, cattle, NCAPG

0963 (W067) Association of DNA methylation levels with tissue-specific expression of adipogenic and lipogenic genes in Longissimus dorsi muscle of Korean cattle. M. Baik*[1], T. T. T. Vu[2], M. Y. Piao[1], and H. J. Kang[1], *[1]Dep. of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, South Korea, [2]Chonnam National University, Gwangju, South Korea.*

The epigenetic factor such as DNA methylation status may regulate adipogenesis and lipogenesis, affecting intramuscular fat (IMF) deposition of *longissimus dorsi* muscle (LM) in beef cattle. In steers, the LM consists mainly of muscle tissue. However, the LM in Korean cattle steers also contains IMF. We compared the gene expression levels between the IMF and muscle portions of the LM steers after separation of the tissues. Real-time PCR analysis showed that mRNA levels of both adipogenic peroxisome proliferator-activated receptor γ isoform 1 (*P*PARγ1) and lipogenic fatty acid binding protein 4 (FABP4) were higher ($P < 0.01$) in the IMF portion than in the muscle portion of the LM. DNA methylation at specific sites within regulatory regions of gene is known to regulate transcription. We determined DNA methylation levels of regulatory regions of the PPAR γ1 and FABP4 genes by pyrosequencing of genomic DNA isolated from the IMF and muscle portions of the LM. DNA methylation levels of two CpG sites out of three from regulatory region (+144 ~ +225) of PPARγ1 gene were lower ($P < 0.05$) in the IMF portion than in muscle portion of the LM. DNA methylation levels of all five CpG sites from regulatory regions (−9664 ~ −9469) of FABP4 gene were also lower ($P < 0.001$) in IMF portion than in the muscle portion. Thus, mRNA levels of both PPARγ1 and FABP4 genes were inversely correlated with DNA methylation levels of regulatory regions of CpG sites of the corresponding gene. In conclusion, our findings suggest that DNA methylation status regulates tissue-specific expression of adipogenic and lipogenic gene expression in IMF and muscle portions of LM tissues of Korean cattle steers.

Key Words: intramuscular fat, adipogenesis, DNA methylation

0964 (W068) Changes in the cattle cervical transcriptome between estrus and luteal phase. D. Gonzalez-Peña Fundora*, P. Cardoso, M. B. Wheeler, and S. L. Rodriguez Zas, *University of Illinois at Urbana-Champaign.*

During the periestrous phase, the cow cervix undergoes changes associated with hormonal phases that affect the secretions. The cervical mucus fluctuates from fluid and abundant, allowing the sperm transport at estrus, to dense and thick, creating a barrier that minimize pathogen colonization and infection during pregnancy or luteal phase. The corresponding changes in the transcriptome have not be fully characterized.

The objective of this study was to identify the genes that are differentially expressed between the estrus (n = 4) and luteal (7 d postestrus, n = 5) phases in the cervical tissue of synchronized beef heifers. An RNA-Seq platform (Illumina Genome Analyzer II) was used to identify and quantify the transcripts. Single-end reads were mapped to the *Bos taurus* reference genome (Baylor Btau_4.6.1/bos Tau7). In total, 14,419 transcripts from 13,822 genes were tested and 1163 transcripts from 1150 genes were differentially expressed between the luteal and estrus phases (False Discovery Rate adjusted, $P <$ 0.05). Among these, angiotensinogen (AGT) and potassium voltage-gated channel, subfamily F, member 1 (KCNF1) were overexpressed, while cartilage oligomeric matrix protein (COMP) and chloride channel accessory 1 (CLCA1) were under-expressed in the luteal relative to the estrus phase. These results are consistent with known gene functions. AGT produces the enzyme angiotensin II that has been associated with the corpus luteum. KCNF1 regulates the epithelial electrolyte transport and COMP plays a role in cell proliferation, apoptosis, and regulation of cell movement and attachment. Also, the activity of CLCA1 decreases during the luteal phase when mucus thickens. Functional analysis of the differentially expressed genes using DAVID identified six category clusters (enrichment score > 3 equivalent to average category $P <$ 0.001). These categories included cartilage development and condensation, inflammatory responses, defense responses, and sterol-cholesterol biosynthetic. These functional categories suggest that changes during the estrus cycle are associated with changes in molecular pathways that in turn may affect the morphology, function and penetrability of the cervix.

Key Words: RNA-seq, cervix, cow

0965 (W069) Physical and chemical and fatty acid profile in the steers beef with different genetic predominance fed with diets containing substitutions levels of corn by pearl millet.

R. M. D. Silva[*1,2,3], J. T. Pádua[2], J. J. R. Fernandes[2], R. Z. Taveira[1], R. L. Missio[4], P. S. Pacheco[5], D. A. Fausto[6], and J. Restle[2], *[1]Universidade Estadual de Goiás, São Luis de Montes Belos, Brazil, [2]Universidade Federal de Goiás, Goiânia, Brazil, [3]FAPEG, Goiânia, Goiás, Brazil, [4]Universidade Tecnológica Federal do Paraná, Pato Branco, Brazil, [5]Universidade Federal de Santa Maria, Rio Grande do Sul, Brazil, [6]ESALQ/USP, Piracicaba, São Paulo, Brazil.*

This study aimed to evaluate the steers crossbred meat fatty acid profile with European (E) or Zebu (Z) genotypic predominance fed with high concentrated diets (80%) containing levels of ground millet grain in replacement of ground corn grain (0, 33, 66, and 100%). Twenty-four steers of each genetic predominance were feedlot during 96 d and slaughtered at 24 mo of age. The experimental design was completely randomized design with treatments in a 4x2 factorial arrangement using six replicates. The initial pH (6.68) and final carcass pH values (5.9), the final carcass temperature (9.72°C), the fluid loss during thawing (9.7%) and cooking (26.6%), color (3.7 points), texture (3.1 points), marbling (4.5 points), the shear strength of the muscle fibers (8.1 kgf) and moisture (72.9%), crude protein (23.0%), and ether extract content (1.5%) of the meat were not affected by the substitution of corn grain by millet grain ($P >$ 0.05). Meat characteristics were not influenced by genetic predominance, except the marbling, which was higher (4.99 vs. 3.95 points) in European animals. The final pH was correlated with thawing liquid loss (r = -0.36) and meat color (r = -0.62). The replacement of corn grain by millet grain in diet did not affect the steers meat quality ($P >$ 0.05). Increasing the proportion of millet in the diet it linearly increased the arachidic (C20:0), heneicosanoic (C21:0), α linolenic (C18:3 n-3), and di-homo γ linolenic (C20:3 n-6) fatty acids. European bulls meat showed less content of myristic (C14:0), heneicosanoic (C21:0), and γ linolenic (C18:3 n-6) fatty acids. The total concentration of saturated (45.2%), monounsaturated (41.2%), and polyunsaturated (8.7%) fatty acids and monounsaturated/saturated (1.09) and polyunsaturated/saturated (0.18) relationship were not affected by the factors studied. Zebu cattle fed high concentrate produce meat with higher levels of hypercholesterolemic fatty acids that European cattle. The millet grain precentage increase in the diet of European and Zebu crossbred steers improves the ratio between *n-6*/*n-3* fatty acids (0% = 13.90, 33% = 13.79, 66% = 11.67, 100% = 10.58) (P = 0.042). These results indicate that the millet grain used in a complementary way for other strategies, such as providing protected polyunsaturated fatty acids (PUFA) ruminal fermentation, may allow getting a closer relationships ω6/ω3 to the recommended.

Key Words: intramuscular fat, meat tenderness, nutition

0966 (W070) Major loci associated with growth traits on BTA14 in Hanwoo (Korean cattle).

S. W. Lee[*1], K. Y. Chung[1], U. H. Kim[1], B. W. Choi[2], D. Lim[2], Y. M. Cho[2], C. G. Dang[1], H. C. Kim[1], S. H. Yeon[1], H. S. Kang[1], and C. Gondro[3], *[1]Hanwoo Experiment Station, NIAS, RDA, Pyeongchang, South Korea, [2]Animal Genomics & Bioinformatics Division, NIAS, RDA, Suwon, South Korea, [3]University of New England, Armidale, Australia.*

Genome-wide single marker regression using Bovine 50K BeadChip was performed on growth traits from 1012 Hanwoo steers in Hanwoo (Korean cattle). SNPs were excluded from the analysis if they failed in over 5% of the genotypes, had median GC scores below 0.6, had GC scores under 0.6 in less than 90% of the samples, deviated in heterozygosity more than three standard deviations from the other SNPs and were out of Hardy-Weinberg equilibrium for a cutoff p-value of $1E^{-5}$. Unmapped and SNPs on sex chromosomes were also

excluded. A total of 32,696 SNPs were used in this analysis. To test an association between SNP and QTL, single marker regression analysis was implemented in this study. SNP was assumed to be in LD with QTL in close proximity and the effect evaluated was additive effect (QTL allele substitution effect). The Bonferroni-corrected genome wide significant association ($P < 1.5 \times 10^{-6}$) was applied to detect significant SNPs for the GWAS. The GWAS identified one major QTL for body weight at 6, 12, 18, and 23 mo ranging 23Mb to 25Mb on BTA14. The most significant SNP was Hapmap32241-BTC-054753 (24Mb, $P = 1.8 \times 10^{-6}$) for BW6, Hapmap27934-BTC-065223 (25Mb, $P = 1.2 \times 10^{-10}$) for BW12, BW18 and BW23 in Hanwoo. The most significant SNPs accounted for 8 to 10% of additive genetic variance, which is quite large proportion against total additive genetic variance. The Hapmap27934-BTC-065223 has 12.97 kg of allele substitution effect in body weight at 12 mo (BW12). The results revealed that growth traits was affected by major QTL with large effect and many other SNP with small effects with the normal distribution.

Key Words: GWAS, major loci, BTA14

0967 (W071) SNP located on three candidate genes influencing growth, performance and carcass traits in a population of steers sired by Braunvieh, Charolais and Simmental bulls. M. D. Garcia*, S. Mizell, and T. Page, *Louisiana State University, Baton Rouge,.*

The objective of the current study was to evaluate the association of single nucleotide polymorphisms (SNP) on three candidate genes for growth, performance, carcass traits in 39 steers sired by Braunvieh, Charolais, and Simmental bulls. Single nucleotide polymorphisms from three candidate genes including the Thyroglobulin gene (TG), the Adiponectin (ADPOQ) gene, and the Insulin-like growth factor 1 (IGF-1) gene were utilized for association analyses. Single nucleotide polymorphisms were selected utilizing SNP that were evenly distributed and represented the total length of the candidate gene. Of the 67 SNP genotyped, 20 were chosen for TG, 20 for ADPOQ, and 27 for IGF-1. Linkage disequilibrium (LD) was not evaluated in the current study due to the small population size; however, LD will be calculated as the genotyped population becomes larger in future studies. The growth traits that were evaluated included, birth weight (BW), hip height (HH), and weaning weight (WW). Carcass quality and composition traits included marbling score (MS), back fat thickness (BF), ribeye area (REA), hot carcass weight (HCW), and yield grade (YG). The PROC MIXED of SAS was utilized to evaluate associations of the 67 SNPs and measured traits. Sire breed and SNP genotype were fit in the model as fixed effects with performance and carcass traits fit as random effects. Associations between traits and SNPs were reported as significant if $P < 0.05$. Multiple SNP from all three candidate genes were identified as being significantly associated ($P < 0.05$) all traits evaluated in the current study. Association analyses for growth traits revealed seven SNP significantly associated with BW (rs109830314, rs383724494 rs378724414, rs381911082, rs383535987, rs384076273, rs109327701), five with HH (rs110553649, rs132813094, rs210258853, rs109327701, rs137651874), 10 with WW (rs109182502, rs110616947, rs377997897, rs379996188, rs380627374, rs378724414, rs109327701, rs136982429, rs137140434, rs137726884), 10 with BF (rs110501231, rs110616947, rs378567477, rs382644882, rs210258853, rs137140434, rs137374423, rs137601357, rs137662301, rs137726884). Association analyses for carcass quality and composition traits revealed two SNP significantly associated with HCW (rs110501231, rs378567477) four with MS (rs378567477, rs378900777, rs383535987, rs137104571), two with REA (rs109830314, rs137651874), and five with YG (rs379467464, rs382252585, rs386026054, rs378724414, rs137601357). Furthermore, a total of eight SNPs (rs109830314, rs110501231, rs110616947, rs378567477, rs378724414, rs137140434, rs137651874, and rs137726884) representing all three candidate genes were significantly associated with growth, performance and carcass quality and composition traits.

Key Words: SNP, candidate genes, beef, growth and performance, carcass traits, snp, growth, carcass, candidate genes

---

0968 (W072) Single nucleotide polymorphisms in the XKR4 and DRD2 genes influence adjusted birth and 205-d weights of calves grazing endophyte-infected tall fescue. *K. M. Ely*[*1], C. J. Kojima[1], A. M. Saxton[1], and R. L. Kallenbach[2], [1]University of Tennessee, Knoxville, [2]University of Missouri, Columbia.*

Tall fescue (*L. arundinaceum Schreb*.) is the most prevalent forage in the Southeastern United States due to the presence of the endophytic fungus *N. coenophialum*. The fungus enhances the persistence of tall fescue, but decreases the productivity of cow-calf herds grazing it. Single nucleotide polymorphisms in the XK, Kell blood group complex subunit-related family, member 4 (XKR4) and Dopamine Receptor D2 (DRD2) genes both yield the genotypes AA, AG, and GG. The A allele of both XKR4 and DRD2 has shown to increase serum prolactin concentrations in Tennessee beef cattle herds grazing endophyte-infected tall fescue. We evaluated the relationship between genotypes of dam and calf and adjusted 205-d weight (A205) and adjusted birth weight (ABW) in a well-managed fall-calving beef herd in Missouri. The ANOVA model included XKR4 and DRD2 genotype (SAS 9.3, Cary, NC). Genotype and allele frequencies for XKR4 were AA = 0.67, AG = 0.30, GG = 0.04, A = 0.82 and G = 0.18 for the dam; AA = 0.64, AG = 0.34, GG = 0.03, A = 0.81 and G = 0.19 for the calf. Since the G allele was sparsely represented in the

population only AG and AA animals were used for the XKR4 analysis. Genotype and allele frequencies for DRD2 were AA = 0.23, AG = 0.46, GG = 0.31, A = 0.46 and G = 0.54 for the dam; AA = 0.25, AG = 0.50, GG = 0.25, A = 0.50 and G = 0.50 for the calf. Dam genotype for DRD2 influenced ABW such that calves from AA and GG animals had lower ABW than those from AG animals ($P < 0.0001$). This is similar to previous findings in a larger herd of animals from Missouri. The AA genotype for the dam at XKR4 was associated with higher ABW when compared to AG dams ($P = 0.08$). Calf genotype for XKR4 influenced A205, such that AA animals were heavier than AG ($P = 0.05$). The AA genotype for the calf at XKR4 was associated with higher ABW when compared to AG calves ($P = 0.07$). No association was observed between calf genotype for DRD2 on ABW or A205. Similarly, no association was observed between dam genotype for XKR4 and A205. Fall-calving dams are grazing fescue at its peak infection level while in mid-gestation; having a beneficial allele for ABW is important for healthy calf weights. As fall-born calves are grazing endophyte-infected tall fescue before weaning, calf genotype at these loci may influence A205. Taken together with previous work, these results indicate a potential for their use as genetic markers for increased productivity of beef cattle grazing endophyte-infected tall fescue.

Key Words: XKR4, DRD2, fescue toxicosis

BREEDING AND GENETICS: COMPANION ANIMAL NUTRITION

0969 (T055) Influence of velocity on Weimaraner trotting stride mechanics. L. Carlisle[1], M. C. Nicodemus[*1], and K. Slater[2], *[1]Mississippi State University, Starkville, [2]Banfield Pet Hospital, Houston, TX.*

The large size of the Weimaraner assists in the breed performing the tasks of a sporting dog. However, the size may also make the breed more susceptible to hip dysplasia. Nevertheless, the Weimaraner compared to other large dog breeds demonstrates a lower rate of dysplasia, which may be due to the preferred slower speed of this breed and resulting stride mechanics. Although kinematic research has been done on other large breeds, gait analysis of the Weimaraner is lacking, and thus, the objective of this study was to determine the influence of velocity on the trotting stride mechanics of the Weimaraner. Six American Kennel Club (AKC) registered Weimaraner dogs were led by the same handler at a slow (st velocity: 1.2–1.7 m/s) and fast (ft velocity: 1.9–2.3 m/s) trot on even, natural footing. Strides (n = 10) were selected for each dog for each trot based on soundness and correctness of gait, consistency of speed, and noticeable foot placement and lift-off. Stride variables were determined by frame-by-frame analysis with video frames of foot placement and lift-off documented. Stride variables were given as a % of stride. Means (SD) were determined for stride variables and t tests ($P < 0.05$) were performed between velocities. Both trots were produced with a diagonal footfall sequence and a similar stride duration (st-0.53 ± 0.10 msec, ft-0.47 ± 0.07 msec) and frequency (st-1.94 ± 0.13 str/sec, ft-2.12 ± 0.09 str/sec), alternating between periods of diagonal bipedal support (st-88 ± 2%, ft-75 ± 5%) and suspension (st-12 ± 1%, ft-25 ± 3%) with less than half of the stride cycle of each limb spent in stance (Fore: st-44 ± 4%, ft-38 ± 2%; Hind: st-44 ± 5%, ft-38 ± 4%). Although stride length significantly increased with speed (st-0.90 ± 0.02 m, ft-0.99 ± 0.04 m; $P < 0.05$), the diagonal limbs remained paired on contact (diagonal advanced placement: st-0 ± 0%, ft-0 ± 0%). The use of suspension at all velocities and the dependence of stride lengthening to increase velocity are distinguishable characteristics of the Weimaraner from other large breeds studied including the Labrador Retriever and German Shepherd. Understanding of canine locomotion through the analysis of the stride mechanics as was done in this study will assist in the clinical examination of gait and the assessment of veterinary locomotive rehabilitation.

Key Words: kinematics, trot, Weimaraner

0970 (T056) Effects of dietary resistant starch on the fasted plasma metabolome of healthy adult dogs. A. N. Beloshapka[*1], K. L. Pappan[2], and K. S. Swanson[1], *[1]Dep. of Animal Sciences, University of Illinois, Urbana, [2]Metabolon, Inc., Durham, NC.*

Fermentable carbohydrates alter gut microbial activity and metabolite production, with many entering the bloodstream and consequently impacting host physiology. The effects of feeding fermentable carbohydrates, such as resistant starch (RS), on the canine plasma metabolome have not been well-studied. The objective of this study was to use a high-throughput metabolomics platform to identify differences in the fasted plasma metabolome of dogs fed increasing RS concentrations. Seven dogs (mean age = 5.3 yr; mean BW = 20 kg) were randomly allotted to one of three treatments (0%, 2%, or 4% high-amylose maize cornstarch (HI-MAIZE260) in an incomplete Latin square design. Treatments were formulated to be iso-energetic and consisted of graded amounts of 100% amylopectin cornstarch, RS, and cellulose, and fed as a top dressing on the food each day. All dogs were fed the same amount of a basal diet throughout the study and fresh water was offered ad libitum. Blood samples were collected after an overnight fast via jugular venipuncture on the last day of each treatment period (d 21) and were subjected to liquid/gas chromatography and mass spectrometry. A total of 288 named biochemicals were identified in plasma, but few statistical differences were noted among treatments. Compared to the controls, RS consumption appeared to alter amino acid metabolism, marked by increased ($P < 0.10$) plasma N-acetylglutamine, 3-hydroxy-3-phenylpropionate, and α-hydroxyisovalerate concentrations and decreased ($P < 0.05$) plasma kynurenine and kynurenate concentrations. Compared to controls, RS consumption also appeared to alter fatty acid and bile acid metabolism, marked by increased ($P < 0.05$) plasma 2-hydroxyglutarate concentrations and decreased ($P < 0.05$) plasma stearamide, cholate, and 1-pentadecanoylglycerophosphacholine concentrations. While RS supplementation produced some changes on the canine plasma metabolome, large, consistent changes were not observed.

Key Words: canine, plasma metabolome, resistant starch

0971 (T057) In vitro effect of diets added with fructooligosaccharides and differing in their protein content and digestibility on dog fecal microbiota. G. Biagi*, M. Grandi, and C. Pinna, *Dep. of Veterinary Medical Sciences, University of Bologna, Ozzano Emilia, Italy.*

Feeding dogs with diets containing high amounts of low-digestible protein may negatively affect the animal intestinal ecosystem, increasing the presence of undesired proteolytic

bacteria. On the other hand, the administration of prebiotics can enhance the activity of beneficial bacteria residing in the canine intestine. The objective of the present study was to evaluate in vitro the effect of diets differing in their protein content and digestibility, and containing or not fructo-oligosaccharides (FOS), on canine fecal microbiota. There were six treatments: 1) Low-protein diet (LPHD, 23% CP); 2) High-protein diet (HPHD, 30% CP); 3) High-protein low-digestible diet (HPLD, 30% CP); 4) Diet 1 + 1.5% FOS (LPHD+FOS); 5) Diet 2 + 1.5% FOS (HPHD+FOS); 6) Diet 3 + 1.5% FOS (HPLD+-FOS). After enzymatically digestion, the undigested fraction of the diets was added to a canine fecal suspension and incubated for 24 h in an anaerobic cabinet (five bottles per diet). From each bottle, a sample of fermentation fluid was collected at 6 and 24 h of fermentation for microbial counts (by FISH) and chemical analyses. Data were analyzed by three-way ANOVA, with protein level and digestibility and FOS as the main effects. At 24 h, FOS resulted in lower ammonia (36.4 vs. 40.3 mmol/l; $P < 0.001$) and iso-valeric acid (0.52 vs. 1.44% of total volatile fatty acids (VFA); $P < 0.05$) and higher total VFA concentrations (47.1 vs. 32.9 mmol/l; $P < 0.001$). Conversely, LD diets resulted in lower VFA (33.9 vs. 43.1 mmol/l; $P < 0.001$). The presence of FOS induced a shift in VFA production, reducing acetic acid (57.1 vs. 73.8%; $P < 0.001$) and increasing propionic and *n*-butyric acids proportions (20.9 vs. 16.4% and 21.0 vs. 7.5%, respectively; $P < 0.001$). With regard to biogenic amines, putrescine concentrations were increased at 6 and 24 h of fermentation by LD diets (+21 and 22%, respectively; $P < 0.05$) and FOS (+18 and 24%, respectively; $P < 0.01$). After 24 h of fermentation, HP diets resulted in lower counts of lactobacilli and enterococci (-0.5 and -0.7 log cells/ml, respectively; $P < 0.05$), whereas LD diets tended to increase counts of *C. perfringens* (+ 0.2 log cells/ml; $P = 0.07$). Results from the present study showed that diets rich in low-digestible protein may exert a negative influence on the canine intestinal ecosystem, increasing the presence of proteolytic compounds and reducing counts of beneficial bacteria. Conversely, administration of FOS may improve canine intestinal health, reducing proteolysis and enhancing VFA production.

Key Words: dogs, fructo-oligoccharides, dietary protein

0972 (T058) The modified Atwater equation does not accurately predict diet ME value of premium food in adult cats. K. D. Berendt*[1], A. K. Shoveller[2], M. Guevara[2], and R. T. Zijlstra[1], [1]*University of Alberta, Edmonton, Canada,* [2]*Procter & Gamble Pet Care, Mason, OH.*

The diet ME value of pet foods is commonly predicted using the Atwater equation, because routine ME measurements are not practical or not feasible ethically or financially. As such, AAFCO recommends the use of the modified Atwater equation [ME = 3.5 × CP (%) + 3.5 × N-free extract (NFE, %) + 8.5 × crude fat (%)] to predict metabolizable energy (ME) of dog and cat foods, which is then used to calculate daily feeding allotment. Previously, the modified Atwater equation underestimated the measured ME value of dog diets; hence, we decided to study this equation in cats. Twelve domestic shorthair cats were used in a quadruple 3 × 3 Latin square. Initial BW averaged 4.4 ± 0.8 kg and ranged from 3.0 to 5.7 kg. Three premium cat diets varying in predicted glycemic index (GI) based on ingredient composition and starch content (36.8, 30.7, and 23.6% for high, medium, and low GI, respectively) were fed for 10 d, with feces and urine collected quantitatively for the last 5 d. Diet, feces and urine were analyzed for GE to measure diet ME value. Predicted GI and ME value of the three diets were inversely related. The greater ME value of the low GI diet ($P < 0.001$) was associated with its greater fat content (22.9, 22.2, and 15.7% ether extract for low, medium and high GI diet, respectively) and energy digestibility (95, 95.4, and 92.9% for low, medium and high GI, respectively). The modified Atwater equation underestimated measured diet ME values by 12% (11.9, 10.8, and 13.6% for high, medium, and low GI, respectively). The traditional Atwater equation [ME = 4 × CP (%) + 4 × N-free extract (NFE, %) + 9 × crude fat (%)] did predict diet ME values accurately (underestimation of 2.0, 1.5, and 4.6% for high, medium, and low GI, respectively). In conclusion, the modified Atwater equation did not accurately predict diet ME value of diets fed to adult cats. The traditional Atwater equation should be used for premium cat diets.

Key Words: metabolizable energy, Atwater, cat

0973 (T059) Association of idiopathic epilepsy with a novel locus in the Belgian Shepherd. A. M. Oberbauer*, and J. M. Belanger, *University of California–Davis, Davis.*

Idiopathic epilepsy in the Belgian shepherd dog is complexly inherited. The objective was to identify novel genomic loci associated with the expression of generalized seizures in the Belgian Tervuren and Sheepdog. Dogs were classified as cases if they met specific seizure criteria and controls if they were over 7 yr of age and had no other health disorder. DNA from cases ($n = 35$) and controls ($n = 58$) from dogs predominantly unrelated at the grandparent level, were subjected to a high-density genotyping array consisting of more than 170,000 evenly spaced single nucleotide polymorphisms (SNPs). Association analyses were conducted using the software package PLINK. Based on 100,000 permutations and removal of non-informative markers and markers with low call rate, five chromosomal regions reached genome wide significance: chromosomes 5 ($P < .034$), 7 ($P < .015$), 24 ($P < .0003$), 29 ($P < .020$) and 37 ($P < .05$). Chromosome 7 showed four significant SNPs between 46,094,658 and 49,666,725 bp (CanFam 3.1). A Sequenom iPlex analysis was conducted using 34 dogs representing 17 cases and 17 controls. Sequenom Assay Design Suite was used to multiplex 65 SNPS covering the region between 45.03 and 48.06 MB. Three SNPs demon-

strated genome wide significance in three genes: two were intronic SNPs ($P = 0.00001$ and $P = 0.04548$) and the third was a missense SNP ($P = 0.0061$) in a novel gene. The mutation in the novel gene changes the codon from proline to arginine. For the novel gene, a 344-bp region was targeted for resequencing uncovering a second missense SNP within the novel gene. The genome wide analysisconfirmed the previously characterized locus found on chromosome 37 and revealed a second locus segregating for epilepsy on chromosome 7. The missense mutation in a novel gene validates the model of a multifactorial genetic regulation of idiopathic epilepsy for the Belgian shepherd, while also suggesting the existence of a previously unidentified neurological regulatory gene. Taken together, the data support the application of genetic selection to reduce the prevalence of this debilitating disorder.

Key Words: idiopathic epilepsy, canine, genome wide association

---

0974 (T060) Amino acid and mineral concentrations of whole grains and grain byproducts used in pet foods. A. N. Beloshapka[*1], P. R. Buff[2], and K. S. Swanson[1], *[1]Dep. of Animal Sciences, University of Illinois, Urbana, [2]Nutro Company, Franklin, TN.*

Whole grains may be valuable components of canine diets, due to the functional ingredients, such as dietary fiber and β-glucans, or the amino acids (AA) and minerals they provide; however, the use of whole grains in pet food has not been thoroughly evaluated. Our objective was to measure the AA and mineral concentrations of various whole grains, processed grains, and grain byproducts that may be incorporated into dog food. Thirty-one grain samples, including: rice samples (brown rice, rice, rice bran, and rice flour); barley samples (barley flake, cut barley, ground pearled barley, malted barley, whole pearled barley, pearled barley flakes, and steamed rolled barley); oat samples (groats, ground oatmeal, ground steamed groats, instant oats, oat bran #1, oat bran #2, oat fiber, oat flour, quick oats, regular rolled oats, steamed rolled oat groats, and steel cut groats); and miscellaneous cereals and pseudocereals (conventional hulled millet, conventional whole millet, conventional quinoa, organic spelt hull pellets, potato flake, sorghum, whole wheat, and whole yellow corn) were analyzed. Total essential (0.65 to 7.51% DMB) and individual AA concentrations were highly variable among ingredients tested: Arginine (0.01 to 1.38% DMB), Histidine (0.02 to 0.47% DMB), Isoleucine (0.07 to 0.62% DMB), Leucine (0.15 to 1.49% DMB), Lysine (0.06–to0.88% DMB), Methionine (0.03 to 0.36% DMB), Phenylalanine (0.08 to 0.77% DMB), Threonine (0.05 to 0.66% DMB), Tryptophan (< 0.04 to 0.20% DMB), and Valine (0.09 to 0.96% DMB). Of the ingredients tested, oat fiber had the lowest concentrations of most essential AA and rice bran had the highest concentrations of most essential AA. Calcium, phosphorus, and magnesium concentrations ranged from 0.0 to 2.22% DMB, 0.04 to 2.03% DMB, and 0.03 to 0.88% DMB, respectively, with rice bran having the highest concentrations of all three minerals. Based on our compositional analysis, whole grains and grain byproducts vary greatly in AA and mineral content. Although these ingredients are commonly used in canine diets, more research is needed to test the effects of feeding whole grains to dogs.

Key Words: whole grains, amino acids, minerals

0975 (T061) Metabolic phenotyping using mass spectrometry-based metabolomics: A cross-sectional pilot study of lean and overweight domestic cats. R. E. Cokeley[1], G. R. Seiler[1], and J. W. McFadden[*1,2], *[1]West Virginia University, Morgantown, [2]Johns Hopkins University, Baltimore, MD.*

Overnutrition and sedentary behavior increases adiposity in domestic cats, a consequence of positive energy balance that can be detrimental to health. Adiposity is a risk factor for feline diabetes mellitus, characterized by insulin resistance. Chromatography and mass spectrometry (MS) technologies in the field termed "Metabolomics" may be a means to identify biomarkers for predicting pre-onset insulin resistance. The objective was to evaluate MS, coupled with gas chromatography (GC) or liquid chromatography (LC), techniques to perform metabolic phenotyping in lean and overweight domestic cats in preparation for a large-scale study aimed at identifying predictive biomarkers for feline insulin resistance. To evaluate methods, lean ($n = 6$; ≤ 4.5 kg) and overweight ($n = 6$; ≥ 6.5 kg), adult (2 to 10 y of age), neutered, client-owned male domestic shorthair cats were enrolled in a cross-sectional pilot study. Cats were not diagnosed with diabetes. Plasma samples were collected by a veterinarian following an overnight fast. For GC/MS, plasma metabolites were methanol extracted, derivatized, and analyzed by a GC tandem MS system. For LC/MS, plasma metabolites were chloroform-methanol extracted and analyzed by high pressure LC coupled to an electrospray ionization source of a triple quadrupole tandem MS system. Normalized data were analyzed using Student's *t* test. For metabolomics data, statistics were performed on the log of the normalized, median-scaled data. To validate analytical methods, total free fatty acids (FA) and glucose were determined by colorimetry. Mean weights and ages for lean and overweight cats were 3.9 ± 0.5 and 7.1 ± 1.0 kg ($P < 0.05$), and 4.2 ± 2.6 and 6.8 ± 2.4 y of age ($P > 0.10$), respectively. Untargeted GC/MS analysis detected 40 metabolites including lactate, urea, glycerol, amino acids, citrate, saccharides, saturated and unsaturated free FA, uric acid, vitamin E, and cholesterol. Overweight cats had a nearly two-fold increase in palmitic acid, stearic acid, and oleic acid ($P < 0.05$), results validated by an 83% increase in total free FA ($P < 0.05$). In overweight cats, glucose levels were increased by 38% (MS; $P < 0.05$) and a similar nonsignificant numerical increase when determined by colorimetry. Cholesterol, vitamin E, and glycerol were elevated in

overweight cats ($P < 0.05$). Targeted LC/MS analysis detected 28 sphingolipids including ceramides, monohexylceramides, and dihexylceramides. Of interest, palmitoyl-linked ceramide level was increased 80% in overweight cats ($P < 0.05$); elevated plasma ceramides are associated with insulin resistance progression in humans. In overweight cats, GC/MS and LC/MS methodologies revealed metabolite phenotypes similar to patterns observed in diabetic humans.

Key Words: feline diabetes mellitus, metabolomics, obesity

0976 (T062) Effects of dietary energy restriction on the hunting behavior and home-range size of free-ranging domestic cats. A. N. DeGrave*, S. K. Carignan, and S. E. Kitts-Morgan, *Berry College, Mount Berry, GA.*

Free-ranging cats pose concern for native small mammals and birds due to their reputation as instinctual predators. Hunting and prey consumption may be altered by food amounts received from humans. This study's objective was to determine the effects of dietary energy restriction on hunting behavior and home-range size of free-ranging cats. Eight free-ranging cats (five female, three male) residing at the Berry College Equine Center were blocked by weight and assigned randomly to receive daily ME requirements for adult cats at maintenance (control; $n = 4$) or 80% of daily ME requirements (restricted; $n = 4$). For 11 mo, cats were individually offered commercial cat food daily with additional colored glitter to identify each cat's feces. Cats were fitted with harnesses and GPS units to construct home ranges. Feline feces were dried at 60°C and analyzed for prey teeth, total hair, and cat vs. non-cat hair. No differences in BW ($P = 0.99$) or DMI ($P = 0.66$) occurred throughout the experiment. Home ranges were constructed using 95% kernel density estimation and analyzed by season. While no differences in home-range size occurred during spring or summer, fall home-range was larger ($P = 0.04$) for control cats (7.35 ha; 95% CI 4.72 to 11.43 ha) compared to restricted cats (3.91 ha; 95% CI 2.67 to 5.73 ha). Likewise, winter home-range was larger ($P = 0.04$) for control cats (6.91 ha; 95% CI 4.71 to 10.12 ha) compared to restricted cats (3.92 ha; 95% CI 2.68 to 5.75 ha). Of 306 fecal samples identified by cat, a similar ($P = 0.83$) percentage of feces from control vs. restricted cats contained hair (92.05% vs. 92.9%). There was a tendency ($P = 0.11$) for total hair weight in control-cat feces (0.55 ± 0.058 g) to be greater than total hair weight in restricted-cat feces (0.42 ± 0.057 g). However, restricted-cat feces had a lower percentage (18.1%; $P = 0.003$) of non-cat hair compared to the percentage (33.1%) of non-cat hair in control-cat feces. The percentage (21.85%) of control-cat feces containing prey bones/teeth was greater ($P < 0.0001$) compared to the percentage (6.45%) of restricted-cat feces containing prey bones/teeth. However, there was no difference ($P = 0.82$) in total bone/teeth weight for control-cat feces (0.061 ± 0.008 g) compared to restricted-cat feces (0.065 ± 0.015 g). These results suggest that cats will not expand home-range or increase prey consumption when energy-restricted. It may be possible that further restriction of energy intake might affect home-range size and hunting of free-ranging cats.

Key Words: cats, hunting, energy

0977 (T063) Differences in the cerebral cortex metabolome of young adult and geriatric dogs. M. R. C. de Godoy*[1], K. L. Pappan[2], and K. S. Swanson[3], *[1]Dep. of Animal Sciences, University of Illinois, Urbana, [2]Metabolon, Inc., Research Triangle Park, NC, [3]Dep. of Veterinary Clinical Medicine, Urbana, IL.*

Aging is responsible for chemical and morphological alterations in the brain (e.g., decreased brain mass, increased ventricular size, demyelination, neuroaxonal degeneration, decreased cholinergic activity, etc.) that lead to cognitive decline and neurodegenerative diseases. The longer lifespan of the canine pet population has increased the prevalence of cognitive dysfunction. A better understanding of the brain aging process would aid in preventing or reversing the progression of cognitive decline and improve the quality of life of geriatric dogs. Therefore, the objective of this experiment was to use untargeted GC-LC-MS to assess the impact of age on the metabolome of the cerebral cortex of dogs. Cerebral cortex samples were collected from 12 geriatric (12-yr-old) and 12 young adult (1-yr-old) beagles and stored at −80°C until GC–MS and LC-MS/MS analyses. A total of 239 named biochemicals were identified, with 101 being altered ($P < 0.05$) geriatric and young adult dogs. Prior transcriptomics analysis of these samples showed that 963 genes were altered due to age, with old dogs having increased expression of genes associated with inflammation, stress response, and calcium homeostasis and decreased expression of genes associated with neuropeptide signaling and synaptic transmission. In the current study, the cerebral cortex of geriatric dogs had a relative deficiency of excitatory amino acids, such as glutamate and γ-aminobutyrate (GABA), compared to young adult dogs. In addition, geriatric dogs had increased concentrations of palmitoylethanolamide (PEA), suggesting greater levels of oxidative stress or inflammation in the brain of these animals. Glutathione metabolism also differed ($P < 0.05$) between geriatric and young adult dogs, with the former having greater concentrations of reduced glutathione. A relative hyperglycemia in the cerebral cortex of geriatric dogs seemed to drive elevations in glycolytic pathway intermediates; lactate and sorbitol which, over long periods of time, could drive undesirable pathological events such as protein glycation and aggregation. Overall, the data suggest that the brains of geriatric dogs have reduced neurotransmitter metabolism and increased inflammation, possibly contributing to the altered neural functional capacity and health status of these animals.

Futures studies should investigate whether a metabolic signature of the aging brain may be detected in the plasma or serum of geriatric dogs. Identification of circulating metabolic biomarkers would allow for more frequent sampling using a non-invasive method and be useful in disease diagnosis and the development of nutritional interventions.

Key Words: age, dog, metabolome

0978 (T064) Use of gelatin as a strengthening agent in dry extruded pet food. A. Simmons*[1], C. G. Aldrich[1], T. Zhou[1], M. Remund[1], T. Putarov[2], S. Alavi[1], E. Maichel[1], and C. K. Jones[1], *[1]Kansas State University, Manhattan, [2]Sao Paulo State University, Sao Jose do Rio Preto, Brazil.*

Recent pet food innovations have increased protein and decreased cereal inclusions in diets, which has diminished product durability and negatively changed texture. Low-bloom gelatin is a pure protein that is used to improve some pelleted feeds. The objective of this project was to determine the effect of low bloom gelatin (Pro-Bind Plus 100) on kibble physical properties. Two experiments were conducted on a Wenger X-20 single screw extruder. In Exp. 1, a total of six total treatments were extruded: 0, 5, 10, or 15% gelatin inclusion at 400 RPM and 15% gelatin inclusion at 300 or 500 RPM. Chicken by-product meal was removed to add gelatin and maintain an iso-starch formulation. In Exp. 2, a total of six treatments were extruded: 0 vs. 10% gelatin inclusion; 300 vs. 500 RPM; and 15 vs. 30% hydration ratio, meaning the ratio of water added in the extruder vs. the preconditioner. Extrudates were analyzed for moisture, expansion ratio, specific length, piece density, hardness (TA-XT2, Stable Micro Systems), and pellet durability index (PDI; Holmen NHP 100, Tekpro). Results were analyzed using the GLIMMIX procedure of SAS. Product hardness showed a good positive correlation with PDI. Hardness and PDI improved with gelatin inclusion ($P < 0.05$; 5.15 vs. 9.35 kg; 64.5 vs. 96.9%). It was surmised that the increase in kibble strength and durability was caused partially by the strengthening effect of gelatin on the solid matrix. Lower product expansion also had an important role in increasing hardness and durability, as radial expansion ratio increased at 10% gelatin inclusion ($P < 0.05$; 4.27 vs. 6.65 mm^2/mm^2) but decreased at 5 and 15% gelatin inclusion ($P < 0.05$; 4.27 vs. 3.31 or 2.40 mm^2/mm^2, respectively). Increase in screw speed from 300 to 400 rpm and decrease in hydration ratio from 30 to 15% (impying greater degree of pre-conditoning) led to a slight increase in expansion ratio, suggesting that altering processing parameters may overcome the negative imapct of gelatin on radial expansion. Additionally, specific length (a measure of longitudinal expansion) increased at 15% gelatin inclusion ($P < 0.05$; 42.11 vs. 48.30 mm/g), and as less of the total water content was added in the extruder ($P < 0.05$; 37.62 mm/g vs. 41.16). These results suggest that gelatin had a binding effect on finished product. This binding may be helpful in high protein formulation, especially those reducing the use of functional cereal grain starches.

Key Words: gelatin, pet food, extrusion

CSAS GRADUATE STUDENT POSTER COMPETITION

0979 (M057) Effect of dietary supplementation with linseed oil on the miRnome profile of the bovine mammary gland. R. Li[*1,2], F. Beaudoin[1], X. Zhao[3], C. Lei[2], and E. M. Ibeagha-Awemu[1], *[1]Agriculture and Agri-Food Canada, Sherbrooke, QC, [2]Northwest A&F University, Xi'an, China, [3]McGill University, Ste Ann De Bell, PQ, Canada.*

Linseed is particularly rich in α-linolenic acid (C18:3n3) and its supplementation in diets induces an increase in milk unsaturated fatty acid content (along with decrease in milk saturated fatty acids) with potential milk fat depression. The specific role of microRNAs (miRNAs), important post-transcriptional regulators of gene expression, in this dietary adaption remains unknown. Using next generation sequencing, the miRnome of the bovine mammary gland in response to dietary supplementation with 5% linseed oil on dry matter bases was studied. Thirteen high-producing Holstein dairy cows in mid-lactation were fed a control ration (total mixed ration of corn and grass silages) for 28 d followed by a treatment period (control diet supplemented with 5% linseed oil) of 28 d. Milk component yields including fat (%) were measured on a weekly basis. Mammary biopsies on three cows were performed on d 14 (control period) and on d +7 and +28 (treatment period). Results show a significant decrease ($P < 0.0001$) in milk fat yield (%) during the treatment period (3.02 ± 0.17) as compared to the control period (3.62 ± 0.17). Nine libraries were constructed and subjected to 50bp smallRNA sequencing. A total of 103,796,305 raw reads were obtained and 93,218,009 retained after adaptor trimming and quality filtering. Of these, 69,210,197 (74.25%) were mapped to the bovine genome. A total of 338 known miRNAs (82.6% of mapped reads) were identified with more than one count per million in at least six libraries. Furthermore, 223 novel hairpins encoding for 212 novel miRNAs were identified. Five miRNAs (bta-miR-148a, miR-143, miR-26a, miR-30a-5p, and miR-10b) were most highly expressed, accounting for 54.93% of reads of identified known miRNAs. As compared to d 14 (control period), 10 miRNAs were significantly regulated (five up-regulated: bta-miR-4286, mir-199c, miR-199a-3p, miR-98, and miR-23b-3p; five downregulated: bta-miR-484, miR-96, miR-200a, miR-335, and miR-2299–5p) at d +28 ($P < 0.01$), while no significant regulation was detected at d +7 ($P > 0.01$). About 5541 genes were predicted to be targeted by differentially expressed miRNAs. Function enrichment analysis showed significant enrichment of target genes for functions related with lipid metabolism ($P < 0.01$). In conclusion, our study revealed that several miRNAs were differentially expressed during the milk fat depression introduced by linseed oil supplementation, suggesting that these miRNAs could be important regulators of mammary lipid synthesis. Furthermore, novel miRNAs identified in this study will greatly enrich the bovine miRnome repertoire and also act as targets for further study of bovine mammary gland biology.

Key Words: microRNA, linseed oil, bovine mammary gland

0980 (M058) Effect of co-expression of Lc and C1 flavanoid regulatory genes in alfalfa on nutritive value and ruminal methane production. R. G. Heendeniya Vidanaral[*1], M. Y. Gruber[2], Y. Wang[3], D. A. Christensen[1], J. J. McKinnon[1], B. Coulman[1], and P. Yu[1], *[1]University of Saskatchewan, Saskatoon, Canada, [2]Agriculture, and Agri-Food Canada, Saskatoon, SK, [3]Agriculture and Agri-Food Canada, Lethbridge, AB.*

An alfalfa progeny was developed by transforming Lc and C1 genes which are regulatory genes associated with flavonoid pathway in Zea maize. The transformation objective was to promote anthocyanidin accumulation in alfalfa leaves and stems, thus reducing the extent and rate of protein degradation in the rumen and potentially rumen methane production. The objective of this study was to evaluate the effect of co-expression of Lc and C1 genes on 1) protein, energy and feed milk values, and 2) methane gas production relative to single gene transformed alfalfa and non-transgenic parent plants. Alfalfa samples were collected at late-bud stage from populations of single gene transformed (C1, Lc1, and Lc3), double gene transformed (Lc1C1 and Lc3C1), parental non-transgenic (NT), and a commercial cultivar (AC-Grazeland: ACGL) maintained in growth chambers at the Saskatoon Research Centre, Agriculture and Agri-Food, Canada. Samples were chemically analyzed according to AOAC methods, and energy and protein values were determined using NRC (2001) and CNCPS (v.6.1) models. Fermentation gases were obtained from in vitro batch culture and analyzed by gas chromatography for methane. Rumen degradable protein was higher ($P < 0.01$) by 2% in double gene alfalfa comparing to single gene alfalfa, but no differences ($P > 0.05$) were observed in digestible rumen undegradable protein. In comparison to single gene alfalfa, co-expression of Lc and C1 genes increased ($P = 0.01$) net energy by 50 kcal for both lactation and growth and thereby increasing ($P < 0.01$) the feed to milk conversion efficiency by 80 g of milk per kg of alfalfa dry matter. The double gene alfalfa tended to have lower ($P = 0.07$) total gas production than NT alfalfa and significantly lower ($P < 0.05$) methane production by 3.5 L per kg DM than single gene alfalfa. In conclusion, C1 gene when co-expressed with Lc gene improved the feeding value of alfalfa and reduced in vitro methane production.

Key Words: Lc-C1 transgenic alfalfa, energy and protein, methane

0981 (M059) Predicting milk fat concentration from nutrient content and DCAD of the diet.

L. Fadul-Pacheco*, D. Pellerin, P. Y. Chouinard, and E. Charbonneau, *Université Laval, Québec, Canada*

The farm-gate price of milk in Canada is based on composition, which provides incentive for producers to increase fat content. The objective of this study is to determine the extent to which changes in nutrients and DCAD can predict milk fat percentage. Data recorded by Valacta (Dairy Production Center of Expertise Quebec-Atlantic) for the years 2009 to 2011 was used and originally comprised 3481,705 test-day records (275,758 cows and 3140 herds). Records used for the regression analysis were restricted to those from Holstein cows, between one and 305 DIM, taken during winter months, reducing the number of admissible records for the analysis to 306,191 (134,236 cows and 2658 herds). Lactations were divided into early (1 to 50 DIM), peak (51 to 100 DIM), and established lactation (101 to 305 DIM). Statistical analysis were performed using PROC HPMIXED of SAS with herd and cow (herd) as random effects. Independent variables were included in the final equation when $P \leq 0.05$. The variables used as covariates in the regression were: milk production (kg/day), DIM, and estimated breeding value for fat composition (EBV_FAT). Variables tested to explain milk fat concentration were: NDF from forage + 0.5 x NDF from concentrate (NDF_NRC), NFC, amount of buffers (BUFF; kg/day), amount of fat supplements with more than 80% of palmitic acid (PALM80; kg/day), and DCAD. In the final analysis for the 3 yr, multiple regression in early lactation (n = 24,987; R^2 = 0.44) included, in addition to the covariates, the following variables: NDF_NRC (quadratic) and PALM80. For peak lactation (n = 29,317; R^2 = 0.42) the variables were DCAD, NDF_NRC, BUFF and PALM80. For established lactation (n = 100,706; R^2 = 0.64) NDF_NRC, NFC (quadratic), BUFF and PALM80. All the equations accounted for a significant effect of year. When the regression was split by year, all the variables remained the same, while the DCAD (quadratic) was also added to the model for established lactation in all 3 yr, but with different optimal value (2009: > 330 mEq/kg MS; 2010: 210 mEq/kg MS; 2011: > 380 mEq/kg). In summary, the equations were able to predict up to 64% of milk fat variation based on the combination of different nutrients, especially NDF_NRC (quadratic) and PALM80. Based on the variations in optimal values between years, it could be concluded that the impact of the DCAD on milk fat concentration can be influenced by the nutritional quality of feed ingredients.

Key Words: lactating dairy cows, milk fat, DCAD.

0982 (M060) Evaluation of methane prediction equations for beef cattle fed high forage or high concentrate diets.

P. Escobar[*1,2], K. A. Beauchemin[3], and M. Oba[4], *[1]University of Alberta, Lethbridge, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, AB, [3]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, [4]University of Alberta, Edmonton, Canada.*

Enteric methane (CH_4) emission is the major contributor to greenhouse gases from beef cattle farms. Many equations are available to predict enteric CH_4 emissions from beef cattle, but the predictions vary substantially amongst equations. The aims of this study were to: 1) construct a database of enteric CH_4 emissions for beef cattle fed forage and grain-based diets from published literature, and 2) identify the most precise and accurate extant CH_4 prediction models for beef cattle fed diets varying in forage content. The database was comprised of treatment means of enteric CH_4 production from in vivo beef studies published from 2000 to 2013. Criteria for selecting data to include in the database were: animal description, intake, diet composition, and measurement of enteric CH_4 production. Missing values were estimated using feed composition tables, nutritional software or by calculation from the diet description. Fifty-one equations that predict CH_4 production from diet composition were evaluated. Precision and accuracy of the equations was evaluated using the concordance correlation coefficient (r_c), bias correction factor (C_b) and root mean square prediction error (RMSPE, g/d), and then ranked highest to lowest based on r_c. Statistical analysis was performed using JMP and SAS. The final database contained 39 studies and 163 treatment means that were divided into two subsets: a subset comprised of data from diets containing 40% or more forage and a subset comprised of data from diets containing less than 40% forage (dry matter basis). Using the complete database, equations with highest r_c were: G (Ellis et al., 2009), IPCC (2006) and J (Ellis et al., 2009), with r_c: 0.71, 0.67, 0.63, C_b: 0.98, 0.98, 0.98, and RMSPE: 55.0, 57.7, 61.4, respectively. For the high forage dataset, equations with highest r_c were IPCC (2006), G (Ellis et al., 2009), and Nonlinear 2 (Mills et al., 2003) with r_c: 0.75, 0.75, 0.71, C_b: 0.96, 0.99, 0.95, and RMSPE: 47.9, 51.7, 52.5, respectively. For the low forage dataset, equations with highest r_c were 9b (Ellis et al., 2007), G and P (Ellis et al., 2009), with r_c: 0.52, 0.48, 0.47, C_b: 0.67, 0.81, 0.81, and RMSPE: 56.0, 64.0, 62.0, respectively. Ranking of extant CH_4 prediction equations for their accuracy and precision differed with forage content of the diet. When used for cattle-fed low-forage diets, extant CH_4 prediction models were generally imprecise and lacked accuracy.

Key Words: beef cattle, enteric methane emission, models

0983 (M061) Non-protein nitrogen improves feed efficiency of growing pigs fed a diet deficient in non-essential amino acid nitrogen. W. D. Mansilla*[1], J. K. Htoo[2], and C. F. de Lange[1], [1]*University of Guelph, ON, Canada,* [2]*Evonik Industries AG, Hanau-Wolfgang, Germany.*

In pig diets the balance between essential amino acids (EAA) and total N should be considered, especially when large amounts of crystalline EAA are supplemented and N levels are reduced. When lowering dietary N, the dietary supply of non-essential amino acids (NEAA) is reduced and the need of N for endogenous synthesis of some NEAA may be increased, requiring N from either catabolism of excess EAA and NEAA or non-protein nitrogen (NPN). The objective of the present study was to determine the effect of supplementing NPN, in the form of ammonium salts, in diets deficient in NEAA-N on performance of growing pigs. In total, 48 gilts (initial BW of 15.2 ± 1.3 kg) were randomly assigned to 4 diets: 1) positive control (PC; 13.39% CP), not deficient in EAA and NEAA-N, and all N was supplied from intact protein (casein and soybean meal) or crystalline EAA; 2) negative control (NC; 10.19% CP), supplying the same amount of potentially limiting EAA as PC, but deficient in NEAA-N; 3) NC with 3 g/kg added ammonium (Low NPN); and 4) NC with 6 g/kg added ammonium (High NPN), the latter containing the same amount of digestible N as PC. Pigs were grouped in two pigs per pen with six pens per treatment. BW gain and feed intake were monitored weekly during 3 wk, and blood samples were taken on d 14 and 21 to determine plasma urea concentration. Wk 1 yielded poor growth performance and was considered a week of adaptation. During wk 2 and 3, BW gain was not affected by NPN ($P > 0.10$), while feed intake tended to decrease with increasing dietary NPN ($P = 0.06$). Gain:feed improved linearly with supplementation of NPN in diets ($P < 0.05$; 0.45, 0.47, and 0.51 for NC, Low and High NPN during wk 2 and 3). Gain:feed for High NPN was similar to that for PC ($P > 0.10$: 0.51 and 0.52 for High NPN and PC; wk 2 and 3). Plasma urea concentration was Low and not different between diets ($P > 0.10$). Dietary supplementation with NPN, in the form of ammonium salts, can improve pig performance when pigs are fed diets deficient in NEAA-N.

Key Words: growth, nitrogen, pigs.

984 (M062) Impact of the fatty acids in the diet on milk fat content: Analysis from a database of commercial farms. H. Mannai*, P. Y. Chouinard, L. Fadul-Pacheco, D. Pellerin, and E. Charbonneau, *Université Laval, Québec, Canada.*

Controlled trials have shown that milk fat content can be affected by dietary fatty acids. The purpose of this study was to evaluate the impact of dietary fatty acids on milk fat content in commercial dairy herds using multiple regression procedure. Data recorded by Valacta (Dairy Center of Expertise, Québec-Atlantic) from 2009 to 2011 were used for the analysis. The fatty acid content in feed ingredients (16:0, 16:1, 18:0, *cis* 18:1, *trans* 18:1, 18:2 and 18:3), not originally in the database, were obtained from CNCPS V6.1, INRA Tables of Feed Composition, and peer-reviewed articles. Test-day records from Holstein cows in early- (1 to 50 DIM) and peak- (51 to 100 DIM) lactation during winter months were used, giving 2491 records over the 3-yr period from 1585 cows and 143 herds. Statistical analyses were performed using the PROC MIXED of SAS with herd and cows (herd) as random effects. Independent variables were included in the final equation when $P \leq 0.10$. The variables used as covariates in the regression were DIM and estimated breeding value for fat composition (EBV_FAT). Variables tested to explain milk fat concentration were: forage NDF + 0.5 × concentrate NDF content (NDF_NRC), NFC content, buffer intake (BUFF), and intake of previously listed individual fatty acids. Multiple regressions for data from early lactation records ($n = 390$; $R^2 = 0.43$) included, in addition to the covariates, the variables 18:0 (quadratic), *cis* 18:1 (quadratic), 18:2, and BUFF. For peak-lactation records ($n = 422$; $R^2 = 0.49$) the variables included were 16:0 (quadratic), 16:1, 18:0 (quadratic), *trans*18:1 (quadratic), 18:2 (quadratic), NFC (quadratic), NDF_NRC (quadratic), and BUFF. The nonlinear relationships observed for several fatty acids retained in the model could be explained by the heterogeneity of fatty acid sources on commercial farms (forages, cereal grains, oil seeds, fat supplements in the form of triglycerides, free fatty acids or calcium salts, etc.), and their interaction with numerous feed ingredients. The current study gives insight into the relationships between individual dietary fatty acids and milk fat content in the context of commercial milk production.

Key Words: dietary fatty acids, milk fat, lactating dairy cows

0985 (M063) Pregnancy and lambing rates in anestrous ewes bred to a new synchronization protocol and laparoscopic timed artificial insemination (TAI). S. B. Turner*[1], M. B. Gordon[1], T. Gowan[2], J. A. Small[2], and D. M. W. Barrett[1], [1]*Faculty of Agriculture, Dalhousie University, Truro, NS, Canada,* [2]*Agriculture and Agri-Food Canada, Truro, NS.*

Reproductive performance in seasonally anestrous ewes is poor even after the application of conventional controlled breeding techniques. Estradiol-17β (E_2) has been shown to synchronize follicular wave emergence in anestrous ewes treated for 12 or 14 d with a medroxyprogesterone acetate sponge. The objective of this study was to determine the effects of an E_2 treatment administered 6 d after CIDR insertion on E_2 concentrations, estrus, pregnancy rates, and lambing rates in ewes bred out of season. Ewes from three farms (Farm A: $n = 22$; Farm B: $n = 48$; Farm C: $n = 28$) received

CIDRs (d -12) followed by an injection of eCG (500 IU; d 0) at CIDR removal and an injection of sesame oil without (1 mL; Control) or with E_2 (350 µg; d −6) 6 d before CIDR removal. Treatments were balanced for breed, age, parity, and BCS. Blood samples were taken from half of the ewes on d −6 and 0 to determine E_2 concentrations. On d 1 ewes were exposed to rams to observe estrus. Ewes were subjected to laparoscopic TAI on d 2. Pregnancy was diagnosed by transabdominal ultrasonography on d 50. Estrus, pregnancy rates, and lambing rates were analyzed using logistic regression. Day of lambing and E_2 concentrations were analyzed using ANOVA. The percent of ewes observed in estrus within 36 h of CIDR removal was similar between treatments (E_2: 24.5%; Control: 34.7%; $P > 0.05$). Pregnancy rates were similar between treatments (E_2: 40.8%; Control: 40.8%; ± $P > 0.05$) and were higher on Farm C than Farm B (Farm A: 45.5%; Farm B: 22.9%; Farm C: 67.9%; $P < 0.05$). Lambing rates were also similar between treatments (E_2: 34.7%; Control: 34.7%; $P > 0.05$) and were higher on Farm C than Farm B (Farm A: 40.9% Farm B: 16.7%; Farm C: 60.7%; $P < 0.05$). Relative to CIDR removal, ewes lambed earlier on Farm B (Farm A: 141.7 ± 1.3 d; Farm B: 136.6 ± 1.4 d; Farm C: 143.2 ± 0.9 d; $P < 0.05$) and ewes treated with E_2 lambed earlier (E_2: 138.9 ± 1.0 d; Control: 142.2 ± 1.0 d; $P < 0.05$). Concentrations of E_2 were similar between treatments on d −6 (E_2: 1.5 ± 0.1 pg/mL; Control: 1.6 ± 0.1 pg/mL; $P > 0.05$) and d 0 (E_2: 1.6 ± 0.1 pg/mL; Control: 1.3 ± 0.1 pg/mL; $P > 0.05$). Differences were mainly observed among farms potentially due to differences in breed, BCS, semen, or management practices. The addition of an E_2 treatment during a CIDR-eCG heat synchronization protocol does not clearly increase pregnancy and lambing rates in seasonally anestrous ewes.

Key Words: anestrus, ewes, controlled breeding

0986 (M064) Effect of duration on feed and energy substrate on the digestive physiology of finishing feedlot cattle. F. Joy*, J. J. McKinnon, S. Hendrick, and G. B. Penner, *University of Saskatchewan, Saskatoon, Canada.*

The objective of this study was to determine the effect of dietary energy substrate and days on feed (DOF) on apparent total tract digestibility, rumen fermentation, short-chain fatty acid (SCFA) absorption and the arterial glucose clearance rate. Eight ruminally cannulated, cross-bred growing heifers were randomly allocated to one of the two dietary treatments. The control (CON) diet consisted of 75.2% barley grain, 9.8% canola meal, 9% mineral-vitamin supplement, and 6% barley silage (DM basis). To evaluate the effect of energy source, a high-lipid byproduct pellet was included to replace 60% of the barley grain and canola meal (HLP). Diets were similar in NEg (5.15 MJ/kg) and CP (13.7% DM). The study consisted of four consecutive 40-d periods with collections occurring in the last 6 d of each period. Dry matter intake did not differ among periods but the HLP group tended to eat less ($P = 0.09$). The ADG was greater for CON ($P < 0.05$) than HLP and ADG decreased with advancing DOF. The ADG of CON was greater than HLP during first and the last periods (Trt×Period; $P = 0.024$). Heifers fed HLP tended to have greater mean ruminal pH (6.10 vs. 5.96; $P = 0.07$) than CON, but pH was not affected by DOF. The CON heifers had a greater digestibility for DM, OM, CP and NDF ($P < 0.05$) and the digestibility for DM, OM, CP, NDF and starch increased with advancing DOF ($P < 0.05$). Crude fat digestibility of CON increased with DOF while that of HLP decreased (Trt × Period; $P < 0.05$). Total SCFA concentration in the rumen was greater ($P = 0.006$) for CON (141.5 vs. 128.08 mM/dL) than HLP and it tended to decrease with DOF ($P = 0.098$). The molar proportion of acetate increased and butyrate decreased with increasing DOF ($P < 0.05$) but propionate was not affected. The rate of SCFA absorption was not affected, but the passage rate of chromium over period was decreased ($P < 0.026$). The arterial clearance rate of glucose was not affected by treatment or DOF. These data suggest that replacing 60% of the barley grain and canola meal with high lipid byproduct pellets negatively affects total tract digestibility and performance. Moreover, regardless of diet, with advancing DOF digestibility increases and SCFA concentration decreases without corresponding changes in SCFA absorption and, as such, these changes do not explain the reduction in G:F with advancing DOF.

Key Words: beef, digestibility, feeding-duration

0987 (M065) A prepartum diet supplemented with rolled canola seed reduced pituitary sensitivity to GnRH in dairy cows during second week postpartum. *R*. Salehi*[1], M. G. Colazo[2], M. Oba[1], and D. J. Ambrose[2], [1]*University of Alberta, Edmonton, Canada,* [2]*Alberta Agriculture and Rural Development, Edmonton, Canada.*

Cows fed a prepartum diet supplemented with rolled canola seed (high in oleic acid, OLA) had longer interval from calving to first ovulation than cows fed diets supplemented with either linola (high in linoleic acid, LA) or flax (high in linolenic acid) (Colazo et al., 2009; JDS, 92:2562). We hypothesized that the delayed ovulation in canola-fed cows occurred through suppression of pituitary LH since adding OLA to culture medium suppressed GnRH-induced LH release from porcine pituitary cells in-vitro (Barb et al., 1995; JAS, 73:1416). To test our hypothesis, pregnant Holstein cows, blocked by BCS, were assigned to 1 of 3 prepartum diets supplemented with canola (high OLA, $n = 10$), sunflower (high LA, $n = 10$), or control (no oilseed, $n = 11$) from 35 d before expected calving date until parturition. The concentrate portion of OLA- and LA-diets contained 0.99 kg rolled oilseeds providing 0.27 kg/d OLA or 0.31 kg/d LA. Average DMI ± S.E. (kg/d) was higher in control (15.30 ± 0.63) than in canola (13.54 ± 0.54), sunflower (13.31 ± 0.57) diets. Blood was sampled during the

first (6 ± 1.00 d, n = 15) or second (9 ± 1.20 d, n = 16) week postpartum, every 15 min for 6 h to measure LH pulsatility. Thereafter, 100 μg GnRH was administrated im and blood was sampled for 4 h to measure induced LH release. Treatments did not affect LH pulsatility during the first and second week postpartum. Mean, minimum, maximum LH, pulse amplitude, and frequency were 0.30, 0.11, 0.82, 0.40 ng/ml, and 4.24 pulses per 6 h, respectively, and they were not affected by treatments or weeks. GnRH-induced LH release was not influenced by dietary treatments during the first week postpartum, but cows fed a prepartum diet high in OLA had lower mean LH (1.70 ± 0.20 ng/mL) than in control (2.40 ± 0.20 ng/mL; P = 0.02) during the second week postpartum, but it did not differ from LA (1.80 ± 0.20 ng/mL; P > 0.05); LA vs. control, P = 0.09. After GnRH administration, diets did not affect LH peak (3.39 ng/ml), interval to peak (47.40 min) or area under curve (7.01 ng/ml per 4h). In summary, although, prepartum diets did not affect pulsatile and GnRH-induced LH release during the first week postpartum, cows fed a prepartum diet supplemented with rolled canola had lower mean GnRH-induced LH than those fed no oilseed.

Key Words: oilseed, prepartum, luteinizing hormone

0988 (M066) Utilization of high lipid byproduct pellet in the finishing diet of feedlot steers to improve carcass traits and reducing feed costs.

F. Joy*[1], J. J. McKinnon[1], P. Gorka[2], and G. B. Penner[1], [1]*University of Saskatchewan, Saskatoon, SK, Canada,* [2]*University of Agriculture in Krakow, Krakow, Poland*

Two studies were conducted to evaluate the rate and timing of provision of a high-lipid high-fiber byproduct pellet (HLP) as a partial replacement for barley grain in diets for feedlot cattle. In study 1, steers (n = 288; BW = 378.4 ± 0.50 kg) were randomly allocated to one of 24 pens, and pens were assigned to one of four treatments. The study period was divided into three equal periods of 49 d each, namely P1, P2, and P3. A barley-based diet (CON; 75.2% barley grain, 9.8% canola meal, 9% mineral and vitamin, and 6% barley silage; DM basis) was compared to a diet where HLP replaced 60% of the barley grain and canola meal, relative to the CON. Steers received the HLP diet for 0 (CON147), 147 (HLP147), the last 98 (HLP98), or the last 49 d (HLP49). Steers fed CON had greater ADG (1.96 vs. 1.83 kg/d; P < 0.01), but DMI was not affected. The HLP147 had greatest DMI and least G:F during P1, but least DMI in P3 (Trt × Period; P < 0.01). Hot carcass weight of CON and HLP49 were the heaviest (P < 0.05), and HLP49 tended to have the greatest percentage of carcasses in yield grade 1 (P = 0.07). Carcass quality grade was not affected. In the second study, steers (n = 264; BW = 441.3 ± 0.19 kg) were randomly allocated to one of 24 pens and fed for 120 d. Diets were similar in composition to study 1 except that the HLP replaced 30% of the barley grain. Treatments included feeding steers the HLP diet for 0 (CON), 120 (HLP120), and the last 60 (HLP60), and the last 60 d along with additional canola oil (HLP60CO). There were no differences for DMI and ADG (12.6 and 2.0 kg/d, respectively). The G:F for HLP120 was less than the other treatments (0.149 vs. 0.158; P = 0.001). Hot carcass weight was greater for CON and HLP60 than HLP120 and HLP60CO (386 vs. 377 kg). The HLP120 tended to have the greatest proportion (P = 0.06) of yield grade 1, with HLP60CO tending to be the lowest (62.5 vs. 37.9%). Carcass quality was not affected. Partially substituting barley grain with HLP in the second half of the finishing period may improve carcass yield grade without negatively affecting growth performance and feed efficiency relative to a barley-based diet.

Key Words: beef, byproduct, pellet, carcass

DAIRY FOODS: **TECHNICAL SESSION 1: CHEESE / YOGURT**

0989 (M067) Physicochemical and sensory characteristics of processed cheese manufactured from goat's milk fed diet supplemented with sunflower seed or sunflower oil. A. G. Mohamed*[1], T. A. Morsy[2], and S. Kholif[2], [1]*National Research Center, Cairo, Egypt,* [2]*National Research Center, Cairo, Egypt.*

Oilseed lipids are important sources of unsaturated lipids. Among oilseeds, linseed, soybeans, and sunflower seed are used both in farms and experimental work. Moreover, the enhancement of unsaturated fatty acids and conjugated linoleic acid (CLA) in milk products is important for human health. The aim of this work was to improve the fatty acid profile of processed cheese by using milk from goats fed with different supplements, namely, sunflower seed or sunflower oil. Fifteen lactating Damascus goats, in early lactation, were divided into three groups using complete randomized design for a 90-d experimental period. The treatments were: 1) control ration consisted of concentrate feed mixture: bersem clover (1:1 dry matter bases); 2) control +50 g/head/d sunflower seed; and 3) control +20 mL/head/d sunflower oil. Pooled milk from each treatment was used in the manufacture of processed cheese. It was manufactured by using cheese base that was prepared by acidifying goats' milk with diluted lactic acid until coagulation. Cheese samples were stored at 7°C for 3 mo. The results demonstrated that experimental additives increased ($P < 0.05$) the total unsaturated fatty acids and CLA in the processed cheese. In all additives decreased ($P < 0.05$) the total saturated fatty acids and omega 6:omega 3 ratio and increased ($P < 0.05$) the polyunsaturated fatty acids contents of the processed cheese fat. Processed cheese flavors, color, and physical properties such as melting index, oil separation, and penetrometer reading were not significantly affected by the experimental treatments. It can be concluded that sunflower seed or sunflower oil addition to lactating goats ration increased the nutritive value of processed cheese.

Key Words: goat's milk, processed cheese, fatty acids profile.

0990 (M068) Fatty acid profile of sheep cheeses that are commercialized in Chile. E. Vargas-Bello-Pérez*, C. Ugalde, P. Toro-Mujica, R. Vera, and C. Aguilar, *Pontificia Universidad Católica de Chile, Santiago, Chile.*

The fatty acid (FA) content of sheep cheeses is an important characteristic for consumers due to its role in human health. In Chile, there is an incipient internal market for sheep cheeses due to the fact that the demand for these cheeses is not widespread; however, its production is expected to be increased in the forthcoming years. The present study was performed to characterize the FA profile of sheep cheeses that are commercialized in Chile. Thirty-two sheep cheeses were collected from supermarkets of five different cities from which 21 were Chilean and 11 imported from Europe (Spain and France). Results showed that C10:0, C14:0, C16:0, C18:0, C18:1 t11, and C18:1c9 represented around 78% of the total FA profile detected in cheeses. Short-chain (C4:0-C6:0) and medium-chain (C8:0–12:0) FA content was lower in Chilean cheeses than European. Saturated, monounsaturated and polyunsaturated FA contents did not differ between cheeses. The n6:n3 ratio was lower in Chilean cheeses than European (2.8 and 5.9). The atherogenicity index was not different between cheeses; however, the thrombogenic index was lower in Chilean cheeses (2.7) than European (2.9). The results indicated that the FA profile of Chilean cheeses was desirable from a human standpoint.

Key Words: cheese, fatty acids, thrombogenic index

0991 (M069) Investigating the impact of distiller's dried grains with solubles on the quality of milk and Swiss cheese. V. Manimanna Sankarlal*, E. D. Testroet, and S. Clark, *Iowa State University, Ames.*

Late blowing in Swiss cheese, a result of unwanted gas production during ripening, is unacceptable to consumers, is impossible to slice, and causes economic loss to manufacturers. Cheese processors have raised concerns that feeding distiller's dried grains with soluble DDGS to cows leads to this defect, in part because of *Clostridium tyrobutyricum*. In this study, the effect of feeding DDGS on composition and quality of milk and Swiss cheese was studied. Thirty healthy mid-lactation ISU Dairy Farm Holstein cows were assigned randomly to one of three dietary treatment groups (10 cows per treatment group): 1) total mixed ration (TMR) with no DDGS; 2) TMR with 10% substitution with DDGS; and 3) TMR with 20% DDGS. One complete milking from all cows within a treatment was collected and pooled for cheese-making trials, twice within each of 3-mo-long treatment periods. Additionally, individual milk samples from three milkings of a day were collected weekly, and proximate analysis was performed on pooled individual milk samples. Cheese milk was filtered, standardized to 0.88 fat:protein, and pasteurized before addition of starter cultures and coagulant. Curds were cut, fore-worked, worked, and post-worked according to a baby Swiss cheese recipe, followed by pressing and brining (10°C, 12 h). The 3.5 kg blocks were vacuum packed and allowed to ripen (10°C, 7 d; then 22°C, 21 d), then cooled (4°C, 60 d). The milk and DDGS were analyzed for *C. tyrobutyricum* using selective media. After incubation up to 48 h in modified RCM lactate medium, tubes containing DDGS did not show gas formation, whereas most of the tubes containing milk showed gas formation, which indicates that DDGS were not the source of *C. tyrobutyricum*. Milk fat content decreased as % DDGS in diet increased ($P < 0.05$). Sol-

ids nonfat, protein, and lactose content of milk of cows fed 10 and 20% DDGS were only slightly higher than from control diet. After ripening (> 60 d), baby Swiss cheese had typical propionic acid Swiss cheese aroma. Regardless of diet treatment, pinholes, slits, and cracks were seen throughout most cheeses. DDGS feeding increased the amount of long-chain unsaturated fatty acids and decreased short-chain and most medium-chain fatty acids. Although feeding cows DDGS modified milk composition and subsequent cheese composition, DDGS alone should not be blamed as a source for *C. tyrobutyricum*or for late blowing in Swiss cheese.

Key Words: *C. tyrobutyricum,* Swiss cheese

0992 (M070) Evaluation of unidentified structural features in hard, aged cheeses and soft, washed rind cheeses by powder X-ray diffractometry.

G. F. Tansman*[1], P. S. Kindstedt[1], and J. M. Hughes[2], *[1]Dep. of Nutrition and Food Sciences, University of Vermont, Burlington, [2]Dep. of Geology, University of Vermont, Burlington.*

Hard, aged cheeses and soft, washed rind cheeses sometimes develop structural features that can be detected visually and texturally by mouthfeel, but which are incompletely characterized. The objectives of this research were to evaluate visible spherical features embedded within the bodies of aged Parmigiano Reggiano and Gouda cheeses, and granular features at the surfaces of three artisanal washed rind cheeses using powder X-ray diffractometry (PXRD). All cheese samples were purchased from local retail sources. Discolored spherical features up to *ca.* 5mm in diameter, which were readily visible against the darker cheese matrix, were extricated from the matrix of Parmigiano Reggiano and Gouda cheeses, defatted in acetone, ground to a powder, and analyzed by PXRD. Samples of the cheese matrix that surrounded the spheres were also prepared similarly and analyzed by PXRD for comparison. Granular features at the surface of washed rind cheeses were scraped off, defatted in acetone, ground, and analyzed by PXRD. The resulting X-ray diffraction patterns were compared with those in a database of over 1 million known crystals to establish crystal identities. The discolored spherical features from both Parmigiano Reggiano and Gouda cheeses diffracted X-rays in a manner characteristic of leucine; however, the surrounding cheese matrix did not diffract X-rays. The formation of numerous large (5-mm diameter) crystalline leucine entities may have important implications for the rheological properties of Parmigiano Reggiano and Gouda cheeses, which warrant further study. The washed rind cheeses exhibited surface grittiness that was perceptible in the mouth. Surface scrapings from three different washed rind cheese varieties yielded X-ray diffraction patterns that were all unique from one another. Two cheeses produced diffraction patterns that could not be identified, whereas the third displayed the presence of calcite crystals. None of the surface scrapings contained appreciable quantities of previously documented cheese crystals such as brushite, tyrosine, or calcium lactate. Due to the outward migration of calcium in washed rind cheeses, it is possible that the unidentified diffraction patterns represent crystalline calcium salts in novel forms that have not been documented. Based on anecdotal reports from cheesemakers and cheese mongers, we hypothesize that these surface crystals are responsible for distinctive visual and mouthfeel characteristics that appeal to consumers of artisanal washed rind cheeses.

Key Words: cheese, crystal, X-ray

0993 (M071) Quality of milk and Minas fresh cheese of pasture cows suplementted with licuri cake.

A. C. C. Ferreira*[1], R. L. Oliveira[2], J. F. Vieira[3], T. M. Silva[2], A. M. Barbosa[2], S. M. P. L. Jaeger[3], and D. D. Amaral[2], *[1]Universidade Federal da Bahia, MI, [2]Universidade Federal da Bahia, Salvador, Brazil, [3]Universidade do Reconcavol da Bahia– UFRB, Cruz das Almas, Brazil.*

This is study aimed to determine the best level of licuri cake for the diets of pasture dairy cows. This was done by the evaluating the quality of milk and Minas frescal cheese. Eight crossbreed cows were distributed in four Latin square simultaneously, on the Farm of Federal University of Bahia (UFBA), Brazil, in August to October 2012. The concentrated feeding consisted of soybean meal, ground corn, mineral salt, ammonia, urea, and licuri cake at 0, 20, 40, and 60% dry matter. Contents of fat, protein, lactose, total solids and solids not fat in milk and cheese were not affected ($P > 0.05$) by licuri cake in the diet (Table 0993). The decrease in the yields of components in the milk is related to the low energy content of the diet and low intake of dry matter. Furthermore, the amounts of fat and protein vary according to race, climate, management, and other factors. The percentage of milk fat had lower values in cows that had given birth at a younger age. In the summer months, the fat content (3.41 to 3.49%) was lower than in the winter months (around 3.7%).

Key Words: byproduct, supplement, ruminant nutrition

Table 0993. Fat content, crude protein, lactose in milk and cheese, and total solids (TS) solid not fat (SNF) in milk from cows on pasture supplemented with licuri cake

	Levels of Licuri cake (% DM)					*P*–Value	
Variable	0	20	40	60	SEM1	Linear	Quadratic
Fat (%)	2,22	2,31,	2,38	2,77	0306	00696	04645
Protein (%)	3,11	3,11	3,11	3,09	0060	08501	09560
Lactose (%)	4,63	4,63	4,64	4,62	0042	09256	08643
TS (%)	10,92	11,00	11,07	11,44	0296	00802	04745
SNF (%)	8,69	8,68	8,68	8,67	0082	08567	09655
Minas freshcheese							
Fat (%)	17,20	18,22	19,12	18,41	0298	01835	02528
Protein (%)	23,64	27,33	22,96	23,55	0058	03821	01973
pH	6,45	6,40	6,47	6,40	0754	06322	07385
Humidity (%)	59,94	57,19	58,78	57,86	0054	01544	02123

[1] SEM = standard error of mean. The cheeses were, on average, 18.2% fat and 58.4% moisture. Cheeses of this study can be classified as lean and high humidity. The licuri cake included in the concentrate until 60% of cows grazing did not alter the parameters of milk quality and frescal cheese.

0994 (M072) Microbial stress responses and gene expression during aging of cation-substituted full fat cheddar cheese. B. Ganesan*, S. Muruganandam, and D. J. McMahon, *Western Dairy Center, Utah State University, Logan*

Sodium replacement is a potential alternative to direct Na reduction in foods, wherein an equally salty cheese will attract consumers without the risk of high sodium intake. However bacteria in Cheddar cheese responsible for cheese flavor development may experience a different form of stress and respond differently when Na is, for example, substituted by K. We are yet to understand how salt change is likely to alter flavor formation in cheddar cheese. We proposed to study whether bacteria continue to experience NaCl stress even with Na reduction or with use of different NaCl mixtures with less Na in full fat cheddar cheese containing different fat levels. We investigated how starter bacteria respond to stress from different NaCl combinations during aging of cheddar cheese. To study starter bacterial stress, gene expression studies were done by qPCR targeting six known NaCl stress-related genes (three induced, three repressed by NaCl stress, based on literature) for starter lactococcal subspecies in cheeses with different NaCl combinations. Five cation combinations with different levels of Na replacement– 100% Na (control with 2.2% total salt), 75:25 and 50:50 Na:K, 50:40:10 of Na:K:Ca, and low sodium (0.7% total salt)– were chosen for the analyses. Starter lactococci survived well in response to stress, with initial variations post salting due to cations diminished over aging ($P < 0.05$). Initial responses of the dual enolase genes of lactococci matched known responses from other studies, with *enoA* being induced more by high NaCl and *enoB* repressed by high NaCl ($P < 0.05$), respectively. Expression of *dnaK*, which encodes a molecular chaperone and is known to be induced immediately with acid and NaCl stresses, steadily plateaued and remained high (> 10^6 copies) throughout 6 mo of aging. Initial stress response to other cations varied between the six genes, with only the cheese substituted with 50:40:10 of Na:K:Ca exhibiting lower transcript induction ($P < 0.05$) of all stress response genes. This indicates that Ca even at low levels plays a role in mitigating lactococcal stress. Notably, RNA extracted for gene expression directly from cheeses was devoid of any cross-contaminating genomic DNA, which confirmed that only transcripts were detected. The presence of detectable mRNA even after 6 mo of cheddar cheese aging confirms that lactococci are still physiologically active independent of their exhibiting growth on media plates. This study presents a novel perspective on cation-controlled gene expression through cheese aging.

Key Words: lactococci, cation substitution, gene expression

0995 (M073) Characteristics of yogurt manufactured using reconstituted yogurt cultured milk powder compared to yogurt powder. L. Song*[1], and K. J. Aryana[2], [1]*Louisiana State University, Baton Rouge,* [2]*Louisiana State University Agricultural Center, Baton Rouge.*

For the manufacture of commercial yogurt powder the yogurt has to go through drying process which substantially lowers the yogurt culture counts, so the potential health benefits of the yogurt culture bacteria are deminished or lost. Also, on reconstitution, commercial yogurt powder does not taste like yogurt, it is sour and off-flavored. The objective was to enumerate *Streptococcus thermophilus* and *Lactobacillus bulgaricus* of reconstituted yogurt cultured milk power and reconstituted commercial yogurt powder up to 8 wk and to elucidate their physicochemical and sensory characteristics. Commercial yogurt powder (CYP) was the control and yogurt-cultured milk powder (YCMP) was the treatment. Freeze-dried yogurt starter culture (*Lactobacillus bulgaricus* and *Streptococcus thermophilus* at ratio 1:1) was added to milk powder at 10^7 cfu/g on reconstitution. Microbial and physicochemical characteristics of the reconstituted CYP and YCMP were analyzed daily for the first week and then weekly for a period of 8 wk (at 1, 2, 3, 4, 5, 6, 7, 14, 21, 28, 35, 42, 49, and 56 d) after reconstitution. Three replications of each treatment were conducted. Sensory consumer testing of CYP and YCMP on reconstitution was conducted with 100 consumers of yogurt. Data were analyzed by PROC GLM of SAS. YCMP had 5 log cfu/ml higher counts of *Streptococcus thermopilus* compared to the control (CYP) at 56 d. Also, *Lactobacillus bulgaricus*-counts of YCMP at 28 d was 6.55 log cfu/ml and at 56 d was 5.35 log cfu/ml while the CYP at 28 d onward had no counts. YCMP also had significantly higher apparent viscosity, pH, appearance, sensory color, aroma, taste, thickness, overall liking, consumer acceptability and purchase intent compared to CYP. YCMP had better overall characteristics than CYP.

Key Words: yogurt, powder, reconsituted

0996 (M074) Impacts of different types of exopolysaccharides on the physical and rheological properties of yogurts. U. Pachekrepapol*[1], J. A. Lucey[2], and D. S. Horne[2], [1]*Dep. of Food Science, University of Wisconsin–Madison, Madison,* [2]*Wisconsin Center for Dairy Research, Madison.*

Exopolysaccharides (EPS) produced by some starter cultures are often used to modify yogurt texture. Our goal was to study the impact of different EPSs on yogurt properties. Reconstituted skim milk was inoculated with eight strains of *S. thermophilus*; ST1-UWM (non-EPS producer used as a control) and seven EPS producing strains. Due to the different acid producing ability of each strain, milks were supplemented with different amounts of peptone, and the inoculation rates were var-

ied to achieve a similar acidification rate for all strains. Milks were fermented at 40°C until pH 4.6 was reached. Small amplitude oscillatory rheology was performed to monitor yogurt gel formation. Gel permeability and whey separation were determined. Microstructure of the yogurt gels was studied using fluorescence microscopy. EPS from each strain were isolated for molar mass determination using size exclusion chromatography– multi-angle laser light scattering (SEC-MALLS), and for repeating unit structure determination using nuclear magnetic resonance spectroscopy (NMR-spectroscopy). Gelation pH of each yogurt was significantly different. The yogurt made from the control strain had significantly lower gelation pH (pH ~ 5.10) than yogurts made from EPS-producing strains (pH ~ 5.17 to 5.29). Storage modulus (G′) of the control gel at pH 4.6 (G′ ~ 97 Pa) was significantly lower than the other yogurts made from EPS-producers (G′ ~ 151 to 191 Pa) except the yogurt made from ST-143 strain (G′ ~ 67 Pa). Permeability and whey separation of each yogurt were significantly different with the control yogurt having higher permeability and whey separation than other yogurt gels. The microstructure of the control yogurt showed finer and smaller pore sizes compared to other gels. The yields of EPS produced from each strain varied between 34 and 95 mg dry material/L, with ST-143 being the highest EPS producer. The molar mass of the isolated EPS ranged from 0.13 X 10^6 to 1.74 X 10^6 g/mol. The structures of the repeating units showed that all EPS were different in terms of sugar compositions, linkages and conformations. Since all samples had similar milk composition, heat treatment, and rate of acidification, this study shows that EPS produced during yogurt fermentation modifies the gelation mechanism and physical properties of the yogurt gels.

Key Words: EPS, yogurt, rheology

0997 (M075) Substituting KCl for NaCl in fresh queso fresco. D. L. Van Hekken*[1], D. X. Ren[1,2], and M. H. Tunick[1], [1]*USDA, ARS, ERRC, Dairy & Functional Foods Research Unit, Wyndmoor, PA,* [2]*Institute of Dairy Science, College of Animal Science, Zhejiang University, Hangzhou, P.R., China.*

Reducing the sodium level in cheese is challenging when a signature salty flavor is expected, such as in high-moisture Queso Fresco (QF). Fresh starter-free QF was fine milled and dry salted at different levels of NaCl and KCl to obtain total NaCl levels of 1.5 to 2.0%. The treatments contained 1.5/0, 2.0/0, 1.0/0.5, 1.0/0.75, 1.0/1.0, and 1.5/0.5% NaCl/KCl. Texture profile analysis and small amplitude oscillatory shear analysis were conducted on d 7, and salt intensity levels were evaluated by trained sensory panelists at d 6. Texture profile analysis indicated that the QFs were similar in hardness (16.7 ± 1.8 N) with the 1.0/0.5 QF being the softest and similar in cohesiveness (0.17 ± 0.01) with the 1.5/0/5 QF being the least cohesive. Chewiness was highest in the 1.5/0 QF and lowest for the 1.5/0.5 QF (224 and 144 J, respectively). Increasing the total NaCl in the cheese increased the elastic and viscous moduli although the 1.5/0 QF was higher than the 1.0/0.5 QF and the 1.5/0.5 had the highest values. This suggested that the use of KCl may function differently in the matrix of QF, a weak body cheese that is expected to crumble easily. Five of the six QF had saltiness intensity scores 1.0 to 1.5; the 2.0/0 QF had a score of 2. Panelists selected 2 as the target saltiness for QF. The metallic off-flavor commonly associated with KCl was not an issue at levels used in this study. The replacement of NaCl with KCl in the ranges tested had only slight effects on the textural properties, did influence the viscoelastic properties, and did not match the saltiness intensity of NaCl.

Key Words: sodium, cheese, queso fresco

0998 (M076) Effect of potassium sorbate and sodium benzoate concentrations on growth of cheese starter cultures. D. Olson*, E. Gonzalez, M. Ponce, and K. J. Aryana*, Louisiana State University Agricultural Center, Baton Rouge.*

Potassium sorbate and sodium benzoate are commonly added to foods as antimicrobials. The objective was to determine if varying concentrations of potassium sorbate or sodium benzoate affect the growth of DVS R-604 cheese starter cultures at a 10^{-4} dilution in peptone and M17 broth containing 5% (w/v) lactose. Potassium sorbate and sodium benzoate concentrations used were 0% (control), 0.01%, 0.05%, 0.1%, 0.2%, 0.5%, and 1%. Counts on M17 agar containing 5% (w/v) lactose were performed immediately after inoculation of cheese starter culture and at 1, 2, 3, and 4 d of storage. Immediately after inoculation, concentration of potassium sorbate or sodium benzoate did not affect counts of cheese starter cultures in either peptone or M17 broth containing 5% (w/v) lactose. For cheese starter cultures grown in peptone, the counts after 1 d in the presence of 1% potassium sorbate or 1% sodium benzoate were lower than in the presence of the lower concentrations of these antimicrobials. Also, the decrease of these counts over 4 d of storage was greater in the presence of 0.5% and 1% potassium sorbate or sodium benzoate than in the presence of lower concentrations of these antimicrobials. For cheese starter cultures grown in M17 broth containing 5% (w/v) lactose, the counts increased between 100 and 1000-fold during the first d of storage after inoculation in the presence of potassium sorbate or sodium benzoate at concentrations of 0.2% or less. However, this increase was less than 100-fold in the presence of 0.5% and 1% potassium sorbate and 1% sodium benzoate. Between d 1 and 4 of storage, the counts in M17 broth containing 5% (w/v) lactose decreased between 10- to 100-fold in the presence of potassium sorbate or sodium benzoate at concentrations of 0.2% or less, but this decrease was smaller in the presence of 1% potassium sorbate. Concentrations of 0.5% and 1% potassium sorbate and sodium benzoate were more effective than lower concentrations for decreasing the counts of cheese starter cultures grown in

either peptone or M17 broth containing 5% (w/v) lactose, but this greater effectiveness was observed in different ways in peptone versus M17 broth containing 5% (w/v) lactose.

Key Words: cheese starter culture, potassium sorbate, sodium benzoate, growth.

0999 (M077) Influence of submicronization of sodium chloride on the sensory characteristics of surface salted cheese crackers. *M. Moncada*, C. Sabliov, C. Astete, and K. J. Aryana, Louisiana State University Agricultural Center, Baton Rouge.*

Reducing the particle size of sodium chloride crystal would increase its dissolution rate leading to a more efficient transfer of the ions to the taste buds and hence perhaps a saltier perception of foods. The objective was to evaluate the effect of developed submicro salt on the sensory characteristics of surface salted cheese crackers. The cheese cracker treatments consisted of three different salt sizes (regular, micro, submicro salt) and three different concentrations (2, 1.5 and 1% w/w). A Balanced Incomplete Block Design was used to conduct the consumer analysis of cheese crackers for submicro salt (2, 1.5 and 1%), microsalt (2, 1.5 and 1%) and regular 2% (control as used by industry) using 476 participants in total at wk 1 and 4 mo. At 4 mo, submicro salt treatments (2, 1.5, and 1%) resulted in having significantly ($P < 0.05$) more preferred saltiness scores compared to control (regular 2%). At 4 mo, submicro salt (1.5 and 2%) showed significantly ($P < 0.05$) more preferred just-about-right saltiness scores compared to control (regular 2%). The consumers purchase intent increased by 25% for the submicro salt 1.5% after they knew about the 25% reduction in sodium content of the cheese cracker. The reduction of 25 and 50% salt content in cheese cracker through use of submicro particulated salt did not adversely influence sensory color, aroma, crunchiness, overall liking and acceptability scores, which were the same compared to control (regular 2%) and microsalt treatments (2, 1.5, and 1%). Compared to the micro salt, the sub micro salt particle size was reduced 10 times and yet there was no increase in saltiness of crackers with submicro salt. This may be because instead of taking salt directly it was taken as a surface salting on a product containing protein, fat and other biomolecules which, masked the saltiness of the surface salted cheese crackers. Reduction in sodium chloride particle size by 10-fold may increase its surface area but not the saltiness of surface salted cheese crackers.

Key Words: submicronization, salt, cheese cracker

1000 (M078) Submicronization of sodium chloride and its effect on the physicochemical and microbiological characteristics of surface salted cheese crackers. M. Moncada*, C. Sabliov, C. Astete, and K. J. Aryana*, Louisiana State University Agricultural Center, Baton Rouge.*

Reducing particle size of salt to submicron range increases its surface area. The objective of this study was to develop submicro salt (sodium chloride) by using a nanospray drying method and using the developed submicro salt in surface salted cheese crackers and evaluating their physicochemical, and microbiological characteristics. The sodium chloride solution (3% w/w) was sprayed through the nozzle size of 4 μm with air flow of 125 l/min, pressure of 3800 Pa, head temperature of 95°C and spray percentage of 90%. The processing parameters were optimized to ensure formation of the smallest size submicrosalt, as measured by Scanning Electron Microscopy and Dynamic Light Scattering. The cheese cracker treatments consisted of three different salt sizes (regular, microsalt and submicrosalt) and three different concentrations (2, 1.5, and 1%). The 9 (three sizes x three concentrations) different cheese cracker treatments were tested for salt concentration and sodium content at wk 1. Water activity (A_w), yeast and mold counts, texture-fracturability, and color were determined at wk 1 and 4 mo of storage. Completely Randomized Design (CRD) was used for salt and sodium content and CRD with repeated measures was used for A_w, yeast and mold counts, texture-fracturability, and color. The 80% of the submicro particles produced by the nanospray dryer B-90 was between 500 nm to 1900 nm. Yeast counts and A_w in all treatments increased from 1 wk to 4 mo. Submicrosalt treatments (2, 1.5, and 1%) had positive effect in yeast reduction at 4 mo compared to regular salt (2, 1.5, and 1%). There was no mold growth in all treatments at all times. The L*, b*, C* and h* values in all treatments increased significantly ($P < 0.05$) from 1 wk to 4 mo. The sodium chloride micro and submicro particles maintained low counts in yeasts, no counts in molds and did not adversely influence quality attributes.

Key Words: submicro, salt, cheese cracker

1001 (M079) Influence of various health beneficial spices on some characteristics of yogurt culture bacteria and *Lactobacillus acidophilus* and sensory acceptability of spicy probiotic yogurt. *M*. Sánchez-Vega, and K. J. Aryana**, Louisiana State University Agricultural Center, Baton Rouge.*

Garlic and ginger have a beneficial influence on averting cardiovascular diseases. Onion and turmeric decrease the risk of diabetes and have anticancer properties. *Streptococcus thermophilus*, *Lactobacillus bulgaricus,* and *Lactobacillus acidophilus* are lactic acid bacteria that produce lactase and reduce the symptoms of lactose malabsorption. Earlier work has

shown the influence of spice extracts but the influence of pure spice juice on yogurt culture bacteria is not known. Characteristics of yogurt culture bacteria were measured by suspending freshly thawed cultures into 0.1% peptone water (growth), MRS-Thio broth with oxgall (bile tolerance) and skim milk (*P*rotease activity) with 1% (v/v) of freshly extracted spice juice. Fresh spices were obtained locally and spice juice was extracted using a juice extractor. Bile tolerance was measured by enumeration in presence of bile and protease activity was measured by a spectrophotometric assay. A probiotic blueberry yogurt was made that incorporated 0.05% of individual spice juice. Apparent viscosity of probiotic blueberry yogurt was measured using a viscometer with a helipath and Wingather 32 software. A T-C spindle was used at 20 rpm and 100 data points were acquired per sample. Physico-chemical characteristics of spicy probiotic yogurts containing the three bacterial cultures used were determined. Differences of least square means were used to determine significant differences at $P < 0.05$ for main effects and interaction effects. Consumer acceptability test was conducted using 100 consumers. A nine point scale was used to evaluate overall appearance, color, aroma, taste, texture and overall liking of the product. Results indicated that all spices except turmeric improved the bile tolerance of *L. bulgaricus*. Ginger, turmeric and onion had the best overall influence on the protease activity of *S. thermophilus*. Turmeric improved the protease activity of *L. bulgaricus*. Ginger and turmeric improved the protease activity of *L. acidophilus*. All four spices decreased the pH of the spicy yogurt, while garlic, ginger and turmeric increased the titratable acidity of the spicy yogurt. Onion and ginger increased the apparent viscosity of the spicy yogurt. The control yogurt obtained 80% acceptance and the ginger yogurt obtained 84% acceptance, and both of these yogurts obtained the highest intent of purchase. Ginger can be used in spicy yogurt manufacture for direct consumption while all four spices have potential for a new product line of yogurts for cooking, marinating and dips enabling potential health benefits from both spices and probiotic bacteria.

Key Words: spice, fermented, culture

1002 (M080) Yogurt characteristics as effected by added lactose. B. Mena, and K. J. Aryana*, *Louisiana State University Agricultural Center, Baton Rouge.*

Enrichment of yogurt with lactose addition may increase growth of the yogurt starter culture (*Streptococcus thermophilus* and *Lactobacillus delbrueckii* ssp. *bulgaricus*) and enhance yogurt physicochemical and sensory attributes. The objectives of this study were: to determine the influence of added lactose on 1) the growth of the yogurt starter culture during yogurt´s shelf life, 2) the physicochemical characteristics of yogurt during shelf life, 3) the final lactose content of yogurt during its shelf life, and 4) the sensory attributes of yogurt. Fat-free plain set-type yogurt was manufactured using 0, 1, 3, and 5% w/w added lactose to accomplish objectives 1, 2, and 3. For objective 4, a blueberry yogurt was manufactured using the same lactose levels. Analyses for plain set-type yogurt were done at 7 d intervals during 35 d of storage period. Three replications were conducted. Sensory evaluation was conducted by 100 consumers of yogurt on d 3 of its manufacture. Data were analyzed using PROC MIXED model of SAS 9.3 program. Significant differences between means were analyzed at $\alpha = 0.05$ using Tukey adjustment. Addition of lactose to yogurt at 5% w/w significantly increased growth of *Streptococcus thermophilus* ST-M5 but had no effect on growth of *Lactobacillus bulgaricus* LB-12. Lactose added at 5% w/w showed significantly the highest lactose content during entire storage period as expected, the lowest pH values, and also the highest syneresis values over storage period of 35 d. Lactose addition had no effect on appearance and color of blueberry yogurt. Samples containing added lactose showed significantly higher scores for taste, sourness and sweetness. Lactose added at 3 and 5% w/w had significantly the highest overall liking scores. Acceptability of yogurts and purchase intent markedly increased with the addition of lactose. Added lactose in yogurt manufacture favorably influenced some attributes of yogurt.

Key Words: added lactose, yogurt, probiotic properties, starter culture, lactic acid bacteria

---

1003 (M081) Influence of added lactose on some probiotic properties of yogurt culture bacteria. B. Mena, and K. J. Aryana*, *Louisiana State University Agricultural Center, Baton Rouge.*

Lactose is a source of energy for lactic acid bacteria in dairy fermented products. Acid tolerance and bile tolerance are important probiotic properties. The influence of lactose on acid tolerance and bile tolerance of yogurt culture bacteria is not known. The objective was to determine the influence of lactose on acid and bile tolerance of yogurt starter culture *Streptococcus thermophilus* ST-M5 and *Lactobacillus bulgaricus* LB-12. Acid tolerance was conducted on pure cultures of *S. thermophilus* in M17 broth at pH 2.00 and *L. bulgaricus* in MRS broth at pH 2.00 both at 30 min intervals for 2 h of incubation. Bile tolerance of pure cultures was determined using MRS-THIO broth with 0.3% oxgall for *L. bulgaricus* and MRS broth with 0.3% oxgall for *S. thermophilus*. Dilutions were plated every hr for 12 h. Three replications were conducted. Data were analyzed using PROC MIXED model of SAS 9.3 program. Significant differences between means were analyzed at $\alpha = 0.05$ using Tukey's adjustment. With use of lactose at 3 or 5% (w/v), the *Streptococcus thermophilus* ST-M5 had significantly higher acid tolerance than control at 120 min. In presence of lactose at 3 or 5% (w/v), the *Lactobacillus bulgaricus* LB-12 had significantly higher acid tolerance than control at 60, 90, and 120 min. Lactose, when used at 5% (w/v), significantly improved bile tolerance of *L. bulgaricus* compared to control. With use of lactose at 1%

(w/v), *S. thermophilus* had significantly higher bile tolerance compared to control at 2 h of incubation. Use of lactose at 5% (w/v), favorably influenced acid tolerance of *S. thermophilus* and the bile tolerances of *S. thermphilus* and *L. bulgaricus*.

Key Words: added lactose, acid tolerance, bile tolerance, starter culture

1004 (M082) Evaluation of the perten dough lab for production of imitation mozzarella cheese.

A. Kommineni[*1], S. Patel[1], A. C. Biswas[1], C. Marella[2], and L. Metzger[3], *[1]Dairy Science Dep., South Dakota State University, Brookings, [2]Dairy Science Dep., California Polytechnic State University, San Luis Obispo, [3]Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

The functional properties of imitation mozzarella cheeses (IMC) are influenced by the equipment and manufacturing procedure used to produce them. To test new formulations a pilot scale twin screw cooker with a batch size of 4.5kg is routinely utilized. However, in situations such as when experimental ingredients are being evaluated, a smaller batch size is desired. The Dough lab (Perten Instruments, Hagersten, Sweden) is a commercial twin screw heating and blending system that is used for dough rheology applications. As compared to a typical pilot scale twin screw cooker the dough lab has a batch size of 600 g. The objective of this study was to compare imitation mozzarella cheese (IMC) manufactured with the Perten dough lab (PDL) to IMC made with a pilot scale Blentech twin screw (BTS) cooker (cheese Therm cooker- Blentech Corporation, Santa Rosa, CA). Initially a typical control IMC was produced in the BTS cooker using a cook temperature of 90°C, a cook time of 4 min and 30s ec and at a stirring speed of 140 rpm. The same IMC formulation was then produced with the PDL using four different stirring speeds (75, 100, 115, and 125 rpm) at a cook time of 4 min and 50 sec and a cook temperature of 90°C. Of the IMCs made in PDL at four stirring speeds, the utilized 115 rpm had similar functional properties as compared to IMC made in the BTS. IMC was then manufactured in triplicate using the PDL operated at 115 rpm stirring speed and samples were analyzed for chemical (Fat, Protein and Moisture) and functional (Texture Profile Analysis (TPA)— Hardness, Melt and Stretch) properties. Method comparison statistics (mean comparison, graphical representation, repeatability) were used to evaluate the agreement between the two methods. The TPA-hardness, schreiber melt and stretch characteristics of the IMCs made with PDL were similar to the IMC produced in the BTS. The results indicate that the Pertain Dough Lab can be used to produce a 600-g batch of IMC that has functionality similar to IMC produced in a pilot scale twin screw cooker.

Key Words: dough lab, twin screw cooker, imitation cheese

1005 (M083) Genome analysis of two *Lactobacillus curvatus* strains that have emerged as dominant non-starter lactic acid bacteria in cheese.

C. J. Oberg[*1], T. S. Oberg[2], J. R. Broadbent[2], M. D. Culumber[1], D. J. McMahon[3], and J. L. Steele[4], *[1]Dep. of MIcrobiology, Weber State University, Ogden, UT, [2]Dep. of Nutrition, Dietetics, and Food Sciences, Western Dairy Center, Utah State University, Logan, [3]Western Dairy Center, Utah State University, Logan, [4]University of Wisconsin, Madison.*

Recent studies concerning cheese microbiology have revealed *Lactobacillus curvatus* becoming an increasingly common component of the non-starter lactic acid bacteria (NSLABs) population in aged cheddar cheese. We recently sequenced the genome of two *Lb. curvatus* strains, WSU1, isolated from aged cheddar cheese manufactured at Utah State University, and LFC-1, isolated from aged cheddar cheese manufactured at the University of Wisconsin–Madison. Whole-genome shotgun sequencing was performed on both isolates and assembled into draft genome sequences. Preliminary genome annotation was performed using the RAST algorithm (rast.nmpdr.org). Initial genetic comparisons between the predicted coding sequences of the two strains showed similar genome content with strain WSU01 having 312 unique predicted proteins, and LFC-1 having 297 unique proteins using a 90% amino acid identity threshold. Both strains have genes encoding enzymes for cellobiose utilization, and the ability to ferment ribose and N-acetylglucosamine. Although both strains have genes for lactose utilization, API sugar panel results showed that only LFC-1 fermented lactose. Further analysis showed that LFC-1 also has genes that encode enzymes for maltose and trehalose fermentation, along with genes for citrate utilization. To understand why *Lb. curvatus* has become a dominant NSLAB in cheddar cheese, genome sequences were analyzed to identify possible mechanisms. Both genomes contain genes for a putative sakacin-like bacteriocin and genes for a propanediol utilization pathway, which converts 1,2-propanediol to propanol and propionic acid. To test for propionate production, both strains were grown to carbohydrate exhaustion in MRS media (*P*H 5.2), after which 50 mM lactate was added. Cultures were incubated under strict anaerobic conditions for 22 d with samples taken after 0, 5, and 22 d and analyzed for propionate using GC–MS. Lactate concentrations were also measured using an enzymatic assay. Results revealed that both WSU1 and LFC-1 produce a fivefold increase in propionate after 22 d. Previous studies on propionate production in other lactic acid bacteria show that lactate was converted to 1,2-propanediol, but lactate in both WSU1 and LFC-1 did not show a decrease in concentration during incubation. This observation opens the possibility that in *Lb. curvatus*, 1,2-propanediol is produced by another pathway and warrants further investigation since high levels of propionic acid have been found in aged cheddar cheese where *Lb. curvatus* is a dominant NSLAB.

Key Words: NSLABs, cheese, genomes

1006 (M084) Use of a water-in-oil-in-water (w/o/w) double emulsion to simulate the full-fat cheese physical properties in a 30% reduced-fat cheese.

L. Liu*[1,2], D. Clayton[2], and D. J. McMahon[2], *[1]Key Laboratory of Dairy Science, Ministry of Education, Northeast Agricultural University, Harbin, China, [2]Western Dairy Center, Utah State University, Logan.*

Reduced-fat cheeses have greater hardness and elasticity than full-fat cheeses because of the reduction in number of fat particles that can interrupt long-range interaction within the casein protein matrix structure of cheese. Our objective was to produce a water-in-oil-in-water ($W_1/O/W_2$) double emulsion as the carrier for butterfat that, when used in the manufacture of cheese, would provide similar physical properties to a full-fat cheese but have 40% less fat. The $W_1/O/W_2$ emulsion was made by making a 1% (wt./vol.) solution of inulin in boiling 0.5% (wt./vol.) NaCl solution, and adding this solution in a 40:60 ratio into anhydrous milk fat (containing 8% (wt./wt.) polyglycerol polyricinoleate) at 50°C using low shear. This formed the primary W_1/O emulsion. The W_1/O emulsion was then mixed with high shear (5000 rpm for 1 min) in a 20:80 ratio with a 2% (wt./wt.) aqueous solution of whey protein concentrate to form the $W_1/O/W_2$ emulsion. A single oil-in-water emulsion was prepared as a control using milkfat emulsified into the whey protein solution and designated as O/W_2. Immediately after emulsion preparation, the control (O/W_2) and double ($W_1/O/W_2$) emulsions were added separately (in triplicate) into pasteurized skim milk at 31°C and then made into cheese FFCON and WOW32, respectively) using a standard procedure for full fat cheddar cheese. Mean (± SE) composition for FFCON cheeses was 354 (± 3) g/kg moisture, 333 (± 3) g/kg fat, 17.2 (± .5) g/kg salt and pH 5.37 (± .02), while for the WOW32 cheese it was 424 (± 6) g/kg moisture, 228 (± 2) g/kg fat, 17.6 (± 0.7) g/kg salt and pH 5.30 (± .02). Rheological properties (at 25°C) were analyzed after 1 mo of storage. Storage modulus (G') and loss modulus (G") for both cheeses were linear over the range of 10^{-3} to 10^{-1} percent strain. The WOW32 cheese was slightly softer ($P < 0.1$) than the FFCON cheese with mean G' between 0.1% and 0.01% strain of 112 kPa and G" of 33 kPa compared to G' and G" of the FFCON cheese of 177 and 52 kPa, respectively. This softening of the WOW32 cheese compared to the FFCON cheese was considered beneficial as normally a 30% fat reduction causes cheese to become firmer. We successfully produced a cheese with 30% less fat and similar (slightly softer) properties to a full fat cheese, with the extra moisture in the WOW32 cheese attributed to moisture coming from the W_1phase of the $W_1/O/W_2$ double emulsion.

Key Words: cheese reduced-fat emulsion

DAIRY FOODS: **TECHNICAL SESSION 2: ANALYTICAL / PROCESSING**

1007 (T065) Incidence of thermoduric bacteria and spores on selected Midwest dairy farms.

K. P. Buehner*[1], S. Anand[2], and A. D. Garcia[1], *[1]Dairy Science Dep., South Dakota State University, Brookings, [2]Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Thermodurics can be present in milk even after pasteurization. The objectives of this study were to identify the origin and common species of heat-resistant bacteria occurring during summer and winter on Midwest dairy farms. Bulk tank milk samples were taken from 10 dairy farms along the South Dakota section of Interstate 29 with herd sizes ranging from 650 to 3500 lactating dairy cows. Milk samples were profiled for the prevalence of thermoduric bacteria (TDB) and spore counts (SC). In addition, corn silage samples and swabs of the milking clusters were taken at nine of the 10 dairies to profile the potential sources of TDB and SC. The samples were taken three times during winter (January to March) and summer (June to August), to track seasonal changes in the bacterial flora. During winter the average TDB counts in bulk tank milk were 2.61 log compared to 2.76 log TDB counts in summer. The SC was 1.03 log in winter, which is half the 2.06 log SC present in summer season ($P < 0.0001$). Corn silage sampled in winter contained 7.57 log TDB compared to an increased 10.77 log TDB during summer sampling. Concentrations of SC in corn silage reached an average of 6.3 log in winter compared to 11.81 log for summer ($P < 0.001$). The seasonal effect was evident with an increase in summer counts across the board for TDB and SC both, in the feed and bulk tank. *Bacillus licheniformis* was the predominant species identified in 62.4% of winter (85 total) and 49.4% of summer (83 total) samples. *Bacillus subtilis* made up 9.4% of the remaining winter isolates followed by *Bacillus sonorensis* at 8.2%, conversely, *B. sonorensis* made up 12% of summer isolates followed by *Bacillus pumilus* at 10.8%. *Bacillus licheniformis* is a ubiquitous microbe and was isolated from both TDB and sporeformer categories in all three sample types. There were larger increases in SC than TDB indicating summer conditions potentially increase the ability of sporeforming bacteria to proliferate over TDB. In conclusion, samples from bulk tank milk, milking cluster swabs, and corn silage at each of the 10 sites indicated *B. licheniformis* was the major contaminant regardless of season. In this experiment corn silage was determined as the major source of both TDB and SC over the milking clusters and relative to the levels in bulk tank milk showing significant higher concentrations in summer than winter.

Key Words: spores, thermoduric bacteria, corn silage, *Bacillus*

1008 [Withdrawn]

1009 (T067) Mechanisms and ways for improving heat stability of Micellar casein concentrates.

S. G. Sutariya*, H. G. Patel, and G. H. Meletharayil, *South Dakota State University, Brookings.*

Heat stability of proteins is the major hurdle in designing high protein containing heat stable foods and beverages with long shelf-life. Micellar casein concentrate (MCC) can be an ideal ingredient for such products. As MCC typically has > 90%w/w casein and is devoid of whey proteins, the mechanism of it's heat stability is expected to be different compared to milk powders and MPC. However, little is known about heat stability of MCC solutions, particularly at higher protein concentrates. The objective of the present study was to explore the mechanisms of heat stability of MCC and also investigate the effects of different additives on heat stability of MCC. Aliquot of MCC (12, 14, and 16% w/w protein) were prepared by diluting concentrated MCC retentate with glass distilled water. Experiments were designed with following treatments: 1) no treatment (control), 2) addition of sodium phosphate (SP) at 1, 5, 10, 25, 50 mML^{-1}, 3) addition of sodium citrate (SC) at 1, 5, 10, 25, and $50mML^{-1}$. The time required for visual precipitation or aggregation (generally referred as heat coagulation time (HCT) was measured using oil-bath at 140 and 120°C. The visual observations, calcium-ion activity and particle size were also measured. The HCT of control samples was 49 sec. The colloidal state of casein micelle, calcium activity and voluminosity of casein micelles seemed responsible for poor heat stability of MCC. Addition of SP. and SC at low level (1 mM) improved HCT by 15s compared to control samples., whereas their addition at 5, 10, and 25 mM exhibited significant improvement ($P < 0.05$) in heat stability at all protein concentration showing no aggregation when heated for more than 3 min at 140°C or 120°C. The color was also changed from opaque to translucent. However, increasing level of SP. and SC to 50 mM decreased both HCT and turbidity of samples. The addition of SP. and SC shifted the casein-mineral equilibria leading to decrease in free Ca-ion concentration as well as dissociation of colloidal calcium phosphate from casein micelle and increased negative charges of the casein micelle and hence increased repulsion, which contributed to increase in heat stability of MCC. The results of this study showed significant ($P < 0.05$) improvement in the heat stability of micellar casein concentrate using additives such as SP. and SC, which show promise to make shelf-stable MCC with higher protein content.

Key Words: micellar casein concentrate, heat stability, calcium chelators

1010 (T068) Influence of carboxymethylcellulose molecular weight on physicochemical properties and stability of whey protein-stabilized emulsions. S. Zhang*, and B. Vardhanabhuti, *University of Missouri, Columbia.*

Complexation of protein with polysaccharides at pH near the isoelectric point (*P*I) of protein has been widely used to improve the stability of oil-in-water emulsions. This is attributed to the fact that protein–polysaccharide complex formed a thick, dense and homogenous layer surrounding the droplets to prevent the flocculation. However, little is known about the effect of molecular properties of polysaccharides on emulsification properties of protein. The objective of this study is to assess the influence of carboxymethylcellulose (CMC) molecular weight on physicochemical properties and stability of whey protein-stabilized emulsions. Emulsions containing 5 wt% oil, 0.5 wt% protein and 0 to 0.5 wt% CMC (molecular weights of 270 k, 750 k, and 2500 kDa) were obtained by emulsification of oil with aqueous WPI–CMC solution at pH 7.0 through homogenization at 12,000 rpm for 1 min, followed by ultrasonic processing for 5 min. The emulsions were then slowly acidified to pH 5.2. Droplet size, zeta-potential, and rheological properties of emulsions were measured to characterize their physicochemical properties. Creaming index along with protein surface coverage were used to measure the stability of emulsions. In the absence of CMC, WPI emulsions were prone to flocculation. WPI–CMC emulsion showed improved stability, but was highly dependent on the molecular weight and concentrations of CMC. Addition of less than 0.1% CMC enhanced the adsorption of protein at the interface and increased the repulsion between droplets, resulting in more stable emulsions compared to WPI emulsions. Further addition of CMC did not change the surface coverage of protein, but increased the viscosity of the continuous aqueous phase, further contributing to the stability of emulsions. Emulsions with low molecular weight CMC showed much faster creaming rate than those with high molecular weight CMC during 15 d of storage. This is likely due to combined effects of higher protein surface coverage on the droplets and increased viscosity of the aqueous phase. The flow behavior of emulsions changed from shear-thinning to Newtonian and back to shearthinning, however, the concentrations where these changes occurred were dependent on the molecular weight of CMC. This study demonstrates that complexation of whey protein with high molecular weight CMC improves the surface properties of protein and enhances the repulsion between droplets, contributing to the stability of the emulsions. The outcomes could be applied to improve the stability of food emulsions having pH values near the pI of protein.

Key Words: CMC, molecular weight, emulsion

1011 (T069) Induction of pitting on stainless steel 304 and 316 by *Bacillus sporothermodurans*. S. Gupta[*1], and S. Anand[2], [1]*South Dakota State University, Brookings,* [2]*Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Stainless steel (SS) undergoes corrosion in both polished and unpolished regions of dairy evaporators and dryers leading to product quality and economic concerns. The objective of this research was to investigate microbially induced corrosion (MIC) or pitting on SS 304 and 316 by a common milk contaminant; *Bacillus sporothermodurans*. These bacteria and their spores can persist on the SS milk contact surfaces in evaporators and dryers in the form of biofilms and may induce corrosion due microbial metabolic products such as enzymes, exopolymers, organic and inorganic acids and hydrogen sulfide. Many sulfate reducing bacteria (SRB) are active under oxygen stress and contribute to oxygen reduction reactions, thus influencing corrosion. In this study, polished and unpolished SS coupons (1'x1') of grades 304 and 306 were used to form biofilms of a dairy origin strain 10599 of *B. sporothermodurans* (Deutsche Sammlung von Mikroorganismen und Zellkulturen). This strain was found to exhibit sulfate reduction, as well as, proteolytic activities. About 10^7 cfu/mL of the overnight grown culture were inoculated in sterile 11% reconstituted non-fat dry milk (NFDM) in a Petri dish, in which sterile SS coupons were immersed. The incubation was performed at 30°C, being the optimum growth temperature of the culture. The suspension medium (NFDM) was replaced at regular intervals based on its pH drop to 5.0. bacterial counts from the spent media were taken at weekly intervals, while the biofilm counts were taken after every 2 wk to monitor the culture viability. The data were statistically analyzed to compare means. The counts in spent media and biofilms ranged from 10^5–10^6 cfu/mL and 10^2–10^4 cfu/cm^2, respectively. The coupons were examined using scanning electron microscope (SEM) for any corrosion or pit formation. Energy dispersive x-ray spectroscopy (EDS) was used to find the elemental composition of the control SS surface and was compared with that of the pits. From SEM observations and EDS data, it was established that pitting of surfaces for both grades of SS with biofilms got induced from wk 4 onward. These pits were distinct for the two grades; some pits were deep, while others were on the surface with corrosion products deposited over them. Elemental increase in sulphur and oxygen on the pit surfaces further confirmed the induction of corrosion. In conclusion, the biofilms of *Bacillus sporothermodurans* induced corrosion on the surface of stainless steel of both grades.

Key Words: corrosion, *Bacillus,* stainless steel, pitting

1012 (T070) Protective effect of lactic acid bacteria against H_2O_2–induced oxidative stress in Caco-2 cells. S. Liu[1], C. Man[2,3], X. Peng[1], W. Zhou[1], M. Guo[*4], and Y. Jiang[1,2,3], *[1]Dep. of Food Science, Northeast Agricultural University, Harbin, China, [2]Synergetic Innovation Center of Food Safety and Nutrition, Harbin, China, [3]National Dairy Engineering and Technology Research Center, Northeast Agricultural University, Harbin, China, [4]University of Vermont, Burlington.*

Oxidative stress can be defined as an imbalance between production of free oxygen radicals and reactive oxygen metabolism or repair the organism damage. A number of studies indicate that lactic acid bacteria (LAB) possess antioxidant activity due to their ability to regulate the activity of antioxidant enzymes during the cell metabolizing. The objective of this study was to establish a model of oxidative stress in human colon carcinoma cell line, Caco-2 cells, and to compare the protective effect of *Lactobacillus plantarum* NDC75017, *L. plantarum* ATCC14917 and *L. acidophilus* NCFM against hydrogen peroxide (H_2O_2)-induced oxidative stress in Caco-2 cells. The Caco-2 cells were divided into five groups: control group; oxidative stress group; *L. plantarum* NDC75017-protected group; *L. plantarum* ATCC14917-protected group and *L. acidophilus* NCFM-protected group. Caco-2 cells were exposed to 500 μM H_2O_2 in FBS-free DMEM for 30 min to induce oxidative stress, and then the three protection groups were respectively treated with 1×10^7 cfu/ml *L. plantarum* NDC75017, *L. plantarum* ATCC14917 and *L. acidophilus* NCFM suspended in FBS-free DMEM. After 4 h of incubation, the activity of intracellular antioxidant enzymes was measured. Superoxide dismutase (SOD) and catalase (CAT) activity were measured with the commercial kits based on colorimetric method, and the colorimetric reactions were determined at 450 nm and 405 nm, respectively. The data showed that CAT activity increased by 81% in oxidative stress group compared with control group, however no significant difference was observed in CAT activity between oxidative stress group and protection groups. SOD activity decreased by 33% in oxidative stress group compared with control group. All the three strains of the protection groups provided protection ($P < 0.05$) against H_2O_2–induced SOD activity reduction in different degrees, in which *L. plantarum* NDC75017-protected group showed the most significant increase in SOD activity by 44%. The results revealed that when the Caco-2 cell was suffering oxidative stress, the activity of intracellular antioxidant enzymes such as SOD and CAT would increase substantially. Some strains of LAB have positive effects on relieving oxidative stress and regulating intracellular antioxidant enzymes activity. Particularly *L. plantarum* NDC75017, which was isolated from traditional yogurt in Inner Mongolia of China, provided the greatest protection against H_2O_2–induced SOD activity reduction of the three strains, may have potential applications for use in the food industry. *This work was supported by National Science and Technology Project (2011AA100902).*

Key Words: oxidative stress, antioxidant enzyme, lactic acid bacteria

1013 (T071) fatty acid composition of cultured butter with probiotic *Lbc. acidophilus* La-5 produced in winter time. O. Tsisaryk[*1], L. Musiy[1], O. Golubets[2], and S. Shkaruba[2], *[1]Lviv National University of Veterinary Medicine and Biotechnologies, Ukraine, [2]Ukrmetrstandart, Kyiv, Ukraine.*

The objective of our study was to determine the fatty acid composition of sweet butter (SB) and cultured butter (CB) after *Lbc. acidophilus* was added to the starter. Control butter was churned from sweet cream (SB). Starters Flora Danica (*Lac. lactis, Lac. cremoris, Leu. cremoris, Lac. diacetilactis and Lbc. acidophilus La-5*), provided by Chr. Hansen, were used. Four groups of CB were produced: group 1, cream fermented at 30°C for 6 h by Flora Danica (CB1), 1:1 Flora Danica and La-5 (CB2) and La-5 (CB3); group 2, cream fermented at 37°C for 6 h by Flora Danica (CB4), 1:1 Flora Danica and La-5 (CB5) and La-5 (CB6); group 3 (Alnarps Winter method), left for 2 h at 8°Ñ, heated up to 20°Ñ and starter Flora Danica (CB7), 1:1 Flora Danica and La-5 (CB8) and La-5 (CB9) were added and fermented for 8 h, then cooled down to 12°Ñ and left for 10 h; group 4, starter Flora Danica (CB10), 1:1 Flora Danica and La-5 (CB11) and La-5 (CB12) were added to the butter grain. The experiment was replicated three times. Butter samples were stored at 20°C before the fatty acid analysis by GLC. The FAME were separated in a chromatography column (Hewlett-Packard 6890, 100 m × 0,25 mm × 0,2 μm [HP-88] 88%-cyanopropyl aryl-polysilixane, Agilent Technologies). The total content of the trans-9 isomers was 1.22 g in SB, whereas in CB2 the value was the lowest, i.e., 1.02 g/100 g of fatty acids. The total content of trans-11 isomers was the highest in CB2 (7.92 g/100 g) vs. 7.56 g/100 g of fatty acids in the SB ($P < 0.05$). Trans-11 C18:1 content increased from 5.19 in SB to 5.28–5.41% in the CB, the highest value observed for CB2 ($P < 0.05$). The percentage of cis-9,trans-11 CLA was the highest for CB2, CB5, CB6, CB8, when Flora Danica was combined with La-5, and for pure La-5 at 37°C (the optimal inoculation temperature for this strain). The total percentage of unpaired and branched-chain fatty acids was the same for all samples, but the percentage of medium-chain saturated fatty acids (C12-C16) slightly decreased from 37.34% in the SB to 37.0% in CB7 and CB9. CB1 and CB2 possessed the best taste, flavour and texture. Thus, adding La-5 into starter for cultured butter stimulates the 11-trans isomerisation of fatty acid and provides probiotic properties of cultured butter.

Key Words: butter, cultured butter, La-5, fatty acid

1014 (T072) Development of dairy products enriched with healthy lipids. J. Moats[*1,2], M. Epp[2], and D. Christensen[2], *[1]O&T Farms Ltd., Regina, SK, Canada, [2]University of Saskatchewan, Saskatoon, Canada.*

This study investigated the effects of feeding an extruded flaxseed product to dairy cattle on the fatty acid profile and sensory attributes of milk and Havarti cheese. The health benefits associate with certain lipids such as n-3 PUFA have been well documented. However, increasing the availability of these nutrients in dairy products for human consumption remains a challenge due to rumen biohydrogenation. Finding a mechanism for improving the fatty acid profile of dairy products without compromising sensory attributes would prove beneficial to the North American consumer. The hypothesis was: Feeding an extruded flaxseed product to dairy cattle would improve the fatty acid profile of milk and Havarti cheese without compromising sensory attributes. The objectives were: 1) to produce milk with elevated levels of n-3 through dietary means, 2) to produce Havarti cheese from control and n-3 milk, and 3) to evaluate the fatty acid profiles and sensory attributes of the milk and cheese. Six Holstein cows were offered a control diet followed by a treatment diet supplemented with an extruded flaxseed product with 70% flaxseed (LinPRO-R70) at 9% of TMR DM for 28 d. After the 28 d, milk samples were collected for compositional, fatty acid, and sensory analysis. Bulk milk samples were also collected and used to make Havarti cheese. Milk analysis showed a significant difference ($P < 0.01$) in total n-3 in the n-3 milk (1.25% FAME) compared to control milk (0.67% FAME). In a blind triangle test, sensory panelists were unable to identify source of milk indicating they were unable to detect any sensory differences between the control milk and the n-3 milk ($P < 0.01$). After 30 d of ripening, Havarti cheese was sampled for compositional, fatty acid, and sensory analysis. A significant difference in total n-3 ($P < 0.01$) was observed when comparing the n-3 cheese to control cheese. Cheese sensory results indicate that there were no differences in taste, texture or overall acceptability of the n-3 cheese compared to the control cheese. This trial suggests that including extruded flaxseed in the ration of dairy cattle may provide an opportunity for development and marketing of n-3 enriched dairy products.

Key Words: n-3, cheese, extruded flaxseed

1015 (T073) Evaluation of dulce de leche produced with different starches. F. Silva[1], H. Ferreira[2], M. Pinto[3], R. Stephani[2], A. Carvalho[*1], and Perrone[1], *[1]Federal University of Viçosa, Brazil, [2]Gemacom Tech, Juiz de Fora, Brazil, [3]Fedarl University of Viçosa, Brazil.*

Dulce de leche is technologically framed as preserved milk by evaporation and adding sugar. It usually presents creamy or pasty consistency, homogeneous texture, no lumps or flakes, bright caramel brown color, obtained by Maillard reactions and caramelization, peculiar aroma, and distinctive flavor, not too sweet or cloying. It presents good solubility in the mouth, and no perceptible sensory crystals. Starch is one of the main optional ingredients and can be used in its native form or modified. It can contribute to improve consistency and yield due to water retention, or assist in lactose crystallization control, by reducing the perceived appearing of crystals. The aim of this study was to evaluate the composition and properties of dulce de leche obtained with different types of modified starches, added in different concentrations of soluble solids during manufacturing. In this work, formulations of dulce de leche were prepared with different values of soluble solids concentration (39, 48, and 56°Brix). Yield, color, physicochemical composition, texture, crystal formation and sensory evaluation of dulce de leche were evaluated. Starch configures an important optional ingredient to production of dulce de leche, since increase shelf life without changes in texture, composition and yield characteristics of the product. Analysis revealed that the addition of starch reduced the formation of lactose crystals sensorially perceptible in almost all replications over the storage period. Further, dulce de leche with starch presented a good sensory acceptability among the analyzed attributes (color, texture, flavor and overall impression) and only significant difference ($P < 0.01$) was found for color. This was expected as the processes of the Maillard reaction and caramelization are associated with the dimming of the sweet, these reactions are less intense in this treatment.

Key Words: dulce de leche, starch, technology

1016 (T074) Rheological behaviors of edible casein-based packaging films under extreme environmental conditions, using humidity-controlled dynamic mechanical analysis. S. Akkurt[1], L. M. Bonnaillie[2], H. Zhang[1], and P. M. Tomasula[*2], *[1]Rutgers University, Dep. of Food Science, New Brunswick, NJ, [2]Dairy & Functional Foods Research Unit, Eastern Regional Research Center, Agricultural Research Service, USDA, Wyndmoor, PA.*

Thin casein films for food packaging applications possess good strength and low oxygen permeability but low water-resistance and elasticity. Customizing the mechanical properties of the films to target specific behaviors depending on temperature and humidity changes would enable a variety of commercial applications for casein-based films. The mechanical properties of edible films are vitally important to determine possible uses, such as replacement for plastic films. Dynamic mechanical analyses under controlled humidity (DMA-RH) can supply useful information about the mechanical properties and network-structure of hydrophilic protein films, including the storage modulus (E'), loss modulus (E"), deformation (swelling and shrinkage), damping behavior (tan-δ), as well as various transition temperatures and humidities. The dynamic

mechanical properties of solvent-cast (15% solids) calcium-caseinate/glycerol films (CaCas:Gly ratio 3:1) were fully characterized on a broad range of temperature (T = 5–90°C) and humidity (RH = 0–80%) using DMA-RH technology to study behaviors under normal or extreme environmental conditions. Citric pectin (CP, 0.05 to 1 wt.%) was then incorporated into CaCas films as a crosslinker using three different formulations (A, F, G) to examine CP effects on the properties and macrostructure of CaCas/Gly/CP films, and improve the stability of CaCas film under high humidity or temperature. The mechanical properties of casein films were extremely sensitive to formulation, CP content, T and RH, and DMA-RH technology proved a precise and effective tool to characterize composition/properties trends and point out various transition temperatures during T-ramps at 50% RH, and "transition humidities" during RH-ramps at 20°C. Transition-T and RH were considered to correspond to different critical points at which sufficient plasticization with water and/or heat triggered various rearrangements of the CP/protein/water network, until ultimate film-failure at the "melting point." DMA-RH enabled to precisely characterize shifts in E', E'' and tan-δ, as well as shifts in the various transition-T and transition-RH caused by different formulations or increased CP contents. Generally, the addition of CP improved the environmental stability of CaCas films: after addition of 1% CP, the melting-T increased from ~40°C to ~60°C, and the "melting-RH" from ~58% to ~67%, depending on formulation. F films showed the most drastic improvement with increased CP content, while G films appeared stronger and generally more T- and RH-stable at all CP contents. Improving the strength and environmental stability of casein-based films will broaden their possible range of application, such as use in edible food packaging.

Key Words: calcium caseinate, thin films, DMA

1017 (T075) Evaluation of a laboratory-scale batch crystallizer for lactose isolation from deproteinized whey. S. Beckman*, S. Anand, and L. Metzger, *Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Accurate replication of industrial-scale lactose crystallizations on a laboratory-scale apparatus has been a challenge for researchers wanting to improve lactose yield from dairy streams. The objective of this experiment was to develop a repeatable method for lab-scale batch crystallization of lactose from concentrated deproteinized whey (DPW). Commercial DPW powder was reconstituted to 60% total solids (wt/wt) in 80°C distilled water and held with agitation for 15 min for complete solubilization of lactose. The 80°C reconstituted DPW solution was immersed in an ice water bath to rapidly (15 min) cool to 50°C. Once the temperature reached 50°C, seed crystals were added (0.027 g per 100 g solution) to the DPW solution, mixed thoroughly, and held at 50°C with agitation for 1 h. After 1 h at 50°C, the solution was split into two portions by weight, and poured into lab-scale crystallizers. The crystallization apparatus consisted of a glass beaker with a PTFE magnetic stirrer and vanes for agitation. Stirring rate was maintained at 100 rpm throughout the cooling profile. The immersed crystallizer temperature was maintained by immersing a coil attached to a recirculation water bath into the bath surrounding the crystallizer. Crystallizers were cooled from 50 to 20°C at a rate of -0.130 ± 0.007°C per min. At the end of crystallization, the crystallizer was decanted and crystals were harvested from the bottom of the beaker for analysis. Recovered lactose crystals were observed microscopically (40×) to determine mean crystal size. Micrographs of lactose crystals were analyzed using image analysis software provided by the manufacturer of the microscope. A minimum of 10 crystals from each micrograph were measured for height, recorded as the length (μm) of the longest side, and duplicate micrographs were analyzed to improve accuracy. Three crystallizations were performed using the same lot of DPW reconstituted to 60% total solids. Results indicated that mean lactose crystal length obtained using this method were 21.36 ± 7.42 μm, with some larger (> 90 μm) crystals present in low numbers. Many small (< 10 μm) crystals were observed (not enumerated), which indicates the presence of secondary nucleation during cooling. The crystal sizes obtained using this method were small compared to what is encountered in industry. Small crystals would be easily lost during subsequent refining steps, decreasing yield. An optimized cooling profile, agitation speed during cooling, and crystal isolation scheme should be considered for future developments of this method.

Key Words: lactose, crystallization, lab-scale

1018 (T076) Dispersibility, suspension ability, solubility, and gelation properties of rehydrated frozen highly concentrated micellar casein. Y. Lu[1], D. J. McMahon[*1], and L. Metzger[2], [1]*Western Dairy Center, Utah State University, Logan,* [2]*Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Highly concentrated micellar casein (HCMC), a potential ingredient of protein fortified food, is a gel at cold temperature containing ~20% casein with whey proteins and lactose removed by microfiltration (and diafiltration) of skim milk. Dispersibility, suspension ability, solubility, and gelation properties of rehydrated frozen HCMC were characterized. Thawed HCMC was reconstituted to 3% protein with water or trisodium citrate buffer and adjusted to pH 7 then mixed using 1 min of high shear (7500 rpm) at 4, 12, 20, and 50°C, or 30 min of low shear (800 rpm) at 4, 20, and 50°C, followed by 18 h storage at 4°C. Dispersibility was defined as percentage by dry weight of HCMC that did not pass through a 250-μm sieve. Material that was 100% dispersible was centrifuged for 5 min and tested for suspension ability (using 80 *g*) and solubility (using 20,000 *g*). Protein in the supernatant was measured and

suspension ability and solubility calculated as percent protein that was not sedimented during centrifugation. The HCMC was also rehydrated with cream to obtain casein-to-fat ratio of 0.8 with casein levels from 9.3% to 12.5%, adjusted to pH 7.0, then stirred at 800 rpm for 30 min at 50°C, Gel modulus (G', G'') was measured at 50°C followed by cooling at 1°C/min to 5°C. At temperatures $\leq$ 20°C, HCMC was only partially dispersible in water (e.g., 60% dispersibility using high shear at 4°C), while at 50°C it was 100% dispersible. Mixing at $\leq$ 20°C followed by overnight hydration at 4°C also produced 100% dispersibility. Suspension ability at 50°C was ~90%, while mixing HCMC at $\leq$ 20°C followed by overnight hydration yielded only 50 to 60% suspension ability. Solubility followed a similar trend with HCMC having ~85% solubility at 50°C and only ~30% solubility at $\leq$ 20°C. Mixing HCMC in 60 mM trisodium citrate increased dispersibility, suspension ability and solubility of HCMC at 4°C to 97, 75, and 75%, respectively. Gelation temperature of the HCMC-cream mixture, defined as temperature at which G' = G'' was positively correlated (R^2 = 0.71) with casein level. Gelation occurred at ~35, ~25 and ~15°C with 12.5, 10.5, and 9.5% casein, respectively. This process was reversible with a hysteresis effect observed depending on whether the mixture was being heated or cooled. With a 10.5% casein HCMC-cream mixture exhibiting G' at 15°C of 30 Pa during cooling and 160 Pa during warming.

Key Words: casein, microfiltration, gelation

DAIRY FOODS: **TECHNICAL SESSION 3: FLUID MILK**

1019 (W073) Interaction of bovine and caprine milk α-caseins with tea polyphenols.
A. Mora-Gutierrez*, and R. Attaie, *Prairie View A&M University, Prairie View, TX.*

Tea (*Camellia sinensis*) is one of the most commonly consumed beverages. The anticarcinogenic properties of the many phenolic compounds of tea, including catechins, have been shown to inhibit tumor formation in rats. The anticarcinogenic properties of these phenolic compounds have been attributed to their antioxidant activity. However, the antioxidant activity of tea polyphenols may be affected when adding milk to tea. In this work, 7.6 mg/L bovine or caprine milk α-casein and 7.7 μM tea polyphenols (catechin, epicatechin, epicatechingallate, epigallocatechingallate, epigallocatechin and theaflavin) were added to an emulsion of linoleic acid (40 mM) prepared using a borate buffer (0.1 M, pH 8.5) and containing 0.1 M of sodium dodecyl sulfate. Interaction of bovine and caprine milk α-caseins with tea polyphenols in sodium dodecyl sulfate micelles was studied by a lipid peroxidation method. It was found that the antioxidant activities of the smaller catechins (catechin, epicatechin and epigallotocatechin) were higher in the presence of bovine and caprine milk α-caseins. The antioxidant capacity of epigallocatechin was greatly enhanced ($P < 0.05$) by milk α-casein (21.3% by bovine milk α-casein and 25.2% by caprine milk α-casein). The larger and bulkier polyphenols from tea (epicatechingallate, epigallocatechingallate, and theaflavin) did not significantly increase ($P < 0.05$) the lipids protecting effect. These results suggest that bovine and caprine milk α-caseins have the potentials to be used as natural ingredients to increase the antioxidant activity of tea polyphenols.

Key Words: bovine and caprine milks, α-casein, antioxidant activity, tea polyphenols

1020 (W074) Comparison of Jersey And Holstein-Friesian milk composition and coagulation properties.
J. H. Bland*, C. C. Fagan, and A. S. Grandison, *University of Reading, UK.*

Holstein-Frisian milk is increasingly blended with Jersey milk by cheesemakers to improve cheese yield. However, to date, no study has investigated the impact of blending on milk composition and properties. The objective of this study was to compare the composition and milk coagulation properties of Jersey and Holstein-Friesian milk produced in the United Kingdom. In addition, the effect of blending the two types of milk at different ratios (0 to 100% Jersey milk in Holstein-Friesian at 10% intervals), was evaluated. This knowledge could assist cheesemakers in optimising the blending process. Raw bulk milk composition from both breeds was measured every 3 mo over a year ($n = 55$). Significant variations in fat, protein, fat to protein ratio, casein, casein to protein ratio, fat globule size (D(4.3), D(0.5) and span), casein micelle size and titratable acidity were observed ($P < 0.05$). However, no significant difference in lactose, urea, somatic cell count, calcium ions, fat globule surface area mean particles D(3.2) and pH were seen. Blending the milks resulted in a linear trend for all significant variables with the exception of the fat globule volume mean diameter D(4.3) and casein micelle size which followed a quadratic trend ($P < 0.05$), which is believed to be due to change in the mineral balance. Coagulation properties were measured using a C-VOR controlled stress rheometer using raw milk at natural pH. Rennet Coagulation Time (RCT) (min) was defined as at the time at which a firmness of 0.5 Pa was attained, Curd Firmness (CF) (Pa) was taken 10 min after coagulation and Curd Firming Rate (CFR) (Pa min^{-1}) was calculated from the time for the gel to firm from 0.5 Pa to 2 Pa. Mean RCT of Holstein-Friesian was 58.7 min compared to 24.0 min for Jersey milk ($P < 0.001$). CF was 2.01Pa compared to 12.50 Pa and CFR 0.14 Pa min^{-1} compared to 0.49 Pa min^{-1} respectively ($P < 0.001$). CFR increased linearly with increase percentage of Jersey milk ($R^2 = 0.940$, $P = 0.003$) whereas RCT and CF followed a quadratic trend with increased percentage of Jersey milk ($R^2 = 0.9903$, $P = 0.007$ and $R^2 = 0.9965$, $P = 0.001$, respectively). This could be linked to the nonlinear trend found in fat globule volume mean diameter D(4.3) and casein micelle size. This study demonstrates that Jersey milk composition and coagulation properties are more suited for cheese making than Holstein-Friesian and additionally indicated that blending the two milk types gave beneficial synergistic effects for cheese.

Key Words: milk composition, milk coagulation, breed

1021 (W075) Light exposure affects milk acceptability and emotional response of college students.
A. M. Walsh, H. Potts*, and S. Duncan, *Virginia Tech, Blacksburg.*

Off flavors in fluid milk result from light exposure due to poor light-blocking characteristics of packaging materials. Even short periods of light exposure cause light-induced oxidation leading to noticeable differences in flavor. There is no direct evidence that light-induced oxidation affects milk acceptability. In this study, effects of fluorescent light exposure (2000 lux) on fluid 2% milk for periods of 8 and 168 h (7 d; 4°C) were determined on oxidative stability of milk, consumer acceptability of the product, and the resulting emotional response from the sensory experience. Oxidative stability was measured by thiobarbituric reactive substances (TBARS) and riboflavin (Rb) assays. Consumer ($n = 53$) acceptability of the product was reduced, as measured with a 9-point hedonic scale and a check-all-that-apply emotional response scorecard. TBARS assays showed significant in-

creases in oxidation by-products by 168 h (P = 0.006). Rb decreased significantly, with 71% loss by 168 h. Although there was no significant chemical evidence of oxidation by 8 h of light exposure, hedonic scores decreased significantly from 7.20 (like moderately) to 5.85 (below like slightly) (P = 0.008). Acceptability decreased severely by 168 h of light exposure (P = 2.15 E-10) with light-exposed milk scoring only a 3.46 (between dislike moderately to dislike slightly). Light-protected milk maintained a score of 7.0 over the 7 d of refrigerated storage. Emotion term selection reflected the acceptability change; across all milk samples the terms calm, content, good and satisfied were shared ($\geq$ 20% frequency of the term used and < 8% difference in percent frequency between samples compared). Unique terms for 'liked' samples (hedonic score: 6 to 9) included friendly, good-natured, happy, interested, peaceful, pleasant, pleased, quiet, safe, warm, and whole. However, 'disliked' samples (hedonic score: 1 to 4; mostly light-exposed milk samples) exclusively shared the term disgusted. Milk that is protected from light maintains a high quality flavor with positive emotional responses whereas the influence of light degradation causes negative sensory and emotional responses. The emotional and flavor acceptability of milk is particularly important in the 18- to 25-yr-old population focused on in this study. This population is establishing independent selection, purchasing habits, and consumption of products that influence future health and well-being. In the tested population, only 24% reported consuming any milk (whole, 2%, 1%, skim) more than once daily. The selection of milk packaging that protects milk nutrients and flavor quality is important consideration for increasing milk consumption.

Key Words: milk, emotion, oxidation

1022 (W076) Fatty acid compositions of low-fat goat milk ice creams formulated with commercial ice cream mix and 3 different levels of caprine milk fat. C. E. McGhee, B. P. Gupta*, and Y. W. Park, *Fort Valley State University, Fort Valley, GA.*

Low-fat ice cream has been a popular frozen dairy food among the consumers due mainly to health concerns. However, scientific research on nutritional quality of caprine milk ice cream has been very scarce. The objective of this study was to determine fatty acid compositions of three types of low-fat goat milk ice creams. Three batches of three different low-fat caprine milk ice creams were manufactured using skim (0.46%; SIC), 2.0% (2IC) and whole (3.65%; WIC) goat milk by addition of a commercial ice cream mix (0.25% fat) in fluid goat milk. The soft-serve goat ice creams were made using Sani Serv ice cream machine (A5223P, Mooresville, IN), and all experimental fresh ice creams were stored at -18°C in a freezer for 0, 2, 4, and 8 wk. Fatty acids compositions of all experimental ice cream samples were analyzed using a GC–MS (Thermo Electronic TRACE GC Ultra, Austin, TX) equipped with an automatic sampler (Thermo Electronic AS-3000) and a fused silica capillary column (0.25 mm i.d. x 0.25μm × 60 m; SP-2380 Supelco, Bellefonte, PA). The results showed that concentrations of fatty acids C4:0, C6:0, C8:0, C12:0, C14:0, C16:0, C16:1, C18:0, C18:1, C18:3, C24:0 in the ice creams were significantly (P < 0.05 or 0.01) affected by the three different levels of fat treatments, while those of C10:0, C14:1, C18:2, C20:0, C22:0 acids were not influenced by the fat treatment. The C12:0, C16:0 and C18:1 acids were the most abundant fatty acids in the experimental goat ice creams, while C12:0 (lauric acid) revealed the highest concentration among all 16 fatty acids. There were no differences in levels of individual fatty acid between storage periods, where the same trend of storage effect occurred in all 16 fatty acids. The fat level x storage interaction effects were also not significant on fatty acid contents of all three goat ice creams. It was concluded that the highest content of lauric acid among all fatty acids was probably due to the existence of coconut oil in the commercial ice cream mix, which was used in the manufacture of goat milk ice creams in this study.

Key Words: goat milk, ice cream, fatty acids

1023 (W077) Application of non-nutritive natural sweeteners to skim chocolate milk. *X*. E. Li*, K. Lopetcharat, and M. Drake, *Southeast Dairy Foods Research Center, NCSU, Raleigh, NC.*

The additional sugar content of chocolate milk has raised health concerns, and artificial non-nutritive sweeteners have been used to reduce sugar and calories. However, artificial sweeteners lack appeal to parents for purchase of chocolate milk for their children. Natural non-nutritive sweeteners may be viable alternatives to sweeten chocolate milk. The objective of this study was to evaluate stevia or monk fruit extract as the sole or partial sweetener source for skim chocolate milk. Magnitude estimation scaling (MES) with 14 trained panelists was used to create power function curves for the sweet taste of stevia and monk fruit extract in water and skim chocolate milk. The iso-sweetness of 150 mM sucrose chocolate milk, the lowest acceptable sweetness level for young adult consumers in a previous study, from stevia or monk fruit extract were calculated and confirmed by a 2-alternative forced choice (AFC) test with 25 panelists. Due to other taste and flavor attributes of the two natural non-nutritive sweeteners, iso-sweetness from a mixture of sucrose and natural non-nutritive sweetener were also investigated. Chocolate milks (sweetened with sucrose, stevia, monk fruit, stevia:sucrose blend, or monk fruit:sucrose blend) were manufactured and evaluated by young adult consumers (n = 120) for overall and sweet taste liking. Chocolate milks that were sweetened by natural non-nutritive sweeteners alone received lower liking scores compared to chocolate milks sweetened by sucrose or sucrose:non-nutritive sweetener blends (P < 0.05). The results demonstrate that natural non-nutritive sweeteners can be successfully applied in choco-

late milks with no change in liking from sucrose when applied as blends replacing up to 50% of sucrose.

Key Words: chocolate milk, flavor, sugar reduction

1024 (W078) Cross-linking of milk proteins can reduce its susceptibility to plasmin-induced hydrolysis.

H. Bhatt*[1,2], A. Cucheval[2], C. Coker[2], H. G. Patel[3], A. Carr[1], and R. Bennett[1], *[1]Massey University, Palmerston North, New Zealand, [2]Fonterra Research & Development Centre, Palmerston North, New Zealand, [3]South Dakota State University, Brookings.*

Plasmin-induced proteolysis is a major problem in milk and dairy beverages and must be controlled, as it leads to flavor (bitterness) and texture (gelation, sedimentation) defects. Plasmin cleaves proteins at the carboxyl site of lysine-X and arginine-X bonds with a preference for the lysine-X bond. We therefore hypothesized that cross-linking of milk proteins and modification of lysine residues through transglutamination and the Maillard reaction would reduce the susceptibility of milk proteins to the action of plasmin. Lysine residues on the β-casein backbone were cross-linked with glutamyl residues to different extents by transglutamination and lysine-sugar-lysine cross-linking was achieved through the Maillard reaction. The modified systems were then hydrolyzed by plasmin. The extents of cross-linking and the hydrolysis reaction were monitored by quantifying the formation of the different hydrolyzed products, e.g., γ-casein and proteose peptones, using sodium dodecyl sulfate polyacrylamide gel electrophoresis and reverse phase high performance liquid chromatography. Cross-linking of lysine residues with glutamyl residues by transglutamination and lysine-sugar-lysine cross-linking through the Maillard reaction clearly affected plasmin-induced hydrolysis negatively and reduced the susceptibility of b-casein to plasmin-induced hydrolysis. This could have been due to 1) the modification of lysine making it unrecognizable to the substrate-binding pocket of plasmin, and 2) the cross-linking preventing the release of hydrolyzed peptides. In terms of controlling plasmin-induced hydrolysis, it appeared that Effect 1 played a more major role in Maillard reaction cross-linking and that Effect 2 played a more major role in transglutamination. It can be concluded from this study that the cross-linking of proteins may be a useful tool for controlling the plasmin-induced hydrolysis of milk proteins and therefore for minimizing the texture- and flavor-related defects that are caused by the release of hydrolyzed peptides.

Key Words: plasmin, transglutamination, Maillard reaction

1025 (W079) Optimization of γ-aminobutyric acid production of *Lactobacillus plantarum* and determination of flavor substances in γ-aminobutyric acid-enriched fermented milk.

L. Li[1], C. Man[2,3], T. Li[1], Y. Shan[2,3], Y. Deng[1], M. Ding[1], M. Guo*[4], and Y. Jiang[1,2,3], *[1]Dep. of Food Science, Northeast Agricultural University, Harbin, China, [2]National Dairy Engineering and Technology Research Center, Northeast Agricultural University, Harbin, China, [3]Synergetic Innovation Center of Food Safety and Nutrition, Harbin, China, [4]University of Vermont, Burlington.*

Gamma-Aminobutyric acid (GABA) is a nonprotein amino acid with positive physiological properties to animals and human. Two objectives were achieved in this work: 1) optimization of the GABA production of *Lactobacillus plantarum* NDC 75017 isolated from traditional yoghourt in Inner Mongolia of China, and 2) exploration of the flavor variations of GABA-enriched fermented milk by this strain in shelf life. High performance liquid chromatography (HPLC) and o-phthaldialdehyde (OPA) precolumn derivatization were used to determine the GABA concentrations in MRS culture media under different fermented conditions. GABA maximum accumulation increased to 3.004 folds of the original production in the following optimized condition: 75 mM L-solium glutamate (L-MSG), 20 μM pyridoxal 5'-phosphate (*P*LP), 3 mM $CaCl_2$, 3% inoculation in MRS and 48 h fermentation with the initial pH value of 4.5. In the above condition, *L. plantarum* NDC 75017 was cultured to be the starter of GABA-enriched fermented milk and it was stored in 4°C for 21 d. Six typical flavor substances were measured by spectrophotometry and HPLC at 11 point-in-time during the whole storage. Diacetyl increased gradually from 3.226 to 4.975 mg/L. Acetaldehyde went up at first, peaked at the third day with 8.9 g/L and went down slowly to 7.259 g/L at last. Citric acid, pyruvic acid, lactic acid and formic acid contents of fermented milk were stable without significant variations and the concentrations of them at the end of storage were 132.772 mg/L, 10.782 mg/L, 109.268 mg/L and 82.757 mg/L, respectively. Compared to general fermented milk products, lower content of diacetyl and lactic acid but higher concentration of formic acid showed in the GABA-enriched fermented milk and other three flavor substances were similar between them. Results in the present study suggested that the optimized GABA-producing *L. plantarum*NDC 75017 could be the potential starter applied in the manufacture of fermented milk or other dairy products with healthcare functions and unique flavors. *This work was supported by National Science and Technology Project (2011AA100902) and National Natural Science Foundation of China (31171718).*

Key Words: γ-aminobutyric acid, *Lactobacillus plantarum*, fermented milk

1026 (W080) Comparison of odd and branched chain fatty acids profiles of cow, yak, buffalo, Jersey cattle, goat, camel and horse milk fat. L. Ma[1,2], D. P. Bu[2], J. T. Chen[2], and J. Q. Wang[*2], *[1]Inner Mongolia Agricultural University, Huhhot, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

To unravel the expression profile of odd and branched chain fatty acids (OBCFA) in cow (n = 20), yak (n = 20), buffalo (n = 20), Jersey cattle (n = 20), goat (n = 20), camel (n = 8) and horse (n = 8) milk samples which were collected around the fourth month of lactation for each species from February to April 2013, composition and variation were detected by gas chromatography-mass spectrometry selected scan mode (GC–MS/SCAN) (7890N-5975C, Agilent Technologies Co., Ltd., USA). Descriptive statistics and Duncan's multiple comparison of OBCFA profiles were obtained by SAS 9.1 via GLM model (SAS Institute Inc., Cary, NC). All OBCFA data sets were analyzed by principal component analysis (PCA) using the Unscrambler 9.8 (CAMO SOFTWARE AS, Oslo, Norway) and submitted to further hierarchical clustering using Cluster 3.0 software (USA). Significant differences in milk OBCFA composition of different species were observed. In cow, yak, buffalo and Jersey cattle milk, the highest composition of OBCFA were *iso*-C15:0 and C15:0, in goat milk were C15:0 and *anteiso*-C17:0, while in horse and camel milk were *iso*-C15:0 and *anteiso*-C17:0, respectively. Among various species milk, *anteiso*-C13:0 accounted for the smallest percentage of OBCFA. Total OBCFA composition was highest in yak milk. Most of the individual OBCFA were significantly highest in yak milk, except for *anteiso*-C17:0 which was a little lower than in camel milk. However, most individual OBCFA and the total amount of OBCFA in horse milk were significantly lower than in other species' milk. The cluster analysis result showed that cow, buffalo, Jersey cattle and yak milk samples comprised a major sample cluster, and goat milk added to this group yielded another cluster. Camel and horse milk were in another major cluster. In addition, principal component analysis (*P*CA) result could also be used to group different species according to OBCFA and demonstrate an effective way to distinguish between yak milk and others' milk. It was concluded that milk from different species had its special OBCFA profile.

Key Words: odd and branched chain fatty acids, species milk, gas chromatography-mass

1027 (W081) Detection and comparison of major and trace elements from different species milk by inductively coupled plasma–mass spectrometry. L. Ma, D. P. Bu, J. T. Chen, and J. Q. Wang**, State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Milk contains lots of nutrients, such as proteins, lipids, carbohydrates, vitamins and elements. As a complex biological fluid and an excellent source of macro and micro nutrients, milk can play an important way in meeting the nutritional requirements for individuals. The content of nine major and trace elements in cow (n = 20), yak (n = 20), buffalo (n = 20), Jersey cattle (n = 20), goat (n = 20), camel (n = 8) and horse (n = 8) milk samples which were collected around the 4thmonth of lactation for each species from February to April 2013 in China have been determined by inductively coupled plasma–mass spectrometry (ICP–MS) (Agilent 7700X, Agilent Corporation, United States) after microwave digestion. Descriptive statistics and Duncan's multiple comparison of protein contents were obtained by SAS 9.1 via GLM model (SAS Institute Inc., Cary, NC). To check the applicability of the proposed method to the analysis, two certified reference materials available for powder skim milk (GBW10017) and for cabbage power (GBW1001) were analysed to obtain satisfactory results in all cases. The result showed that the contents of major elements (Na, Mg, K, Ca, Fe) and trace elements (Mn, Co, Zn, Se) in different species milk were significantly different. All of the major elements were lowest in horse milk. Much higher concentrations of Mg and Ca were found in buffao milk. The content of Fe was highest in cow milk. Na and K were found highest in camel milk and goat milk, respectively. The concentrations of trace elements (Mn, Co, Zn, Se) were almost higher in cow milk than in other species milk, except for Se, which was a little lower than in buffalo milk. The content of Co was found nearly the same in cow, yak, buffalo, Jersey cattle, camel and horse milk, except for in goat milk, which was a little lower. In addition, Se was not detected in horse milk. It was concluded that the contents of major and trace elements in milk from different species were various and the trace element of Se was not detected in horse milk in this study.

Key Words: major and trace elements, species milk, inductively coupled plasma–mass spectrometry

1028 (W082) Identification of microRNA in fresh milk of cow and goat. D. P. Bu[1], L. Ma[1], X. M. Nan[1], J. J. Loor[2], and J. Q. Wang[*1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]University of Illinois, Urbana.*

MicroRNAs (miRNAs) are a class of small RNA molecules (~22 nt) that inhibit translation or induce degradation of pro-

tein-coding mRNAs containing complementary sequences to mRNAs. Recent studies have demonstrated the presence of miRNAs in body fluids such as serum, plasma, saliva, urine and milk. The objective of this study was to identify the differences of microRNA profiles between cow whey and goat whey. Cow whey samples and goat whey samples without milk fat, somatic cells and major proteins were obtained by a series of centrifugations and filtrations. miRNA was isolated and the quantity of RNA measured. Isolated miRNAs were amplified and sequenced by Solexa sequencing technology. After bioinformatics analysis, 381 loci possessed the typical stem-loop structures matched to the known miRNA hairpins and a total of 34 loci with novel hairpins were identified as novel miRNAs in cow whey. In goat whey, a total of 111 microRNAs were obtained, of which 13 were novel microRNAs. Among all the microRNAs detected in cow and goat whey, 29 miRNAs were common between these species. Overall, the miRNA profile of cow whey and goat whey differed significantly.

Key Words: fresh milk, whey, microRNA

1029 (W083) Sodium azide and potassium dichromate not suitable preservative of raw milk for detection β-lactamase by cylinder plate method. Y. Zhang[1,2,3], N. Zheng[1,2,3], F. Wen[1,2,3], S. Li[1,2,3], S. Zheng[1], and J. Wang[*1,2,3], *[1]Ministry of Agriculture– Laboratory of Quality and Safety Risk Assessment for Dairy Products, Beijing, China, [2]Ministry of Agriculture– Milk and Dairy Product Inspection Center, Beijing, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Upon selecting the appropriate sample of raw milk, keeping the stability of physicochemical property of β-lactamase relevant compounds is essential for its successful detection and identification in systematic analysis. However, there is no particular standard pre-treatment procedure for detection of β-lactamase in raw milk. This study examined the storage time of refrigeration (4 h, 8 h, 24 h, 48 h) and freeze (1 d, 7 d, 30 d), the temperature (25°C, 40°C, 60°C) and times (1, 3, and 5) of thawing for freeze sample and the kinds of preservative (sodium azide, potassium dichromate, sodium thiocyanate, bronopol, methanol) using cylinder plate method. Milk sample, collected from individual cow and negative for β-lactamase testing by cylinder plate method, was divided into 10 aliquot of the milk sample, two aliquot of the milk sample adding nothing were the control group, eight aliquot of the milk sample adding 4 U/mL β-lactamase were the experiment group. Refrigeration time within 48 h and freeze time within 30 d had no influence on the detection result of β-lactamase, thawing temperature below 60°C and thawing times below five times for freeze sample were also no influence. β-lactamase could not be detected when adding sodium azide and potassium dichromate in raw milk, whereas sodium thiocyanate, bronopol and methanol had no effect, suggesting sodium azide and potassium dichromate were not suitable preservative of raw milk for detection β-lactamase by cylinder plate method.

Key Words: pre-treatment, β-lactamase, raw milk

1030 (W084) Discrimination of reconstituted milk and over-processed milk in pasteurized and UHT milk. H. Wang[1,2,3], N. Zheng[1,3], F. Wen[1,3], H. Wang[2], X. Guo[1,3], S. Li[1,3], and J. Wang[*1,3], *[1]Ministry of Agriculture– Laboratory of Quality and Safety Risk Assessment for Dairy Products, Beijing, China, [2]College of Animal Science and Technology, Yangzhou University, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

The objective of the present study was to distinguish over-processed milk and reconstituted milk by comparing the heat treatment indicators in raw milk, over-processed milk and raw milk plus reconstituted milk under both pasteurized and ultra high temperature (UHT) conditions. The contents of furosine and lactulose, as well as the ratio of lactulose to furosine were investigated. Lactulose was detected using UV spectrophotometer by enzymatic method (ISO 11285/2004) with modifications and furosine was detected by using high-performance liquid chromatography (HPLC) according to ES ISO 18329/2012. The content of furosine was less than 12 mg/100 g protein, when the milk was pasteurized from pure raw milk; if the content of furosine was more than 12 mg/100 g protein, it can be considered as reconstituted milk when L/F was less than 1, otherwise it could be regarded as over-processed milk when L/F was higher than 1. If it was produced from pure raw milk under UHT conditions, the content of furosine would be less than 140 mg/100 g protein; if the content of furosine was more than 140 mg/100 g protein, it can be considered as reconstituted milk when L/F was less than 2, otherwise it could be regarded as over-processed milk when L/F was higher than 2. Our results suggest that over-processed milk and reconstituted milk in pasteurized and UHT milk might be differentiated by the content of furosine and the ratio of lactulose and furosine (L/F).

Key Words: reconstituted milk; over-processed milk; lactulose/furosine

1031 (W085) Caseinomacropeptide index (cmp), microbiology and protein content of UHT chocolate milk-whey-based drinks in Brazil. F. P. Paula[1], L. M. Melgaço[1], A. B. Jardim[1], C. F. A. M. Penna[2], L. M. Fonseca[1], M. R. Souza[2], M. P. Cerqueira[2], and M. O. Leite[*2], *[1]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, [2]Universidade Federal de Minas Gerais* (*School of Veterinary Medicine), Belo Horizonte, Brazil.*

Ultra high temperature (UHT) milk-whey-based-drinks are obtained by processing a mix of milk and cheese whey. In Brazil, this may additionally be added of food ingredients, vegetable fat, and other milk derivatives. The intake of this product is popular among children in Brazil, and it is commonly used to replace milk consumption. Consequently, nutritional concerns emerge because of the low protein content due to whey addition. The objective of this work was to evaluate the protein content and microbial contamination, and to estimate the caseinomacropeptide index (CMP) of this beverage. Fifty-six samples of UHT chocolate milk-whey-based drinks from seven dairy plants, and eight production lots each were collected in the city of Belo Horizonte, MG (Brazil) and analyzed for protein content (Kjeldahl), CMP index by high performance liquid chromatography (HPLC) and count of aerobic mesophilic bacteria (total plate count). Descriptive statistics was used. All samples were in compliance with Brazilian standards for aerobic mesophilic countings (< 1.0 CFU/mL). Average CMP index (mg/L), and protein content (g/100 g) for the seven brands are showed in Table 1031. Samples with higher CMP index were correlated with lower protein content (Pearson correlation of -0.7 at $P = 0.07$), as expected. Although protein content results were in compliance with Brazilian legislation, the low levels found in several samples are indicative of potential low protein intake by children with high consumption of this food.

Key Words: milk-whey-based-drinks, caseinomacropeptide index, protein content, microbiology

Table 1031.

Brand	CMP (mg/L)	Protein (g/100g)
A	912.5+	1.15+
B	646.31+	2.06+
C	611.24+	2.93+
D	566.64+	2.04+
E	498.93+	1.73+
F	332.67+	2.93+
G	328.23+	2.49+

1032 (W086) Stability of vitamin a palmitate in raw skim milk and apple juice on exposure to ultraviolet light. M. S. Mohan[*], and F. Harte, *University of Tennessee, Knoxville.*

Vitamin A palmitate is commercially fortified in milk. Earlier studies have indicated that the vitamin A fortified in milk is associated with the casein micelles in milk. Our objective was to study whether casein micelles protect vitamin A palmitate from degradation on exposure to ultraviolet (UV) radiation. For this purpose raw skim milk and apple juice was fortified with vitamin A palmitate (1.4 mM) after dispersing in ethanol (2.44% v/v ethanol in sample) with rotary homogenization at 10, 000 rpm for 3 min. The vitamin A milk and juice samples were then subjected to strong UV radiation (365 nm, intensity at the surface of transilluminator 5300μW/cm^2) for 0, 5, 10, 15, and 20 min. The vitamin A was extracted with hexane and quantified by using a normal phase HPLC at 325 nm. Vitamin A milk samples were subjected to size exclusion chromatography (SEC) and the fractions pertaining to the same peak at 280nm were pooled, then freeze dried and analyzed for vitamin A content. There was rapid degradation of vitamin A palmitate in juice samples, with a reduction of 59% of vitamin A of the initial amount added, on exposure to 20 min of UV light. The vitamin A content was 100%, 97%, 88%, 67% and 41% (± 4%) of the initial amount added, on subjecting to UV exposure for 0, 5, 10, 15, and 20 min, respectively. While the vitamin A in milk samples degraded only 6% over 20 min of UV exposure, with a degradation pattern 100%, 100%, 99%, 97% and 94% (± 4%) of the initial amount added, on subjecting to UV exposure for 0, 5, 10, 15, and 20 min, respectively. The difference in the percentage of vitamin A between milk and juice was especially significant after 15 and 20 min of UV light exposure ($P < 0.01$). The quantification of vitamin A in the SEC fractions indicated that vitamin A palmitate associated only to casein micelles in milk with a recovery of 42% of the initial amount added within the casein section. The results indicate that the association of vitamin A palmitate and casein micelles in raw skim milk samples provide a protective effect to vitamin A palmitate against degradation on exposure to UV light.

Key Words: vitamin A palmitate, ultraviolet, casein, milk

1033 (W087) Effect of abomasal ferrous lactate infusion of dairy cows on milk proteins. A. Wang[*1], A. M. Dietrich[1], S. Duncan[1], K. F. Knowlton[1], and W. Slade[2], *[1]Virginia Tech, Blacksburg, [2]University of North Carolina at Chapel Hill, Chapel Hill.*

Water makes up more than 80% of the total weight of milk. However, the influence of water chemistry on milk quality has not been extensively studied. Heavy metals in bovine drinking water may affect the synthesis of milk and subsequent milk quality. The objective of this study was to determine the in-

teraction of ferrous lactate infusion in dairy cows, representing the intake of iron through drinking water, on qualitative changes in protein composition of their milk. Four ruminally-cannulated cows each received aqueous infusions of ferrous lactate at 0, 200, 500 or 1250 mg of Fe/d in a Latin Square design. A wash-out period (7 d) existed between each infusion period (7 d). Raw milk was collected at d 6 of each infusion period and was homogenized and pasteurized before analysis. two-dimensional electrophoresis (2-DE) coupled with matrix-assisted laser desorption/ionization time-of-flight/time-of-flight (MALDI-TOF/TOF) high-resolution tandem mass spectrometry analysis was applied to characterize the milk proteins. About 56 protein spots were identified and represented the major and minor casein and whey proteins. Although the protein compositions were similar across cows, the intensity of specific protein spots such as α-S1-casein and k-casein showed differences among different cows. Within-cow comparison demonstrated diminished spot intensity and less focusing along the pI gradient for some spots with increasing ferrous infusion. Such variation may indicate that high iron in bovine drinking water affects some cows more than others. Cow D presented the most stable and consistent protein spots both in position and intensity throughout the infusion period. The content of copper and iron in milk from this cow was consistent and was very near the four cow average. In contrast, milk from cow C presented more α-S1-casein spots when consuming high iron-contaminated water then when consuming regular drinking water; the iron and copper concentration in her milk decreased with increasing infusion concentration. However, cow A lost several α-S1-casein spots when drinking high ferrous sulfate concentration water. The iron-binding protein, lactoferrin was observed at both control and high ferrous infusion periods for cows. There is qualitative evidence that iron in drinking water may affect milk proteins differently in different cows.

Key Words: proteins, lactoferrin, iron

1034 (W088) Effect of high hydrostatic pressure processing on in vitro digestion of milk proteins and fats. D. X. Ren[1,2], D. L. Van Hekken[1], M. H. Tunick[1], and P. M. Tomasula[*1], *[1]USDA, ARS, ERRC, Dairy and Functional Foods Research Unit, Wyndmoor, PA, [2]Institute of Dairy Science, College of Animal Science, Zhejiang University, Hangzhou, P.R., China.*

The use of high hydrostatic pressure processing (HPP) is increasing in popularity in the food industry. Its ability to modify milk proteins and fats suggests that it may be useful in creating foods that suppress appetite; however, its effect on the digestibility of proteins and fats is unclear. The objective of this study was to compare the change in clot size with time during in vitro simulated fasting gastro-intestinal digestion of protein and fat for HPP-treated raw whole milk (WP), homogenized raw whole milk (WHP), and skim milk (SP) to that of untreated raw whole (WR) and raw skim milk (SR), and WR and SR milk treated by HTST pasteurization (72°C, 15 s) with or without homogenization. HPP was conducted at 600 MPa (3 min, 21°C). Milk digestion procedures followed the 2012 U.S. Pharmacopeia using simulated gastric fluid (SGF) for 1 h followed by simulated intestinal fluid for 2 h. The average particle size of WR 8.5 ± 0.3 μm remained unchanged with all processing treatments while the average particle size of SR increased from 1.3 ± 0.3 μm to 4.6 ± 0.6 μm with HPP treatment only. The clots that formed on addition of SGF for WR and SR and with the various processing treatments were then followed for 3 h using a light-scattering particle-size analyzer. The clot sizes of processed WR samples were > those for the raw samples but were not different after 3 h. The clot size for SR was < that for SP. after 3 h but the amounts of SR and SP. protein digested were not different ($P < 0.05$). In vitro % protein digestibilities of WR and SR were similar regardless of treatment, ranging from 85 to 90%, except for HPP-treated WR and SR which ranged from 62 to 70%. Free fatty acid release (FFAR) decreased in the order WHP > WR > WP, indicating that WHP was the most digestible due to the increased surface area for enzyme contact and fat breakdown. Stearic and oleic acids, located on the outside of the triglyceride molecule, degraded approximately twice as fast as the other fatty acids. FFAR for WP was 40% < that of WR. Results indicate that HPP processing may possibly be used to moderate in vitro protein and fat digestion of milk.

Key Words: high pressure processing; digestibility; free fatty acids

---

1035 (W089) Effect of storage temperature on the physio-chemical properties of skim milk powders treated with chelators. V. Sikand[*1], P. S. Tong[1], S. Vink[1], and S. Roy[2], *[1]Dep. of Dairy Science, California Polytechnic State University, San Luis Obispo, [2]Dep. of Statistics, California Polytechnic State University, San Luis Obispo.*

The objectives of this study were to determine the impact of storage temperature on functional properties– solubility, opacity and heat stability compared to freshly manufactured skim milk powder (SMP) samples treated with mineral chelators. This study was conducted by adding 5, 15, and 25 mM sodium citrate dihydrate (SCD), sodium polyphosphate (SPP) and disodium EDTA (DSE) to skim milk concentrate (30% total solids) and adjusting the concentrate to 6.65 pH before spray drying. One set of sample bags were stored at room temperature (22°C). The second sets of bags were kept at 37°C for 3 mo. The experiment was repeated twice. Samples were tested for solubility index (SI) and reconstituted to contain 9% TS and tested for opacity by using a Hunter Lab Colorimeter. Heat stability was determined by measuring the heat coagulation time (HCT) at 140°C as the time required for visible flocculation for samples. SI indicated high solubility of all SMP

samples. However, lower values for SI were observed for samples treated with 5mM SPP. and DSE (0.13 mL) as compared to samples treated with SCD (0.3mL). Furthermore, low SI values were observed with an increasing level of chelating agents regardless of chelator type. No significant difference was observed in SI of samples stored at 37°C as compared to SI tested for freshly manufactured samples. A decreased opacity (L* value) or an increase in the lightness of samples was found with increasing levels of mineral chelating salt treatment ($P < 0.001$). Furthermore, lower L* values were observed in samples stored at 37°C ($P < 0.001$) as compared to freshly manufactured samples. Heat stability studies showed that SMP (PH 7.0) treated with 5mM DSE or SCD chelators had higher HS (> 30 min) as compared to the SPP. (16 min). Samples treated with 15mM SPP. showed significantly higher HS (20 min) as compared to SCD or DSE treated samples. Samples showed poor HS (< 5 min) chelator type at 25mM concentration level. Slightly lower HCT values were observed for samples stored at 37°C ($P < 0.001$) as compared to freshly manufactured samples, regardless of any concentration level. The results from this study showed that storage temperature may impact the functional properties.

Key Words: SMP, chelators, solubility, heat stability

1036 (W090) Effect of sunflower oil, vitamin E and selenium inclusion in the diet of dairy cows on the sensory acceptability of milk. L. F. D'Abreu*, C. Rodrigues, A. Saran Netto, J. L. Guimarães, M. A. Silva, and N. D. P. Lopes, *School of Animal Science and Food Engineering, University of São Paulo, Pirassununga, Brazil.*

The objective of the present study was to evaluate the effect of sunflower oil, vitamin E and selenium inclusion in the diet of dairy cows on the acceptance of sensory attributes of milk. Thirty-two Jersey cows in early lactation were divided into four experimental groups in a complete randomized design. The animals were randomly assigned to receive one of the following diets: 1) control (C, $n = 8$); 2) 3.5 mg selenium/kg dry matter (DM) + 3000 IU vitamin E/kg DM (SE, $n = 8$); 3) 4% inclusion of sunflower oil (total diet DM basis) (O, $n = 8$), 4) 4% inclusion of sunflower oil (total diet DM basis) + 3.5 mg selenium/kg DM + 3000 IU vitamin E/kg DM (OSE, $n = 8$). Before sensory evaluation, the milk was pasteurized. Sixty untrained tasters received the samples in complete blocks and used a nine-point hedonic scale for acceptance testing regarding the attributes color, odor, flavor and mouthfeel of milk and a scale of intensity difference of odor and flavor for the test of difference from the control. Data were submitted to ANOVA analysis of variance and Tukey test was conducted to compare means, to the level of 5% of significance using the PROC MIXED of SAS version 9.1. In the test of difference from the control, no difference ($P > 0.05$) between milk from cows fed the C diet and those from cows fed the SE, O and OSE diets was observed for the evaluated attributes- odor and flavor. The acceptability of the commercial milk color was higher ($P < 0.05$) when compared to the other dietary treatments (8.10 *vs*. C = 6.56; SE = 5.73; O = 6.51; OSE = 7.03). The attributes odor, flavor and mouthfeel showed no effect of dietary treatment ($P > 0.05$) in acceptance by the consumer. These results demonstrate the feasibility to produce milk from cows supplemented with sunflower oil, selenium and vitamin E.

Key Words: antioxidants, consumers acceptance, dairy

EXTENSION EDUCATION POSTERS

1037 (T077) Potential bull buyers perceive increased value to their operations when purchasing bulls from the Florida Bull Test. D. D. Henry*, V. R. G. Mercadante, F. M. Ciriaco, P. M. Mercadante, T. Schulmeister, N. DiLorenzo, and G. C. Lamb, *University of Florida, Marianna.*

The primary purpose of the Florida Bull Test is to serve as an educational aid for the improvement of beef cattle production. The test aims to: 1) provide the commercial cow/calf producer a source of bulls that have been tested for animal performance (i.e., ADG, DMI and feed efficiency), that were thoroughly evaluated at the same location, and that have passed stringent health requirements; 2) provide an opportunity for seed stock producers to advertise their breeding programs through testing and marketing bulls; and 3) promote awareness and understanding of the latest animal breeding concepts and tools while showcasing superior beef cattle genetics in Florida. The test standardizes environmental conditions for evaluating postweaning performance. In doing so, it provides useful records for bull consignors to better evaluate breeding programs and creates a local source of performance-tested bulls. Since the inception of the test, 14 annual bull tests have been completed with 1205 bulls tested from more than 14 different breeds. Mean sale average has ranged from $1,283 (in 2001) to $3,274 (in 2013). Before initiation of the 2014 Florida Bull Test sale a survey was conducted among potential buyers on their perception of the value that purchasing a bull may be to their operation. Of the 77 completed surveys, 54% indicated that they had purchased between one and six bulls from previous Florida Bull Test sales. Buyers originated from Alabama (n = 21), Florida (n = 47), and Georgia (n = 9). The primary factors identified by potential buyers when considering to purchase a bull were prioritized as follows: 1) breed, 2) performance and rank in the test, 3) sale price of the bull, 4) phenotype, 5) feed efficiency, and 6) pedigree. The mean perceived increased value per calf sired by bulls purchased from the Florida Bull Test was $58.05, but ranged from $0 to $125 per calf. We concluded that potential buyers value bulls purchased from the Florida Bull Test and these bulls are perceived to increase the value of their offspring at weaning.

Key Words: beef cattle, survey, bull test

1038 (T078) 300-d grazing discovery farm. T. R. Troxel*[1], M. S. Gadberry[1], J. A. Jennings[1], S. M. Jones[1], K. J. Simon[1], J. G. Powell[2], D. S. Hubbell, III[3], and J. D. Tucker[3], *[1]Dep. of Animal Science, University of Arkansas, Little Rock, [2]Dep. of Animal Science, University of Arkansas Division of Agriculture, Fayetteville, [3]University of Arkansas Livestock and Forestry Research Station, Batesville.*

The objectives of the 300d grazing discovery farm were to reduce hay feeding to 60 d or less, 90% net calf crop, average weaning weight of 249 kg and implement management practices common and available to cattle producers. The demonstration pastures consisted of 17.7 ha of common bermudagrass (*Cyndodon dactylon*), two 10.6-ha pastures of toxic endophyte-infected Kentucky-31 tall fescue (*Festuca arundinacea*), 10 ha of Ark-Plus novel-endophyte tall fescue, and 10 ha of Ark-Plus fescue/common crabgrass mix. Red (*T. pretense* L.) and white (*T. repens* L.) clovers were interseeded into fescue pastures. Each pasture contained water sources and were subdivided with electric fence. In yr 1 the cow herd was predominately Balancer females (38 multiparous cows) bred to Balancer bulls with a fall calving season. Two horned Hereford bulls were used in yr 2 to 5. The breeding seasons were approximately November 21 to January 26. The grazing protocol for each yr was fescue/clover in spring, bermudagrass for summer and early fall, fescue/clover for late fall and stockpiled fescue in winter. The primary management practices implemented were rotational grazing, strip grazing stockpiled forages during winter and a short defined breeding and calving season. The length of the grazing season for yr 1, 2, 3, 4, and 5 was 337, 311, 330, 323, and 279 d, respectively, and averaged 316 ± 20.4 d (mean ± SD). The mean mature cow net calf crop for yr 2, 3, 4, and 5 was 90 ± 7.0%; 24% points improvement compared to yr 1. The overall adj. 205-d BW increased ($P < 0.05$) from yr 1 and 2 (190 and 208 kg, respectively) to yr 3, 4, and 5 (225, 222, and 233 kg, respectively). All calves were weaned during the first 2 wk of May. The weaning weight of yr 1 was 213 ± 21.4 kg. The weaning weight goal (249 kg) was achieved for yr 2, 3, and 5 and was 255 ± 39.2, 273 ± 40.4 and 259 ± 31.0 kg, respectively, and was 241 ± 35.7 in yr 4. The average calving season was 59 ± 9.4 d for 5 yr. By incorporating rotational grazing, strip grazing stockpiled forage and a short breeding and calving season a 300 d grazing with acceptable beef cattle performance can be achieved in Arkansas.

Key Words: 300 d grazing, beef cattle, rotational grazing, stockpiled forage, weaning weight

1039 (T079) Case study: Fermentation profile, physical form, and starch digestibility of whole-plant corn silage harvested with novel processing.
L. F. Ferraretto, L. M. Vanderwerff*, and R. D. Shaver, *University of Wisconsin, Madison.*

Samples collected from two self-propelled harvesters (SPFH) at harvest were evaluated for fermentation profile, physical form, and ruminal in situ starch digestibility (StarchD; 12-h incubations on undried, unground samples) in whole-plant corn silage (WPCS). One SPFH was fitted with conventional type rolls with greater roll-speed differential than normal (CRGD). The other SPFH was fitted with intermeshing-disc type rolls (IMDR). The CRGD samples were from three theoretical lengths of cut (TLOC; 1.91, 2.24 and 2.54 cm; 3-mm roll-gap setting) on two hybrid types (leafy [LFY] and dual-purpose [DP]). The IMDR samples were from three TLOC (1.70, 1.91 and 2.54 cm) at two roll-gap settings (1.5 and 2.5 mm) on one hybrid. Unfermented samples were analyzed for processing score (CSPS) and mean particle length (MPL). Fermentation profile and StarchD were measured on fermented samples (30-d; vacuum-sealed bags). Data were analyzed using PROC MIXED of SAS with the Fixed effects of TLOC, hybrids and their interaction or TLOC, roll-gap settings and their interaction for CRGD and IMDR, respectively. For CRGD, CSPS tended ($P < 0.06$) to decrease while MPL increased ($P < 0.001$) with increasing TLOC. Fermentation profile and StarchD were unaffected ($P > 0.10$) by TLOC. Greater CSPS and reduced MPL were observed ($P < 0.05$) for LFY than DP. In addition, LFY had ($P < 0.01$) lower pH and greater total VFA concentrations. Starch digestibility tended ($P < 0.10$) to be greater for LFY than DP (79.9% vs. 71.2%). The difference in DM content between hybrids ($P < 0.01$; 31.2% vs. 35.2% for LFY and DP) may partially explain the differences between hybrid types. For IMDR, CSPS tended ($P < 0.10$) to be greatest for 1.70 cm TLOC. Greatest MPL was observed ($P < 0.05$) at the 2.54 cm TLOC. Measurements of pH were similar ($P > 0.10$) among TLOC, although total VFA concentration was lower ($P < 0.01$) for the 1.91 cm TLOC. A roll-gap set at 1.5 mm increased CSPS and decreased MPL compared to the 2.5 mm setting ($P < 0.001$). Total VFA concentration was similar ($P > 0.10$) and pH lower ($P < 0.01$) for the 2.5 mm treatment. Roll-gap and TLOC setting did not affect ($P > 0.10$) StarchD. Hybrid type and settings for TLOC and roll-gap influenced WPCS physical form and 30-d fermentation profile, while StarchD differed by hybrid type but not TLOC and roll-gap settings.

Key Words: corn silage, processing, starch digestibiity

1040 (T080) Initial assessment of producers' experiences, perceptions and attitudes about mastitis and bulk tank somatic cell count management in the Southeast.
S. M. Schexnayder[1], P. D. Krawczel*[1], M. Fly[1], L. E. Garkovich[2], C. S. Petersson-Wolfe[3], J. M. Bewley[2], S. H. Ward[4], G. M. Pighetti[1], R. A. Almeida[1], M. Arnold[2], S. C. Nickerson[5], A. DeVries[6], and S. P. Oliver[1], *[1]University of Tennessee, Knoxville, [2]University of Kentucky, Lexington, [3]Virginia Tech University, Blacksburg, [4]Mississippi State University, Starkville, [5]University of Georgia, Athens, [6]University of Florida, Gainesville.*

Impacts of mastitis, including reduced quality milk and productivity, negatively affect the profitability and sustainability of dairies in the Southeast (SE). The Southeast Quality Milk Initiative (SQMI), an integrated research, extension, and education project involving six land grant universities in the SE, aims to reduce mastitis and lower bulk tank somatic cell counts (SCC) through cost-effective control strategies. The first aim of this project was to identify social, psychological, and economic barriers limiting adoption of practices known to effectively control mastitis. To address this aim, a qualitative survey was conducted to identify producers' attitudes, their perceptions of control, the normative factors that influence their behavior towards mastitis control, and their attitudes on the ease of use, utility, and cost of associated control practices. In total, thre focus groups (two in Kentucky and one in Virginia) and 18 personal interviews (Producers in Tennessee and Virginia) were conducted. Participants represented a range of farm size (40 to 1200 cows), dairy experience (2 to 55 yr as owner or manager), bulk tank SCC (100,000 to > 600,000/ml; with either decreased or unchanged average SCC in the last 3 yr), and operational types. At each focus group and in personal interviews, a specific set of questions was posed. All content was subsequently reviewed for patterns and similarities. Producer responses were then grouped into key points. Findings summarized here are those that occurred frequently and were emphasized by producers through their input. Main trends are as follows: 1) Shortcomings remain in producer understanding of effects of subclinical mastitis on milk quantity and quality, 2) Producers' long-term objectives drive their investment of time and financial resources into mastitis management, 3) Uncertainty existed on the efficacy and cost-effectiveness of various mastitis control practices, 4) Producers wanted to know the bulk tank SCC that was most cost-effective in terms of the balance among associated costs of labor, management, penalties, and incentives, 5) Culling has been a favored mastitis management practice recently, 6) On-farm demonstrations of effective practices were the preferred means of communication and 7) Frustration resulted when implemented practices failed to control mastitis outbreaks. This information will be utilized to develop strategies for countering non-adoption rationales and form the foundation of a survey subsequently

distributed to approximately 2000 dairy producers in the SE. *This work was supported by a grant award from USDA-NIFA-AFRI (2013–68004–20424).*

Key Words: qualitative survey, mastitis, behavior, dairy production

---

1041 (T081) The status of milk quality at the start of the Southeast Quality Milk Initiative.

G. M. Pighetti[1], C. S. Petersson-Wolfe[2], J. M. Bewley[3], S. C. Nickerson[4], S. H. Ward[5], A. DeVries[6], P. D. Krawczel[*1], R. A. Almeida[1], M. Fly[1], S. M. Schexnayder[1], L. E. Garkovich[3], M. Arnold[3], and S. P. Oliver[1], *[1]University of Tennessee, Knoxville, [2]Virginia Tech University, Blacksburg, [3]University of Kentucky, Lexington, [4]University of Georgia, Athens, [5]Mississippi State University, Starkville, [6]University of Florida, Gainesville.*

The quality of milk produced in the Southeast (SE), based on somatic cell count (SCC) and standard plate count (SPC), is consistently lower than the rest of the United States. Reduced milk quality increases costs while decreasing revenues and efficiency. The combined effect of these factors contributes to the declining dairy industry in the SE. Understanding factors that have the greatest impact on milk quality will provide a background for programs aimed at helping producers improve their operations and was the underlying basis for the establishment of the Southeast Quality Milk Initiative (SQMI). Our overall goal is to enable dairy farmers to move toward production systems compatible with a sustainable industry. To accomplish this, we will integrate outreach, education, and research initiatives focused on improved milk quality, lowered disease costs, and greater revenues on farm. As part of this process, we established the baseline status of milk quality at the start of the project on dairy operations in FL (n = 126), GA (n = 221), KY (n = 753), MS (n = 82), TN (n = 404), and VA (n = 814), which are the partnering states of the SQMI. SCC and SPC bulk tank milk data for 2012 were evaluated from records maintained by state regulatory agencies. At least one SCC and SPC were collected each month from each dairy farm with a Grade A permit and data were summarized using the Timeseries procedure of SAS. Most SPC samples (65%) had < 5000 colony forming units (CFU)/ml and 82% fell within the recommended range (< 10,000 CFU/ml). The SE SCC averaged 324,204 ± 174,083 cells/ml (mean ± SD). The annual mean SCC of individual states ranged from 279,603 ± 160,665 to 417,146 ± 210,692. For herds enrolled in DHIA, which comprised 30–44% of the total herds within a state, annual mean SCC was approximately 50,000 fewer cells/ml. Considerable state-by-state variation occurred in frequency of samples, with SCC > 400,000 cells/ml having the greatest effect evident in the summer months. At this time, 20 to 60% of samples from individual states were > 400,000 cells/ml. In summary, milk quality in the SE lags behind the US as a whole, and hot, humid summers of the region present one of the major challenges to producing quality milk. Continued evaluation of this information will provide a basis to evaluate the success of the SQMI. *This work was supported by a grant award from USDA-NIFA-AFRI (2013–68004–20424).*

Key Words: Mastitis, extension, milk quality

1042 (T082) Hedonic pricing models for Angus bulls sold at auction following performance testing at Oklahoma Panhandle State University.

D. L. Stephens[*1], P. K. Camfield[1], and T. C. Schroeder[2], *[1]Oklahoma Panhandle State University, Goodwell, [2]Kansas State University, Manhattan.*

Selection of a herd sire has always been of paramount importance given the initial financial investment and their contribution and effect on the genetic make-up of a beef herd. Data was collected from the nation's longest consecutively run bull test conducted at the University Farm of Oklahoma Panhandle State University (OPSU). The Bull Test and Bull Sale data utilized were collected from 2008–2013. Performance data were collected over a 112-d test period with data collection occurring at 28-d intervals. The top 70 bulls from each year's test were selected based on a performance index of 1/2 ADG and 1/2 weight per day of age (WDA), and a semen quality and motility score of excellent and sold at auction. Angus bulls were the focus of the study as they represented the vast majority of individuals sold. Three hedonic pricing models were created. The initial hedonic model contained production data that included BW, ADG, WDA, Julian age, final test weight, ultrasound data, and a dummy variable for sale year. The second model utilized production data and added genetic variables in the form of production EPDs (Calving Ease Direct (CED), BW, Weaning Weight, and Yearling Weight) and maternal EPDs (Calving Ease Maternal, Maternal Milk). The third model included the variables from the first and second model with the inclusion of carcass EPDs (Marbling, Ribeye Area [REA] and FAT). Year was significant in all three models however; there was less of an effect on price as more variables were included. In model one, the production factors that were of significance were: ADG ($P < 0.01$), BW ($P < 0.01$) and final test weight ($P < 0.01$). In the second model, ADG, BW, and final test weight retained their significance at the $P < 0.001$ level. The only production EPD that was significant ($P < 0.05$) was CED. In the third model, years, ADG, and BW were still significant ($P < 0.01$). Final test weight ($P = 0.070$) and CED ($P = 0.132$) had substantial changes. The carcass EPD rib eye area had a P-value of 0.057. Producers who are placing bulls on test can utilize the given information to assist with their selection. It cannot go unsaid that while single trait selection can be very detrimental; ADG was significant across all models. The study indicates that performance and growth

are of utmost importance to buyers, followed by birth weight consideration because a live calf is the start to a potentially profitable calf crop.

Key Words: hedonics, Angus, EPD

1043 (T083) Survey of management practices used in the implementation of artificial insemination and estrous synchronization programs in the United States. S. K. Johnson*[1], and G. Dahlke[2], [1]*Kansas State University, Colby,* [2]*Iowa State University, Ames.*

Artificial insemination (AI) and estrous synchronization (ES) remain underutilized tools by US beef producers. Little information is available on actual management practices used by producers who use these technologies and the value they have within their operation. An online survey tool was developed concerning a variety of production practices, synchronization methods and available tools used with AI and ES. A link to the survey was promoted through electronic extension publications, contact lists and cooperating news media. Producers that participated could enter a drawing for AI supplies at the completion of the survey. The survey was accessed by 546 individuals and 425 completed the survey. Responses came from 42 states. Average number of owned cows that were AI was 67 cows (range 0 to 1750) and 34 owned heifers (range 0 to 1500). Respondents represented commercial herds (56%), seedstock herds (67%), having both commercial and seedstock (44%), commercial heifer development (14%), AI Technicians (18%) and DVMs (18%). A majority of producers used AI for both cows and heifers (87%) with 8% use on heifers only and 5% on cows only. The proportion of respondents that always, usually, sometimes, rarely or never ES was 46%, 26%, 28%, 6%, and 4%, respectively. The frequency of use of AI after observed estrus, estrus AI followed by clean-up timed-AI and strict fixed-time AI was 42%, 25% and 34%, respectively and was similar between cows and heifers. A majority of respondents (97%) were familiar with the recommended protocols for synchronization of estrus and ovulation provided by the Beef Reproduction Task Force. Recommendations from these guidelines were generally used by 65% and sometimes or occasionally used by 20%. The estimated difference in value between AI-sired calves and natural service sired calves was highly variable and averaged $465 ± 689 per head. The most common ways that AI contributed to profitability were through value of replacement heifers (60%), seedstock production (46%), reduced calving difficulty (42%), and premium of calves sold at weaning (35%). Sex-sorted semen had been used by 27% of respondents for use in heifers to make heifers (43%), cows to make heifers (47%), or cows to make bulls (8%). Pregnancy rates to sex-sorted semen were reported to be about as expected (61%), better than expected (12%) or worse than expected (27%). Despite improvements in fixed-timed AI protocols, many producers still depend on AI after observed estrus.

Key Words: artificial insemination, estrous synchronization, management practices

---

1044 (T084) Effect of on-farm dairy Beef Quality Assurance (BQA) training on worker knowledge of BQA and welfare-related practices. A. E. Adams*[1], J. K. Ahola[1], M. Chahine[2], A. L. Ohlheiser[1], and I. N. Roman-Muniz[1], [1]*Colorado State University, Fort Collins,* [2]*University of Idaho, Twin Falls.*

A training program in Beef Quality Assurance (BQA) practices, which included BQA core components and guidelines, was developed for use on dairy farms. The objective was to determine if on-farm dairy BQA training has an effect on dairy worker knowledge of BQA and welfare-related practices. Twelve dairies in Colorado and Idaho (six per state) participated in this pilot project, with 3 dairies in each state receiving BQA training. Training was provided to all employees (including owners and managers) on the dairies that received it, was conducted by experts in dairy BQA via Spanish-language materials, and was consistent across all dairies. To gauge knowledge of various BQA and welfare-related practices, dairy employees were administered a brief exam before receiving training, and again immediately after. Scores were compared between the pre- and post-exams using the TTEST procedure in SAS, with a significant improvement in overall test score occurring in both states ($P < 0.0001$). Respondents ($n = 28$) scored an average of 53.1 (out of 100) before receiving training, which improved to 76.0 after the training (mean improvement = 22.9). In addition to improvement in worker knowledge, one dairy added a full-time hoof trimmer to their staff after receiving the BQA training, indicating the training made them realize the importance of lame cow identification and management on dairy cow welfare and BQA. The change in producer perception of the importance of lameness on an operation, as well as improvement in dairy worker knowledge, suggests that BQA training programs have the potential of impacting dairy owner and/or employee behavior in a positive manner. Further research, including a larger sample size and follow-up visits to gauge employee knowledge retention, is needed to investigate the long-term effect of on-farm BQA training on dairy worker knowledge and management practices. A training program that benefits both BQA and welfare practices would be an excellent tool for the dairy industry, and would foster continuous improvement in these areas within the industry.

Key Words: beef quality assurance, dairy cows, training

1045 (T085) Monetary impact of heat stress on dairy and beef industries in the US. B. Scharf*, D. Liu, J. M. Leath, S. A. Kelly, T. X. Nguyen, Y. Shi, M. Schrader, G. D. Martin, P. A. Eichen, and D. E. Spiers, *University of Missouri, Columbia.*

Heat stress continues to be a major economic problem for the livestock industry. Over 10 yr ago, St-Pierre et al. (2003) reported annual economic losses totaling $897 and 369 million for dairy and beef, respectively. Utilizing this publication, economic impact figures were adjusted for 1) inflation using a cumulative rate of 24.78% (US Inflation Calculator), and 2) 2012 USDA figures for the dairy and beef industry inventories by state. For dairy, estimated annual state-by-state financial loss per cow and average farm were calculated. For beef, only estimated loss per cow was found because information on average herd size by state was not available. Annual losses were primarily determined by loss in productivity (i.e., weight gain for beef and milk production for dairy). In terms of economic loss per cow from heat stress, loss to the beef industry is overwhelmed by the dairy industry, with the top 10 dairy states having 25 times greater loss than average loss among the top 10 beef states. Average annual economic losses across all states on a per cow basis for dairy producers was $89.01, while national annual losses for beef producers was only $3.05. Texas had the highest beef loss per cow in 2012 ($19.25), which was nearly double the second highest loss state which occurred in Oklahoma ($10.59). In comparison, the dairy industry showed an annual per-cow losses of $366.85 and $308.03 per animal for Louisiana and Texas, respectively. Of total loss due to heat stress in the contiguous 48 states, the top 10 states account for 85% and 68% of the losses for beef and dairy industries, respectively. Economic losses per farm showed significant variation due to differences both in level of heat strain and average herd size (ranging from 2357 dairy cows per farm in New México to 66 in Missouri). Texas (872 dairy cows per farm), once again had the highest economic losses at $268,601 per farm while the national average per farm was $33,245 (national average of 187 dairy cows per farm). When ranked according to a combination of total economic loss due to heat stress, per-cow losses, and severity of heat stress, Texas, Kansas, Nebraska, and Oklahoma are the states where heat abatement systems would have the largest economic impact.

Key Words: heat stress, beef, dairy, livestock economics

1046 (T086) Phosphorus status of grazing beef cattle in Virginia's Chesapeake Bay watershed. S. J. Neil*[1], K. J. Mize[1], D. D. Harmon[1], J. K. Smith[2], and M. A. McCann[1], *[1]Virginia Polytechnic Institute and State University, Blacksburg, [2]Virginia Tech, Blacksburg.*

Phosphorus is one of the nutrients identified in EPA's TMDL plan for the Chesapeake Bay watershed. Major research and extension efforts in Virginia have focused on reducing P losses from concentrated animal feeding operations, however approximately 400,000 beef cows graze pastures in Virginia's Chesapeake Bay watershed. To better characterize farm P status, fecal, forage and soil samples were collected from beef cattle farms in the watershed. One hundred twenty producers from 11 counties cooperated with sample collection ($N = 166$). Samples were analyzed for total P (TP) and inorganic P (*P*i) using the molybdovanadate yellow and blue methods, respectively. Soil test P values were characterized as low (12%), medium (37%), high (35%), and very high (16%) based on Virginia Cooperative Extension Soil Test guidelines. Phosphorus content of pasture forage grab samples (mean = 0.34%; SD = 0.12) was lowly correlated with soil P ($r = 0.18$; $P < 0.0001$) and fecal TP ($r = 0.15$; $P < 0.0001$). Forage TP levels were compared with Beef Cattle NRC (2001) P requirements for a 545-kg cow (*P*eak milk, 13.6 kg per d). All forage samples were sufficient in P content to meet a dry cow's requirements, while 98% met the requirements for late gestation and 88% met the requirements for peak lactation. Farm mineral supplements were categorized into four levels of P content (< 1.0 [nil], 1.0 to 2.5 [low], 3.0 to 5.0 [medium] and > 6.0% [high]). Forage P content did not affect mineral selection by producers. The mean forage P content of the mineral categories was 0.30, 0.36, 0.32, and 0.40%, respectively. The mean fecal TP (0.56%, 0.65%, 0.79%, and 0.97%, respectively) and Pi levels (0.33%, 0.41%, 0.55%, and 0.68%, respectively) significantly differed between producers that fed a nil and low P mineral, and those that fed mineral in the medium and high categories ($P = < 0.001$ for TP and Pi). Soluble P (defined as Pi/TP*100) tended to increase across mineral categories going from nil to high. All farms surveyed required little or no P supplementation in regard to cow P requirements. These results indicate that reducing mineral P may be capable of limiting soluble P losses from supplementation of beef cattle.

Key Words: phosphorus, beef cattle, Chesapeake Bay

1047 (T087) Assessment of farm nutrient management and phosphorus supplementation practices of beef cattle producers in Virginia's Chesapeake Bay watershed. S. J. Neil*[1], K. J. Mize[1], D. D. Harmon[1], J. K. Smith[2], and M. A. McCann[1], *[1]Virginia Polytechnic Institute and State University, Blacksburg, [2]Virginia Tech, Blacksburg.*

Concerns over the environmental impact and resource usage of agricultural operations have pressured producers to explore nutrient management as an option to improve sustainability and profitability on the farm. The objective of this study was to determine the level of phosphorus supplementation and nutrient management practices among cow/calf producers in Virginia's Chesapeake Bay watershed. Surveys were collected from 67 producers in 10 counties. Total cattle populations (unweaned calves excluded) of sampled farms ranged

from six to 2810 with a mean of 162 (SD = 359). Seventeen percent of producers had no defined calving season, while 21% practiced fall calving, 31% practiced spring calving, and 31% calved in both spring and fall seasons. Nutrient management plans (NMP) are one of the more prevalent strategies currently employed in the Chesapeake Bay watershed in an attempt to minimize whole farm environmental impact and enhance nutrient conservation on the farm by limiting soil erosion and runoff. Fifty-five percent of participants had implemented NMP at the time of survey completion. In relation, twenty-five percent of all producers sampled forage to determine nutrient content. The majority of producers that sampled forage (94%; $\chi^2 = 17.1$; $P < 0.0001$) currently utilized nutrient management plans. Participants ranked criteria for mineral supplement selection. Responses were weighted based on participant designated ordinal ranking of criteria (three for primary, two for secondary and one for tertiary criteria). Interpretation of response distribution suggests that the primary criterion for mineral supplement selection was price (20.6%), followed by local availability (17.8%) and trace mineral content (17.5%). Sixty-nine percent of producers supplemented a commercial complete mineral mix and 22% used a trace mineral salt block. Eighty percent of producers provided a high magnesium (Mg) mineral (> 10% Mg) at some point during the year for an average of 9.5 mo (SD = 3.5). Eighty two percent of participants indicated willingness to reduce mineral phosphorus supplementation levels if forage analyses revealed that feed and forage resources were capable of meeting phosphorus requirements, while 15% indicated uncertainty, and 3% indicated unwillingness. Survey results suggest that producers are willing to monitor and reduce farm nutrient losses if research shows that over-supplementation is a problem. A concurrent study is underway to assess the extent of nutrient over-supplementation on beef operations in Virginia's Chesapeake Bay watershed.

Key Words: phosphorus, beef cattle, Chesapeake Bay

1048 (T088) An economic impact decision support tool for farm specific estimation of not covering horizontal silos storing corn silage.

B. A. Wadsworth*, D. M. Amaral-Phillips, and J. M. Bewley, *University of Kentucky, Lexington.*

In a horizontal silo (i.e., bunkers and trenches), considerable silage is exposed to environmental elements and, if left uncovered, results in significant feed shrink and economic loss. Depending on the silo dimensions and silage density, 25% of the total volume of corn silage may be within the top 1 m of silage. The objective of this project was to create a producer-friendly dashboard tool (SAP America, Inc. Newtown Square, PA) to highlight the cost of not covering a horizontal silo storing corn silage. Farm-specific inputs of the dashboard tool are adjustable by the end user and include silo dimensions, dry matter of the silage, price of shelled corn/bushel, and total cost to cover silage including price of cover and labor. Bunker silage volume was calculated using silo dimensions including: 1) wall height (height of the silage next to the wall), 2) mean width (width of the silo measured half way up the silo), 3) filling ramp length (length of front filling ramp measured horizontally), 4) dome height (height of the silage above the top of the wall), 5) back ramp length (length of the back silage ramp measured horizontally), and (6) wall length (wall length at the top of the silo). Bunker silage volume calculations were generated from Brian Holmes's Investment and Annual Costs of Forage Storage Calculator (www.uwex.edu/ces/crops/uwforage/bunkersilovolume10–18–08.xls) from the University of Wisconsin–Madison. The dashboard tool outputs lost revenues from not covering a silo. This was calculated by silage price per ton (price of shelled corn/bushel × 8), multiplied by dry matter lost, and subtracting the cost of covering silage. To demonstrate model utility, total bunker silage amount was set at 1494 metric tons, dry matter density was 6.35 kg/m^3, price of corn was $5.00/bushel, total price of plastic was $485/horizontal silo, and total labor cost was $100 for covering the silo. With these inputs, the total lost revenues from not covering the silo was $1,100/year. Dairy producers may use this model as a decision support tool to highlight lost revenue from not covering silos.

Key Words: silage covering, economic dashboard, extension tool

---

1049 (T089) A producer assessment of precision dairy farming technology use, usefulness, and pre-purchase considerations.

M. R. Borchers*, and J. M. Bewley, *University of Kentucky, Lexington.*

A survey to identify producer perception of precision dairy farming technologies was distributed in March 2013 through written publications and email. Responses were collected in May 2013 ($n = 109$) and statistical analysis was performed using SAS (SAS Institute, Inc. Cary, NC). Herd size, producer age, and role on the farm were collected and analyzed but significant differences were not found ($P > 0.05$). Producers were asked to indicate parameters currently monitored on their farm from a predetermined list and producers most often selected daily milk yield (52.3%), cow activity (41.3%), and not applicable (producers not currently implementing technologies; 1.2%). Producers were asked to rank the same list on usefulness using a 5-point Likert Scale (1, not useful to 5, useful). Least-squares means were calculated using the GLM procedure of SAS and producers indicated (mean ± SE) mastitis (4.77 ± 0.47), standing heat (4.75 ± 0.55), and daily milk yield (4.72 ± 0.62) to be most useful. Pre-purchase technology selection criteria were ranked using a Likert Scale (1, not important to 5, important) by producers and benefit to cost ratio (4.57 ± 0.66), total investment cost (4.28 ± 0.83), and simplicity and ease of use (4.26 ± 0.75) were found most important. Producers were categorized into United States or an other countries category based on their farm location. Significant differences

($P < 0.05$) were identified between country and the adoption of technologies monitoring: animal position and location, body weight, cow activity, daily milk yield, lying and standing time, mastitis, milk components, rumen activity, and rumination with other countries being higher in all cases. Producers were categorized based on technology use (using technology vs. not using technology) and least-squares means were calculated across technology usefulness with daily milk yield (using technologies: 4.83 ± 0.07, vs. not using technologies: 4.50 ± 0.10) and standing heat (using technologies: 4.68 ± 0.06, vs. not using technologies: 4.91 ± 0.09) differing significantly ($P < 0.05$). Least-squares means were calculated for technology use categories on producer pre-purchase considerations and availability of local support (using technologies: 4.25 ± 0.11, vs. not using technologies: 3.82 ± 0.16) differing significantly ($P < 0.05$). Using this data, technology manufacturers can better design and market technologies for producer needs.

Key Words: producer perception, survey, precision dairy farming technologies

---

1050 (T090) Sustainable year-round forage production and grazing/browsing management education program. U. Karki*[1], L. B. Karki[2], N. Gurung[1], R. Lemus[3], S. Hart[4], K. Cearley[5], S. Enloe[6], E. Jolley[7], and M/Edmonson[6]. [1]*Tuskegee University, Tuskegee, AL,* [2]*PadmaDal Memorial Foundation, Auburn, AL,* [3]*Mississippi State University, Starkville,* [4] *Langston University, Langston, OK,* [5]*Texas AgriLife Extension Service, Amarillo, TX,* [6]*Auburn University, Auburn, AL;* [7]*Natural Resources Conservation Service, Auburn, AL.*

Pasture-based goat production is becoming popular among the small-scale livestock farmers in the Southern region. However, most farmers have not adopted sustainable forage programs. As a result, they depend on hay and supplementary feedstuff to sustain their herd during times of reduced forage availability. Moreover, there is not much information available on pasture development/improvement and sustainable grazing/browsing management for goats. The goal of this project was to develop a comprehensive education program to increase the productivity, quality, and production duration of pastures as well as to improve the management of existing pastures for sustainable goat production. Project objectives were: 1) to develop training curricula, and 2) to train field-level extension and technical assistance personnel and goat farmers on sustainable year-round forage production and grazing/browsing management. Tuskegee University and PadmaDal Memorial Foundation were collaborating in this project. Other key partners in the project were Alabama Natural Resources Conservation Service, Auburn University, Mississippi State University, Langston University, and Texas A&M AgriLife Extension Service. The project outputs were 1) ready- to-use training curricula in the form of a handbook- sustainable year-round forage production and grazing/browsing management for goats in the Southern Region, which is now freely available to the public at Tuskegee University website: http://www.tuskegee.edu/sites/www/Uploads/files/About%20US/TUCEP/Livestock%20Program/Year- RoundPasture_Handbook.pdf, 2) an educational video to complement the handbook (under review), and 3) trained field-level extension and technical-assistance personnel and extension specialists (22) serving the goat producers in different Southern states and lead goat farmers (4). Short-term impact results showed 29% increase in the knowledge of trainees. The medium-term impact results revealed that majority of the trainees applied the learned skills and knowledge either to educate their clientele more effectively (professionals) or improve their farm operation (farmers).

Key Words: curricula, goats, training

1051 (T091) Assessment of the potential for compost bedded pack barns in sustainable organic dairy farming systems. H. A. Mussell*, J. L. Taraba, K. L. Jacobsen, and J. M. Bewley, *University of Kentucky, Lexington.*

Compost bedded pack barns (CBP) take full advantage of composting and manure management to provide a clean, comfortable environment for cows. Although most CBP research has been conducted on conventional dairy farms, organic dairy farms could also benefit from CBP due to increased cow comfort, natural airflow, and manure storage. To assess the potential for CBP use on organic dairy farms, a survey was distributed to through multiple email lists to organic dairy producers across the United States. Twenty-seven surveys were returned. Mean herd size (mean ± SD) was 95.05 ± 78.71 cows. Mean SCC was 182,250 ± 61,605 cells/mL. Twenty-seven percent of producers housed their milking herds in a straw bedded pack, 23% in free stalls, 23% used a year-round pasture based system, 18% used CBP tilled daily, 5% used CBP that were not tilled daily and 5% used tie stall barns. Fifty percent of herds spent 19 to 23 h on pasture/d. Thirty percent spent an average of 12 h/d on pasture. Twenty percent of herds spent 24 h/d on pasture. The number of months that cows spent in a housing system for 24 h/d ranged from > 4 mo (30%), 3 to 4 mo (15%), < 2 mo (15%) or never in a housing system (30%). Organic dairy producers evaluated how effectively CBP, tie stalls, freestalls, straw-based bedded packs and pasture systems meet the needs of organic dairy herds by using a scale of 1 to 5 (1, poorly meets the needs of organic dairy herds to 5, well-suited for meeting the needs of organic dairy herds). Compost bedded pack barns (4.06 ± 0.64) were the highest ranked system, followed by straw bedded packs (3.84 ± 0.90) pasture based systems (3.39 ± 1.20), and tiestalls (2.72 ± 1.23). Using a scale of 1 to 5 (1, strongly disagree to 5, strongly agree), benefits of the CBP were ranked as shelter (4.47 ± 0.51), cow comfort (4.42 ± 0.69), access to fresh air (4.17 ± 0.99), and ventilation (4.17 ± 1.04). Compost bedded pack barns appear to be a viable housing option for organic dairy farms.

Key Words: compost bedded pack barns, organic, cow comfort

1052 (T092) Development and utilization of the AI Cowculator: A decision-aid application to determine whether to utilize fixed-time artificial insemination (TAI) or purchase herd sires for natural service. V. R. G. Mercadante*[1], D. D. Henry[1], F. M. Ciriaco[1], P. M. Mercadante[1], J. C. Rodgers[2], N. DiLorenzo[1], and G. C. Lamb[1], *[1]University of Florida, Marianna, [2]Zoetis, Florham Park, NJ.*

The development of reliable, efficient and economic TAI protocols has resulted in the opportunity for increased use in commercial cattle production systems. However, producers do not have access to simple decision-aid tools using their own data to determine whether implementing a TAI program or purchasing herd sires is more economically feasible. Therefore, we conducted an experiment to generate an economic model that determined that for every cow exposed to a TAI protocol a cattle producer will gain an additional $49 per cow after weaning. Utilizing this economic model we developed the AI Cowculator smartphone and tablet application for iOS and Android systems. Since inception, the AI Cowculator has been downloaded 1025 times in 38 states and four countries. Features of the application include: 1) a simple calculator to assist producers decide whether to utilize AI or purchase a herd sire. The calculator includes 18 entries divided into three categories (natural service sires costs, herd related costs, and artificial insemination related costs). The output includes a partial budget and provides users an opportunity to email the results to a single email account; 2) a push-pin locator that allows users to locate representatives who perform AI services or suppliers of semen and AI suppliers; 3) a resource icon that allows users to access helpful material for reproduction planning including TAI articles by the Beef Reproduction Task Force, a list of extension documents on beef production and future cattle prices; 4) a gallery of pictures and estrus synchronization protocols recommended by experts in the field; 5) a YouTube icon that provides a demonstration on the use of the AI Cowculator; and 6) a social media icon that directs to Facebook and Twitter pages and allow users to share their results. The AI Cowculator Facebook page is updated weekly with relevant reproductive management information and provides technical assistance to users of the application. Information posted on the AI Cowculator Facebook page has reached more than 5000 users of social media and has been liked by more than 310 people.

Key Words: smartphone application, decision aid tool; artificial insemination

FOOD SAFETY

1053 (T093) Regulatory process for food additives used in animal foods. S. A. Benz[1], R. Christensen[*2], and M. G. Alewynse[2], *[1]Center for Veterinary Medicine, FDA, Woodbine, MD, [2]Nutrition & Labeling Team, Center for Veterinary Medicine, FDA, Rockville, MD.*

Animal food, both livestock feed and companion animal food, is composed of many different ingredients. With recent changes in ingredient availability, there is increasing interest in the use of novel ingredients in animal food. These ingredients may be intended to be a source of nutrients or, like enzymes, may affect the characteristics of the food itself. Under Federal law, ingredients that are not generally recognized as safe (GRAS) for an intended use are considered food additives that must be approved by the Food and Drug Administration (FDA) before they can be used in animal food. The food additive petition (FAP) process is the means to get approval of food additives and it is described in Title 21 of the Code of Federal Regulations Part 571 (21 CFR 571). Within FDA, the Center for Veterinary Medicine (CVM) approves animal FAPs when a firm demonstrates that the ingredient is safe and achieves its intended purpose. In a petition, the safety of the substance at the intended use rate must be addressed for both the animal and the environment. For food producing species, the safety of human food obtained from the animals must also be addressed. When FDA approves a FAP, a regulation in 21 CFR 573 is established addressing the safe use of the substance in animal food. In September 2013, FDA published Guidance for Industry #221 on the Recommendations for the Preparation and Submission of Animal Food Additive Petitions. This draft guidance describes the types of information to be included in a petition, including: the name and all pertinent information concerning the food additive itself; chemical identity and composition of the additive; manufacturing methods and controls; intended use, use level and labeling; data establishing the intended effect (physical, nutritional, or other technical effect); a description of validated analytical methods to determine the amount of the food additive in the food; safety evaluations for the animal and humans consuming animal products; proposed tolerances for the food additive; proposed regulation; and environmental assessment. With the guidance, CVM seeks to provide the animal industry with knowledge of the types of information that are required to establish the safety of the use of an ingredient to help to ensure a safe animal food supply.

Key Words: FDA, food additive, guidance

1054 (T094) Persistence of *Escherichia coli* O157:H7 in feces from cattle fed diets with or without wet distillers grains with solubles. E. D. Berry[*], J. E. Wells, and V. H. Varel, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Feeding wet distillers grains with solubles (WDGS) to cattle can increase prevalence of *E. coli* O157:H7, but mechanisms for this increase are not fully understood. The objective of these experiments was to examine the persistence of *E. coli* O157:H7 in feces from cattle fed diets with or without WDGS. In the first study, fresh feces from steers fed 0, 20, 40 or 60% WDGS were collected and combined (6 to 8 animals/composite, $n = 8$ separate composites/diet treatment). Feces composites (600 g) were inoculated with a five-strain mixture of streptomycin-resistant *E. coli* O157:H7, incubated at room temperature, and sampled periodically up to 14 d. Feces samples were diluted and plated to determine *E. coli* O157:H7 levels. Compared to levels seen with diets containing WDGS, *E. coli* O157:H7 levels in feces from cattle fed 0% WDGS rapidly decreased ($P < 0.05$), from 6.28 $\log_{10}$ cfu/g on d 0 to 2.48 $\log_{10}$ cfu/g by d 14. From the same initial levels, *E. coli* O157:H7 in feces from cattle fed 20, 40, and 60% WDGS were 4.21, 5.59, and 6.13 $\log_{10}$ cfu/g of feces on d 14, respectively. A second study evaluated survival of *E. coli* O157:H7 in feces from cattle fed 0 and 40% WDGS. Steers were fed in eight pens (75 to 77 per pen; 4 pens/WDGS treatment). Feces were collected from 5 to 6 animals in each pen, both before and after the corn source was switched from high-moisture corn (HMC) to dry-rolled corn (DRC). Feces samples were combined within pen, inoculated, incubated, and analyzed for *E. coli* O157:H7 as described above, and examined in triplicate at 0, 1, 2, 4, and 7 d. Within corn source, *E. coli* O157:H7 persisted at higher levels ($P < 0.05$) in 40% WDGS feces at d 7. For 40% WDGS feces, *E. coli* O157:H7 persisted at higher levels ($P < 0.05$) at d 7 in feces when cattle were fed HMC compared to DRC. Greater persistence of *E. coli* O157:H7 in the feces and environment of cattle fed WDGS may play a role in the increased prevalence of *E. coli* O157:H7 seen in these animals, by increasing the risk for recolonization of animals. This work further suggests potential dietary approaches for reducing the occurrence and numbers of this pathogen in cattle fed WDGS. *USDA is an equal opportunity provider and employer.*

Key Words: *E. coli* O157:H7, distillers grains, cattle

1055 (T095) Characterization of Shiga toxin-producing *Escherichia coli* isolated from feces of cattle in commercial feedlots. T. W. Alexander[*1], T. A. McAllister[1], K. Stanford[2], T. Reuter[2], and E. Topp[3], *[1]Agriculture and Agri-Food Canada, Lethbridge, AB, [2]Alberta Agriculture and Rural Development, Lethbridge, Canada, [3]Agriculture and Agri-Food Canada, London, ON.*

Shiga toxin-producing *Escherichia coli* (STEC) are potential food and waterborne zoonotic pathogens. The objective of this study was to characterize the general population of *E. coli* (EC) in feedlot cattle and determine the proportion that is STEC. Four commercial feedlots with approximately 1,000 pens were sampled over a three-year period. Thirty percent of the pens were randomly selected for study enrollment. Pens were sampled when they had been filled with cattle and again after cattle had been on feed for > 60 days. Sampling consisted of collecting 1 to 2 g of material from 20 fresh fecal pats on pen floors and combining them into a single mixed sample per pen. In total, 291 pens were sampled and processed for EC isolation at both time points. A total of 3,578 EC were isolated and stored after plating pooled fecal pats onto MacConkey agar. Isolates of EC were then screened by multiplex real-time PCR for the virulence genes *stx*1, *stx*2, and *eae*. Isolates positive for *stx*1 or *stx*2 were further characterized for i) variants of *stx* using PCR, ii) susceptibility to 15 antimicrobials using broth dilution, and iii) genetic relatedness after pulsed-field gel electrophoresis (*P*FGE) of Xba1 restricted DNA. In total, 60 (1.7%) isolates tested positive for *stx*1 (N = 27), *stx*2 (N = 30) or a combination of *stx*1 + *stx*2 (N = 3) genes. The most prevalent *stx* variant was *stx*1d, followed by *stx*2a, *stx*2g, *stx*1a, *stx*1a + *stx*2a, and *stx*2b (N = 18, 15, 8, 7, 3, and 2, respectively). Undefined *stx*1 and *stx*2 variants were present in 2 and 5 isolates, respectively. Seasonality and time of isolation did not affect prevalence of total *stx*1 or *stx*2 ($P > 0.05$). However the majority of isolates with *stx*1d (15/18) and *stx*2g (7/8) were detected at > 60 days. Only 10 STEC (0.3%) also tested positive for *eae*. Sampling time point did not affect the prevalence of antimicrobial-resistant STEC ($P > 0.05$). Overall, 69.8% of STEC were resistant to at least one antimicrobial. The most prevalent resistance was to tetracycline which was common to all resistant STEC. From PFGE, 46 subtypes were observed. These data indicate STEC from feedlot cattle are diverse and their prevalence is low among the general population of EC. In addition, the majority of STEC were *eae*-negative, thus unlikely to be associated with outbreaks of hemolytic uremic syndrome.

Key Words: STEC, *Escherichia coli*, cattle

1056 (T096) Development of an ultrasensitive aptasensor for the detection of aflatoxin B1. X. Guo[1,2,3], F. Wen[1,4], N. Zheng[*1,3,4], Q. Luo[2], and J. Wang[1,4], *[1]Ministry of Agriculture—Laboratory of Quality and Safety Risk Assessment for Dairy Products, Beijing, China, [2]College of Animal Science and Technology, Xinjiang Agricultural University, Urumchi, China, [3]Ministry of Agriculture - Milk and Dairy Product Inspection Center, Beijing, China, [4]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

Contamination of feed and food by aflatoxin B_1 (AFB_1), one of the most toxic of the mycotoxins, is a global concern. To prevent food safety scares, and avoid subsequent economic losses due to the recall of contaminated items, methods for the rapid, sensitive and specific detection of AFB_1 at trace levels are much in demand. In this work, a simple, ultrasensitive, and reliable aptasensor is described for the detection of AFB_1. An AFB_1 aptamer was used as a molecular recognition probe, while its complementary DNA played a role as a signal generator for amplification by real-time quantitative polymerase chain reaction (*P*CR). Under optimal conditions, a wide linear detection range (5.0×10^{-5} to 5.0 ng mL^{-1}) was achieved, with a high sensitivity (limit of detection (LOD) = 25 fg mL^{-1}). In addition, the proposed aptasensor exhibited excellent specificity for AFB_1 compared with eight other mycotoxins, with no obvious Ct value change. This aptasensor can also be used in quantifying AFB_1 levels in Chinese wildrye hay samples and infant rice cereal samples, demonstrating satisfactory recoveries in the range of 88–127% and 94–119%, respectively. This detection technique has a significant potential for high-throughput, quantitative determination of mycotoxin levels in a large range of feeds and foods.

Key Words: aflatoxin B_1, aptasensor, feed and food safety

1057 (T097) Cytotoxicity induced by ochratoxin A, zearalenone and α-zearalenol: Effects of individual and combined treatment. H. Wang[1,2,3,4], N. Zheng[1,2,3], S. Li[1,2,3], F. Li[4], and J. Wang[*1,2,3], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture - Milk and Dairy Product Inspection Center (Beijing), Beijing, China, [3]Ministry of Agriculture - Laboratory of Quality and Safety Risk Assessment for Dairy Products, Beijing, China, [4]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China.*

Mycotoxins, a series of secondary metabolites generated from moulds, mainly come from food and feed contaminated in the field, during drying and subsequent storage. Among all

the mycotoxins, ochratoxin A (OTA), zearalenone (ZEA) and α-zearalenol (α-ZOL) have evoked great concern owing to their high occurrence and serious harm to human health. The co-occurrence of OTA, ZEA and α-ZOL was found in animal feed and milk. The previous reports indicated that the co-occurrence of mycotoxins could increase their cytotoxicity. The aim of the present study was to investigate the cytotoxicity of combined mycotoxins of OTA, ZEA and α-ZOL on human Hep G2 cells by using the tetrazolium salt (MTT) assay and the isobologram analysis. Statistical analysis of data was carried out using SAS9.2, statistical software package. Our results demonstrated the significant ($P < 0.05$) cytotoxic effects of the two-toxin combination and the three-toxin combination on Hep G2 cells in a time- and concentration-dependent manner. The IC_{50} (inhibit concentration equal to 50%) values of Hep G2 treated with individual mycotoxin after 24 h, 48 h and 72 h of exposure were 1.86-8.89 μM, 29.48-55.79 μM, 20.91-52.30 μM for OTA, ZEA and α-ZOL, respectively. The combined indexes (CI) were 2.73–7.67 for OTA+ ZEA and 1.23–17.82 for OTA+ α-ZOL after 24 h, 48 h and 72 h of exposure at all inhibit concentration(IC) levels (IC_{10}-IC_{90}), indicated an antagonism. The CIs of ZEA+ α-ZOL were 1.29–2.55 after 24 h and 72 h of exposure (IC_{10}-IC_{90}), indicated an antagonism. The CIs of ZEA+ α-ZOL were 0.74-1.68 after 48 h of exposure, indicated an antagonism (IC_{10}-IC_{40}), additive effect (IC_{50}-IC_{70}) or synergism (IC_{80}-IC_{90}). The CIs were 1.41–14.65 for OTA+ ZEA+ α-ZOL after 24 h, 48 h and 72 h of exposure (IC_{10}-IC_{90}), indicated an antagonism. In conclusion, OTA was more toxic than ZEA and α-ZOL. The combined mycotoxins of OTA and ZEA, OTA and α-ZOL, OTA, ZEA and α-ZOL showed antagonism. And the combined mycotoxins of ZEA and α-ZOL showed antagonism, additive effect and synergism at different concentrations. But the result of combined mycotoxins affected by type of cell used endpoint of cytotoxicity, analysis assay of interaction, and other factors. So interaction of combined mycotoxins should be determined or re-validated in continuously toxicological data.

Key Words: ochratoxin A, zearalenone, α-zearalenol

1058 (T098) Efficacy of various levels of mycotoxin adsorbent to reduce aflatoxin M1 levels in milk of lactation cows fed aflatoxin B1. M. Dehghan banadaky[*1], R. Motameny[2], and S. Parhizkar[3], [1]*Dep. of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran,* [2]*Azad University, Tehran, Iran,* [3]*University of Tehran, Karaj, Iran*.

The aim of this study was to compare the ability of various levels of adsorbent Biotox (Biochem GmbH, Lohne, Germany) to reduce Aflatoxin in milk of Holstein cows. Twenty-four lactating Holstein cows in mid lactation were assigned to one of three treatments ($n = 8$) for 35 d. Diet formulated according to the nutrient requirements of dairy cattle (NRC, 2001). The following treatments were investigated 1- Aflatoxin diet plus 60 g/d/cow of Biotox (Biochem GmbH, Lohne,. Germany), 2- Aflatoxin diet plus 20 g/d/cow of Biotox and 3- Aflatoxin diet without mycotoxin adsorbent (Control). Aflatoxin diet provided 350 μg/d/cow of AFB. Individual dry matter intake and milk yield were recorded daily. Milk samples were collected at each milking time weekly. Blood samples (10 ml) were collected weekly from the coccygeal vein and centrifuged to separate plasma. Quantification of aflatoxin (B1 or M1) in TMR samples, milk and plasma done using microtitre plate enzyme linked immunosorbent assay (ELISA) method. Weekly data were analyzed using the PROC MIXED of SAS as repeated measurement data. Aflatoxin M1 concentrations for the Biotox60, Biotox20 and control (no adsorbent) treatments averaged 338.0, 439.0 and 490.1 ng/kg, respectively. Compared to the control group, AFM1 concentrations in milk were reduced ($P = 0.015$) by the addition of 20 and 60 g/d/cow of Biotox. Aflatoxin M1 excretion via milk, as calculated from milk AFM1 concentration and total milk volume produced, was 9.87, 12.87 and 14.66μg/d/cow in the Biotox60, biotox20 and control treatments respectively. Biotox significantly decreased AFMI excretion in milk ($P = 0.033$). Transfer rate of AF from feed to milk (TR), as calculated from [(excretion of AFM1/AFB1 consumption) × 100] averaged 2.90, 3.85 and 4.22% for the Biotox60, biotox20 and control treatments respectively. Biotox in 60 g/day dose significantly decreased Aflatoxin TR ($P = 0.029$). The results of the analysis of variance on plasma AFM1 showed that treatment did not affect plasma AFM1, but numerical increase in plasma AFM1 of control group showed. Results of the current study indicate that the Biotox was effective in reducing milk AFM1 concentrations, AF excretion, and AF transfer from feed to milk, but this efficacy was improved in higher dosage (60g/day/cow) at least in high polluted diets.

Key Words: aflatoxin, transfer rate, milk

1059 (T099) Inhibitory activity of *Staphylococcus aureus* against *Lactococcus* spp. isolated from artisanal Minas cheese. F. F. Ângelo[1], L. M. Fonseca[*2,3], and M. A. V. P. Brito[4], [1]*Universidade Federal da Paraíba/CTDR, João Pessoa, Brazil,* [2]*Universidade Federal de Minas Gerais* (*School of Veterinary Medicine), Belo Horizonte, Brazil,* [3]*University of Wisconsin-Madison/CAPES Est. Senior 18183-12-3, Madison,* [4]*EMBRAPA Gado de Leite* (*CNPGL), Juiz de Fora, Brazil.*

Production of antimicrobial substances by *Staphylococcus aureus* isolated from food has been reported. Since it is a highly prevalent etiologic agent for mastitis in dairy herds, inhibition of starter culture due to *S. aureus* inhibitory activity is possible during the processing of fermented dairy products, such as cheeses. The objective of the current work was to evaluate the antimicrobial substances produced by samples of *S. aureus* isolated from cow's milk during mastitis occurrence and their effect against strains of *Lactococcus* spp. Individual milk samples,

obtained from 54 herds, were analyzed for *S. aureus* presence and isolated strains were tested for inhibitory activity using the deferred-antagonism assay, with *Corynebacterium fimi* (NCTC 7547) as indicator. Proteic nature of the antimicrobial substances was investigated using protease type XIV from *Streptomyces griseus* (Sigma P-5147). Inhibitory spectrum was tested against nine *Lactococcus* spp. strains, previously isolated from artisanal Minas cheese. Descriptive statistics was used. Antimicrobial activity using the deferred-antagonism assay was detected in 262 (40%) of the 655 *S. aureus* strains tested. All 262 strains were inactivated by a proteolytic enzyme tested, indicating their proteic nature, a characteristic of bacteriocins. From 262 positive strains, 55 were selected based on the diameter of inhibition zone (> 10mm) for inhibitory activity against *Lactococcus* spp. Noteworthy, 42 strains (76%) presented some inhibitory activity against *Lactococcus* spp., and one strain of *S. aureus* presented inhibitory activity against five *Lactococcus* spp. strains. The results indicate that some *S. aureus* strains inhibit samples of *Lactococcus* spp. isolated from artisanal Minas cheese. Additional work is recommended to investigate further implications of this finding.

Key Words: *Staphylococcus aureus*, bacteriocins, mastitis

1060 (T100) Microbiological quality and safety of commercial local yogurt products in Giza Governorate, Egypt.

M. M. Motawee[*1], and S. A. Ibrahim[2], *[1]National Organization for Drug Control and Research, Giza- Egypt, Egypt, [2]North Carolina A&T State University, Greensboro.*

Yogurt is the most popular dairy product in Egypt. The popularity of yogurt can be attributed to its sensory characteristics and nutritional value. The microbiological characteristics of yogurt also contribute greatly to in the quality and shelf life of the final product. Thus, the objective of this study was to examine the microbiological quality and safety of yogurt products available in the local market in Giza Governorate, Egypt. One hundred yogurt samples were collected from local stores and stored in refrigerators prior to microbiological examination which was done within 24 h. Samples were stored under chilled conditions for 14 d at 7ºC ±1 and examined for yogurt culture viability, psychrophic bacteria (*Pseudomonas*), *Salmonella, Staphylococcus, E. coli, Aspergillus, and Bacillus*. The identification of each isolate was molecularly conformed using 16s rRNA. Our results showed that the yogurt culture maintained 6-7 log CFU/ml during the chilled storage. The psychrophic bacteria ranged from 5-6 log CFU/ml, whereas the other tested groups ranged from 2-4 log CFU/ml. The population of the tested bacteria did not change during chill storage. Our findings demonstrated that pathogenic bacteria could survive in commercial yogurt products. However, the presence of yogurt culture could help prevent foodborne illness in consumers. Our research demonstrates the importance of having standardized hygienic quality control practices in place to ensure the highest yogurt quality. Therefore, the implementation of HACCP or an equivalent safety protocol is paramount in preventing future outbreaks of foodborne illness in such popular dairy products in Egypt.

Key Words: yogurt, foodborne, quality.

1061 (T101) Stability of 10 β-lactam antibiotics in raw milk under different storage conditions.

H. Wang[1,2,3], N. Zheng[1,3], F. Wen[1,3], H. Wang[2], and J. Wang[*1,3], *[1]Ministry of Agriculture - Laboratory of Quality & Safety Risk Assessment for Dairy Products, Beijing, China, [2]College of Animal Science and Technology, Yangzhou University, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

B-lactam antibiotics are used to cure mastitis which inflicts severe economic losses in dairy farming. However, improper use of antibiotics may lead to residues in milk, which could be toxic and dangerous for human health, and may cause allergic reactions and antimicrobial resistance. At present, several methods for detecting the residue of β-lactam require milk samples to be sent back to a testing laboratory and stored until further analysis. In this study, we attempted to evaluate the stability of 10 β-lactam antibiotics, include amoxicillin (AMOX), cloxacillin (CLOX), oxacillin (OXAC), penicillin G (*P*ENG), nafcillin (NAFC), cefoperazone (*P*ER), cephapirin (*P*IR), ceftiofur (TIO), cefazolin (ZOL) and cefalonium (LON) in raw milk under different storage conditions, such as storage temperature and time, thawing temperature, freeze-thaw cycle times, and the addition of preservatives. Raw milk samples were collected from a local farm in Beijing and transported to our lab as soon as possible. Milk samples were spiked with the Maximum Residue Limits (MRL) levels in China and the antibiotic residues were determined by UPLC-MS/MS. Results showed that most of these antibiotics were quite stable (recovery = 90 ~ 120%) under different storage conditions, and their degradation rate increased with the increasing storage temperature and time, thawing temperature and freeze-thaw cycle times. Among the variables, preservatives played a critical role in the stability of β-lactam. The storage of PIR at room temperature for 1 day in raw milk containing preservatives resulted in a degradation rate up to 41.7%. Above all, the milk samples should be stored at -80ºC less than 7 days so that the β-lactam residues can be analyzed accurately.

Key Words: raw milk; β-lactam; storage conditions

1062 (T102) Risk warning of veterinary drug residues in raw milk based on shewhart control chart.

R. Han[1,2,3], N. Zheng[3,4], Z. Yu[2], X. Qu[1,3,4], S. Li[1,3,4], Y. Zhang[1,3,4], X. Zhou[1,3], and J. Wang[*1,3,4], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Food Science and Engineering, Qingdao Agricultural University, China, [3]Ministry of Agriculture - Laboratory of Quality & Safety Risk Assessment for Dairy Products, Beijing, China, [4]Ministry of Agriculture - Milk and Dairy Product Inspection Center, Beijing, China*.

The aim of this study was to develop a dynamic risk warning method of veterinary drug residues in raw milk. Risk warning methods of veterinary drug concentration above MRLs (C1 risk warning), abnormal detection rates (J-Pn risk warning) and average-standard deviation (X-δ risk warning) were developed based on theory of Shewhart Control Chart. Flumequine and danofloxacin residues data of raw milk from a large dairy company were collected. Fifty raw milk samples were detected in each week and total of 1,000 continuous data of 20 weeks were analyzed. The data were divided into 20 groups according to time series. C1 risk warning was not triggered, because none of samples exceeded MRLs. J-Pn risk warning was used for danofloxacin, because most of samples were not detected. Central line (CL) was calculated with the value of 5.95 and upper control limit (UCL) was 12.82. Control charts indicated that numbers of samples detected in each week were stable and all less than 12.82, so J-Pn risk warning was not necessary in 1-20 weeks. For flumequine, X-δ risk warning was used, because most of samples were detected. The value of CL was 1.5 and UCL was 2.82. Results analyzed by control charts showed average of flumequine in each week were stable and less than 2.82, so X-δ risk warning was not necessary in 1-20 weeks. In this study, abnormality of detection rate and average-standard deviation was also assumed and analyzed.

Key Words: risk warning, veterinary drug residues, Shewhart Control Chart

1063 (T103) Stability of flavonoids in grape seed and grape marc meal extract (GSGME).

M. Würzbach, E. Holl, and B. Eckel[*], *Dr. Eckel GmbH, Niederzissen, Germany.*

A secure food supply is crucial to all consumers. The use of a plant derived component poses a challenge for quality control: environmental factors lead to variations of plant composition, regarding the desired active substances, during the growth period. After harvest the active component should stay stable. The following study investigates the processing and storage stability of plant derived components, using the example of plant derived flavonoids in GSGME (AntaOxE, Dr. Eckel GmbH, Niederzissen, Germany). Flavonoids have shown anti-inflammatory properties and are effective for animal nutrition (Gessner et al., 2013; Fiesel et al., 2013). The stability of flavonoids in GSGME was studied under common processing conditions with different stressors: time of storage (9 mo), standard packaging material and temperature stress to simulate manufacturing processes. Flavonoid content was analysed using the Folin-Ciocalteu-method (Waterhouse, 2003). It was decided to compare storage characteristics in bags which were shut and sewn or open, stored under cool to room temperature (22°C) conditions. Each measurement was taken in triplicate. The samples, with an initial flavonoid concentration of about 86g/kg ± 0.9g/kg, were analysed every 3 mo. To rule out light as a potential influence, some samples were stored in daylight and some in darkness. Heat stability of flavonoids was tested in a cabinet dryer (Heraeus) at different temperatures, ranging from room temperature to 140°C for 4 hr. In the present study, the analysis of the flavonoid content after 3 mo of storage showed a higher concentration (up to 156g/kg ± 1.6g/kg) than before. This increase in flavonoid concentration may be caused by isomerisation. We found no influence of sealing and packaging on flavonoid activity. For the samples stored under daylight conditions, we analysed an increase in flavonoid content of maximum 25% compared to the other groups after 9 mo. For temperatures of 50°C, 75°C and 100°C, the samples showed flavonoid contents above the initial concentration of 86g/kg ± 0.9g/kg. At 120°C and 140°C, the flavonoid content decreased to 70 to 82g/kg. The study showed that both storage up to nine months or temperatures up to 120°C did not lead to a reduction of the initial concentration of flavonoids in GSGME. It even had a positive influence on concentrations. The results indicate that GSGME can be used without any concern with regard to flavonoids. Further studies should be conducted to explain the increase of flavonoids during storage and which molecules are modified during that time.

Key Words: flavonoids, stability, AntaOxE

1064 (T104) Effect of lysozyme or antibiotics on fecal zoonotic pathogens in nursery pigs.

J. E. Wells[*], E. D. Berry, N. Kalchayanand, L. A. Rempel, and W. T. Oliver, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Lysozyme is a 1,4-β-N-acetylmuramidase that has antimicrobial properties. The objective of this study was to determine the effect of lysozyme and antibiotics on zoonotic pathogen shedding in feces in nursery pigs housed without and with an indirect disease challenge. Two replicates of 600 pigs each were weaned from the sow at 26 d of age (d 0), blocked by litter and gender, and then randomly assigned to one of 24 pens in either a nursery room that had been fully disinfected or a nursery room left unclean after the previous group of pigs. Within a room, pigs were randomly assigned to control diets (C; 2-phase nursery regime), control diets + antibiotics (C + A; chlortetracycline and Denegard), or control diets +

lysozyme (C + Lyso; 100 mg/kg diet). Rectal swab samples were collected on d 0 and 28 of treatment, and enriched and cultured for *Campylobacter* spp. and shigatoxigenic *Escherichia coli* (STEC) O26, O45, O103, O111, O121, O145 and O157. Enrichments from rectal swab samples were also analyzed for presence of enterohemorrhagic *E. coli* (EHEC) virulence genes (*hly*A, *eae*, *stx*1, and *stx*2). Overall, the percentage of samples positive for *Campylobacter* spp., *hly*A, *eae*, and *stx*1/*stx*2 on d 0 were 43.8, 27.4, 25.3, and 14.3%, respectively, and all were different on d 28 (70.6, 17.4, 78.7, and 3.0%, respectively; $P < 0.05$). Room hygiene on d 0 had little effect on d 28 results, except the percentage positives for *hly*A was greater (21.6 vs 13.4%; $P < 0.02$) and for *eae* was less (74.7 vs 82.6%; $P < 0.02$) in unclean compared to clean rooms, respectively. Percentage of samples culture positive for *Campylobacter* spp. was lowest for C + Lyso diet, but similar for C and C + A diets (43.2, 83.7, and 84.8.respectively; $P < 0.01$). Diet had little effect on the EHEC virulence genes *hly*A or *eae* ($P > 0.1$), but there was a tendency for lower percentage of samples positive for *stx*1/*stx*2 in C + A or C + Lyso diet groups compared to C diet (5.8, 1.2, and 2.1%, respectively; $P < 0.07$). The STEC types tested were rarely detected and not affected by time, hygiene or treatment ($P > 0.1$). Thus, lysozyme in the diet can reduce fecal shedding of *Campylobacter* spp. from nursery swine. *USDA is an equal opportunity provider and employer*.

Key Words: antibiotics, lysozyme, swine

1065 (T105) Thermophilic spore forming bacilli: attachment and biofilm formation on stainless steel. M. C. Enes Ribeiro[1], G. Theodore Walsh[2], M. Lucia Gigante[1], and R. Jimenez-Flores[*2], *[1]Faculty of Food Engineering, University of Campinas, Campinas, SP, Brazil, [2]Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo.*

Studies suggest that the spores of thermophilic bacilli possibly bind to the stainless steel surface in greater numbers than vegetative cells. The aim of this study was to evaluate the attachment and biofilm formation by spore-forming bacteria on stainless steel. The microorganisms (CM12, SL12, SL9, CM3, CH7, and SH6) were isolated from milk powder plants in the USA and belong to the collection of cultures at DPTC/Cal Poly. To evaluate the spores attachment and biofilm formation, cleaned stainless steel coupons were used. The experiments were carried out using either whole or fat free UHT milk in order to form a fouling film on the coupons surface. The system was kept at 55°C for 20 hours at 200 rpm. After film formation, the coupons were removed from the matrices and immersed into an aqueous spore solution held at the same conditions to verify the ability of attachment and biofilm formation. Spores were enumerated after heat treatment (80°C/12 minutes) for either 5 minutes or for 20 hours. In addition, a SDS-PAGE gel was performed in order to verify the proteins present in the spores. The effect of the matrices (fat free or whole milk), microorganisms (six different strains), time of exposure (5 minutes or 20 hours), and their interactions on the spores attachment and biofilm formation were evaluated by ANOVA and Tukey's test for comparison between means ($P < 0.05$). Although, the spore strain and the time of exposure significantly affected the attachment and biofilm formation, none of the interactions among the factors were significant. Spores attachment ranged from 3 to 4 log cfu/cm^2. The highest average attachment was observed by SL12 and SH6 (4.01 and 4.08 log cfu/cm^2, respectively), while CM12 and SL9 showed the lowest average attachment (3.42 and 3.52 log cfu/cm^2, respectively). The strains that showed the lowest average attachment (CM12 and SL9) also presented less protein in band density around 25 and 50kDa when compared to the other four strains in the SDS-PAGE. Despite the attachment after 5 minutes was significantly higher than 20 hours, the difference observed was only 0.12 log cfu/cm^2. The results suggest that these matrices did not interfere with the spores attachment and biofilm formation. This could be a strain-dependent characteristic since spores protein may play an important role on attachment. *Acknowledgments: CNPq, CAPES.*

Key Words: dairy, spores, biofilm

1066 (T106) The consumer profile of certified beef in the XXI century. M. E. A. Canozzi[1], J. Magero[1], R. C. T. Mesquita[1], J. O. Barcellos[2], D. Streit Júnior[1], and L. Kindlein[*1], *[1]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil, [2]Universidade Federal Do Rio Grande Do Sul, Porto Alegre, Brazil*.

The beef production chain has been reinvented as a consequence of changes in perceptions and importance of its various players. The emergence of the current model, which combines quality and food safety, was in the late twentieth century. It was due to the expansion of the international trade in meats and an awareness of the connection between health crises and animal derived products. These changes in the supply chain and the difficulty of the consumer to judge quality and food safety favored the emergence of the certification processes in the beef market. The aim of this study was to characterize the publications and evaluate the consumer profile of certified beef. A systematic search of descriptive and/or sensory research published between 2002 and 2012 was performed. Three hundred twenty-seven indexed papers were found in the literature on the proposed subject. Only 34 papers were selected for (10.4%) in depth evaluation, based on its importance and meta-analysis methodology. Over these ten years there was a gradual increase in the number of publications. Concerning the spatial distribution of publications, the highest proportion was from the European continent (46.2%), followed by North (23.1%) and South America (15.4%). More than half of the analyzed articles (60.5%) studied traceability, and less repre-

sentative was animal welfare and geographical origin (11.6%/each). There was a predominance of studies on accreditation type most sought or demanded by consumers (35.8%), followed by willingness of the consumer to pay a premium price (33.9%) and the relationship between socio-demographic characteristics and certification type (30.7%). The consumer demand for certified beef in the 21st century increased after the health crises and the quality differential became a relevant point in the buying decision. This process was influenced by social and demographic characteristics.

Key Words: food certification, meta-analysis, traceability

1067 (T107) Identification of horsemeat presence in beef commercial butcheries using the polymerase chain reaction (PCR) technique. G. Aranda-Osorio*[1], B. Alarcón-Zúñiga[1], M. Huerta-Bravo[1], O. Hernández-Mendo[2], and G. Reséndiz-González[1], *Departamento de Zootecnia, Universidad Autónoma Chapingo, México, [2] Colegio de Postgraduados, Montecillo, México.*

The objective of the present study was to determine the presence of horsemeat in beef commercial butcheries through the use of the polymerase chain reaction (PCR) technique. Statistically, horsemeat is not consumed in México, however, the country occupied important places in the world as producer (4º with 64,695 ton) and exporter (4º with 14,026 ton), remaining an important amount (a little more than 50,000 ton) that should be commercialized into the domestic market, thus the question is if some portion of this amount is commercialized as beef in one of the biggest markets in the country, México City. To give answer to this question, there were sampled 22.5% of the Delegational markets of México City (the City is divided in 16 Delegations, each one have different numbers of markets, depending on their size and population). From a completely random design there were selected two butcheries per market, in each butchery, there was asked (bought) for a portion of specific cut of beef, approximately 250 g of "aguayón" (*Biceps femoris*), although it was not always the case. Once the sample was obtained, it was immediately identified and kept on ice for transportation to the meat lab, once arrived to it, the samples were prepared: from the center of the meat cut (to avoid contamination) a subsample of 1 g was deposited in a vial and freeze (-80ºC) until lab analysis. The PCR technique used was based in the methodology reported by Matsunaga *et al.* (1999). Fortunately, the results showed that only 5.5% of the samples were positive to equine. Horsemeat is as nutritious a beef, and has the advantage of being a lean meat, thus less saturated fatty acids, less probability of cardiovascular problems, although, the key point is the fraud to the consumer.

Key Words: DNA identification, meat substitution

FORAGES AND PASTURES: FORAGES AND PASTURES 1: SILAGES AND FORAGES IN DAIRY PRODUCTION SYSTEMS

1068 (M085) The influence of wilting on the quality of *Leucaena leucocephala* silage. T. Clavero[*1], and R. Razz[2], [1]*Universidad Del Zulia, Maracaibo, Venezuela,* [2]*Universidad del Zulia, Maracaibo, Venezuela.*

An experiment was conducted in the northwest of Venezuela in order to evaluate the ensiling properties of *Leucaena leucocephala* using laboratory silos. Factors studied were wilting for 0 and 3 h and ensiling time of 0, 7, 14, 21, and 35 d.The silos were kept in the room set at 25ºC and samples were taken from three silos at each sampling time for chemical analyses. Data were analyzed as a randomized design with a 2 x 5 factorial of wilting and ensiling time, respectively, with three replications. Means were compared by Tukey test. Response variables were: DM, cellulose (C), pH , total nitrogen (TN), ammonia (NH_3) and NH_3/TN. Increasing ensiling time of high moisture *Leucaena* resulted in losses of DM in the silage, unwilted silage contained 52.3% DM at the end of ensiling time while wilting silage showed 59.9% of DM. Ensiling *Leucaena* from 0 to 35 days resulted in decreased ($P < 0.05$) C content in 9.5% for high moisture silage in contrast to 6.5% for wilted. This could have been due to the cumulative activity of plant cell respiration and some facultative bacteria in the fresh ensiled forage. The pH increased ($P < 0.05$) while TN, NH_3 and NH_3/TN decreased ($P < 0.05$) with reduced moisture content of ensiled *Leucaena.* The concentrations of fermentation end-product decreased with wilting, showing that low moisture restricted fermentation. The reduction in TN content in wilted silage was expected due to breakdown of true protein during sun-drying and ensiling process. Wilting resulted in decreased ($P < 0.05$) NH_3 and NH_3/TN when compared to high moisture silage. Concentrations of NH_3 and NH_3/TN in high moisture silage were 35.3 and 24.6% greater, respectively than wilted silage. However, levels of NH_3 were less than 80-100 g/kg TN which is commonly used to represent well fermented silage. All silages in the current experiment achieved satisfactory preservation.

Key Words: *Leucaena leucocephala*, wilting, silage, quality

1069 (M086) Comparison of milk fatty acid profiles of dairy cows grazing cool-season perennial ryegrass or birdsfoot trefoil pasture on a commercial organic dairy farm. R. G. Christensen[1], J. S. Eun[*1], V. Fellner[2], A. J. Young[1], and J. W. MacAdam[1], [1]*Utah State University, Logan,* [2]*North Carolina State University, Raleigh.*

This experiment investigated milk fatty acid (FA) profiles of grazing dairy cows on a commercial organic dairy farm during 2 grazing seasons in 2012 and 2013. Eighteen multiparous cows in mid-lactation were assigned to one of 2 intensively rotated grazing treatments in a completely randomized design: cool-season perennial ryegrass (RGP) vs. birdsfoot trefoil pasture (BFTP). Cows received 2.27 kg of concentrate (flaked barley grain and vitamin and mineral supplement) twice per day following milking. Experiment lasted a total of 10 wk, with 2 wk for adjustment to pasture treatments and 8 wk for data and sample collection. Samples of pasture forages and milk were taken at wk 2 and 6 and were analyzed to determine their FA profiles. In 2012 and 2013, averaged concentration of C18:3 n-3 (42.6 and 53.5 g/100 g) was the greatest in pasture forage FA followed by C16:0 (20.5 and 15.7 g/100 g) and C18:2 n-6 (13.9 and 13.5 g/100 g), respectively. The most noticeable difference of pasture forage FA profiles in 2012 and 2013 was that in 2012 proportion of C18:3 n-3 in RGP increased from wk 2 (39.8 g/100 g) to wk 6 (47.1 g/100 g), whereas its proportion in BFTP was similar at wk 2 and wk 6. In contrast, proportion of C18:3 n-3 in RGP and BFTP decreased from wk 2 (57.3 and 55.1 g/100 g) to wk 6 (51.9 and 49.6 g/100 g), respectively. Concentration of *trans*-11 C18:1 in milk was very low in RGP and BFTP in both grazing seasons, suggesting limited impacts of pasture on the biohydrogenation activity for the pastures tested. Dairy cows grazed on RGP and BFTP showed similar concentrations of *cis*-9, *trans*-11 conjugated linoleic acid in milk fat throughout grazing seasons. Cows grazed with BFTP increased concentration of C22:6 (n-3; docosahexaenoic acid) at wk 6 in 2012 and 2013 compared to those grazed with RGP. However, pasture treatment did not affect ratio between polyunsaturated FA and saturated FA in two grazing seasons. Overall results in this experiment indicate that source of pastures did not affect major milk FA profiles, and some minor changes in FA profiles may have resulted from pasture FA profiles in two grazing seasons.

Key Words: birdsfoot trefoil pasture, lactating dairy cows, milk fatty acids

1070 (M087) Lactational response of Holstein cows to brown midrib or leafy-floury corn silage.

S. Y. Morrison*[1], K. W. Cotanch[1], C. S. Ballard[1], H. M. Dann[1], E. O. Young[1], R. J. Grant[1], and C. I. Key[2], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Healthy Herd Genetics & Nutrition, LLC, Oneida, NY.*

The objective of this experiment was to measure the response of lactating Holstein cows to total mixed rations containing either brown midrib-3 (BMR; Mycogen F2F387) or an experimental leafy-floury hybrid (LF; Healthy Herd Genetics HHG39HF13) bred for improved NDF and starch digestibility compared with similar leafy corn hybrids. Sixteen cows (6 primiparous; 10 multiparous) averaging 130 ± 16 days in milk were assigned to one of two dietary sequences in a crossover design with 28-d periods (21 d adaptation and 7 d collection). Each diet contained 49% BMR or LF corn silage, 9.8% haycrop silage, and 41.2% concentrate mix (DM basis). The BMR silage contained 30.2% DM, 7.3% CP, 41.5% NDF, 60.2% 24-h NDF digestibility, 31.0% starch, and 77.5% 7-h starch digestibility (DM basis). The LF silage contained 31.9% DM, 7.8% CP, 42.6% NDF, 47.5% 24-h NDF digestibility, 30.3% starch, and 73.0% 7-h starch digestibility which was unexpectedly low. The BMR diet contained 17.2% CP, 32.2% NDF, and 24.6% starch, and the LF diet was similar with 17.8% CP, 33.5% NDF, and 23.0% starch. Data were analyzed as a crossover design using the PROC MIXED of SAS with model effects of diet, sequence, and period, with cow within sequence as a random effect. Compared with the LF diet, the BMR diet resulted in greater DMI (29.7, 27.2 kg/d, SE = 0.9; $P < 0.001$), greater SCM yield (47.0, 41.7 kg/d, SE = 1.4; $P < 0.001$), and greater SCM/DMI (1.59, 1.54, SE = 0.04; $P < 0.01$). Chewing during eating and ruminating was greater for the LF versus the BMR diet (89, 84 min/kg NDF intake, SE = 3; $P < 0.001$). Compared with the LF diet, the BMR diet resulted in greater total tract OM and NDF digestibility (81.4, 77.7%, SE = 0.6; 63.8, 55.4%, SE=0.8; $P < 0.001$), although starch digestibility was similar for the LF and BMR diets (99.0, 98.9%, SE = 0.1; $P < 0.001$). Compared with the BMR diet, the LF diet resulted in higher fecal pH (6.92, 6.71, SE = 0.03; $P < 0.001$), lower fecal starch (0.82, 1.15%, SE = 0.09; $P < 0.008$), and lower fecal P (0.53, 0.63, SE = 0.02; $P < 0.001$). The LF hybrid assessed in this experiment constrained DMI and milk production compared with the BMR hybrid. To achieve dietary fermentable carbohydrate content similar to BMR, a LF hybrid will require higher NDF and starch digestibility than the hybrid evaluated in this experiment.

Key Words: leafy-floury corn silage, brown midrib corn silage, dairy cattle

1071 (M088) Production response of lactating cows to diets based on corn or forage sorghum silage produced from first or second harvest.

J. K. Bernard*, *University of Georgia, Tifton.*

The objective of the trial was to compare the production response of lactating Holstein cows to corn or forage sorghum silage produced from two crops. Corn was planted in April and harvested in July (CS1). A second crop was planted in July and harvested in November (CS2). A brachytic dwarf forage sorghum was planted in April, harvested in July (FS1), fertilized, and harvested a second time in November (FS2). All forage was ensiled in plastic bags and stored until the production trial began. Silages contained (DM basis) 8.0, 8.5, 9.0, and 9.5% CP; 39.0, 38.3, 54.2, and 55.1% NDF; 3.55, 2.83. 7.72, and 7.77% acid detergent lignin; and 48.1, 47.7, 31.5, and 29.1 NFC, for CS1, CS2, FS1, and FS2, respectively. Forty-eight mid-lactation Holstein cows (153.5 DIM, 36.5 kg milk, and 3.2% fat) were assigned randomly to one of for diets differing in forage source. Cows were fed individually once daily behind Calan doors for 5 wk. Diets were balanced to provide equal concentrations of protein, fiber, and energy. No differences were observed in DMI, milk yield, or milk composition among treatments: 23.1, 21.1, 21.0, and 19.9 kg/d DMI; 34.5, 34.4, 34.9, and 35.1 kg/d milk; 3.34, 3.22, 3.40, and 3.52% fat; and 2.73, 2.63, 2.61, and 2.65% protein for CS1, CS2, FS1, and FS2, respectively. Concentrations of MUN (mg/dl) were higher ($P = 0.03$) for FS1 and FS2 compared with CS1 and CS2 (16.2, 16.3, 11.6, and 13.9, respectively). Results of this trial suggest that brachytic forage sorghum silage can support similar as corn silage. Forage harvested from the regrowth of brachytic forage sorghum also supported similar performance as the first harvest. The higher MUN observed for diets based on forage sorghum reflects most likely reflects differences in fermentable carbohydrate compared with corn silage diets.

Key Words: corn silage, forage sorghum, milk yield

1072 (M089) Feeding strategy and pasture quality relative to nutrient requirements of grazing dairy cows in the Northeastern U.S.

A. N. Hafla*[1], K. J. Soder[1], A. F. Brito[2], R. Kersbergen[3], F. Benson[4], H. Darby[5], and M. D. Rubano[1], *[1]USDA-Agricultural Research Service, University Park, [2]University of New Hampshire, Durham, [3]University of Maine Cooperative Extension, Waldo, [4]Cornell University Extension, Cortland, NY, [5]University of Vermont, Albans.*

Pasture samples ($n = 229$) collected during the grazing season from 14 organic dairy farms in 2012 (*P*A, ME, NY, NH, VT) and from 11 of the same farms in 2013 (PA, ME, NY, NH) were analyzed for nutritional composition. Frequency analysis was used to determine the proportions of pasture samples that met minimum NE_L, CP, and macro-mineral requirements according to the NRC (2001) model for a 680 kg Holstein, producing

25 kg milk/d with 3.5% milk fat and 3.0% milk protein. The Large Ruminant Nutrition System (LRNS, Version 1.0.24) was used to describe feeding strategies that accompanied grazing on eight of the participating farms. Four farms had moderate conserved feed input (> 20% diet DM not from pasture; MF), and fed corn silage, grass/legume balegae or haylage, and/or a grain mix and dry hay, two farms supplemented pasture with a grain mix (GS), and two farms fed forage only (*P*asture and dry hay; FO). Management and production information used in the LRNS model were specific to environmental conditions, nutrient concentrations of feeds, cow type, and level of production for each farm. If pasture was the only diet component, energy was the most limiting nutrient, with 39% of pasture samples failing to meet the minimum NRC NE_L requirement. Only 7% of pasture samples did not meet the minimum CP requirements. Calcium, P, and S did not meet minimum NRC requirements in 35, 18, and 10% of pasture samples, respectively. Average concentrations of Mg and K were in excess of 156 and 1,113% of dietary requirements. Milk production was observed to be higher on MF farms (23 kg/d), but was comparable on GS and FO farms, averaging 15 kg/d for both. Proportion of DMI from pasture was related to feeding strategy and ranged from 51 to 79% on MF farms, 84 to 96% on GS farms, and 91 to 100% on FO farms. Metabolizable protein provided by the total diet (*P*asture and supplementation) exceeded the requirements at the specified level of production and environmental conditions except for 1 farm (the MF farm with the lowest amount of DMI coming from pasture). Rumen N balance was negative for both GS farms (-18 and -33 g/d). Overall, the forage quality of pastures evaluated was high. Additionally, varying feeding strategies allow farmers to use resources such as pasture, homegrown forages, and grains to meet individual goals of milk production.

Key Words: pasture, grazing, dairy

1073 (M090) Use of biological additives to improve lactic fermentation tropical silages.

L. Bernal[*1], R. Herrera[2], P. Avila[3], H. Jimenez[2], M. Cuchillo[3], and S. D. Martens[4], *[1]La Salle University, Bogotá, Colombia, [2]Corpoica, Bogota, Colombia, [3]International Center for Tropical Agriculture, Cali, Colombia, [4]Saxon State Office for Environment, Agriculture and Geology, Department of Animal Production, Köllitsch, Germany.*

The objective of this study was to assess different biological additives to favor lactic acid fermentation. This trial aimed also to obtain the optimal proportions of sorghum/soybean to ensure good fermentation quality for silage making using a fast in vitro fermentation test (Rostock fermentation test; RFT). Different combinates of a grass (*Sorghum bicolor* L. variety H70) and legume (soybean *Glycine max* variety Panorama 29) were tested against biological additives. Test used sorghum and soybean and their combinations (100/0, 33/67, 67/33, 0/100) with or without biological additives. Inoculates were evaluated for their acidification ability: enzymatic complex from anaerobic rumen fungi (*Orpinomyces* sp), clarified rumen fluid, Lactic acid bacteria (LAB)-epiphytic S738 (from sorghum), LAB-epiphytic S739 (from soybean), LAB from CIAT bacteria collection (S66.7), commercial silage inoculant (SilAll4×4-Brazil) and a control. Fifty grams of fresh minced material and 200ml of distilled water of forage were incubated into sterile glass in triplicate at 37°C for 48 hours and the pH was measured at 0, 20, 28, 44, and 48 hours to determine the dynamics of fermentation. Completely randomized in a 4x6 factorial design was used. Forage inclusion level (four levels) and the type of additive (six additives and control) were arranged. Significant difference ($P < 0.001$) was found at the level of forage inclusion and the additive used ($P < 0.05$). The treatments including biological additives showed lower pH value than control treatment (5.5). Best results were obtained (pH = 3.7) for the sorghum/soybean at 100/0% inclusion, followed by the mixture of sorghum/soybean 67/33 (pH = 4.2) while the pH for the rest of treatments value were above 5.0. The best additive was the bacterial strain (S738) (pH <4.0). The enzymatic complex (pH 5.0), clarified rumen fluid (pH 5.3) and silall4x4 (pH 5.2) have reasonable pH values for ensilability. The highest pH value (5.7) was for soybean 100% ($P < 0.05$). Results show that biological additives such as epiphytic bacterial strains isolated from sorghum have potential to improve fermentability. Larger sorghum inclusion in the mixture facilitated lactic fermentation for silage making.

Key Words: pH, Rostock fermentation test, grass, legume.

1074 (M091) Quality evaluation of five varieties of corn for silage production in crop-livestock-forest integration system in the Cerrado region.

M. C. A. Santana[*1], A. A. Pinheiro[1], V. A. Silva[1], J. T. C. Pacheco[1], A. C. Fernandes[1], I. D. Carneiro[1], V. C. Modesto[2], and J. Cavali[3], *[1]Emater, Goiânia, Brazil, [2]UNESP, Jaboticabal, Brazil, [3]Universidade Federal de Rondônia - Unir, Rondonia, Brazil.*

The intercropped of corn within the integrated crop- livestock-forest system can be seen in the establishment of forage with lower costs and diversify, producing silage for animal feed. Thus, we evaluated the qualitative characteristics of five cultivars of maize intercropped with *Brachiaria brizantha* cv. Marandu for silage production in integrated crop-livestock-forest system. The experimental design was a randomized block with three replications and five treatments. Maize cultivars used were: EMGOPA 501, AL Bandeirantes, BRS Caimbé, PL 6880, BRS 1060. To assess the qualitative characteristics were estimated: number of grains per ear; number of kernels per row; number of rows per ear; grain weight per ear and weight of 100 grains. There were no significant differences in the variables studied. The intercropped of forage maize cultivars do not influence on the qualitative characteristics of corn for silage.

Key Words: intercropped, Marandu, tropical region

Table 1074. Means for number of grains per ear (NE); number of kernels per row (NR); number of rows per ear (NRE); grain weight per ear (GWE) and weight of 100 grains (W100G).

	NE	NR	NRE	GWE (g)	W100G (g)
EMGOPA501	532.6	358.0	12.6	178.34	34.09
AL BAND[1]	479.8	366.0	13.2	187.24	38.80
BRS CA[2]	540.0	349.7	15.6	179.98	32.64
PL 6880	443.4	316.0	14.0	171.13	37.54
BRS 1060	549.6	386.0	14.2	189.39	34.44
CV (%)	12.8[ns]	11.5[ns]	12.4[ns]	12.1[ns]	5.68[ns]

ns - non significant.
[1]Cultivar- AL Bandeirantes.
[2]Cultivar - Caimbé.

1075 (M092) Impact of hybrid and growing location on yield and composition of corn plants harvested for silage. D. Bolinger[1], L. Nuzback[*2], and F. N. Owens[2], *[1]DuPont Pioneer, Perrinton, MI, [2]DuPont Pioneer, Johnston, IA.*

Relative effects of hybrid, growing location, and DM at harvest on corn silage yield and composition have not been clearly defined. Their impacts on yield, plant and grain composition at silage harvest, and potential milk yields were examined using corn plants and grain from five Pioneer hybrids grown in each of 15 environmentally diverse Michigan locations in 2013 all harvested at silage maturity. Nutrient compositions were determined at a commercial laboratory; milk yields were predicted from Milk 2006 equations. Relationships were evaluated using regression and GLM procedures of SAS. Whole plant DM, grain DM, starch, and NDF ranged from 24.2 to 47.8, 49 to 76, 17.2 to 39.6, and 37.1 to 49; 24 hour NDF disappearance ranged from 36.3 to 55.6 percent of NDF; DM yield ranged from 8 to 23 metric ton (MT) per hectare while milk ranged from 1444 to 1873 kg per MT. Growing location altered ($P < 0.01$) every measurement. Harvest DM had quadratic effects on milk per hectare and on yields of DM, starch and NDF, each peaking at 41% DM; hence relative nutritional values can be biased if hybrids differ in DM content even when harvested on the same date. Among environmental measures, growing degree days prior to harvest (range 1916 to 2367) was related ($P < 0.05$) negatively to sugar but positively to starch content of plants. Precipitation (36 to 65 cm during the season) was related ($P < 0.02$) positively to yield and milk per hectare but negatively to crude protein content and NDF digestibility. Locations that received less than 41 cm of rain had lower ($P < 0.05$) plant yields and milk per hectare but greater ($P < 0.05$) NDF digestibility (48.3 versus 45.8 percent of NDF) and CP, fat, and prolamin content of grain. Greater plant weight was associated with increased kernel density and yield of milk and DM per hectare. Hybrids with greater drought tolerance had greater ($P < 0.04$) starch content of plants and grain and greater starch availability from grain but lower NDF digestibility. The growing environment and harvest DM generally had greater impact on silage yield and nutritive value than hybrid choice among the corn silage hybrids tested.

Key Words: corn silage, location, harvest

1076 (M093) Impact of corn plant maturation and planting density on nutrient composition and potential milk yield. L. Brown[*1], L. Nuzback[2], B. Redenius[2], P. M. Walker[3], and F. N. Owens[2], *[1]DuPont Pioneer, Bloomington, IL, [2]DuPont Pioneer, Johnston, IA, [3]Illinois State University, Normal.*

Stage of maturity and planting density can alter weight and nutrient composition of corn plants within the silage harvest window and thereby alter both yield and the nutritional value of corn silage. To appraise effects of maturity and plant density on yield and nutrient composition, nine Pioneer silage hybrids (109- to 115-d relative maturity) were planted in a single field near Lexington, IL, with 69000 and 84000 plants per hectare. Duplicate sets of five representative plants were harvested at 3 to 4 day intervals within the silage harvest window (28 to 42 percent DM), weighed and chopped. Duplicate subsamples were dried (48 h at 15 C) and assayed by calibrated NIR procedures for CP, starch, sugars, NDF, and NDF digestibility. Averaged across harvest dates, hybrids differed ($P < 0.01$) in all measurements. The 21 percent increase in plant density decreased ($P < 0.05$) starch content of plant DM by 1.5 percentage points and milk per ton by 2.5 percent, but increased ($P < 0.01$) yields of DM, milk, NDF, digestible NDF, and indigestible NDF per hectare by 7.2, 7.0, 9.0, 8.0, and 10 percent. Across hybrids, linear and quadratic regressions against harvest DM were significant ($P < 0.05$) for starch content, protein content, milk per ton (each increasing at a decreasing rate), and sugar content (decreasing to a plateau). As plant DM percentage increased, yield of DM increased but NDF digestibility declined ($P < 0.01$) slightly (0.09 points for each 1 percentage increase in plant DM. In corn silage test plots, all hybrids typically are harvested on a single date regardless plant moisture content. Among these nine hybrids, ranking for milk per hectare remained reasonably similar across this DM range; milk per ton ranking changed markedly, especially when plant DM was below 34 percent, although rank of the top (a BMR) and bottom hybrids remained similar. In conclusion, increasing planting density increased corn silage yield with some sacrifice in starch percentage. Hybrid ranking for milk per ton differed with harvest DM. To prevent ranking bias, hybrids in silage test plots should be harvested at multiple moisture contents.

Key Words: corn plant maturity, planting density, hybrid ranking

1077 (M094) Gas production and volatile fatty acids of corn stover silage added with yeast culture and fermented apple pomace. C. Rodríguez-Muela*, N. H. Ruiz, P. F. Mancillas-Flores, O. Ruiz-Barrera, A. Corral, C. Arzola-Alvarez, A. Ramírez-Godínez, and E. Santellano, *Universidad Autónoma de Chihuahua, México.*

Silage is a forage conservation method based on fermentation of carbohydrates to produce lactic acid under anaerobic conditions. Solid state fermentation (SSF) is a process of microbiological growth on solid materials under aerobic conditions. With the objective of improving the nutritional value of corn stover through the combination of SSF and silage, three treatments were driven during 28 d using 48 plastic bags as a microsilos each with 2 kg of: (T1) corn stover alone; (T2) corn stover + yeast culture produced by SSF (10% as feed basis) and (T3) corn stover + fermented apple pomace produced by SSF (69% as feed basis). Treatments were added with water to obtain 35% of DM during the ensilage. Gas production (GP) and volatile fatty acids (VFAs) were determined in the samples obtained on 14d of the ensilage, following 96 h incubation in buffered rumen fluid using the in vitro fermentation technique. Data were analyzed by PROC GLM of SAS. Results are shown in Table 1077. The addition of yeast culture and apple pomace increased GP volume ($P < 0.01$) with values of: 58.17 ± 0.69, 63.57 ± 0.69 and 85.96 ± 0.69 ml*0.2g^{-1} MS of T1, T2 and T3, respectively. VFA´s differed between treatments ($P < 0.01$). Acetate-propionate ratio increased from 1.8:1 to 2.4:1 ($P < 0.05$) during the in vitro fermentation. Results may be derived from a change in rumen fermentation. It was conclude that the addition of fermented apple pomace or yeast culture improve GP and VFAs parameters of corn stover silage.

Key Words: yeast culture, silage, corn stover

Table 1077. Parameters of gas production and volatile fatty acids, determined in the samples obtained on 14 d of the ensilage, following 96 h incubation in buffered rumen fluid using the in vitro fermentation technique

Evaluated Variables	T1	T2	T3
Total Gas Volume (ml*0.2g^{-1} MS)	58.17 ± 0.69^{c}	63.57 ± 0.69^{b}	85.96 ± 0.69^{a}
Parameter A (ml*0.2g^{-1} MS)	30.05 ± 1.30^{b}	30.21 ± 1.30^{b}	39.42 ± 1.30^{a}
Parameter B (h)	3.46 ± 0.07^{a}	3.03 ± 0.07^{b}	2.55 ± 0.07^{c}
Parameter C (mL/h)	0.026 ± 0.00^{b}	0.028 ± 0.00^{a}	0.028 ± 0.00^{a}
Acetic Acid (mM/mL)	103.06 ± 0.09^{c}	114.06 ± 0.09^{b}	120.26 ± 0.09^{a}
Propionic Acid (mM/mL)	43.33 ± 0.07^{c}	46.70 ± 0.07^{b}	48.59 ± 0.07^{a}
Butiric Acid (mM/mL)	16.12 ± 0.06^{c}	17.60 ± 0.06^{b}	18.16 ± 0.06^{a}

^{a,b,c} Means with literal different between columns indicate statistical difference ($P < 0.05$), Parameter A = asymptote of gas production, Parameter B = average time of gas production after incubation, Parameter C = constant determining the change of profile.

1078 (M095) Effect of a chemical additive on fermentation and aerobic stability of high-moisture corn. T. C. Da Silva, M. L. Smith*, S. A. Polukis, A. M. Barnard, and L. Kung Jr., *University of Delaware, Newark.*

The objective of this experiment was to evaluate effect of a chemical additive on fermentation and aerobic stability of high moisture corn (HMC). Ground HMC (~63% DM) was untreated, or treated with 2 L of Safesil (SAFE, sodium nitrite, potassium sorbate, and sodium benzoate, Salinity Agro, Halmstad, Sweden)/t of fresh HMC, 3 L of SAFE/t, or 4 L of SAFE/t. Lab silos (7.5 L, 4 silos/treatment/time point) were prepared (density of 672 kg of DM/m^3) and ensiled for 21 and 90 d at 22 ± 2 °C. Data were analyzed as a 4 × 3 factorial arrangement of treatments with main effects of Safesil (4 levels) and days of ensiling (0, 21 and 90 d), and their interaction, using the software JMP, version 10. Numbers of yeasts were similar ($P > 0.05$) among treatments in fresh HMC (log 6.9 to 7.1 log cfu/g) but decreased ($P < 0.01$) substantially after ensiling (< 3.3 log cfu/g). Numbers of yeasts were similar ($P = 0.33$) among treatments after 21 d of ensiling but after 90 d they were lower ($P < 0.01$) in HMC treated with SAFE (< 2 log cfu/g for all levels) compared to untreated HMC (3.22 log cfu/g). Compared to untreated HMC, addition of SAFE to HMC at all levels did not affect the concentrations of organic acids (lactic, acetic, and propionic) or pH at any ensiling time. In contrast, treatment with SAFE markedly decreased ($P < 0.01$) the concentrations of ethanol in HMC after 21 and 90 d (< 0.25% of DM for all SAFE levels) when compared to untreated HMC (1.02 and 0.76% of DM, respectively at d 21 and 90). Treatment with SAFE markedly improved ($P < 0.01$) the aerobic stability of HMC after 30 d (89 h for untreated HMC vs. > 500 h for HMC treated with SAFE at all levels) and after 90 d of ensiling (77 h for untreated HMC vs. > 500 h for HMC treated with SAFE at all levels). This was the first evaluation of Safesil on HMC in North America and it showed that this additive, even when added at a relatively low level (2 L/t) effectively improved the aerobic stability of HMC and reduced concentrations of ethanol without altering the concentrations of organic acids or pH.

Key Words: high moisture corn, fermentation

1079 (M096) The effect of chemical additives with antifungal properties on the fermentation and aerobic stability of corn silage. M. C. Windle*, C. Merrill, M. C. N. Agarussi, L. O. Rosa, and L. Kung Jr., *University of Delaware, Newark.*

The objective of this study was to evaluate chemical additives with antifungal properties on the fermentation and aerobic stability of corn silage harvested at two maturities: 32% DM (LDM) and 38% (HDM) whole-plant DM. At each harvest, plants were obtained from five random locations within the

field and further divided into four piles and treated with a) no additive, b) 1.5 L of Safesil (Salinity Agro, Halmstad, Sweden; active ingredients of sodium nitrite, potassium sorbate, and sodium benzoate)/t of fresh forage, c) 2 L of Safesil/t, or d) 2 L of Crop Saver (CS, CNH America LLC, Racine, WI; 64.5% propionic acid). Each pile was treated with a total volume of 0.03% vol/wt of liquid (water alone for the no additive treatments). Forage from each pile was ensiled in 7.5-L lab silos (packing density of about 220 kg of DM/m^3). Silage data were analyzed as a 2 (maturity) × 4 (additive) factorial arrangement of treatments after 120 d of storage (22 ± 2°C) using the software JMP. At both harvest DM, compared to untreated silage, treated silages had similar ($P > 0.05$) concentrations of lactic and acetic acids, CP, ADF, NDF, starch and pH. Treatment with CS increased ($P < 0.01$) the concentrations of propionic acid silage in silage in both maturities compared to other treatments. In LDM silages, treatment with Safesil did not affect ($P > 0.05$) the concentrations of ethanol but treatment with CS resulted in a higher ($P < 0.01$) concentration of ethanol when compared to untreated silage. In HDM silage, concentrations of ethanol were lower ($P < 0.01$) in a dose dependent manner for silages treated with Safesil but unaffected by CS. Compared to untreated silage, aerobic stability was improved ($P < 0.01$) for both maturities treated with CS (66 vs. 93 h in LDM silage and 59 vs. 116 h for HDM silages). Treatment with Safesil was even more effective resulting in aerobic stabilities ($P < 0.01$; average of > 450 h in LDM silages and average of > 350 h in HDM silages) that were markedly better than both untreated and CS. This study was the first to show that Safesil has the potential to markedly improve the aerobic stability of corn silage in North America.

Key Words: silage, aerobic stability, corn silage

1080 (M097) Effect of *Lactobacillus plantarum* MTD1, potassium sorbate or their combination on production of volatile organic compounds and aerobic stability of corn silage.

M. C. Windle*[1], C. Merrill[1], M. L. Smith[1], S. D. Hafner[2], F. M. Mitloehner[3], R. Franco[3], and L. Kung Jr.[1], *[1]University of Delaware, Newark, [2]Hafner Consulting LLC, Washington, DC, [3]University of California–Davis, Davis.*

Silages have the potential to contribute to poor air quality through emission of volatile organic compounds (VOC), especially ethanol. Silage additives may be useful for reducing VOC production, but few studies have evaluated them for this purpose. The objective of this experiment was to test the effects of a biological and a chemical additive on production of VOC and aerobic stability of corn silage. Whole plant corn (37.5% DM) was chopped, processed and treated with *L. plantarum* MTD1 (LP, Ecosyl, Ltd., Stokesly, UK) at a rate of 1 × 10^5 cfu/g fresh forage basis, potassium sorbate (0.1% fresh forage basis, PS), a combination of LP and PS (LPPS), or distilled water (untreated, CTRL). Forage was packed in 7.5 L bucket silos at a density of about 230 kg DM/m^3, in quadruplicate, and ensiled at 21-23°C for 119 d. Silage data were analyzed by analysis of variance as a completely randomize to design using the software JMP. Measurements with a headspace GC method showed that both PS and LPPS reduced ($P < 0.05$) production of ethanol and ethyl acetate by more than 75% below CTRL. Treatment LPPS also reduced production of three other significant VOCs: 1-propanol, methyl acetate, and valeraldehyde. Lactic acid was slightly elevated by LPPS ($P < 0.01$) compared to other treatments, but the concentration of acetic acid was similar among treatments. Compared to CTRL, the additives had no effects ($P > 0.05$) on CP, soluble CP (% of CP), ADF and NDF. Due to contaminated media, the numbers of yeasts in silage could not be accurately determined and thus are not reported. However, there was a trend ($P < 0.07$) for improved aerobic stability (48, 49, 169 and 218 h, respectively, for CTRL, LP, PS, and LPPS). In conclusion, a combination of *L. plantarum* MTD1 and potassium sorbate appears to be a very effective additive for reducing production of several important VOCs (including the most important compound: ethanol) in corn silage. Potassium sorbate alone appears to have nearly the same effect on overall VOC production.

Key Words: corn silage, inoculant, volatile organic compounds

---

1081 (M098) The effects of strains of yeasts or *Lactobacillus buchneri* 40788 on the fermentation, production of volatile organic compounds (VOCs) and aerobic stability of corn silage.

R. M. Savage*[1], M. C. Windle[1], S. D. Johanningsmeier[2], and L. Kung Jr.[1], *[1]University of Delaware, Newark, [2]USDA-ARS Food Science Research Unit, Raleigh, NC.*

Several yeasts and *Lactobacillus buchneri* 40788 were evaluated for their effects on the fermentation, production of VOCs and aerobic stability of corn silage. Freshly chopped and processed corn plants were treated with a) no additive, b) *Saccharomyces cerevisiae* -1, c) *S. cerevisiae* - 2, d) an experimental yeast known to produce acetaldehyde under aerobic conditions, or e) *L. buchneri* 40788 (LB, 4 x 10^5 cfu/g of fresh forage). Yeasts were inoculated at 1 x 10^6 cfu/g of fresh forage. All microbes were from Lallemand Animal Nutrition, Milwaukee, WI. Silos (7.5 L, forage density of 224 kg of DM/m^3) were ensiled for 70 and 151 d between 21 to 23 °C. Five replicates were opened for each treatment at each time point. Silage data were analyzed by analysis of variance as a 2 x 5 factorial arrangement of treatments with main factors of days of ensiling, inoculation and their interaction. Silages were analyzed for numbers of yeasts, fermentation end products, aerobic stability and VOCs (d 151 only). The VOCs were determined by solid phase microextraction (SPME) coupled to non-targeted, comprehensive two-dimensional gas chromatography-time-of-flight mass spectrometry (GC´GC-ToFMS). Relative to silage with no ad-

ditive, treatment with yeasts did not affect any of the measured parameters. In contrast, when compared to all other treatments, treatment with LB resulted in a higher concentration ($P < 0.05$) of acetic acid (1.58 vs. 0.52 to 0.81% at d 70 and 2.24 vs. 0.94 to 1.22% at d 151) and 1,2 propanediol at both openings, and lowered the concentration ($P < 0.05$) of ethanol (0.37 vs. 1.18 to 1.52%) after 151 d. The VOC profile of corn silage was markedly altered by LB. Approximately, 25% of the volatile compounds detected in corn silage differed in the LB treated silage ($P < 0.0067$). Decreases were observed in several ethyl esters of medium chain fatty acids along with increases in various esters of acetic acid. Aerobic stability was numerically greater for LB than other treatments after 70 d of ensiling and statistically greater ($P < 0.05$, > 450 h) than other treatments (50 to 120 h) after 151 d of ensiling. This is the first study to show that not only does inoculation with LB improve aerobic stability in corn silage, but it has marked effects on VOC compounds.

Key Words: corn silage, volatile organic compounds, *Lactobacillus buchneri*

1082 (M099) Isolation and identification of lactic acid bacteria in forage peanut silage. L. D. Rufino[1], E. S. Leandro[1], K. G. Ribeiro[1], H. C. Mantovani[1], T. C. Silva[1], and O. G. Pereira[*2], *[1]Universidade Federal de Viçosa, Minas Gerais, Brazil, [2]Universidade Federal de Viçosa, Minas Gerais, Brazil.*

Cultivars of *Arachis pintoi* species are widespread in tropical and subtropical areas in Brazil. There are a limited number of reports about the use of tropical leguminous for ensiling process mainly with regard to the autochthonous population of lactic acid producing bacteria (LAB). Therefore, the objective of the present study was to isolate and identify the LAB by the partial sequencing of the 16S rDNA gene in silage of *Arachis pintoi* cv. Belmonte with 0, 3, 7, 14, 28, and 56 days of fermentation. Forage was ensiled in triplicate by vacuum packing the forage in plastic bags and stored at room temperature. Silage samples were mixed with 225 mL of saline solution and serial dilutions were performed. The dilutions were then plated in MRS agar by using Pour plate technique. Plates were incubated at 37°C for 48 h. After incubation period 40 colonies were randomly selected for streak in MRS agar and then incubated at 37°C for 48 h. Selected isolates were tested for catalase, Gram staining and morphology analysis. The isolates characterized as catalase negative and gram positive were selected to be identified by 16S gene rDNA sequencing. The PCR analysis was performed by using GoTaq DNA polymerase kit and a set of primers 1378/P027. The amplified fragment was purified and sequenced. Among the 40 isolates, only 17 isolates had sequences with identity equal to or greater than 97% with sequences already available in GenBank database. From these 17 sequences the *Lactobacillus plantarum, Lactobacillus paraplantarum, Pediococcus pentosaceus,* and *Lactobacillus casei subs. Casei* were detected. The majority of the isolates were identified as *Pediococcus pentosaceus*. The sequence of isolates obtained in the current study was not matched with the sequences of 16S rDNA of *L. plantarum* or *Pediococcus pentosaceus* already available at Genbank. The lack of matching among the sequences of the isolates obtained in this study with the sequences available at Genbank does not mean that they are not from the same specie. Microorganisms are susceptible to constant mutations varying according to the environment conditions. The accumulation of these mutations may be the reason of the difference among the sequences of different strain. *Sponsored by FAPEMIG, CNPq and INCT-CA.*

Key Words: *Lactobacillus plantarum*, legume silage, *Pediococcus pentosaceus*

1083 (M100) Evaluating top losses in Argentine corn silages. L. O. Abdelhadi[*1], G. Marley[2], and J. M. Barneix[3], *[1]Est. El Encuentro, Research & Extension in Ruminant Nutrition, Brandsen, Buenos Aires, Argentina, [2]Sil-All Global Product Manager, Gloucestershire, United Kingdom, [3]Sil-All Argentine Product Manager, Lincoln, Buenos Aires, Argentina.*

The aim of the study was to quantify how much of the quantity and quality is being lost from the top of corn silages when compared with silo mass across Argentina. Fifty corn silages were sampled in Buenos Aires, Santa Fe and Entre Rios provinces. Composite samples (three sub-samples each) were taken in each silo (from 44 to 488 d since the silages were done), from the core (CS: between 50 to 100 cm inside) or the top (TS: within 50cm), refrigerated until freezing and analyzed for pH, DM, OM and Ashes. Measures of packing density was done by sampling site plus particle size separation using the PSP and finally OM losses were calculated as the difference between % and tons found in the top compared with the core. Data were analyzed as RCB design, using each silo as Block (50), within each block the treatment was the sampling location (CS and TS) and ANOVA by variable was obtained using α 0.05. Of total sampled silages 33, 16 and 1 were storage in stack, bunker and pile silos, respectively; most covered using white and black (36) or black (7) standard plastic and seven uncovered. No one used additives or special covering systems for the surface. Results are presented in Table 1083.

From silos which originally had as a mean 8382 m^3, exposed surface averaged 1398 $m^{3,}$ which involved about 291 tons of OM within each silo. Of exposed OM, we estimated that 23.9% is being lost in the top, averaging 69 tons of OM in each of the sampled silages. When we tried to relate OM losses with days after ensiling or packing density, low relationships were detected; suggesting that practices around covering and uncovering were responsible of top losses.

Key Words: corn silage, top losses

Table 1083.

Item	Top n = 50	Core n = 50	*SE*
DM, %	32.4	31.9	0.112
OM, as %DM	78.7b	93.2a	0.141
ASHES, as %DM	21.3a	6.8b	0.141
pH	5.44a	3.84b	0.002
PS, % >0.75 in	13.41	13.50	1.06
PS, % 0.31 to 0.75 in	70.26	69.41	1.07
PS, % 0.07 to 0.31 in	15.89	16.65	0.22
PS, % <0.07 in	0.43	0.44	0.003
Packing density, kgDM/m^3	264.7b	294.2a	11.86

[ab] Means within a row with unlike letters differ ($P < 0.01$). PS = Particle size.

1084 (M101) Corn silage analysis as influenced by sample size. I. M. Malebana[1], D. J. R. Cherney[*2], and W. J. Cox[2], *[1]Agricultural Research Council, Pretoria, South Africa, [2]Cornell University, Ithaca, NY.*

Sampling variability is a major concern when dealing with chopped corn forage that contains as much as 50% grain. Commercial laboratories prefer to minimize the quantity of corn forage that needs to be processed for analysis. Sample size and particle size of chopped forage will influence sampling variability. Our objective was to evaluate the effect of sample size collected for processing, on variability of results of forage analyses. Samples of chopped corn forage were collected from four field replicates of seven corn hybrids, in 8.3 m^2 plots at four sites in NY. The 112 fresh samples collected were mixed and subsampled to produce samples of 50, 100, 150, 200, 400 and 600 g. Subsamples were immediately ensiled in vacuum-sealed polyethylene bags for 30 d. An additional 600 g fresh subsample was immediately dried at 60 °C, and another 600 g subsample was ensiled for 30 d and then evaluated for particle size distribution. The pH of all ensiled samples was < 3.9, indicating proper ensiling. Particle size distribution using the Penn State particle separator was similar to the distribution recommended for corn silage. Crude protein, NDF, ADF, IVTD and NDFD values were analyzed using SAS PROC MIXED. Standard deviations were calculated for each site/species/size combination to evaluate variability due to sample size collected. Ensiled samples (600 g) were not different from fresh samples (600 g) for NDF, but were significantly higher ($P < 0.05$) in ADF and CP, and significantly lower ($P < 0.01$) in IVTD and NDFD. Crude protein, NDF, ADF, and NDFD all decreased quadratically with increased sample size, while IVTD increased quadratically with increased sample size. Standard deviations for all variables decreased quadratically with increased sample size. Based on both actual values and variability, a 400 g sample produced similar results to a 600 g sample, but smaller sample sizes produced both different and more variable values for all parameters evaluated.

Key Words: neutral detergent fiber digestiblity, sampling variation, vacuum-sealed mini-silos

Table 1084.

	Standard deviations (%)				
Size, g	CP	NDF	ADF	IVTD	NDFD
50	0.61	3.09	1.76	2.35	4.88
100	0.58	2.52	1.56	2.03	4.07
150	0.56	2.23	1.43	2.06	3.84
200	0.55	2.18	1.32	1.96	3.89
400	0.52	2.27	1.36	1.72	3.87
600	0.52	2.25	1.42	1.77	3.54

1085 [Withdrawn]

1086 (M103) In situ degradation characteristics of sorghum silage treated with fibrolytic enzymes. A. Coronado[*1], K. C. McCuistion[1], J. L. Foster[2], G. Schuster[1], and Z. Lopez[3], *[1]Texas A&M University - Kingsville, Kingsville, [2]Texas A&M AgriLife Research-Beeville Station, Beeville, [3]Dow AgroSciences, Knoxville, TN.*

Sorghum (*Sorghum bicolor* L.) silage utilization in beef and dairy cattle diets has increased in recent years due to the increased water efficiency and acceptable feeding values when compared to corn silage. The objective of this study was to determine if fibrolytic enzymes would improve the rate and extent of in situ disappearance of photoperiod sensitive sorghum and hybrid silage varieties with or without the brown midrib (BMR) trait: forage sorghum (FS), BMR forage sorghum (FS-BMR), sorghum-sudangrass (SS), and BMR sorghum-sudangrass (SS-BMR). The experiment was a 4 × 2 factorial design with two replicated periods. Each sorghum silage variety ($n = 4$) was grown, harvested, chopped, and treated with water (control) or a fibrolytic enzyme (50:50 mixture of Cellulase Plus and Xylanase Plus) prior to the ensiling process. Mini-silo buckets were sealed, maintained at 23ºC for 150 d, dried, subsampled, ground to 4 mm, and weighed into duplicate Dacron bags for the in situ trial. An additional silage subsample was taken and stored at -20ºC for subsequent pH determination. Three ruminally cannulated Angus steers (308 ± 24 kg) had ad libitum access to sorghum-sudangrass hay ('Haygrazer'), mineral, and water for 14 d prior to incubation periods. Sorghum silage samples were incubated in situ for 0, 4, 8, 16, 24, 48, or 72 h to determine rate and extent of DM disappearance. Sorghum silage yields were low due to drought. SS yielded the most ($P < 0.01$; 5.3 Mg of DM/ha) compared to SS-BMR (3.8 Mg of DM/ha), FS (3.8 Mg of DM/ha), and FS-BMR (3.7 Mg of DM/ha). All silage reached a pH between 3.1 and 3.5, suggesting that proper ensiling did occur. There were no interactions between treatment and forage variety for DM ($P \geq 0.21$) in the in situ trial. The lag and undegraded residue fraction was not different between varieties ($P > 0.81$). Non-BMR silage had a greater potentially degradable fraction ($P < 0.01$); however, BMR varieties had a

greater wash loss (A; $P < 0.01$) and extent of digestion (ERD; $P < 0.01$). Enzyme treated forage also had a greater A fraction ($P = 0.03$) and ERD ($P = 0.03$), indicating that fibrolytic enzymes can improve silage ruminal degradation. Selecting a sorghum variety containing the BMR trait or using a fibrolytic enzyme can improve silage degradation characteristics.

Key Words: sorghum silage, brown midrib, fibrolytic enzymes

1087 (M104) Effect of ensiling time on fermentation profile and starch digestibility in whole plant corn silage from two different hybrid types.

L. F. Ferraretto[*1], R. D. Shaver[1], S. Massie[2], R. Singo[2], D. M. Taysom[3], and J. P. Brouillette[4], *[1]University of Wisconsin, Madison, [2]Renaissance Nutrition Inc, Roaring Springs, PA, [3]Dairyland Laboratories Inc, Arcadia, WI, [4]Dow AgroSciences, Mycogen Seeds, Indianapolis, IN.*

The objective of this study was to evaluate the effect of ensiling time and hybrid type on fermentation profile, soluble CP (% CP), ammonia-N (% N) and ruminal in vitro starch digestibility (ivStarchD; 7 h incubations on dried and 6 mm ground samples) in whole plant corn silage (WPCS). Samples from 8 hybrids (4 leafy [LFY] and four brown midrib [BMR]; Mycogen Seeds, Dow AgroSciences LLC, Indianapolis, IN) were collected at harvest, vacuum-sealed in plastic bags and ensiled for 0, 30, 120 and 240 d. Samples were stored at room temperature in the dark and immediately frozen to stop the fermentation until processed for analysis. Samples were analyzed for fermentation profile, CP, soluble CP, ammonia-N, starch and ivStarchD at Dairyland Laboratories Inc. (Arcadia, WI). Data were analyzed using Proc Mixed of SAS with the Fixed effects of ensiling time, hybrid type and their interaction. Regressions to determine linear relationships between ivStarchD and ammonia-N and soluble CP contents were performed using Proc Reg in SAS. Contents of DM and starch (DM basis) were unaffected ($P > 0.10$) by ensiling time or hybrid type and averaged 39.3% and 40.0%, respectively. Fermentation profile, ammonia-N, soluble CP and StarchD were similar ($P > 0.10$) between hybrid types. Measurements of pH did not differ ($P > 0.10$) even though lactate, acetate and total VFA concentrations were greater ($P < 0.01$) for WPCS fermented for 30, 120 and 240 d compared to unfermented samples. Gradual increases were observed ($P < 0.001$) from 0 to 240 d for Soluble CP (33.5, 41.2, 48.9 and 54.5% of CP for 0, 30, 120 and 240 d, respectively) and ammonia-N (2.6, 4.6, 6.0, and 7.9% of N for 0, 30, 120 and 240 d, respectively). Likewise, the ivStarchD measurements increased with ensiling time ($P < 0.001$; 50.2, 58.5, 65.8, 71.4% of starch for 0, 30, 120 and 240 d, respectively). Positive relationships between ivStarchD and ammonia-N ($R^2 = 0.67$; $P = 0.001$) and soluble-CP ($R^2 = 0.55$; $P = 0.001$) were observed. Fermentation profile, ammonia-N, soluble CP and ivStarchD were influenced by ensiling time but not hybrid type. Ammonia-N and soluble CP were both good indicators of ivStarchD in WPCS.

Key Words: corn silage, ensiling time, starch digestibility

1088 (M105) Fermentation profile, chemical composition and microbial population in silages of Stylosanthes Campo Grande with microbial inoculant and pelletized citrus pulp.

W. F. D. Souza[1], K. G. Ribeiro[2], S. A. Santos[1], T. C. Silva[2], V. P. Silva[2], and O. G. Pereira[*3], *[1]Universidade Federal da Bahia, Salvador, Brazil, [2]Universidade Federal de Viçosa, Minas Gerais, Brazil, [3]Universidade Federal de Viçosa, Minas Gerais, Brazil.*

We evaluated the chemical composition, fermentation profile and microbial population of silages of Stylosanthes cv. Campo Grande with and without microbial inoculant and different levels of pelletized citrus pulp (0, 3, 6, 9 and 12% fresh forage basis), in different fermentation periods. The plant was harvested at 120 days after sowing, in the flowering stage. Subsequently, this material was chopped in a stationary forage machine and the combinations between the treatments were applied. Treated forages were packed in bag silos that were vacuumed to remove air, heat-sealed, and stored for 1, 3, 7, 14, 28 and 56 d. The microbial inoculant utilized was Sil All C4 (Alltech, Brazil), containing *Lactobacillus plantarum*, *Pediococcus acidilactici, L. salivarius* and *Enterococcus faecium*, at a rate of 1×10^5 cfu/g fresh forage basis. Data were analyzed by analysis of variance as a $5 \times 2 \times 6$ factorial arrangement of treatments with main effects of pelletized citrus pulp (PCP), the presence or absence of inoculant (I), time of ensiling (T) and their interaction, using the procedure MIXED of SAS software, version 9.1. The DM content increased linearly ($P < 0.05$) as the PCP levels were increased. The PCP × I interaction had an effect ($P < 0.05$) on the CP content, with highest values observed in the inoculated silages. Interactions PCP × I and PCP × T affected ($P < 0.05$) the NH₃-N content of silages. The pH and the concentrations of lactic, acetic, propionic and butyric acids were affected ($P < 0.05$) by the PC × I × T interaction. Maximum population of lactic acid bacteria (9.59 cfu/g) was recorded on the first day of fermentation in the non-inoculated silage, whose population decreased linearly over the fermentation period ($P < 0.05$). The population of enterobacteria was greater on the first day after ensiling, but from the fourth day its presence was not detected in all treatments. Interactions PCP × I and PCP × T affected the CP content of the silages, whereas the NDF and ADF levels of the silages were only affected ($P < 0.05$) by the PCP levels. Addition of inoculant and pelletized citrus pulp to Stylosanthes at ensiling increases lactic fermentation and restrict the butyric fermentation, providing better quality silage. Sponsored by FAPEMIG, CNPq and INCT-CA.

Key Words: acetic acid, lactic acid, lactic acid bacteria

1089 (M106) Recombined, late harvested ensiled alfalfa leaves and stems give comparable performance to normally harvested alfalfa silage. R. D. Hatfield*[1], M. B. Hall[1], R. E. Muck[1], W. J. Radloff[1], and K. J. Shinners[2], *[1]U. S. Dairy Forage Research Center, USDA-ARS, Madison, WI, [2]Biological Systems Engineering, University of Wisconsin, Madison.*

Increased use of the perennial forage, alfalfa, on dairy farms could be accomplished by reducing the number of harvests, separately storing leaves and stems, and feeding at a ratio that maintains lactation performance. More use of alfalfa could also decrease the environmental impact of dairies. We compared the impact on lactation performance of normally harvested alfalfa silage (early bud stage) with a blend of separately harvested and ensiled alfalfa leaves and stems obtained from more mature plants (full bloom stage). Forty-four primiparous cows were randomly assigned to one of two diets using a randomized complete block design with a 2-week covariate period followed by a 3-wk experimental period. Lactation performance was measured in the last week of each period. Experimental diets were formulated to provide similar concentrations of crude protein (CP) and neutral detergent fiber (NDF) by blending two whole-plant alfalfa silages (WP), or by blending separately ensiled alfalfa leaves and stems (LS). Urea (0.27%), as diet dry matter (DM), was added to LS to give equivalent CP. Diets were 60% forage, 17.2% CP, 24% starch, 26% ensiled alfalfa, and 34% corn silage on a DM basis. Milk production, energy-corrected milk production, and efficiencies of use of DMI and N did not differ between treatments. Milk urea nitrogen differed between treatments, but by less than 1 mg/dl. This may be due to slightly lower digestibility of LS vs. WP, or to the addition of urea, which likely differed from the soluble protein present in WP. Blending leaves and stems gave similar production performance as normally harvested alfalfa silage, but with the advantage that harvesting alfalfa leaves separate from stems allows large biomass accumulation in the field and fewer harvests.

Key Words: forage, alfalfa, dairy

Table 1089.

Measure	WP	LS	SED	*P*-value
DMI, kg	23.8	23.9	0.62	0.82
Milk, kg	42.5	41.1	1.11	0.23
ECM, kg	45.2	44.3	1.37	0.52
MUN, mg/dl	10.7	11.5	.26	<0.01
ECM/DMI	1.92	1.86	0.09	0.50

1090 (M107) Changes in the structural carbohydrates of corn stover silage added with yeast culture and fermented apple pomace. N. H. Ruiz*, C. Rodríguez-Muela, D. Díaz-Plascencia, O. Ruiz-Barrera, A. Corral, A. Ramírez-Godínez, and C. Arzola-Alvarez, *Universidad Autónoma de Chihuahua, México.*

With the objective of improving the nutritional value of corn stover silage by adding yeast culture or solid-state fermented apple pomace, three treatments were evaluated during 28 d using 48 plastic bags as microsilos each 2 Kg of: (T1) corn stover alone; (T2) corn stover plus yeast culture (10% as feed basis) and (T3) corn stover plus fermented apple pomace (69% as feed basis). Treatments were added with water to obtain 35% (DM). Values for DM, pH, temperature (t), in vitro dry matter digestibility (IVDMD), NDF, ADF, cellulose and lignin were obtained at d 0, 7, 14 and 28 of ensiled time. Data were analyzed by PROC GLM of the SAS. Table 1090, shows the values at 28 d of ensiled. The addition of yeast culture or fermented apple pomace decreased ($P < 0.01$) the pH, increased ($P < 0.01$) the temperature and the DM decreased ($P < 0.01$) across the sampling time. The IVDMD was highest ($P < 0.01$) with the addition of fermented apple pomace. NDF, ADF, cellulose and lignin concentrations decreased with the ensiled time; and the lowest values were shown in T2 and T3. We conclude that the addition of yeast culture or fermented apple pomace improved the nutritional value of silage corn stover.

Key Words: yeast culture, fermentation, silage

Table 1090. Means of the structural carbohydrates of corn stover silage by adding yeast culture or solid-state fermented apple pomace at 28 d of ensiled

Variables	T1	T2	T3
pH	5.18 ± 0.07[b]	4.73 ± 0.07[c]	5.32 ± 0.07[a]
Temperature (°C)	26.00 ± 0.49[b]	26.73 ± 0.5[a]	27.17 ± 0.49[a]
Dry Matter (%)	37.85 ± 0.44[a]	30.68 ± 0.44[c]	35.56 ± 0.44[b]
In vitro Dry Matter Digestibility (%)	48.09 ± 0.34[c]	52.10 ± 0.34[b]	56.06 ± 0.34[a]
NDF (%)	82.76 ± 1.14[a]	77.10 ± 1.14[c]	80.56 ± 1.14[b]
ADF (%)	65.01 ± 0.58[a]	59.44 ± 0.58[c]	62.33 ± 0.58[b]
Cellulose (%)	57.24 ± 0.77[a]	54.30 ± 0.77[b]	55.05 ± 0.77[b]
Lignin (%)	7.0 ± 0.48[a]	3.0 ± 0.48[b]	2.3 ± 0.48[b]

[a,b,c.] Means with literal different between columns indicate statistical difference ($P < 0.05$)

1091 (M108) Effects of different additives on chemical composition, fermentation characteristics and aerobic stability of barley silage. Y. Joo[1], D. Kim[1], H. Lee[1], S. M. Amanullah[1], S. C. Kim[*1], and I. H. Choi[2], *[1]Division of Applied Life Science (BK21Plus, Insti. of Agri. & Life Sci.), Gyeongsang National University, Jinju, South Korea, [2]Dep. of Companion Animal and Animal Resources Science, Joongbu University, Geumsan-gun, South Korea.*

This study was carried out to determine the effect of various additives on chemical composition, fermentation quality, and aerobic stability of barley silage. Youngyang barley was grown at Animal Research Unit, Gyeongsang National University, Jinju, South Korea, and harvested at 31% DM. Approximately 500 kg of barley forage were chopped and divided into 4 piles and applied with one of four treatments which were *L. plantarum* (LP, $1.2x10^3$ cfu/g), *L. buchneri* (LB, $1.2x10^3$ cfu/g), fermented persimmon extract (FPE, 1% of fresh forage) and essential oil (EO, 1% of fresh forage). Barley forage was ensiled into 10 L bucket silo in quadruplicate for 0, 1, 3, 7, 48 and 100 day periods. The ANOVA followed by Tukey test was performed using SAS 9.3. The concentrations of CP and ether extract were highest (7.23, 3.83% of DM, respectively, $P < 0.05$) in FPE silage ensiled for 100 days, while crude ash, NDF, ADF and hemicellulose concentrations were highest (51.8, 30.0, 21.8% of DM, respectively, $P < 0.05$) in LB silage. The in vitro digestibility of DM was highest in EO silage (62.5%, $P < 0.05$), while *in vitro* NDF digestibility was highest ($P < 0.05$) in LB (33.7%) and FPE silages (34.5%), respectively. The pH was not affected, but ammonia-N was highest ($P < 0.05$) in EO silage (0.22%), followed by FPE (0.20%), LB (0.17%) and LP (0.13%) silage. The LP silage had highest ($P < 0.05$) lactate but lowest acetate from the early stage of fermentation (3, 7 and 48 d) to the end (100 d), and so happened in the case of lactate to acetate ratio. In contrary, LB silage showed the reverse pattern in lactate and acetate compared to LP silage. Together with acetate (5.17%), LB silage also had highest ($P < 0.05$) propionate concentration (0.42% of DM) and thus resulted in highest aerobic stability (348 h, $P < 0.05$) in this silage. The yeast count was highest (5.25% of DM, $P < 0.05$) in LP silage with concomitant lowest aerobic stability (254 h, $P < 0.05$). The lactic acid bacteria (LAB) were highest (6.45 $\log_{10}$cfu, $P < 0.05$) in EO silage. The mold was not detected in any treatments. In conclusion, LB efficiently improves the aerobic stability, while LP has lowest aerobic stability as well as in vitro digestibility of NDF. On the other hand, FPE and EO substantially improve aerobic stability, preserved protein efficiently as well as improved the in vitro digestibility of DM and NDF.

Key Words: barley silage, additives, aerobic stability, fermentation quality

1092 (M109) Effects of bacterial inoculation on the fermentation and aerobic stability of whole crop soybean silage. B. D. Nkosi[*1], R. Meeske[2], T. Langa[1], T. F. Mutavhatsindi[1], and I. M. Malebana[1], *[1]ARC-Animal Production Institute, Irene, South Africa, [2]Outeniqua Research Farm, Western Cape Dep. Agric., George, South Africa.*

This study was done to evaluate the effects of microbial inoculation on the fermentation and aerobic stability of whole-plant soybean. Soybean cultivars, Pannar [333 g dry matter (DM)/kg, 64.3 g water-soluble carbohydrate (WSC)/kg DM, 177 g crude protein (CP)/kg DM] and Link [268 g DM/kg, 70 g WSC/kg DM and 170 g CP/kg DM] were harvested at R6 growth stage and chopped to 20 mm theoretical length. The materials were treated with or without Lalsil Fresh LB, a heterofermentative lactic acid bacteria (LAB) inoculant. Treatments were produced in a 2X2 factorial design as: 1) pan control (no additive), 2) link control (no additive), 3) Pan Lalsil and 4) Link Lalsil. The treatments were ensiled in 1.5 L anaerobic jars and kept in room for 90 d. Triplicate samples per treatment were collected on d 0, and 90 for determination of chemical composition and fermentation characteristics. Samples of d 90 were subjected to aerobic stability test where 500 g of sample from each jar was loosely packed in an open plastic jar that was covered with two layers of cheesecloth and kept at 28°C. A temperature probe was placed in the geometric centre of the silage mass for each jar and also in the room where the jars were stored to record temperature. The room temperature and the temperature in each jar were simultaneously recorded at 1 h intervals for 5 d and CO_2 production was measured after the 5 d exposure. The CO_2 production and number of hrs silage remained stable were indicators for aerobic stability. The inoculated silage had lower ($P < 0.005$) contents of DM, fibre and lactic acid compared to the control. The pH, ammonia-N and acetic acid content of the inoculated silage were higher ($P < 0.05$) compared to the control. The aerobic stability of silage was improved ($P < 0.05$) with inoculation as indicated by reduced CO_2 production and increased number of hrs compared to the control. The interaction between cultivars and treatments were significant ($P < 0.05$) in all parameters measured, except for the pH and energy content. Further work is needed to test these silages on ruminant growth and nutrient digestion.

Key Words: inoculant, heterofermentation, silage

1093 [Withdrawn]

1094 (M111) Quality and fermentation profile of sugar cane silage treated with chemical and microbial additives. L. L. Cardoso, M. I. Marcondes*, K. G. Ribeiro, O. G. Pereira, T. E. Silva, and D. G. Ferreira, *Universidade Federal de Viçosa, Minas Gerais, Brazil.*

The objective of this study was to evaluate the composition and fermentation profile in sugar cane silage treated with chemical and microbial additives. The treatments consisted of sugar cane silage (SCS); Sugar cane silage with *Lactobacillus buchneri* (SCSLB); Sugar cane silage with *Lactobacillus plantarum* and *Pediococcus pentosaceus* (SCSLPPP); Sugar cane silage with *Lactobacillus plantarum* and *Propionibacterium acidipropionici* (SCSLPPA); Sugar cane silage with 0.5% lime (SCSCaO0.5); sugar cane silage with 1.0% lime (SCSCaO1.0); Sugar cane silage with 0.5% urea (SCSU0.5); sugar cane silage with 1.0% urea (SCSU1.0). Additives commonly used by Brazilian producers were studied. A completely randomized design was used, with eight treatments and four replicates, with inoculants before ensiling. The sugar cane was chopped and ensiled in 20 kg buckets containing Bunsen valves, and opened 180 days after ensiling. It was observed that the sugar cane silage treated with urea markedly increased protein levels and reduced levels of insoluble nitrogen in acid detergent in the silage. However, the concentration of ammonia nitrogen was also increased ($P < 0.05$). Lime 0.5% and urea 0.5% (5.8 and 5.6, respectively) promoted minor gas losses ($P < 0.05$) in relation to the addition of *Lactobacillus plantarum* and *Pediococcus pentosaceus* in the sugar cane silage (9.8% DM). Effluent average production was not affected by treatments ($P > 0.05$), but it can be considered high in comparison to other works using sugar cane silage. Increased dry matter recovery ($P < 0.05$) was observed in the control silage (87.2%) and SCSCaO0.5 (87.2%) compared to SCSLPPP (81.9%), possibly due to increased gas production seen in this treatment. SCSCaO0.5 (9.21% DM) also promoted the highest yield of lactic acid ($P < 0.05$). The addition of 1% lime increased production of propionic and butyric acids ($P < 0.05$). It was found that the inoculation with *Lactobacillus plantarum* and *Propionibacterium acidipropionici* increased ethanol ($P < 0.05$) content (3.55% DM), and the lowest ethanol concentration was observed in SCSCaO0.5 (0.69% DM). Yeast population ($P < 0.05$) was lower in SCSU1.0 (1.4 log cfu/g) compared to SCSLPPP (4.6 log cfu/g), but both did not differ from control (3.9 cfu/g). Therefore, none of the treatments was effective in controlling yeast. It is concluded that the silages studied presented appropriate profile for fermentation, low yeast population concentration, low ethanol concentration and high recovery of dry matter.

Key Words: effluent, ethanol, yeast

FORAGES AND PASTURES II: FORAGES IN BEEF PRODUCTION SYSTEMS

1095 (T108) Reducing winter feeding needs in southern arkansas through the use of best management grazing principles. B. Stewart*[1], P. Beck[1], L. Sullivan[1], M. Sims[1], and J. Jennings[2], [1]*University of Arkansas SWREC, Hope,* [2]*Dep. of Animal Science, University of Arkansas, Little Rock.*

Research is being conducted at the University of Arkansas Southwest Research and Extension Center in Hope, AR, to determine the impacts of best management principles (BMPs) on production and winter feed requirements of spring calving cows (n = 72, BW = 547 ± 33.2 kg) grazing warm-season based pastures (n = 9, 4.7 ha pastures). The BMPs used include rotational grazing to improve pasture utilization; stockpiled bermudagrass, to extend grazing into the fall and early winter; and complementary cool-season annual grass plantings, to provide high quality forage in the spring. This research compares low management (CG, continuous grazing at a moderate stocking rate of 0.8 ha/cow) and intensive management at moderate (MR, 0.8 ha/cow) and high stocking rates (HR, 0.4 ha/cow). Stockpiling was managed by fertilization of 0.25 ha/cow of bermudagrass in early August with 168 kg ammonium nitrate/ha and deferring grazing until November. Pregnancy rate data were analyzed using the Chi-square test and cow performance data were analyzed by ANOVA using the PROC MIXED of SAS (SAS Inst. Inc., Cary, NC). Stockpiled bermudagrass produced over 5,800 ± 500 kg forage DM/ha which was adequate to hold cows grazing these pastures until late February. During calving, from mid-February to mid-April, cows on MR and HR grazed cool-season annuals and stockpiled bermudagrass or fed hay on alternating days. Cows on CG pastures were fed hay an average of 74 ± 7.3 d compared with 43 ± 7.3 d for HR and 0 for MR (P = 0.04). Pregnancy rates at weaning were similar (P = 0.99) across treatments averaging 85%. Growth performance of calves was reduced (P = 0.04) by both rotational grazing and increased stocking rate, with weaning weights of calves from CG (251 ± 9.1 kg) being greater than MR (222 ± 9.5 kg) which was greater than HR (212 ± 7.2 kg). However, total weaning weight per hectare was 68 and 90% greater (P = 0.01) for HR compared with CG and MR, respectively. With rotational stocking there was the opportunity to harvest excess forage as hay in both the moderate (9,418 kg/pasture) and high (2,206 kg/pasture). In this system every year will be different and flexibility of management will be key. Using rotational grazing, stockpiled bermudagrass, and complementary cool-season annual grasses can drastically reduce stored winter feed requirements and simultaneously increase carrying capacity and total net return.

Key Words: bermudagrass, cool-season annuals, cow calf, rotational grazing

1096 (T109) Bale diameter and feeder design effects on hay waste. D. Tomczak, N. E. Mertz, and W. J. Sexten*, *University of Missouri, Columbia.*

Forty-eight mid-gestation spring-calving cows were stratified by BW (583 ± 77.2 kg), BCS (5.4 ± 0.6), and age (5.6 ± 2.5 yr) into 6 pens to evaluate influence of bale diameter and feeder design on hay waste. Tall fescue round hay bales (85.5% DM, 8.22% CP, 66% NDF, 152 cm height) were classified as Small (128.3 ± 3.19 cm), Medium (160.7 ± 6.38 cm), or Large (187.7 ± 3.52 cm) diameter, and placed in hay feeders equipped with cradle chain (CONE) or without (RING) in a 3 x 2 factorial design randomly assigned to a 6 x 6 Latin square. We hypothesized hay waste would increase as initial bale diameter increased in RING and not differ in CONE. Bales were placed on the circular end in round bale feeders (230 cm diameter, 170 cm height) with 16 feeding stations and metal sheeting on top (50 cm) and bottom (60 cm). Small, medium, and large bales were replaced every 2, 3, and 5 d, respectively to ensure ad libitum hay access. Waste was collected daily, and residual forage was collected prior to new bale feeding. CONE (15.8%) reduced ($P < 0.10$) waste as a percent of initial bale weight compared to RING (18.3%). Waste was increased ($P < 0.05$) for large (19.4%) compared to small (14.2%), while medium (17.6%) did not differ ($P > 0.05$) from large or small. Bales were not fed for equal number of days, so data were analyzed as an incomplete 6 x 6 Latin square to evaluate feeder effects relative to access time. Waste was not different ($P > 0.10$) due to increased access time to small in CONE however waste was reduced ($P < 0.05$) as access time increased for small in RING. As access time increased to medium and large waste was reduced ($P < 0.05$). In conclusion, CONE tended to decrease waste. Increasing access time due to increased bale diameter increased waste in all cases, except small CONE.

Key Words: hay waste, bale size, bale feeder

1097 (T110) Forage and shade type effects on stocker heifers' performance. G. Scaglia*, *Louisiana State University AgCenter, Jeanerette.*

In the Gulf Coast region, performance of young cattle is restricted by the nutritional value of perennial grasses and weather conditions (temperature and humidity). Natural shade is often limited because of grazing on reclaimed croplands or due to reduced number of trees in pasturelands. The objective of this experiment was to evaluate the performance of yearling heifers continuously stocked on alyceclover (*Alysicarpus vaginalis* L.) or pearl millet (*Pennisetum glaucum*) for 60 d-grazing periods (early-July to September) with artificial or natural shade. In two consecutive years, 36 crossbred heifers (BW= 323 ± 15 kg) were randomly allotted to 12 paddocks (1.3 ha;

750 kg BW/ha) in a factorial arrangement of treatments with 3 replicates each. Portable shades were built with 6.25 cm pipe and welded into a 3 x 3.5 m frame which held a black woven polypropylene cloth providing 80% shade. These shades were available in half the paddocks while trees provide natural shade to the other half of the paddocks. Alycelover (12 kg/ha) and pearl millet (22 kg/ha) were no-till drilled after two applications of herbicide for weed control. Despite these applications, areas with some crabgrass and johnsongrass were present 30-40 d into the grazing season in all pastures. In July and August, THI (temperature humidity index, an indicator of heat load) was above 76 for the entire day and above 79 from 0600 to 2100. The latter indicates severe heat load which can adversely affect animal performance. Dry matter production of pearl millet (1800 kg DM/ha) was greater ($P < 0.05$) than alyceclover (1050 kg DM/ha). Alyceclover's CP concentration (21%) was greater while NDF (53%), and ADF (41%) concentrations were lower ($P < 0.05$) than pearl millet (11, 63, and 53%, respectively), however, animal gains were not limited by forage mass and nutritional value of either forage. There was no interaction between forage and shade type on ADG ($P = 0.84$). Forage type ($P = 0.029$) affected animal performance. Heifers grazing alyceclover gained more (0.94 kg/d) than those grazing pearl millet (0.80 kg/d). No effect of shade was detected ($P = 0.19$). Heifers with artificial shade gained 0.91 kg/d while those with natural shade gained 0.83 kg/d. As determined by our laboratory before and despite adverse environmental conditions, heifers grazing pearl millet or alyceclover performed better than those grazing bermudagrass (0.60 kg/d). Artificial shades like these are a viable alternative to improve animal welfare when natural shade is not available.

Key Words: alyceclover, pearl millet, shade

1098 (T111) Monensin supplementation levels effects on rumen fluid and blood parameters of steers receiving warm-season grass.

J. M. B. Vendramini*[1], R. F. Cooke[2], A. D. Aguiar[1], O. F. R. Cunha[1], A. C. J. Pereira[3], P. D. S. Ferreira[1], and C. B. Zactiti[1], *[1]UF/IFAS Range Cattle Research and Education Center, Ona, FL, [2]Oregon State University - EOARC Burns, Burns, [3]Elanco Animal Health, Greenfield, IN.*

Variable effects of monensin on performance of beef cattle grazing warm-season grasses have been reported in the literature. Lack of response is generally associated with low levels of monesin; thus increasing monesin levels on the animal diet may be an effective management approach to improve its efficiency and positive effects on beef cattle performance. The objective of this study was to evaluate the effects of levels of monensin on rumen fluid and blood parameters of beef steers (*Bos* sp.) receiving warm-season grass. The experiment was conducted in Ona, FL from July to September 2013. Treatments were three levels of monensin, 10, 20, and 30 ppm and control (no monensin) tested in a 4 × 4 latin square with 10 d adaptation period and 5 d of rumen fluid collection and total DM intake evaluation. Blood samples were collected on d 4 and 5 of the collection period. Ground stargrass (*Cynodon nlemfuensis*) hay (9% CP, 51% IVDOM) was offered daily and adjusted to allow 10% refusals. The steers received 0.4 kg of a concentrate supplement (14% CP and 78% TDN) daily. Total DM intake was similar among treatments ($P = 0.64$, mean = 2.0% BW). There was a linear increase ($P < 0.01$) in propionic acid concentration in the rumen (from 16.9 to 19.4 mol/100 mol) with increasing levels of monensin; however, there was no effect of monesin levels on pH ($P = 0.19$, mean = 6.6), acetic acid ($P = 0.14$, mean = 72.3 mol/100 mol), isobutyric acid ($P = 0.47$, mean = 0.73 mol/100 mol), butyric acid ($P = 0.83$, mean = 8.3 mol/100 mol) and NH4-N ($P = 0.53$, mean = 6.8 mg/dL). In addition, there was no effect of monensin levels on blood glucose ($P = 0.75$, mean = 62.0 mg/dL), insulin ($P = 0.82$, mean = 3.5 uIU/mL), IGF-1 ($P = 0.73$, mean = 12.4 ng/mL), and blood urea nitrogen ($P = 0.83$, mean = 26.4 mg/dL). Increasing levels of monensin alone may not be effective to increase performance of beef cattle receiving warm-season grasses with limited nutritive value.

Key Words: ionophore, monensin, warm-season grasses

1099 (T112) Polymers molecularly imprinted with ergotamine: Recognition properties to template and related alkaloids.

M. B. Kudupoje*[1], E. S. Vanzant[2], A. Yiannikouris[3], K. A. Dawson[3], and K. R. McLeod[2], *[1]Alltech-University of Kentucky Nutrition Research Alliance, Lexington, [2]University of Kentucky, Lexington, [3]Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech, Nicholasville, KY.*

Alkaloid toxicities negatively impact livestock health and production. Adsorbent technologies may offer effective means to manage alkaloid toxicities. In this study, molecularly imprinted polymers (MIP) were synthesized and evaluated for specificity of adsorption to various ergot alkaloids. Six different noncovalent copolymers were synthesized from styrene and methyl methacrylate functional monomers with a free radical initiator (2,2'-azobis isobutyronitrile) and three different molar ratios (1x, 2x, 4x) of crosslinker (ethylene glycol dimethacrylate) in toluene. Synthesis was performed in the absence (non-imprinted polymer, NIP) or presence of ergotamine template (MIP), yielding products NIP1x, NIP2x, NIP4x, MIP1x, MIP2x and MIP4x. An isothermal adsorption experiment was conducted in triplicates, with product inclusion of 0.01% w/v, using 5 concentrations (range 65 to 1550 ng/mL) of each of three alkaloids (ergotamine, bromocriptine and methylergonovine) in ammonium citrate buffer (*P*H 6.7, 37°C, 90 min). Samples were centrifuged (10,000 *g* for 10 min) and supernatant was analyzed by UPLC-ESI- MS/MS for quantification of unbound alkaloid. Within each alkaloid, adsorption difference between MIP and NIP interacted

($P < 0.05$) with alkaloid concentration and crosslinker ratio. For most comparisons at 1x crosslinker ratio, adsorption was greater ($P < 0.10$) for NIP than MIP. In contrast, for the few differences ($P < 0.10$) detected for 2x and 4x crosslinker ratios, MIP exceeded NIP adsorption. For both MIP and NIP, adsorption was generally greater for 2x and 4x, as compared with the 1x crosslinker ratio. Differences in adsorption between alkaloids varied with alkaloid concentration and product (alkaloid x concentration x product; $P < 0.05$). In most cases, adsorption was seen in the order ergotamine > bromocriptine > methylergonovine. Products with 4x crosslinker ratios gave the greatest adsorption, and therefore those means are used for comparison of products and alkaloids. Averaged across the different alkaloid concentrations, the respective adsorption for MIP and NIP was 91% and 86% for ergotamine, 75% and 69% for bromocriptine, and 26% and 15% for methylergonovine. Differences in adsorption properties among the six products could be explained by differences in functional groups and conformation, which are altered by template or cross linkers. Cross reactivity with related alkaloids exists due to similarities in structure and functional groups. Future in vitro and in vivo studies are required to determine stability of the polymer-alkaloid complexes, and applicability of polymers as adsorbents in livestock to counteract alkaloid toxicoses.

Key Words: adsorbent, MIP, alkaloid

1100 (T113) Silage and hay of Stylosanthes Campo Grande associated or not to corn silage: Nutrient intake and performance of beef cattle.

L. D. Rufino[1], K. G. Ribeiro[1], S. C. Valadares Filho[1,2], R. M. Martins[3], T. F. Bernardes[4], J. A. G. Azevedo[5], and O. G. Pereira[*2], *[1]Universidade Federal de Viçosa, Minas Gerais, Brazil, [2]Universidade Federal de Viçosa, Minas Gerais, Brazil, [3]University of Florida, Dep. of Animal Sciences, Gainesville, [4]Universidade Federal de Lavras, Minas Gerais, Brazil, [5]Universidade Estadual de Santa Cruz, Ilheus, Bahia, Brazil.*

The conservation of stylosanthes Campo Grande as silage or hay is an alternative to the use of corn as it increases the crude protein level of the diet and improves the soil fertility by nitrogen fixation. The nutrient intake and animal performance of Nellore cattle fed diets containing different roughage sources were evaluated. Experimental treatments were: T1 – corn silage (CS); T2 – silage of stylosanthes Campo Grande (StS); hay of stylosanthes Campo Grande (StH); T4 – 50% of CS + 50% of StS; T5 – 50% of CS + 50% of StH. Diets were isonitrogenous (12.5% of CP on DM basis) and consisted of 50:50 roughage:concentrate ratio. A total of 40 non-castrated cattle with initial average body weight of 360 kg were assigned into a completely randomized design with five treatments and eigth replicates per treatment. The experiment was divided into four periods with a 15 d of adaptation followed by three periods of 28 d each totalizing 99 days of experimental period. Means was compared by orthogonal contrasts and the initial body weight was used as a covariate at the statistical analysis of the data. Statistical analysis was performed by using SAS. Animals fed CS had lower ($P < 0.05$) intake of DM, EE, NDFap and NDFi than those fed StS, 50% of CS + 50% of StS, and 50% of CS + 50% of StH. The diet containing CS also decreased ($P < 0.05$) the intake of CP and NFC compared to diets containing StH or StS associated to CS. Despite of the lower DM intake, cattle fed diets containing CS had greater TDN intake ($P < 0.05$) compared to those fed StS. The average daily gain was greater ($P < 0.05$) in cattle fed CS compared to those fed diets with StS or StH as the only roughage source. However, no difference was observed for animal body weight gain ($P > 0.05$) among diets with CS and StS or StH. These data suggests that the mixture of corn silage with silage or hay of stylosanthes seems to be a great alternative to the use of corn silage for diets of beef cattle at the finishing phase. Sponsored by FAPEMIG, CNPq and INCT-CA.

Key Words: average daily gain, feed conversion, legume silage

---

1101 (T114) Evaluation of nutrient intake, in situ disappearance, and fermentation characteristics of fermented Chaffhaye with alfalfa hay and prairie grass hay in steers.

K. K. Guatam, B. S. Obeidat, S. J. Trojan, and M. A. Ballou, Texas Tech University, Dep. of Animal and Food Sciences, Lubbock.*

The aim of this study was to investigate the nutritive value, fermentation characteristics, and in situ disappearance of Chaffhaye and compare it to an isonitrogenous alfalfa and grass hay diets. Each of the three Holstein (mean ± SD, 533 ± 38.2 kg) and 3 Jersey (622 ± 60.5 kg) rumen fistulated steers were arranged randomly in a replicated 3 x 3 latin square design with a 2-wk adaptation period followed by a 1-wk collection period. Isonitrogenous diets consisted of Chaffhaye (fermented alfalfa hay and molasses, Chaffhaye, Inc, Dell City, TX), alfalfa hay diet (92.6% alfalfa hay plus 6.4% cottonseed meal) and prairie grass hay diet (72.9% prairie hay plus 27.1% cottonseed meal). There was no difference ($P > 0.181$) in ad libitum DMI or the intake of CP. There was a tendency ($P = 0.104$) for steers on the grass hay diet to consume more NDF. In situ NDF disappearance at the 12 and 24 hour incubations were greater ($P \leq 0.0001$) for both the Chaffhaye and alfalfa hay diets compared to the grass hay diet, but at the 96-hr incubation the NDF disappearance for the Chaffhaye was greater ($P = 0.024$) than the alfalfa hay. The CP disappearance of the Chaffhaye was greater ($P \leq 0.043$) than the alfalfa hay diet, which was greater ($P \leq 0.003$) than the grass hay diet at the 0, 6, and 24 hour incubations. Furthermore, at the 48 hour incubation the CP disappearance of the Chaffhaye and alfalfa hay was greater ($P \leq 0.001$) than the grass hay diet. Methane production was reduced ($P \leq 0.024$) in the grass hay when com-

pared to the Chaffhaye and alfalfa hay diets. The rumen pH of Chaffhaye fed steers was slightly greater (6.73 ± 0.062; $P \leq 0.040$) than either the alfalfa hay (6.56) or grass hay (6.47) diet. These data indicate that Chaffhaye has an improved NDF digestibility compared to a prairie grass hay diet and that the soluble CP fraction is greater when compared to an isonitrogenous alfalfa hay or prairie grass hay diet.

Key Words: digestibility, forage, neutral detergent fiber

1102 (T115) Ruminal fermentation characteristics of beef steers grazing grass monocultures versus low- and high-tannin grass-legume mixtures.

C. T. Noviandi[1,2], T. J. Bingham[1], J. S. Eun[*1], D. R. ZoBell[1], B. L. Waldron[3], and M. D. Peel[3], *[1]Utah State University, Logan, [2]Universitas Gadjah Mada, Yogyakarta, Indonesia, [3]Forage and Range Research Laboratory, USDA-ARS, Logan, UT.*

Ruminal fermentation characteristics were investigated with 36 Angus crossbred steers grazing 4 treatments: 1) tall fescue (TF) with no fertilizer (TF–NF), 2) TF with N fertilizer (TF+NF), 3) TF-alfalfa mixture (TFALF), and 4) TF-birdsfoot trefoil mixture (TFBFT). Treatments were tested in a randomized complete block design with 3 pasture replicates, 4 paddocks per pasture, and 3 steers per pasture. Replicated 0.47-ha paddocks were grazed with beef steers from May through September in 2013 for total of 16 wk. Steers grazed for 7 d per paddock on a 28-d rotation interval. Pasture forage samples were collected at 4-wk intervals throughout the experiment. Ruminal fluid samples were obtained from all steers using a Geishauser probe at wk 4, 8, 12, and 16 to measure pH and analyze VFA profiles and ammonia-N (NH_3-N) concentration. Concentration of CP in pasture forages was greater ($P < 0.01$) in mixtures than grass monocultures at wk 4 (12.8 vs. 7.89%), but it was similar after wk 4. In contrast, NDF concentration was lower ($P < 0.05$) in mixtures compared with grass monocultures throughout the grazing season. Ruminal pH was maintained at 6.54 or higher and did not differ across treatments. Starting at wk 8, total VFA concentration increased ($P < 0.05$) in steers grazing the mixtures compared to those grazing monocultures. However, the VFA concentration was not different between TFALF and TFBFT. Acetate proportion increased with mixtures at wk 12, but propionate proportion decreased due to grazing mixtures, resulting in increased acetate-to-propionate ratio at wk 12 ($P < 0.05$). Concentration of NH_3-N was highest with TF+NF at wk 8 and 12, whereas at wk 16, it was highest in steers grazing mixtures followed by TF+NF ($P < 0.05$). Steers grazing grass-legume mixtures resulted in enhanced ruminal fermentation evidenced by increased VFA concentration likely due to greater concentration of nonfiber carbohydrates, which may have supported increased growth performance compared to those grazing grass monocultures. Therefore, grass-legume mixtures for grazing steers can replace N fertilization of TF, and thus it can be a sustainable approach to improve pasture utilization for finishing beef steers.

Key Words: grass-legume mixtures, grazing beef steers, ruminal fermentation

---

1103 (T116) Agronomic assessment and beef cattle nutrition suitability of 31 forage type annual crops in the Peace region of Alberta.

T. A. Omokanye**[*1], M. Hobin[1], I. A. Adeyinka[2], and M. Benoit[1], *[1]Peace Country Beef & Forage Association, Grande Prairie Regional College, Fairview, AB, Canada, [2]National Animal Production Research Institute, Shika-Zaria, Nigeria.*

There is increasing use of forage type annual crops for swath grazing, bale grazing and silage for back grounding and finishing beef cattle in the Peace region of Alberta. There is therefore a need for continued effort for recent data (on agronomic adaptation, forage yield and quality, and animal performance) as new forage type annual crop varieties become available for possible inclusion into the forage based cropping systems of the region. A set of 31 annual crop varieties (16 barley, 3 oat, 5 triticale, 3 soybean, 2 field peas, 1 millet and 1 sorghum) were tested in order to identify crop varieties with superior forage yield and quality for beef cattle production. Forage dry matter (DM) yield varied ($P < 0.05$) from 4162 kg ha^{-1} (forage sorghum) to 10769 kg ha^{-1} (AC Ranger barley). Only 6 of the 31 tested crops had > 10.0 t ha^{-1}. Forage crude protein (CP) was unaffected ($P > 0.05$) and was generally > 10.0% for all crops. The 5 legumes included in the test all had significantly ($P < 0.05$) higher forage Ca content than cereal crops. Forage total digestible nutrients (TDN) generally varied ($P > 0.05$) from 60 to 67%. Crops which produced lower DM also had lower CP DM yield (DM x CP%). All crop varieties exceeded the suggested CP, Mg, K and TDN values for a dry gestating beef cow in the mid- and late-pregnancy stages. But the recommended Ca, P and Na values have not been consistently met by all crop varieties. Conducting cluster analysis procedures on the 31 crop varieties tested, using DM yield, forage chemical composition (7 parameters), energy (4 parameters), estimated digestibly (4 parameters), CP DM yield and Ca:P, hierarchical cluster analysis classified the crops into four distinct clusters of 8, 16, 6, and 1 crop varieties with, respectively, excellent, good, regular and poor degree of agronomic adaptation in the region and suitability for beef cattle.

Key Words: annual crop; forage; nutritive value; beef cattle; cluster analysis

FORAGES AND PASTURES III: GENERAL FORAGES AND FORAGE SYSTEMS

1104 (W091) Effect of plant density on nutritional quality of green chopped corn. G. Ferreira[*1,2], D. Carp[2], M. Alfonso[3], and S. Depino[3], [1]Dep. of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, [2]CREA Lincoln, Asociación Argentina de Consorcios Regionales de Experimentación Agropecuaria, Lincoln, Buenos Aires, [3]*Forratec Argentina, SA, Chacabuco, Buenos Aires.*

The hypothesis of this study was that seeding corn at high plant densities results in greater concentrations of neutral detergent fiber (NDF) and lower concentrations of starch in corn whole plant. Therefore, the objective of this study was to determine the effect of planting density on whole-plant dry matter (DM) yield and its nutritional quality. The study was performed in a commercial dairy farm located in General Villegas, Argentina. Preceding crop was corn for silage. Total rainfalls during fallow and crop season were 719 mm. Two commercial corn hybrids (Dekalb747 and Duo548) were sown at 60,000, 70,000, 80,000 and 90,000 plants/ha^{-1} in four plots using a no-till corn seeder with a pneumatic dosing machine (TX Mega, Agrometal, Argentina). Plots were composed of eight 50-m rows separated by 52 cm. Corn was sown on October 13, 2012 and chopped on February 1, 2013. Crop was fertilized with 90 kg N and 31 kg P2O5 per hectare. Ten consecutive corn plants, randomly selected from each plot, were manually cut at 15 cm above ground, chopped with a forage chopper (TRF 70, Trapp, Brasil) and weighted to determine DM yield. Nutritional quality of chopped corn was determined by NIRS. Because the resulting densities were inferior and more variable than targeted (likely due to soil temperature variation linked to no-till conditions) statistical analysis was performed by linear regression. Average DM concentration of the chopped corn was 31.1 and 34.5% for the Duo548 and Dekalb747 hybrids, respectively. Plant density did not affect whole plant dry weight ($P > 0.51$) in either hybrid (285 and 252 g DM.plant^{-1} for Duo548 and Dekalb747, respectively). Therefore, DM yield was linearly increased with plant density (slope = 237 kg DM.1000 plants^{-1}.ha^{-1}, $P < 0.01$). Contrary to the hypothesis, plant density did not affect either NDF concentration ($P > 0.25$) nor starch concentration ($P > 0.72$) of chopped corn (47.2 and 50.2% NDF and 27.5 and 21.3% starch for Dekalb747 and Duo548, respectively). Estimated DM digestibility was not affected ($P > 0.24$) by plant density in either hybrid (65.5 and 67.2% for Duo548 and Dekalb747, respectively). We concluded that, with abundant rainfalls (i.e., >700 mm), plant density does not affect nutritional quality of corn. Whether plant density affects nutritional quality of corn under lower rainfall regimes still needs to be elucidated.

Key Words: corn, density, quality

1105 (W092) Assessment of in vitro fermentation characteristics of lactation dairy diets consisting of orchardgrass or birdsfoot trefoil pasture forages with different supplements using continuous cultures. R. G. Christensen[1], A. J. Young[1], J. S. Eun[*1], J. W. MacAdam[1], and B. R. Min[2], [1]*Utah State University, Logan,* [2]*Tuskegee University, Tuskegee, AL*

This study evaluated the effects of feeding 2 different pasture forages [orchardgrass (OG) vs. birdsfoot trefoil (BFT)] combined with 3 supplements [no supplement, ground barley (GB), and forage-concentrate mixture (FCMX)] on in vitro fermentation characteristics. The experiment was performed in a 2 (source of pasture forage) × 3 (supplement) factorial design with 3 independent runs of continuous cultures ($n = 3$). Continuous culture apparatus consisted of 700-mL working volume fermentation vessels to measure major fermentation end-products. Each culture was offered a diet of 15 g DM/d in 4 equal portions at 0600, 1200, 1800, and 2400 h, and the supplements (GB and FCMX) were included at 30% DM of total diets. Culture pH averaged 6.15 and was not different across treatments. Total VFA concentration averaged 39.5 m*M* and did not differ among treatments. Feeding different pasture forages did not influence acetate and propionate concentrations. While acetate concentration was similar across treatments, propionate concentration increased with supplementing GB or FCMX, resulting in a decreased acetate-to-propionate ratio due to the supplementations. Ammonia-N concentration tended to decrease ($P < 0.06$) with BFT compared with OG (9.40 vs. 13.5 mg/100 mL), whereas supplementation resulted in no difference in the ammonia-N concentration, regardless of source of pasture forage. Methane production decreased when fermentors were offered BFT compared with OG (8.50 vs. 10.9 mmol/d), but supplementation did not affect the methane production under OG as well as BFT. The positive impacts of feeding BFT pasture forage with decreased ammonia-N and methane concentrations could have resulted from beneficial effects of condensed tannins (4.46% DM) in BFT which manipulate ruminal fermentation pathways by improving utilization of N and energy substrates. Overall results in this experiment indicate that feeding BFT-based dairy diets did not interfere with in vitro ruminal fermentation, and BFT can be an effective forage source to reduce N excretion and mitigate methane emissions.

Key Words: birdsfoot trefoil, condensed tannins, continuous cultures

1106 (W093) Fatty acid profile and oxidative stability of carcass fat from meat goats fed grass-legume forage diets. B. R. Min[*], *Tuskegee University, Tuskegee, AL*

A series of experiment was conducted at the Caprine Research and Education Unit at Tuskegee University to develop and

demonstrate a profitable and sustainable forage-based goat production system with 6 different forage combinations included annual ryegrass (RG) or RG + legume combinations (e.g. Austrian pea (AP), berseem clover (BC), hairy vetch (HV), RG+AP+HV, and RG+HV+AP+BC)) in the winter of 2011 for the Southeastern United States. Forty-eight crossbred goats (*Capra hircus*; BW= 27.46 kg) were randomly assigned to 12 paddocks with 6 forage combinations with 2 replicates *(n* = 4) during 45 days. After grazing ended, goats were transported to Mississippi State University Meat Lab and were slaughtered according to the USDA guidelines and carcass characteristics were determined. Forage biomass and forage chemical composition were measured from February to May. On each occasion four random quadrates (0.25 m^2) per forage paddock were cut using a hand-clipper. There was a forage sampling time x forage combination interaction ($P < 0.01$) for CP and NDF. Forage CP content was higher in March than February and April, but NDF content continuously increased with time. The RW with HV combinations continued to have greater CP content. Animals on RG and BC combinations grew 18% faster and reached expected slaughter weight in less time when compared to RG pasture system. Goats grazing RG+BC and RG+HV+AP had higher ($P < 0.05$) ADG and carcass weights than other forage combinations. Goats grazed on RG-based diet had higher SFA and polyunsaturated fatty acids (PUFA) in intramuscular fats ($P < 0.01$), but were lower in mescenteric kidney fat and subcutaneous fat ($P < 0.05$) compared to legume forage-based diets, respectively. For goats grazing on RG-based diet had significantly higher ($P < 0.05$) omega-3 and omega-6 fatty acids in intramuscular fat content, but were lower in subcutaneous fat ($P < 0.05$) compared to legume forage-based diets. Mono unsaturated fatty acids (MFA) were not affected by diets. These results indicated that goats receiving RG forage-based diets produced carcasses with more PUFA and higher omega-3 and -6 fatty acids in intramuscular fat from Kiko-crossbred male goats.

Key Words: fatty acids, goats, grass, legume

1107 (W094) Effects of moisture level at baling and Fresh Cut brand plus on quantity and quality of alfalfa hay harvested in large rectangular bales. K. E. Griswold*, R. Almada, A. Lipata, and E. Rodberg, *Kemin Animal Nutrition & Health, Des Moines, IA.*

The effects of baling moisture and Fresh Cut brand plus (Kemin Industries, Des Moines, IA), a propionic acid-based preservative, on quantity and quality of alfalfa hay harvested in large rectangular bales were determined in a split plot design. Baling moisture, low (LM, <15%) vs. high (HM, >20%), was the main plot, and control (NT) vs. Fresh Cut Plus (FC+) applied at recommended levels was the subplot. Weight, mold and yeast counts, and nutrient content were determined for fresh (day of baling) and cured (8 wk after baling) bales using composite samples from 6 cores per bale. Data were analyzed using JMP software with models that included the fixed effects of baling moisture, FC+, and the interaction of moisture by FC+. Significance equaled $P < 0.05$ and trends equaled $0.05 < P < 0.10$. Mold and yeast counts were log transformed prior to analysis. Data are presented on DM basis. The interaction of HM baling and FC+ increased ($P < 0.01$) fresh bale weights (709 vs. 644 kg, respectively) and tended ($P = 0.06$) to increase cured bale weights (719 vs. 635 kg, respectively) compared to all other treatments. In cured bales, mold and yeast counts were lower (4.5 vs. 5.4 and 5.1 vs. 5.8, respectively; $P < 0.01$) for HM vs. LM bales. In fresh bales, mold and yeast counts were not affected ($P > 0.10$) by FC+, but were lower (4.7 vs. 5.2 and 5.3 vs. 5.7, respectively; $P < 0.05$) in cured bales compared to NT. There were no effects or interactions ($P > 0.10$) of baling moisture and FC+ on nutrient content of fresh bales. In cured bales, the baling moisture and FC+ interacted to lower ($P < 0.05$) sugar content (4.62 vs. 6.09%, respectively) and concomitantly increase ($P < 0.05$) lignin (5.42 vs 4.59%), ADICP (2.73 vs. 2.41%), and fat (1.77 vs. 1.66%) content, respectively. In cured bales, FC+ lowered ($P < 0.05$) CP (25.2 vs. 25.7%) compared to NT, and HM baling increased ($P < 0.05$) ADF (29.4 vs. 28.1%), NDF (38.4 vs 36.8%), and ash (14.1 vs. 13.6%) content compared to LM, respectively. However, there were no significant ($P > 0.05$) effects of treatments on feeding value of fresh or cured alfalfa as determined by MILK 2006 software. Overall, these results would suggest that baling at high moisture in combination with FC+ treatment allowed for the harvesting and retention of more high quality alfalfa DM in large rectangular bales compared to baling at low moisture with or without FC+ application.

Key Words: alfalfa, moisture, Fresh Cut plus

1108 (W095) Estimation of macronutrients content in mixed swards by near infrared reflectance spectroscopy. A. I. Roca-Fernández*, P. Castro-García, and A. González-Rodríguez, *Agrarian Research Centre of Mabegondo, La Coruña, Spain.*

Near infrared reflectance spectroscopy (NIRS) is a rapid, non-destructive and inexpensive technique for providing chemical analysis of forage and feedstuffs. The aim of this study was to develop NIRS calibration equations to determine macronutrients (P, Ca, Mg and K) content in mixed swards. Two hundred twenty samples were taken from mixed ryegrass (*Lolium perenne* L. and *Lolium multiflorum* Lam.) and clover (*Trifolium repens* L. and *Trifolium pratense* L.) swards located in a grassland area from Galicia (NW Spain). Reference data that were used for developing calibration equations were analyzed using standard laboratory methods widely applied for determination of macronutrients content in swards samples (*P* was measured colorimetrically as molybdovanado-phosphoric acid and Ca, Mg and K were measured by atomic absorption spectrophotometry). All the samples were scanned with monochro-

matic radiation from 1100 to 2500 nm using NIRSystems 6500 (FOSS Analytical AS, Denmark). Predictive equations were developed using modified partial least squares (MPLS) regression with internal cross-validation and scatter correction using standard normal variate (SNV) and detrend. Cross validation was used to avoid overfitting of the equations. The best equations of MPLS regression for the four macronutrients were obtained by using the second derivative of spectra than using the first derivate. The coefficient of determination in calibration (R^2_c), cross validation (R^2_{cv}) and prediction (R^2_p) and the standard error of calibration (SE_C), cross validation (SE_{CV}) and prediction (SE_P) found for each macronutrient were: P (R^2_c= 0.72 and SE_C= 0.43; R^2_{cv}= 0.61 and SE_{CV}= 0.51; $R^2_{P=}$ 0.70 and $SE_{P=}$ 0.46), Ca (R^2_c= 0.90 and SE_C= 1.44; R^2_{cv}= 0.69 and SE_{CV}= 2.50; $R^2_{P=}$ 0.84 and $SE_{P=}$ 1.35), Mg (R^2_c= 0.76 and SE_C= 0.19; R^2_{cv}= 0.58 and SE_{CV}= 0.26; $R^2_{P=}$ 0.60 and $SE_{P=}$ 0.20) and K (R^2_c= 0.82 and SE_C= 3.46; R^2_{cv}= 0.71 and SE_{CV}= 4.37; $R^2_{P=}$ 0.74 and $SE_{P=}$ 2.98). Taking into account RPD values for validation, calculated as standard deviation of reference data (SD) divided by SE_p, a good quantitative prediction of Ca (RPD= 2.27) and approximately of P, Mg and K (RPD= 1.79, 1.66 and 1.95, respectively) were achieved. Nevertheless, these results might be improved by adding samples to the calibration set.

Key Words: minerals, NIRS, ryegrass-clover pastures.

1109 (W096) Fall harvest management of eastern gamagrass. W. K. Coblentz*[1], M. G. Bertram[2], P. C. Hoffman[3], N. M. Esser[4], and J. S. Cavadini[4], *[1]U.S. Dairy Forage Research Center, Marshfield, WI, [2]University of Wisconsin, Arlington, [3]University of Wisconsin, Madison, [4]University of Wisconsin, Marshfield.*

Recent research has suggested that eastern gamagrass (EGG) may be an effective alternative to chopped straw in the blended diets of dairy heifers and cows. Most extension materials discussing appropriate fall management of EGG recommend avoiding harvest within about 6 weeks of first frost. Using this guideline for central Wisconsin, a final harvest of EGG would need to occur before August 15; however, previous research has shown that single-harvest yields of DM are not maximized by that date because of inadequate accumulation of growing degree days. Our objectives were to evaluate yields of DM, plant persistence, and nutritive value for EGG harvested at 15-d intervals between August 1 and November 1. Residual forage growth was burned each May, and all forages were fertilized with 84 kg N/ha annually. Data collected from 2010 through 2013 indicated that yields of DM increased with linear ($P < 0.01$) and quadratic ($P < 0.01$) effects over harvest dates, peaking at > 7400 kg/ha on both the September 15 and October 1 harvest dates. Overall DM yields varied with year, but were greatest ($P < 0.01$) during the final year (2013) of the trial (7967 kg/ha), thereby suggesting stands were not damaged by fall harvests. Percentage of continuous row coverage also was assessed, but was not affected by harvest date ($P \geq 0.22$). Concentrations of NDF increased from 75.8 to 82.0% across harvest dates, exhibiting both linear and quadratic ($P < 0.01$) effects. Similarly, acid-detergent lignin increased from 4.07 to 5.12% between August 1 and November 1, exhibiting only a linear ($P < 0.01$) effect of harvest date. Crude protein declined linearly ($P < 0.01$) across harvest dates, ranging from 7.69 to 3.67%. Energy density also declined linearly ($P < 0.01$) over harvest dates, ranging from 53.2% TDN on August 1 down to 43.9% TDN on November 1. One-time harvests of EGG during fall allowed for improved yields of DM through October 1, and did not affect stand persistence. For harvests timed between August 1 and November 1, EGG will likely range between 75.0 and 82.0% NDF, and exhibit an energy density of approximately 50% TDN. These characteristics, coupled with the consistent observation that EGG haylage is not sortable by dairy heifers or cows, make EGG a potentially attractive alternative to chopped straw.

Key Words: eastern gamagrass, fall harvest management, DM yield

---

1110 (W097) Fertilization of fall-grown oat with urea or bedded-pack manure. W. K. Coblentz*[1], W. E. Jokela[1], and M. G. Bertram[2], *[1]U.S. Dairy Forage Research Center, Marshfield, WI, [2]University of Wisconsin, Arlington.*

Oat (*Avena sativa* L.) shows promise as a fall-forage option for dairy producers in Wisconsin, and potentially opens a window of opportunity for manure spreading that is not associated with production of corn (*Zea mays* L.). Our objectives were to assess the effects of summer applications of commercial N fertilizer or bedded-pack manure containing wood shavings on the DM yield, N uptake and recovery, and nutritive value of fall-grown oat forages. Research plots were fertilized with either bedded-pack manure (23 or 45 Mg/ha, wet basis; 22.9% DM; 1.9% N, DM basis) or urea (46-0-0) at application rates of 0, 20, 40, 60, or 80 kg N/ha, and then seeded to two oat cultivars (Ogle or ForagePlus). Plots were harvested on two dates (early October or November), which simulated grazing and silage applications, respectively. Climatic conditions differed sharply across years, with growth responses limited somewhat by drought during 2012. During both years, DM yield increased linearly ($P \leq 0.03$) with commercial N fertilization, and yields following applications of urea exceeded ($P < 0.01$) forages receiving bedded-pack manure during 2011, but not during 2012 ($P = 0.85$). Overall DM yields were greater in early November compared to early October during both 2011 (3991 vs. 2257 kg/ha; $P < 0.01$) and 2012 (2753 vs. 1997 kg/ha; $P < 0.01$). Apparent percentage N recoveries by oat forages increased linearly ($P = 0.01$) with urea application rate during 2011, and increased with both linear ($P = 0.01$) and quadratic ($P < 0.01$) effects during 2012. However, apparent N recoveries following applications of bedded-pack manures were es-

sentially nil for both years (overall range = -6.2 to 2.6% of N applied). For 2011, concentrations of water-soluble carbohydrates (WSC) were inversely related to urea application rate, declining from 12.4 to 10.1% as fertilization rate increased from 0 to 80 kg N/ha, which was explained by both linear (P = 0.01) and quadratic (P <0.01) effects of application rate. Similar effects were observed for 2012, when WSC declined from 19.3 to 16.3% across the same urea fertilization treatments. Calculated energy density of fall-oat forages remained very high across all treatments; overall means were 67.0 and 70.1% TDN for 2011 and 2012, respectively. These results indicate that fall-grown oat is an energy-dense forage option, but bedded-pack manures containing wooden shavings provide little immediately available N to support forage production.

Key Words: bedded-pack manure, fall-grown oat, N fertilization

---

1111 (W098) Nutrient composition and in vitro digestibility of cultivated and non-cultivated plant species found within a Southwestern forage production operation. J. D. Allen[*1], L. W. Hall[2], and J. English[2], *[1]Northwest Missouri State, Maryville, [2]University of Arizona, Tucson.*

Nutrient quality of non-cultivated plants in hay or grazing pasture may affect animal feeding behavior, digestive efficiency, forage quality, or a combination of these. Understanding nutritive composition of invasive plants may improve forage and weed management. A 2-year study was conducted to determine the nutrient composition and digestibility of invasive plants growing within the boundaries of 3 alfalfa hay fields and 7 grass pastures (9.75 ha) located at the University of Arizona's West Agriculture Campus and Campus Agricultural Center (Tucson). Multiple whole above-ground samples of cultivated and non-cultivated species were collected at a maturity of mid-bloom for non-grasses (n = 53) and pre-shatter for grasses (n = 13). Samples were analyzed for DM, ash, NDF, ADF, ADL, CP, and IVTD. Species from 21 plant families were sampled, with the grass (*Poaceae*) family having the highest specie count (13), and 9 forb families having only 1 specie recorded. Compared to cultivated alfalfa, forb species had greater (P < 0.01) CP (20.2 vs. 15.5 ± 2.85%), ADL (8.5 vs. 3.0 ± 1.74%), and IVTD (75.1 vs. 67.3 ± 3.28%), and grass species had greater (P < 0.01) NDF (53.8 vs. 45.9 ± 3.76%) but lower (P < 0.01) ADF (25.7 vs. 33.6 ± 1.74%). Seven (7) plant families were represented by at least 3 species: amaranth (*Amaranthaceae*; n = 3), sunflower (*Asteraceae*; n = 7), mustard (*Brassicaceae*; n = 7), goosefoot (*Chenopodiaceae*; n = 5), knotweed (*Polygonaceae*; n = 4), nightshade (*Solanaceae*; n = 5), and grass. Within the 7 families, grasses had greatest NDF but least ADL, ash, and IVTD (54.7, 5.7, 11.9, and 64.3%, respectively; P < 0.01). Nightshade species had greatest CP (23.5%; P < 0.01), amaranth species had greatest IVTD and least NDF (84.0 and 29.3%, respectively; P < 0.01), and mustard species had greatest ADL (10.1%; P < 0.01). Greatest variation was observed with DM (SEM range = 2.47 to 16.98%), and least variation was observed with ADL (SEM range = 0.93 to 4.33%). Predominant species observed affecting grazing behavior or hay production included junglerice (*Echinochloa colonum*), bermudagrass (*Cynodon dactylon*), little mallow (*Malva parviflora*), and Palmer amaranth (*Amaranthus palmerii*). Results indicate the presence of non-cultivated plants growing within Southwestern hay and grazing fields may affect forage nutritive quality.

Key Words: forage, in vitro, invasive plants, nutrient composition

---

1112 (W099) Effects of Marandu pastures heights and sources of energy supplements on the weights gains per animal and per area. A. A. Oliveira[1], M. V. Azenha[*2], S. S. Santana[2], C. H. O. Macedo[2], J. P. R. Costa[2], T. T. Berchielli[2], A. C. Ruggieri[3], and R. A. Reis[2], *[1]Unesp, Jaboticabal, Brazil, [2]University of Sao Paulo State, Jaboticabal, Brazil, [3]Sao Paulo State University, Jaboticabal, Brazil.*

The study aimed to evaluate forage allowance based in sward heights, and energy supplementation from different sources in the weight gain of young Nellore bull yearling in pastures of *Urochloa brizantha* cv. Marandu. Grazing system was continuous with variable stocking (put and take animals) to maintain the sward height during the rainy season. Three pasture heights (15, 25, 35 cm) were combined with three supplementation strategies (mineral mixture, protein/energy supplement based in corn meal, and protein/energy supplement based citrus pulp) distributed in eighteen paddocks (two pasture replications). Both energy/protein supplements contained 19.0% of crude protein, and were supplied at 0.3% of body weight/day. Experiment was conducted from January to April. Forage mass, and animal body weight were determined monthly to calculate the forage allowance. One hundred eight animals (259 ± 20 kg) were grazed for 122 d and weighed at the beginning and the end of the trial. Total dry matter intake was evaluated using modified lignin LIPE (eternal marker), and indigestible neutral detergent fiber (internal marker). The type of supplementation did not influence (P > 0.05) any pasture variable evaluated during the experimental period. To maintain pastures heights it was necessary to adjust the stocking rate that decreased linearly (6.64, 5.03 and 4.08 UA/ha^{-1}) in response to the treatments (15, 25 and 35 cm, respectively). Forage allowance, and dry matter intake increased linearly (P < 0.05) in response to the pasture heights, or forage allowance. Gain per unit of land showed a quadratic response associated to lowest weight gains per unit of land (6.94, 6.38, and 5.37 kg/ha/day) in response to pasture heights (forage allowance), but there was a positive response in individual animal weight gain (0.694, 0.874 and 0.953 kg/day). Protein/energy supplementation increased (P < 0.05) weight gain per area and per

animal. Citrus pulp provided greater ($P < 0.05$) stocking rates (5.4 AU/ha), but corn was similar (5.3 AU/ha) to both mineral (5.0 AU/ha) and citrus pulp. Pasture management at 15 cm during the rainy season resulted in highest stocking rate, and consequently more weight gain per area. However, lowest forage allowance reduced forage intake, average daily weight gain, and final body weight at the end of the rainy season. It was concluded that the pasture energy/protein supplementation (0.3% BW) provides a balance between gain per area, per animal, and low risks to pasture degradation and maximum productivity in the system.

Key Words: beef cattle, supplementation, weight gain

1113 (W100) Effect of sowing date on forage yields and quality of Italian ryegrass in early spring-seeded. K. Kim*, *Livestock Institute, Jeollanamdo, South Korea.*

Because Italian ryegrass (IRG) is generally cultivated by winter cropping on a drained paddy field, the harvest season is overlapped with that of rice in some cases. In addition, people may miss the adequate seedtime for IRG because of the rainy season. Therefore, this research has been performed between October 2012 and July 2013 in Kangjin, Korea, to examine the effect of spring-seeding on the yields and quality of IRG, as an alternative seeding when the adequate seedtime is missed. Using Kowinearly species, five test groups were prepared depending on the sowing date: Control group (sowing date: October 20, 2012, which is an optimum seeding-time), T1 (sowing date: February 15, 2013), T2 (sowing date: February 25, 2013), T3 (sowing date: March 5, 2013) and T4 (sowing date: March 15, 2013), and the IRG was harvested in May 31, 2013. The lodging of vegetative period for control group, T1 and T2 was >70%, while that of T3 and T4 was approximately 50%. The plant height by harvesting for control group showed the highest value of 109.5cm, and for T1 and T2 was 102.2 and 103.0cm, while those for T3 and T4 were 98.6 and 93.3cm, respectively, whereby the difference was statistically significant ($P < 0.05$). The fresh yield per ha was 38.0, 26.5, 21.2, 22.3 and 20.4 ton/ha for control group, T1, T2, T3 and T4, respectively, where the control group showed the highest value and the T1 was significantly larger than those for T2~T4 ($P < 0.05$). The yield for dry matter was 31.3, 27.8, 28.8, 24.4 and 22.3% for the control group, T1, T2, T3 and T4, respectively, which is the similar to the fresh yield. On the other hand, the content of crude protein was 7.9, 8.6, 8.7, 9.4 and 12.3% for the control group, T1, T2, T3 and T4, respectively, where a shorter growing period represents the higher crude protein content. The ADF was 36% for the control group and T1 ~ T3, while that for T4 decreased to 33%. The NDF was 66% for the control group and T1 ~ T3, while that for T4 decreased to 61%. According to these findings, it can be summarized that the Spring-seeding of IRG gives <70% yield compared to that by the adequate seeding. However, the optimum seeding time to maximize the forage yield and quality would be before February 25.

Key Words: Italian ryegrass, early spring-seeded, forage yield, forage quality

---

1114 (W101) Relationship between protein structural characteristics and supply of metabolizable protein to dairy cattle from new cool-season forage corn varieties in Western Canada . *N. A. Khan, S. Abeysekara, D. A. Christensen, X. Huang*, and P. Yu, University of Saskatchewan, Saskatoon, Canada.*

The objective of this study was to find out the relationship between protein inherent molecular structural characteristics of cool-season forage corn and supply of metabolizable protein (MP) to dairy cattle. Six new corn cultivars, including 3 Pioneer (PNR) and 3 Hyland (HL), coded as PNR-7443R, PNR-P7213R, PNR-7535R, HL-SR06, HL-SR22, HL-BAXXOS-RR, were sown in 24 plots on in the research fields of Canada-Saskatchewan Irrigation Diversification Centre (Outlook, SK, Canada). The 24 plots were blocked within 4 fields, and all cultivars were sown in each field (4 block x6 varieties). Whole crop samples were collected after a target of 2160 CHU was achieved. The MP supply to dairy cattle, and energy synchronization properties were modeled by the DVE/OEB system and the NRC-2001 model. The parameters evaluated were protein molecular structures in terms of amide I, amide II, amide I to II ratio, α-helix, β-sheet and α-helix to β-sheet ratio, which were determined using vibrational molecular spectroscopy (VMS). The data analysis were performed using SAS with Proc Mixed and Proc Corr. The Normality test was used Proc Univariate with Normal and Plot options. Multivariate molecular spectral analyses were performed with Statistica (StatSoft Inc., Tulsa, OK). The Tukey method was used for multi-treatment comparison. The significant level was declared at $P < 0.05$. There were no significant differences ($P > 0.05$) among the cultivars in molecular-spectral intensities of protein molecular structures. The amide II had a significant positive correlation with truly absorbable rumen undegraded feed protein (ARUP) ($r = 0.30$; $P < 0.001$), and had a significant negative correlation ($r = 0.18$, $P < 0.05$) with truly absorbable endogenous CP (AECP). Whereas, both amide I and amide II, and protein secondary structures (α-helix and β-sheet) were inversely correlated with rumen available N per insoluble rumen available OM ($r = \sim -0.30$; $P < 0.001$). In summary, protein molecular structure in the new cool-season corn varieties significantly link to the supply of metabolizable protein to dairy cattle.

Key Words: corn varieties, supply of metabolizable protein, protein molecular structures

1115 (W102) Evaluation of agronomic characteristics of five varieties of corn in integrated crop-livestock-forest system. A. A. Pinheiro*, M. C. A. Santana, V. A. Silva, J. T. C. Pacheco, A. C. Fernandes, and I. D. Carneiro, *Emater, Goiânia, Brazil.*

This research aimend to evaluate the agronomic characteristics of five cultivars of maize intercropped with *Brachiaria brizantha*cv, Marandu. The experimental design was a randomized block with three replications and five treatments. Maize cultivars used were: EMGOPA 501, AL Bandeirantes, BRS Caimbé, PL 6880, BRS 1060. To assess the agronomic characteristics were estimated: plant height, ear height, ear number per plant and number of plants per meter. Corn EMGOPA 501 showed higher plant height, since the height of the spike was equal to cultivars EMGOPA 501 and PL 6880. The number of spike was higher in cultivars EMGOPA 501, Al Bandeirantes and BRS 1060. BRS 1060 showed fewer plants per linear meter. Considering the whole plant corn, all cultivars showed agronomic traits suitable for silage production, highlighting the variety EMGOPA 501 for plant height and ear height hence.

Key Words: silage, ear, production

Table 1115. Means of agronomic characteristics of five cultivars of maize intercropped with *Brachiaria brizantha* cv. Marandu

	EMGOPA 501	AL Bandeirantes	BRS Caimbé	PL 6880	BRS 1060	CV (%)
Plant height	2.88^{A}	2.48^{B}	1.74^{D}	2.56^{B}	2.04^{C}	7.75
Ear height	1.80^{A}	1.39^{BC}	0.89^{D}	1.56^{AB}	1.18^{C}	12.28
Ear per plant	1.12^{AB}	1.25^{AB}	1.00^{B}	1.00^{B}	1.60^{A}	30.15
Plant per meter	3.87^{A}	3.32^{AB}	3.73^{AB}	3.87^{A}	3.20^{B}	13.53

Letters in rows differ ($P < 0.05$).

1116 (W103) Non-structural carbohydrates in Marandu-grass pastures under different grazing intensities. M. V. Azenha*[1], L. F. Brito[1], A. A. Oliveira[1], E. R. Janusckiewicz[1], E. Raposo[1], S. S. Santana[1], R. A. Reis[1], and A. C. Ruggieri[2], *[1]University of Sao Paulo State, Jaboticabal, Brazil, [2]Sao Paulo State University, Jaboticabal, Brazil.*

Carbohydrates are the source of available energy for growth and plants survival. This concentration is reduced by occurrence of defoliation and subsequent regrowth. Thus, reduction being directly proportional to the intensity and frequency of defoliation. This study aimed to evaluate non-structural carbohydrate content on Marandu-grass pasture managed under three grazing management heights. The heights of 15, 25 and 35 cm were managed by beef steers grazing under continuous stocking. Evaluations of non-structural carbohydrates occurred from January to November, 2011, at the UNESP, Jaboticabal, SP. Data were analyzed by repeated measurements with grazing intensity, period and interaction as sources of variation in variance analysis using proc mixed from SAS. Root and shoot samples were collected monthly with a steel cylinder of 15 cm diameter and 13.7 cm high. The collected samples were washed and processed for further analysis. The non-structural carbohydrates content in shoots was not affected ($P > 0.05$) by grazing heights, season and interaction grazing height and seasons of the year. In roots, the contents were affected by the seasons and the interaction heights and seasons of the year. Concentrations in roots were lower in summer compared to other seasons evaluated. There was linear fit ($P < 0.05$) of grazing heights only in the autumn. Non-structural carbohydrates showed a linear response ($P < 0.05$) and the highest average values observed for the levels of non-structural carbohydrates in the roots occurred in winter (158.61 g.kg^{-1}), followed by those for autumn (114.13 g.kg^{-1}), spring (101.00 g.kg^{-1}), and finally the lowest place in the summer (47.30 g.kg^{-1}). The decrease of values from winter to spring and summer was probably due to the improvement of weather conditions over the spring and summer months, which should have provided higher dry matter accumulation, which, in turn, demanded more organic reserves supply in order to have formed new tissue. Climatic changes conditions, defined by the seasons, provide changes in the levels of non -structural carbohydrates. Marandu-grass pastures grazed to 15 cm did not show a drastic condition management since it does not affect the reserve compounds from plants, when compared with the other hights studied.

Key Words: reserve compound, roots, shoots.

1117 (W104) Production and quality of alfalfa harvested on different stages of maturity in summer and fall. C. Arzola-Alvarez*[1], R. Copado-Garcia[2], O. Ruiz-Barrera[1], C. Rodriguez-Muela[1], A. Corral-Luna[1], A. Castañeda-Correa[1], H. M. Gaytan-Torres[1], and D. Diaz-Plascencia[1], *[1]Universidad Autónoma de Chihuahua, México, [2]Universidad Autonoma de Nuevo Leon, Monterrey, México.*

Alfalfa is a very important forage for the dairy industry. The objective of this study was to determine the effect of maturity on quality of hay of two varieties of alfalfa ("Cuff-101" and "Excellent Multileaf") in two seasons (summer and fall). The production (t/ha) and quality of forage was characterized through the determination of leaf:stem ratio of biomass and its content of dry matter (DM), crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF) and lignin over a range of days to harvest (0, 5, 10, 15, and 20 d following Stage 2) within the two seasons. Data were analyzed as a split-plot experiment, the plots arranged factorially in a randomized complete block design, being the alfalfa varieties and season the main effects, and maturity the subplot term. Results indicated season influenced both production and forage quality, so in fall the production of DM was lower ($P < 0.05$). On d 20 in summer a yield of 5.8 t MS/ha was determined and in fall only

4.9 t MS/ha, without differences among varieties ($P > 0.05$). Dry matter crude protein (CP) content of leaves in fall was 35.0% on d 0, and in summer 29.3% ($P < 0.01$). In summer, CP content of leaves was 32.7% and 29.3% in the whole plant, without differences among them ($P > 0.05$), whereas the content of CP on stem was lower than both (22.6%, $P < 0.01$). On d 20 in summer the leaves had 25.4% CP, stems 20.2% and whole plant 23.7% in Excellent Multileaf, compared to 23.5%, 19.1% and 21.6% CP in Cuff-101, respectively, without those differences among varieties being significant ($P > 0.05$). On d 20 it was determined 23.7% CP in fall, whereas in summer 21.6% ($P < 0.01$). NDF and ADF diminished ($P < 0.01$) in fall. In terms of CP, ADF and NDF in leaves, stem and whole plant, it was concluded that a higher quality alfalfa was growth in fall, without differences among varieties.

Key Words: alfalfa, CP, fiber

1118 (W105) Effect of cultivars and planting dates on bioenergy feedstock characteristics of switchgrass (*Panicumvirgatum*) in South Korea.

B. Kim[*1], M. M. Sargolzehi[2], B. Lee[1], D. Ji[1], J. Peng[1], J. Nejad[1], S. Kang[3], D. H. Min[4], and K. Sung[1], *[1]Dep. of Animal Life System, College of Animal Life Science, Kangwon National University, Chuncheon, South Korea, [2]Dep. of Animal Science, College of Agriculture, Ferdowsi University of Mashhad, Mashhad, Iran, [3]Planning and Coordination Division, National Institute of Animal Science, Suwon, South Korea, [4]Dep. of Agronomy, College of Agriculture, Kansas State University, Manhattan.*

The objective of this study was to determine the best performing switchgrass (*Panicum virgatum*) cultivar under three different planting dates as a bioenergy feedstock source in South Korea. Height, yield, energy content and chemical composition of three switchgrass cultivars, Carthage (CT), Cave-in-Rock (CIR) and Forestburg (FB) were measured from 2009 to 2012. Plots were seeded on April 23, May 4, and May 13, 2009 and were harvested once in November each year. The experimental design applied was randomized complete block (RCBD) in factorial arrangement with three replications. Planting date at three levels and cultivars at three levels were used as experimental treatments. Samples were analyzed for dry matter (DM), crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), crude fiber (CF), ether extract (EE), ash and total digestible nutrients (TDN). Planting dates did not significantly affect characteristics of CT, CIR and FB cultivars ($P > 0.05$). The NDF value of CT, CIR and FB were 81.19, 81.40 and 80.81% (DM basis), respectively ($P = 0.9318$). Also the ADF value was 45.24, 45.99 and 48.99% (DM basis; $P = 0.3558$) for CT, CIR and FB, respectively. Total dry biomass yields of CT, CIR and FB were 16.85, 15.90 and 4.50 ton/ha/year, respectively ($P < 0.0001$). Significant difference was also observed for height among CT, CIR and FB (177.59, 169.98 and 94.89 cm, respectively; $P = 0.0002$). There were no significant differences in energy content ($P = 0.96$) and chemical composition among varieties ($P > 0.05$). It appears that Carthage and Cave-in Rock are better adapted to South Korea climatic conditions than Forestburg as a biomass feedstock source.

Key Words: South Korea, bioenergy feedstock, cultivar, planting date

---

1119 (W106) Morphological composition of Piata palisade grass tillers subjected to strategies of intermittent defoliation.

G. O. Rocha[1], F. H. M. Chizzotti[*1], D. M. Fonseca[1], D. N. Junior[1], M. E. R. Santos[2], and B. M. Pereira[1], *[1]Universidade Federal de Viçosa, Brazil, [2]Universidade Federal de Uberlandia, Uberlandia, Brazil.*

It was aimed to evaluate the morphological composition of tillers of Piata palisade grass (*Brachiaria brizantha* cv. Piata) under different combinations of defoliation frequency and severity. The trial was carried out in Vicosa - MG, Brazil, from December 2012 to March 2013. The treatments consisted to combinations of two post-cutting heights (15 and 20 cm) and two pre-cutting frequencies (95% and 100% light interception, LI_{95} and LI_{100}) and were allocated to experimental units (14 m^2) with three replications according to a 2x2 factorial arrangement in a randomized complete block design. Canopy light interception was measured using a canopy analyser LAI 2000 and sward height using a sward stick. The following variables were evaluated: the number of live and dead leaves per tiller, the length of leaf blades and the length of stem. Data were analysed using the mixed procedure of SAS. The number of live leaves was not affected by management strategies ($P > 0.10$), staying on average 4.5 live leaves per tiller. However, the number of dead leaves per tiller was lower ($P < 0.10$) for swards managed with the LI_{95} than those managed with the LI_{100} (1.25 and 1.79, respectively). Additionaly, swards managed with the LI_{95} had lower ($P < 0.10$) stem length (19.15 cm) than those managed with the LI_{100} (27.76 cm). The length of leaf blade also was lower ($P < 0.10$) with LI_{95} strategies than with LI_{100} (18.04 and 27.43 cm, respectively). There were no effects ($P > 0.10$) of two post-cutting heights (15 and 20 cm) on all variables evaluated. The Piata palisade grass managed with the LI_{95} target had lower number of dead leaves and shorter length of stems and leaves, which corresponds to more favorable sward structure to intake by grazing animals. *Funded by Fapemig.*

Key Words: management, pasture, tropical grass

1120 (W107) Chemical composition and in situ dry matter degradability of tropical forages grasses in Northeastern Brazil. S. S. C. Sanches, R. C. Rodrigues, M. O. M. Parente*, I. G. R. Araújo, C. M. S. Galvão, A. L. Silva Júnior, S. Figueredo, R. A. Araújo, I. Rodrigues, and S. S. Mendes, *Universidade Federal do Maranhão, Chapadinha, Brazil.*

Brazil has an area of more than 220 million ha of pasture, and at least 100 million ha are cultivated pastures. Thus, tropical grasslands represent an important resource for the Brazilian cattle industry. The chemical composition and ruminal in situ dry matter (DM) degradability of nine tropical forages grasses in Baixo Parnaíba, Maranhão were evaluated. The forages were harvested at 35 d of growth and the cutting height was 15 cm of soil. One Santa Inês male sheep (BW 63 kg) cannulated in the rumen was used for feed incubation. Samples of 5 grams of each forage were incubated in the rumen in nylon bags. For each time of incubation four bags were used. The experiment followed a completely randomized design in a 3x9 factorial arrangement (three times of incubation – 6, 24 and 96 h and nine species — *Brachiaria humidicola, Brachiaria* hybrid cv. Mulato, *Brachiaria brizantha* cvv. Piatã, Xaraés and Marandu, *Brachiaria ruziziensis*, *Brachiaria decumbens, Panicum maximum* cv. Massai and *Andropogon gayanus*). The *P. maximum* cv. Massai grass presented higher ($P < 0.05$) protein content (7.4%) than *B. humidicola* and *A. gayanus* (3.3 and 3.6, respectively), whereas the NFD, AFD, cellulose and lignin contents didn't differ among grasses. The content of hemicellulose was lower in *P. maximum* cv. Massai, *B. decumbens*, and *A. gayanus* grasses. Higher values of DM disappearance of tropical grasses were found in 96 hours (mean value 36.16, 55.52 and 80.20% for 6, 24 and 96 h, respectively). *B. decumbens* had higher values of effective digestibility (ED) in three passage rates (PR): 67.7, 57.1 and 51.3% in PR of 2, 5 and 8%, respectively. *B. humidicula* and *P. maximum* cv. Massai grasses had the lowest potential degradability, 78.9% and 77.6%, respectively. The nonlinear model was adjusted satisfactorily to data from DM. The coefficients of determination (R^2) obtained for the curves of degradability in both for age degradability were greater than 93%.

Key Words: *Andropogon gayanus*, *Brachiaria* spp., *Panicum maximum*

1121 (W108) Influence of phenological stage on fresh forage, hay and silage on nutritional value of tall wheatgrass. M. Menghini[1,2], H. M. Arelovich*[1,2,3], M. F. Martínez[1], and R. D. Bravo[1], *[1]Dto. Agronomía, Universidad Nacional del Sur, Bahía Blanca, Argentina, [2]CIC, Bahía Blanca, Argentina, [3]CERZOS, Bahía Blanca, Argentina.*

The objective was to compare the nutritional value of two methods of forage conservation and fresh forage (type of forage=TF) of tall wheatgrass (*Thinopyrum ponticum*) in 5 different phenological stages (PhS). The experimental units were 5 m^2 plots randomly distributed upon a uniform stand of tall wheatgrass in a complete randomized design ($n = 3$). Clipping dates were 113, 142, 163, 190 and 211 d after regrowth related to the stages vegetative (V), booting (B), anthesis (A), milk (M) and dough-grain (D) respectively, on standing fresh pasture (P), hay (H) and silage (S). Clipping was mechanical at 10 cm height and dry matter yield (DMY) was measured. Subsamples from each experimental unit were used for: (1) DM determination of P, (2) preparation of H by drying sheltered at environmental temperature (72 h), and (3) preparation of S in PVC cylinders with 2 kg fresh forage carrying capacity (60 d). All materials were analyzed for NDF, ADF, ADL, soluble non structural carbohydrates (SNSC), IVDMD and CP. Data was analyzed by ANOVA and means compared by Tukey ($\alpha = 0.05$). Results are reported in Table 1121. A significant interaction TF x PhS was found for all variables with the exception of CP and ADL. Only A could be an adequate alternative for S. However, at B, A, M and D the H conservation method would preserve an appropriate nutritive value as well.

Key Words: forage conservation, nutritional value, *Thynopirum ponticum*

Table 1121. Nutritional value (%) for tall wheatgrass at different PhS and for different TF

PhS	TF	DM	NDF	ADF	ADL	SNSC	IVDMD	CP	DMY
V	P	38.0^{a}	70.2	35.7	3.0	15.1^{a}	52.4	12.6	1393^{a}
	H	91.9^{b}	67.5	35.8	2.6	13.1^{a}	54.3	11.3	
	S	41.7^{a}	66.8	37.9	3.7	1.96^{b}	50.9	11.2	
B	P	36.1^{a}	70.3^{a}	36.3^{a}	4.8	23.8^{a}	55.4^{a}	9.5	2047^{a}
	H	91.6^{b}	72.8^{b}	38.5^{b}	5.3	12.4^{b}	47.0^{ab}	10.0	
	S	37.5^{a}	70.9^{ab}	40.1^{c}	6.1	3.5^{c}	38.9^{b}	9.07	
A	P	40.8^{a}	72.1	38.7	5.3	24.2^{a}	50.3	7.3	3215^{b}
	H	92.4^{b}	73.2	39.7	5.5	12.7^{b}	46.3	8.1	
	S	43.4^{a}	71.6	41.2	6.1	1.2^{c}	43.5	7.3	
M	P	51.3^{a}	68.4^{a}	36.9^{a}	5.0	18.8^{a}	49.3^{a}	6.6	3338^{b}
	H	92.1^{b}	71.8^{b}	40.4^{ab}	5.9	16.5^{a}	48.4^{a}	7.0	
	S	50.6^{a}	72.5^{b}	47.0^{b}	7.2	4.9^{b}	40.7^{b}	7.1	
D	P	60.4^{a}	72.1	43.7	6.3	17.7^{a}	46.7	5.5	3812^{b}
	H	92.9^{c}	71.2	44.4	5.9	17.2^{a}	49.8	5.7	
	S	63.9^{b}	71.4	45.3	6.0	11.8^{b}	48.2	5.2	

PhS: phenological stage; TF: type of forage.
^{a,b,c} Differ within each PhS ($P < 0.05$)

1122 (W109) Spatio-temporal evaluation of the nutritive value of *Croton cortesianus* and *Leucophyllum frutescens* through in vitro fermentation kinetics.

A. MS.[1], G. C. M.*[*1], G. R. H.[2], D. G. TG.[1], and J. R. A[1], *[1]Universidad Juárez del Estado de Durango, Durango, México, [2]Universidad Autónoma de Nuevo León, Linares, Nuevo León, México.*

The aim of the study was to evaluate, seasonally, two native shrubs which are commonly selected by white-tailed deer in a semiarid and subtropical area of Northeastern México. Foliage from *Croton cortesianus* and *Leucophyllum frutescens* was sampled from Summer 2004 to Spring 2005 in two country sites: China and Linares in the state of Nuevo Leon, México. In vitro gas production was recorded at 3, 6, 9, 12, 24, 48, 72 and 96h. Kinetic parameters such as the asymptotic gas production (B), rate of gas production (*k*) and lag phase (L) were estimated by the exponential model $G = b \times (1 - e^{-k(t-L)})$. Microbial protein synthesis, ME content and in vitro organic matter digestibility (IVOMD) were also evaluated. Data were analyzed according to a completely randomized design with factorial arrangement. The factors were sampling sites, shrub species and seasons. Kinetic parameters significantly varied among shrubs, sites and seasons ($P < 0.001$). The asymptotic gas production (B) ranged from 127 ml of gas/g DM in *C. cortesianus* in summer 2004 in China country to 237 ml of gas/g DM in *C. cortesianus* in spring 2005 in Linares country. The rate of gas production (*k*) was the lowest ($P < 0.05$) in *C. cortesianus* in summer 2004 (0.035%/h) while the highest (0.144%/h) was collected in autumn 2004 in Linares. Values regarding L ranged from 0.05 to 2.89 h, and were superior ($P < 0.05$) in *C. cortesianus* during autumn 2004 in Linares country. Interactions sites x shrub species x seasons were significant ($P < 0.001$) for all kinetic parameters. Microbial protein synthesis measured as purines varied significantly among shrubs and seasons. Mean values ranged from 1.51 to 11.36 µmol, and were lowest ($P < 0.05$) in *C. cortesianus* in spring 2005 in Linares and highest in *L. frutescens* in autumn 2004 in China. The ME content varied from 0.36 to 2.71 Mcal/kg DM ($P < 0.05$). Estimates of IVOMD ranged from 46.4 to 89.7%. *C. cortesianus* had the greatest IVOMD values in summer 2004 in China ($P < 0.05$). Data suggested that although spatio-temporal fluctuations, variables such as the constant rate of gas production, which might indicate nutrient availability for rumen microorganisms (overall mean = 0.079%/h), digestibility (overall mean = 70.2%) and microbial protein synthesis (overall mean = 7.2 µmol) support the nutritive potential of *C. cortesianus* and *L. frutescens* for white-tailed deer in marginal semiarid regions of northeastern México.

Key Words: gas production, native shrubs, semiarid regions

1123 (W110) Reduction of enteric methane emission by using tannin supplementation in grazing goats.

A. C. Ruggieri[*], N. C. Meister, F. O. Alari, V. C. Silva, N. L. Santos, and E. B. Malheiros*, Sao Paulo State University, Jaboticabal, Brazil.*

This study aimed providing condensed tannin (*Schinopsis quebracho*) to reduce methane (CH_4) emission and if it keeps through time. Twelve Anglo Nubian breed goats were used with an average 56 kg of body weight (BW) in Tanzaniagrass (*Panicum maximum*) pasture with access to water and mineral salt managed under intermittent stocking with 11 hours of grazing period during 5 d. The treatments were: control (without tannin-WT) and addition of tannin (AT). Condensed tannin contained 70% (± 2) as guarantee level in powder form was fed (at 6:00 PM) once a day individually for each animal orally 0.31 g per kg of metabolic BW ($BW^{0.75}$). Tannin was provided for 91 d with three collections of methane with intervals of 30 days and period of feces collection to estimate dry matter (DM) intake. CH_4 emission was estimate by technique tracer gas SF_6 (sulfur hexafluoride). Variables for CH_4 emission were analyzed by SAS software in a completely randomized design with two treatments in a split plot in time with two longitudinal factors (5 d and 3 periods) and 6 replications (animals). F-test ($\alpha = 5\%$) was used for comparisons between treatments and orthogonal polynomial contrast for days and grazing cycles. There was no difference ($P > 0.05$) between treatments for g CH_4 emission per animal (21.88 ± 0.8 and 20.52 ± 0.8); kg DM intake (43.07 ± 2.1 and 42.73 ± 2.0) and percentage of loss of gross energy intake (14.65 ± 0.7 and 14.54 ± 0.7) respectively for WT and AT. The higher DM intake was observed ($P < 0.05$) in WT (562 ± 9.2 g / day) treatment compared to AT (510 ± 8.7 g / day). CH_4 emission calculated in relation to $BW^{0.75}$ resulted in larger ($P < 0.05$) amount in WT (1.13 ± 0.04) than AT (0.96 ± 0.4) group. There was not observed ($P > 0.05$) reducing CH_4 emission per animal through time per CH_4/animal (20.66 g ± 0.8, 1.0 ± 22.51 g and 20.42 g ± 1.2) and per $BW^{0.75}$ (1.03 ± 0.04, 07 ± 0.04 and 1.04 ± 0.06) respectively for the period 1, 2 and 3. The similarity in CH_4 production through time is probably due to the amount of tannin provided staying below the required limits for gas reduction and affecting only the fiber digestibility which caused decrease DM intake but no effect on CH_4emission and consequently through time.

Key Words: CH_4; gas emission reduction; tropical pasture

1124 (W111) Nutritive value of buffelgrass-based diets supplemented with dried distillers grains with solubles and dried citrus pulp. N. C. Vásquez Aguilar*[1], H. Bernal Barragán[1,2], R. G. Ramírez Lozano[1], M. Cerrillo Soto[2,3], M. V. Gómez Meza[1], E. Gutiérrez Ornelas[1,2], and M. Guerrero Cervantes[2,3], *[1]Universidad Autónoma de Nuevo León, San Nicolás de los Garza, México, [2]Red Internacional de Nutrición y Alimentación en Rumiantes, Durango, México, [3]Universidad Juárez del Estado de Durango, México.*

The objective of the study was to evaluate the effect of supplementing small amounts of dried distillers grains with solubles (DDGS) or dried citrus pulp (DCP) upon the nutritive value of buffelgrass (*Cenchrus ciliaris* L)-based diets. Twelve experimental diets were formulated using three qualities of buffelgrass: low (3.0% CP, 70% NDF), medium (5.6% CP, 66.5% NDF) and high quality (12.4% CP, 60.8% NDF) and four levels of supplementation (0%, 10% DCP, 10% 50DCP:50DDGS, and 10% DDGS). Utilized DCP and DDGS contained 3.8% and 30.6% CP, respectively. Sample contents of ash, crude protein (CP, Leco), neutral detergent fiber (NDF), hemicellulose, cellulose, lignin, and ether extract (EE) were determined. The in vitro dry matter digestibility (IVDMD; Daisy^{II}, ANKOM), and in vitro gas production (GP) at 0, 3, 6, 9, 12, 24, 48, 72 and 96 h were measured, and fermentation parameters *a*, *b*, and *c* were calculated. Metabolizable energy (ME) content was calculated from the gas production, protein and ether extract content. Each treatment was replicated four times, and results were evaluated according to a 3 x 4 factorial arrangement of treatments, using SPSS software. There were no significant ($P > 0.05$) grass quality x supplement interactions. Ash and protein contents were respectively 30% and 70% less for low- than for high-quality buffelgrass-based diets. Diets made up of high quality buffelgrass had 14% less NDF content, 7% lower hemicellulose, 19% less cellulose and 29% lower lignin content than diets based on low quality buffelgrass (68.1% NDF, 30.9% hemicellulose, 32.5% cellulose, and 4.7% lignin, DM basis). IVDMD was 81.8% for high quality-, and 67.2% for low quality-buffelgrass-based diets, and inversely correlated (r:-0.832; $P < 0.001$) with NDF content. ME content of diets was 26% higher ($P < 0.05$) in high quality-, than in the low quality-grass based diets (1424 Kcal ME/ kg DM). Addition of DDGS increased ($P < 0.05$) 28% the ether extract and 34% the protein content of buffelgrass. Addition of DCP and DDGS to the diet increased in average 5.5% ($P < 0.05$) the IVDMD of non-supplemented buffelgrass (72.5%). In vitro fermentation parameters *a*, *b*, and *c* were neither affected by grass quality nor by type of supplement ($P > 0.05$). In conclusion, quality of buffelgrass determined the nutritive value of diets; supplementing DDGS increased protein and fat content and DCP improved IVDMD.

Key Words: buffelgrass, dried citrus pulp, dried distillers grains with solubles

1125 (W112) Lignin concentration and its correlation with degradability of tropical grasses. A. Vargas Velásquez*, *Universidade de São Paulo, Pirassununga, Brazil*

Lignin inhibits the degradation of structural carbohydrates in the plant cell wall, thus, a precise and accurate method to determine lignin concentration is desirable. The spectroscopic acetyl bromide lignin (ABL) method has recently been receiving more attention by researchers and in this study it was compared to ADL, KL and permanganate lignin (PL). Five species of grasses, *Brachiaria brizantha* cv. Marandú*, Brachiaria brizantha* cv. Xaraés*, Panicum maximum* cv. Mombaça*, Pennisetum purpureum* cv. Cameroon and *Pennisetum purpureum* cv. Napier, harvested at seven maturity stages were used. Three fibrous preparations: NDF, ADF and cell wall (CW) were used to determine lignin concentrations. Protein (N x 6.25) and ash content were determined in the NDF and CW residues. A completely randomized experimental design with duplicate analysis for the lignin assays was used. A randomized block design was used for the in vitro experiment, with rumen fluid blocked by week. Individual treatments were compared by Tukey´s test ($P < 0.05$). Correlation coefficients between lignin methods and in vitro digestibility values were obtained using PROC CORR from SAS. The mean CW values were higher ($P < 0.05$) than NDF values, 768.1 g/kg versus 713 g/kg, reflecting solubilization of pectin and other neutral detergent soluble cell wall oligosaccharides. The ADL method yielded the lowest mean values ($P < 0.05$) of all methods, 95 g/kg versus 107.6, 116.2 and 199.1 g/kg for KL, PerL and ABL, respectively, which may indicate partial lignin solubilization by the acid detergent solution and/or by the 72% sulfuric acid solution. Results obtained by PerL were higher ($P < 0.05$) than those of ADL, possibly due to hemicellulose and pectin oxidation by potassium permanganate. The values for KL were higher ($P < 0.05$) than those of ADL, possibly due to protein contamination. The highest concentrations were obtained by the ABL method. In vitro dry matter degradability showed high negative correlation with lignin content, -0.8505, -0.9130 and -0.8883 when determined by ADL, PerL and ABL, respectively. A proposed correction factor (2.23) applied to the ADL values resulted in a degradability curve similar to the ABL curve. It is interesting to note that this value of 2.23 is very close to the 2.4 value used in the Cornell Net Carbohydrate and Protein System equations $B_2$and C, to estimate carbohydrate fractions, when adjusting lignin content. The ABL method is an easy, fast and convenient method to determine lignin content in forages.

Key Words: lignin, ABL, digestibility

1126 (W113) Chemical characterization and in vitro fermentation activity of tropical legumes.

I. Scull-Rodriguez[1,2], M. A. Cerrillo Soto[*2,3], O. Olao[1,2], M. Guerrero-Cervantes[2,3], A. Juárez-Reyes[2,3], and R. Herrera-Garcia[1,2], *[1]Instituto de Ciencia Animal, San José de las Lajas, Cuba, [2]Red Internacional de Nutrición y Alimentación en Rumiantes, Durango, México, [3]Universidad Juárez del Estado de Durango, México.*

Leguminous species are relevant as feed resources for grazing ruminants in a diversity of agro-ecosystems. Foliage from *Albizio lebecoide, Ormosia panamensis, Centrosema pubescen, C. pubescen* cv Bani*, Pongania pinnata and Albizia lebbeck* from the oriental region of Cuba was chemically characterized and the in vitro fermentation activity evaluated. Plots from various locations at the Rio Cauto's Valley were demarcated and fifteen plants at a vegetative stage were randomly selected. Small leaves and twigs were collected simulating animal grazing. Samples were composite, dried and milled. Chemical composition, in vitro dry matter digestibility (IVDMD), total polyphenols and antioxidative activity using 1,2-diphenyl-2-picrylhydrazyl (DPPH) were determined. Glass syringes were used and gas production recorded at 0, 3, 6, 9, 12, 24, 48, 72 and 96h after incubation initiated. Inoculum from three rumen fistulated sheep fed alfalfa hay and comercial concentrate (70:30) was utilized. Kinetic parameters such as the asymptotic gas production (*b*) and the rate of gas production (*k*) were obtained by the exponential model $G = b \times (1 - e^{-k(t-L)})$. Data related to kinetic parameters *b* and *k,* chemical composition, total polyphenols and antioxidative activity were analyzed according to ANOVA for a completely randomized design. Significant variation ($P < 0.05$) was registered among legume species in all the studied variables. Except for *O. panamensis*, all species had a CP content greater than 15% ($P < 0.05$). Values related to NDF ranged from 51.1% in *O. panamensis* to 59.1% in *C. pubescens* cv bani. Intermediate values were obtained in *P. pinnata* ($P < 0.05$). In vitro dry matter digestibility varied ($P < 0.05$) from 37.3% in *A. lebbek* to 61.5% in *C. pubescens* cv bani. *Centrosema* species exhibited the greatest asymptotic gas production ($P < 0.05$; mean values for *Centrosema*= 182 ml gas/ g DM). Rate of gas production (*k*) ranged from 0.0154% h^{-1} to 0.0549% h^{-1}. *Centrosema* species had superior *k* values as well ($P < 0.05$). Total polyphenols ranged from 1.62% in *A. lebbeck* to 0.29% in both *Centrosema* species ($P < 0.05$). Accordingly, antioxidative activity (overall mean = 92.7%) was greatest in those species containing superior levels of total polyphenols ($P < 0.05$). Among species, *Centrosema* species were of reasonably good quality (CP, 17.7%, IVDMD, 61.5%, DM basis). Moreover, the greatest values regarding the extent (*b*) and rate (*k*) of gas production observed in such species which indicate better nutrient availability for rumen microorganisms, might support their potential in marginal tropical and subtropical regions.

Key Words: legumes, in vitro gas production, chemical composition

1127 (W114) Modeling dry matter production in *Panicum maximum* grasses.

V. L. N. Brandao[1], M. I. Marcondes[2], F. H. M. Chizzotti[*2], and H. Bandeira[2], *[1]Universidade Federal de Viçosa, Minas Gerais, Brazil, [2]Federal University of Viçosa, Brazil.*

The achievement of DM production models for tropical grasses is almost absent in literature, despite the importance for livestock production, especially when considering climate chances, and it has effects on rain and temperature distribution. Models could be used as tools to adjust stocking rate and strategic planning for pasture during the year. The *Panicum maximum* grasses have high DM production (DMP), 30 ton of DM/ha.year on average, and that's why their use is becoming more common in tropical countries. The objective was to determinate a DMP model, using three cultivars of *Panicum maximum* (Mombaça, Colonião and Sempre-verde), and weather variables.A database was used ($N = 180$) based on pre-defoliation criteria as 95% of light interception, and 50% of height residue. Data were collected between December of 2012 and January of 2014. The variables minimum temperature (ºC, MIN), MIN^2, average temperature, maximum temperature, insolation (hours of light/d), precipitation (PCT, mm/d) and fertilizer (FTZ, kg of nitrogen/d) were tested by Stepwise procedure ($P < 0.010$) to determinate the variables that better determinate DMP. Afterwards, the effect of cultivars on selected variables were also tested. The variables MIN^2, FTZ and PCT were chosen by the procedure Stepwise, and they were affected by the cultivars ($P < 0.040$). The intercept was also affected by cultivar ($P = 0.042$). The adjusted equations are: $DMP_{Mombaça}$ (kg/d) = -92.88 + 0.56×MIN^2 + 10.55×FTZ + 3.52×PCT ($r^2 = 0.73$, MSE = 1198, AIC = 566); $DMP_{colonião}$ (kg/d) = -35.44 + 0.42×MIN^2 + 15.67×FTZ + 0.27×PCT ($r^2 = 0.51$, MSE = 1809, AIC = 570); $DMP_{sempre\text{-}verde}$ (kg/d) = -69.33 + 0.46×MIN^2 + 7.03×FTZ + 4.21×PCT (r^2= 0.63, MSE = 1562, AIC = 694). Colonião was the cultivar most responsible to fertilizer, less sensitive to temperature and had the greater DMP, whereas Sempre-verde was the most responsive to precipitation, which shows that their production is more distributed throughout the year in tropical countries. Finally, Mombaça was the most responsive to temperature, with a production strongly affected by weather condition. Nevertheless, despite Colonião having greatest DMP, data from literature shows that it has a small leaf/steam relationship. This variation on morphological components affects their nutritive value, and that's why it's important to develop models capable of stratifying their components for purpose of complementing DMP models. In conclusion, this model is capable to predicting DMP and it is strongly affected by cultivar.

Key Words: Colonião, Mombaça, Sempre-verde

1128 (W115) Productive performance of *Atriplex canescens* forage for 30 years of exclusion and grazing in different seasons of the year in the north of México. E. Suarez*, *UAAAN, Saltillo, México.*

The shortage of forage in rangeland of northern México is becoming more serious every year. Using some shrubs such as saltbush [*Atriplex canescens* (Pursh) Nutt.], can be a feeding strategy because of its high nutritional value. Additionally, its utilization improves ecosystems. Therefore, the use of shrubs improves the productivity of rangelands. The objective of this study was to determine whether the exclusion and/or livestock grazing affect dry matter production of saltbush scrub parvifolio in northern México. Production of dry matter in kg/ha during the four seasons (2012 to 2013) (free-range grazing vs. exclusion) was determined. The plots are distributed in two sites. To collect forage samples quadrant method was used. The data were analyzed using PROC GLM of SAS. The results were a highly significant difference ($P < 0.0001$) was found between the grazing exclusion treatment and the free grazing treatment during every season of the year, for the grazing exclusion site (spring, summer, fall and winter), means of (97.5, 355, 262.5, 95 kg MS/ha, respectively) were found and for the grazing site (65, 274, 144.5, 52.5 kg MS/ha, respectively). Also, a highly meaningful difference between both grazing exclusion and free grazing treatments of ($P < 0.0022$) was found, whose means are (202.5 and 134 kg MS/ha, respectively). With the above we conclude that the shrubs that remained in grazing exclusion can improve the productivity of rangelands and solve the shortage of fodder in times of crisis. On the other hand, where there had been free grazing, the implementation of management strategies to reduce the negative effects of over-consumption of this shrub by livestock is fundamental.

Key Words: forage, chamizo, fourwing saltbush, grazing, exclusion

GRADUATE STUDENT COMPETITION: ADSA DAIRY FOODS DIVISION POSTER COMPETITION

1129 (M112) The effect of native phospholipids on the flavor and flavor stability of bleached cheddar whey. C. Park*, and M. Drake, *Southeast Dairy Foods Research Center, NCSU, Raleigh, NC.*

Off-flavors due to processing of whey protein ingredients negatively influence consumer acceptance of ingredient applications. Previous research has demonstrated that bleaching of Cheddar whey increases lipid oxidation and off-flavors in liquid whey and resulting whey protein ingredients. Due to the high content of unsaturated fatty acids, native phospholipids have a high potential for lipid oxidation. The phospholipid to neutral lipid content ratio in fat free milk is reported to be significantly higher than in whole milk. The objective of this study was to determine the impact that native phospholipids in Cheddar whey have on the flavor and flavor stability of liquid whey. Liquid Cheddar whey was produced from whole milk, reduced fat milk, and fat free milk. The wheys were then fat separated to the same total fat content, pasteurized, bleached (250 ppm hydrogen peroxide) and stored at 4°C for up to 48 h. The wheys were sampled at 0 h, 24 h, and 48 h. The entire experiment was replicated 3 times. Flavor was analyzed by sensory and instrumental analyses. Phospholipids were quantified by UHPLC with an evaporative light scattering detector using hydrophilic interaction chromatography. Fatty acid profiles of the neutral and polar lipids were analyzed by FAME using GC-FID. All wheys increased in the lipid oxidation compounds pentanal, hexanal, heptanal, and nonanal and cardboard flavor from 0 h to 48 h ($P < 0.05$). Liquid whey produced from fat free milk had higher concentrations of hexanal, pentanal, heptanal, and DMTS as well as increased cardboard flavor intensity after 24 or 48 h compared to other wheys ($P < 0.05$). Phospholipids were significantly higher in the whey made from fat free milk compared to wheys made from whole or reduced fat milk ($P < 0.05$). The polar lipid fraction contained higher concentrations of the unsaturated fatty acids 18:1, 18:2, 18:3, and 20:4 and lower concentrations of saturated fatty acids compared to the neutral lipid fraction. These results identify native phospholipids as a major source of off-flavors in liquid whey due to their unsaturated fatty acid profile and susceptibility to lipid oxidation.

Key Words: whey, phospholipids, flavor

1130 (M113) The effect of norbixin destruction or removal on flavor and functionality of 80% whey protein concentrate. Y. Qiu*, T. Smith, A. Foegeding, and M. Drake, *Southeast Dairy Foods Research Center, NCSU, Raleigh, NC.*

The residual annatto colorant (norbixin) in fluid cheddar cheese whey is bleached to provide a neutral-colored final product. Currently, chemical and enzymatic applications are utilized for bleaching liquid whey. These approaches bleach by free radical formation and can cause off-flavors due to lipid oxidation and protein degradation. The objective of this study was to compare three bleaching/norbixin removal methods: hydrogen peroxide (HP), lactoperoxidase (LP), and microfiltration (MF), and their effects on the flavor and functionality of 80% whey protein concentrate (WPC80). Cheddar cheese whey was manufactured from colored, pasteurized milk. The fluid whey was pasteurized and fat separated. Whey was subjected to 1 of 4 different treatments: Control (no bleaching; 50°C, 1h), HP (250 mg hydrogen peroxide/kg; 50°C, 1h), LP (20 mg hydrogen peroxide/kg; 50°C, 1h), or MF (microfiltration; 50°C, 1h). The treated whey was then ultrafiltered, diafiltered, and spray-dried to 80% whey protein concentrate (WPC80). The entire experiment was replicated three times. Proximate analysis, color, functionality, descriptive sensory and instrumental volatile analysis were conducted on WPC80. Norbixin was decreased by 50, 46 and 95% for MF, HP, and LP bleached WPC80 treatments, respectively ($P < 0.05$). The HP and LP WPC80 had higher cardboard flavor and distinct cabbage flavor compared with the unbleached and MF WPC80. Volatile compound results were consistent with sensory results. The HP and LP WPC80 were higher in lipid oxidation compounds (especially heptanal, hexanal, pentanal, 1-hexen-3-one, 2-pentylfuran, octanal) compared to unbleached and MF WPC80. Protein solubility of WPC80 at various pH values was not different ($P > 0.05$). All WPC80 had > 85% solubility at the pH range evaluated. Gelation under all conditions showed similar trends in small strain viscoelastic properties ($P > 0.05$). Based on bleaching efficacy, flavor and functionality results, MF may be a viable alternative to chemical or enzymatic bleaching of fluid whey.

Key Words: whey bleaching, functionality, flavor

1131 (M114) Storage and temperature effects on the solubility, Maillard browning, and sensory characteristics of milk protein concentrates. T. Smith*, R. Campbell, and M. Drake, *Southeast Dairy Foods Research Center, NCSU, Raleigh, NC.*

Milk protein concentrates (MPC) are a relatively young, increasingly important category of dairy ingredients. MPC production in the US increased by 38% between 2008 and 2012. MPC are a highly functional protein, however, solubility and a mild flavor across storage are required for success. The ob-

jective of this study was to determine the effect of storage time and temperature on the solubility, sensory characteristics, and Maillard browning of low (45%) and high (80%) protein MPC. MPC45 and 80 were manufactured in triplicate and stored at low (4ºC), medium (25ºC) and high (40ºC) temperatures for 0, 1, 3, 6, and 12 mo. Solubility was evaluated by measurement of turbidity and protein at pH 7 before and after centrifugation. Maillard browning was determined by measuring furosine levels by high performance liquid chromatography (HPLC). Descriptive analysis and gas chromatography-mass spectrometry (GC-MS) were also performed to evaluate sensory and volatile compound characteristics. Solubility of MPC45 was higher than MPC80 ($P < 0.05$), and a significant decrease in solubility in both MPC 45 and 80 occurred over time and as temperature increased ($P < 0.05$). Furosine increased with storage time and temperature, and this change was higher for MPC80 than for MPC45 ($P < 0.05$). MPC45 were characterized by sweet aromatic/milky and cardboard flavors while MPC 80 were characterized by lower sweet aromatic/milky and higher cardboard flavors, as well as distinct tortilla/grapey flavor. Cardboard, tortilla/grapey and animal flavors increased with storage time and temperature ($P < 0.05$). Key volatile flavor compounds in MPC were o,p,m 2-amino-acetophenone (tortilla), 2 2-methyl-butanal (green/fruity), 1-octen-3-one (earthy/mushroom), and methional (potato brothy), and concentrations of these compounds increased with storage time and temperature. An understanding of storage and environmental effects on MPC lays the foundation for optimizing quality.

Key Words: milk protein, flavor, solubility

1132 (M115) The salt, pH and thermotolerance of a novel nonstarter lactic acid bacterium that might be associated with slit defect in ripened cheddar cheese. F. Ortakci[*1], J. R. Broadbent[1], C. J. Oberg[1,2], and D. J. McMahon[3], *[1]Dep. of Nutrition, Dietetics, and Food Sciences, Western Dairy Center, Utah State University, Logan, [2]Dep. of Microbiology, Weber State University, Ogden, UT, [3]Western Dairy Center, Utah State University, Logan.*

An obligate heterofermentative lactic acid bacteria, *Lactobacillus wasatchii* WDC04 (WDC04), isolated from an aged Cheddar cheese, was studied for salt, pH and thermotolerance. We investigated the pH and salt tolerance of WDC04 in MRS+1.5% Ribose (MRS-R) under conditions that mimic Cheddar cheese ripening. In addition, the thermotolerance of WDC04 was tested in 2% milk to estimate its pasteurization tolerance. WDC04 was inoculated in MRS-R at two different pH levels (5.2 or 6.5), each containing 0, 1, 2, 3, 4, or 5% salt-in-moisture (S/M) levels (w/w). Growth was monitored by OD_{600} measurements every 8 h under anaerobic conditions at 23°C for 60 h. After 48 h, an OD_{600} of 2.0 was reached in all media except for 5% S/M at pH 5.2 which had an OD_{600} of 1.75. At pH 6.5, WDC04 growth rates were similar at S/M levels of 0, 1, 2, and 3% after 24 hr. Growth rates for 0, 1, and 2% S/M levels at pH 5.2 after 24 h were also similar, while growth rates at S/M levels of 4, and 5% at either pH were slower. Two different thermotolerance tests were performed. Milks containing ~$7x10^6$ CFU/ml WDC04, was heated at 72°C for 15 s followed by a cooling by placing in a water bath at 31°C (set temperature for cheesemaking) for 2 h. In the second heat treatment, WDC04 inoculated milks were heated at 63°C for 30 min with samples collected at 0, 15 and 30 min intervals followed by incubation at 31°C for 2 h. Samples were plated on MRS-R agar in triplicate. There was a 4-log reduction of WDC04 after the 72°C for 15 s heat treatment with $9.2x10^1$ CFU/ml after cooling to 31°C. However, there were no detectable colonies (<10^2CFU/ml) when heated for 30 min at 63°C. This suggests that WDC04 is maybe sufficiently thermoduric for some cells to survive HTST pasteurization but perhaps not LTLT pasteurization. It also appears that WDC04 is able to grow in the same environment that occurs during Cheddar cheese ripening, high S/M (2.5 to 4.5%) and low pH. The ability to survive pasteurization and grow under cheese ripening conditions allow WDC04 to be considered a NSLAB, placing it in a position to be involved with late gas production and slit defect in ripened Cheddar cheese.

Key Words: nonstarter lactic acid bacteria, salt, pH, and thermotolerance

---

1133 (M116) Role of protein interactions on microstructure and rheological properties of Greek-style yogurt. G. H. Meletharayil[*1], H. A. Patel[2], and S. G. Sutariya[1], *[1]South Dakota State University, Brookings, [2]Dairy Science Dep., South Dakota State University, Brookings.*

Disposal of acid whey is a major concern for the manufactures of Greek-style yogurt (GSY) because of its potential environmental impact. An alternate way of preparing GSY is to eliminate de-wheying step by using functional milk proteins and manipulating process-induced protein interactions. The objective of this study was to investigate the influence of micellar and non-micellar casein to globular proteins ratios on the properties of GSY prepared using this alternate process. GSY (7.5% w/w proteins, 15% w/w total solids) were prepared with either milk protein concentrates (MPC) as a source of micellar casein or carbon-dioxide treated milk protein concentrate (T-MPC) as a source of non-micellar caseins. Whey protein concentrates (WPC) and de-proteinized whey was used to adjust the globular protein and total solids level respectively. The casein to whey ratio was adjusted to 4:1, 2.3:1 and 1.5:1. All samples were pre-adjusted to pH 6.5 before heating at 90°C/10 min. Acid gels were prepared using Glucono-δ-lactone to obtain final pH 4.4 after 4 h of incubation at 30°C. The soluble (serum) phases obtained by centrifugation of heated and unheated milk samples at 25,000g/1h were characterized using sodium dodecyl

sulfate polyacrylamide gel electrophoresis (SDS-PAGE). Microstructure and rheological characterization of acid gels were performed using confocal laser scanning microscopy (CLSM) in the fluorescence mode and small amplitude oscillatory rheology (1% strain, 0.1Hz frequency), respectively. ANOVA was used to test the results and statistical significance at $P < 0.05$ was determined, using the statistical software SAS. SDS-PAGE results indicated significantly higher proportion ($P < 0.05$) of soluble disulfide-linked aggregates in serum phase of heated milks prepared from T-MPC. Gels prepared using T-MPC as a source of non-micellar casein had significantly higher ($P < 0.05$) elastic modulus (G') (e.g., 1.12 x 10^3 Pa) compared to gels prepared using MPC (e.g., 6.59 x 10^2 Pa). Acid gels containing T-MPC in different ratios with globular proteins had a significantly higher ($P < 0.05$) G' than acid gels prepared with MPC and WPC. CLSM images revealed that T-MPC gels had smaller, well-connected aggregates with uniform, homogenous pore sizes, which strongly supported the results of rheological characterization. It can be concluded that T-MPC as a source of non-micellar casein is an ideal ingredient to alter the ratio of non-micellar to globular protein ratio and thereby increase the gel strength of Greek-style yogurts. This invention is patent pending and can be used to produce protein structures having different gels strengths suitable for commercial applications.

Key Words: Greek-style yogurt, carbon dioxide, rheology

1134 (M117) Assessment of consumer perceptions and preferences regarding fluid milk at the beginning and end of printed code date. M. E. Paterson*, *Iowa State University, Ame.s*

The objective of this study is to understand consumers' expectations and actual sensory perceptions about fluid milk at the beginning and end of code. Eleven sessions were carried out ($n = 103$). Sessions began with explanation of consent form and the experiment process, then panelists filled out a survey about demographics and milk purchasing and consumption behaviors. Consumers were blindly served two pairs of milk samples (2% within 2 to 3 days of production (fresh) and 2% with 2 to 3 days to end of code (end); skim (fresh and end) and asked to indicate preference and the level of acceptability for each sample using a seven-point scale. All samples tasted by consumers were simultaneously evaluated by a panel of eight judges who were trained to evaluate milk quality attributes on a 15-cm line scale. All milk was from the same source, processed on the same timeline for each session; milk was stored in the warehouse until transport to the sessions. Eighty-five participants (82%) indicated they check for the farthest out code date more than half the time they shop. However, upon tasting, consumers did not have a preference for 2% fresh milk over 2% end, or for skim fresh over skim end ($P > 0.05$). These findings were in agreement with their acceptability scores, which were 4.7 for skim fresh, 4.6 for skim end, 5.1 for 2% fresh and 5.1 for 2% end ($P > 0.05$). Trained panelists did not detect a difference in lacks freshness flavor in skim fresh (1.9 cm) or skim end (1.3 cm). Trained panelists also did not detect a difference in cooked, feed, flat, foreign or oxidized flavors for 2% or skim milk samples. Trained panelists detected a significant difference in lacks freshness flavor of 2% fresh (2.3 cm) and 2% end (0.3 cm) ($P < 0.05$). When the one off-flavored batch of 2% fresh milk was removed from analysis, trained panelists could not distinguish a difference in lacks freshness between 2% fresh (1.0 cm) and 2% end (0.4cm) ($P > 0.05$). After tasting and receiving an educational message about the meaning of code dates, 83% of consumers stated the information would impact their future purchases. These results confirm that although many consumers go out of their way to buy the freshest milk, they cannot distinguish fresh milk from milk at the end of code. Additional research must be conducted to confirm impact of educational messages about code date on purchasing behavior.

Key Words: milk, sensory, code-date

1135 (M118) Performance of cross-linked and calcium-reduced milk protein concentrate ingredients in model high-protein nutrition bars. J. C. Banach*[1], S. Clark[1], L. Metzger[2], and B. P. Lamsal[1], *[1]Iowa State University, Ames, [2]Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

Milk protein concentrate (MPC) and micellar casein concentrate (MCC) have the potential to be the major protein source in high-protein nutrition bars. However, MPCs are known to produce bars that harden too quickly and also result in a crumbly texture. Less is known about the performance of MCC in bars. The objective of this study was to evaluate the performance of transglutaminase (TGase) cross-linked MPC and MCC, and calcium-reduced MPC in high-protein bars. MPC and MCC retentate were treated with TGase at 0.3 units (low; MPC-L and MCC-L) and 3.0 units (high; MPC-H and MCC-H) per g protein. Controls (MPC-C and MCC-C) were not treated with the enzyme. Separately, CO_2 was injected during MPC ultrafiltration to produce calcium-reduced MPC. Retentates were spray-dried to produce ingredients with 72 to 78% protein. Bars were prepared by hand pressing dough containing 30% protein, 8.9% HFCS, 20.7% glycerol, 11% maltitol syrup, and 17.6% palm oil into molds (ID = 21 mm, H = 13 mm) and water activity sample cups. Model bars were stored at 32°C for up to 42 days, during which texture, color, water activity, moisture content, and pH were evaluated. Bar hardness and fracturability were determined with compression, after which a sieve analysis was used to evaluate crumbliness. Data, separated via Tukey's adjusted p-value ($P < 0.05$), are the average of two bar preparations. On day 0, no statistical difference was detected for fracturability and hardness between bars ($P < 0.05$) and crumbliness reduced when cross-linked ingredients were compared with their respective controls ($P < 0.05$). Throughout storage, bars formulated with a commercially

produced native MPC80 were less crumbly and maintained a larger geometric mean diameter after compression. A high-level of TGase helped maintain cohesiveness in MPC-H and MCC-H compared with their controls through day 16 and day 28, respectively ($P < 0.05$). Sample moisture content on the day of preparation was the same ($P > 0.05$), whereas water activity was different ($P < 0.05$). A significant increase ($P < 0.05$) in water activity was seen ~24 h after preparation, but after the initial increase it remained stable within each batch. Moisture content and pH remained fairly constant during storage, while visual color change was apparent within the samples. TGase treated and calcium-reduced milk protein ingredients have altered performance in high-protein nutrition bars, which potentially could lead to improved commercial feasibility.

Key Words: milk protein concentrate, micellar casein concentrate, protein bar

---

1136 (M119) The effects of post-exercise consumption of a kefir beverage on performance and recovery during intensive endurance training. K. V. O'Brien*, *Louisiana State University, Baton Rouge.*

This study was designed to determine whether kefir accentuates the positive health benefits assessed by measures in fitness and/or body composition, as a measure of cardiovascular disease risk as well as the biomarker c-reactive protein (CRP). Thirty-eight adult males and females aged 18 to 24 yr were assigned to one of four groups: 1) endurance training + control beverage (ETC), 2) endurance training + kefir beverage (ETK), 3) active control + control beverage (ACC) or 4) active control + kefir beverage (ACK). The E groups (ETK and ETC) completed 15 weeks of structured endurance training. The AC groups (ACK and ACC) maintained their usual exercise routine. Additionally, each group was assigned to either a kefir (ETK and ACK) or a calorie/macronutrient matched placebo (ETC and ACC) beverage that was consumed twice per week. The kefir beverage and the control beverage were developed and manufactured in the Louisiana State University Creamery and were identical in ingredients used with the only difference being the fermentation of the milk used in the kefir beverage. Pre/post measures included: body mass and composition, waist hip ratio and 1.5 mile run. Serum CRP was measured using an ELISA (Alpco Diagnostics, Salem, NH). A MANOVA was used to identify significant interactions and significance was set at $P < 0.05$. RESULTS: There was a significant time x training group interaction ($P = 0.0124$) with the E groups (ETK and ETC) experiencing an average of 4.11% improvement in 1.5 mile time. There were no significance interactions among groups with respect to all other outcome variable with the exception of serum CRP. Serum CRP increased over time ($P = 0.103$). However, there was also a trend for a time x kefir effect($P = 0.0778$). The ETK and ACK groups experienced less (21.18%, 5.45%) of an increase when compared to the ETC and ACC (22.36%, 64.71%). The endurance training was effective in improving 1.5 mile times and kefir supplementation may have been a factor in attenuating the increase in CRP that was observed over the course of the intervention period. This preliminary study suggests that kefir may be involved in improving the risk profile for cardiovascular disease as defined by CRP.

Key Words: kefir, endurance training, cardiovascular disease

1137 (M120) Manufacture of high protein yogurts with low-Ca MPC. A. Kommineni*[1], C. Marella[2], A. C. Biswas[1], and L. Metzger[3], *[1]Dairy Science Dep., South Dakota State University, Brookings, [2]Dairy Science Dep., California Polytechnic State University, San Luis Obispo, [3]Midwest Dairy Foods Research Center, South Dakota State University, Brookings.*

The purpose of this study was to evaluate and compare the effects of high protein yogurt produced with calcium reduced milk protein concentrate (low-Ca-MPC) and regular milk protein concentrate (MPC). The yogurt properties studied were viscosity, syneresis and quantity of acidifying agent required for the yogurt. Reduced Ca MPC was manufactured from ultra and dia-filtration process of skim milk that was injected with CO2 prior to and during the ultra-filtration process. Three different high protein yogurt formulations containing 8% protein were prepared with regular MPC (T-1), low-Ca-MPC with the pH neutralized to 6.7 (T-2) and low-C-MPC at pH 5.9 (T-3). The MPC was the primary source of protein contributing approximately 97% in the all the formulations and the remaining 3% was coming from de-proteinized whey which was used for balancing the lactose content of each formula. All three treatments were manufactured in triplicate from three replicates of low-Ca MPC and regular MPC. Each yogurt formulation was heat treated to 93°C, held for 6 min and then cooled to 45°C. The formulations were then acidified with Glucono-delta-Lactone (GDL) at 45°C and then incubated for 2 hrs. The amount GDL required to reach a pH of 4.6 for 30g of yogurt was 0.7g, 0.6g and 0.55g respectively for T-1, T-2 and T-3. The T-3 yogurt formulation required 21% less GDL to reach the same pH due to the lower initial pH of the T-3 formulation. The T-2 yogurt formulation also used 14% less GDL than T-1 even though the initial pH of both the formulations was same. The undisturbed low-C yogurt formulations (T-2 & T-3) had approximately 40% higher viscosity than the control T-1 formulations. However after stirring all yogurt formulations had similar viscosities. The control yogurt formulation T-1 also had 10% higher syneresis than T-2 and T-3 yougurts. These results indicate that, the use of low-Ca MPC reduces both syneresis and amount of acid required to ferment yogurt.

Key Words: low-Ca MPC, calcium, yogurt, MPC

1138 (M121) Effect of titanium dioxide, annatto, and homogenisation on the translucency of reduced-fat cheddar cheese. R. A. Ibanez[*1,2] and P. L. H. McSweeney[1], [1]*University College Cork, Ireland,* [2]*University of Wisconsin–Madison, Madison.*

The appearance of cheese is greatly influenced by its composition. Low fat content is usually related to an increase in translucency. Many alternatives have been proposed to modify translucency of cheese, such as the addition of ingredients or through the modification of manufacturing protocols. Colorimetric methods have been used extensively to determine the degree of translucency. The Kubelka-Munk index (K/S) measures the relationship between the reflectance of a thin layer of sample above black and white backgrounds, which indicates the reflectance of a sample of infinite thickness. A method based on the measurement of L* values and the application of K/S was proposed to investigate the effect of titanium dioxide, annatto and homogenisation on the translucency of reduced-fat Cheddar cheese during ripening. Three reduced-fat Cheddar cheeses were manufactured in parallel experiments. For titanium dioxide, levels of 0, 20 or 40 g of TiO_2/100 kg were added to cheesemilks. For annatto, levels of 0, 8.25 and 16.50 ml/100 kg were added to cheesemilks. Cheesemilks were also homogenised at 0, 10 or 20 MPa, using a two stage homogeniser (4:1 ratio) at 40°C. L* values and K/S were obtained with a colorimeter at 20°C for all experimental cheeses during six months of ripening. A high correlation was observed between K/S and L* values (r>0.90). Titanium dioxide, annatto and homogenisation significantly ($P < 0.05$) modified K/S values compared to the control. Ripening significantly increased translucency (i.e., reduced K/S) for all treatments ($P < 0.05$). An increase in K/S was observed when TiO_2 was added ($P < 0.05$). A reduction of the K/S value was observed following addition of annatto ($P < 0.05$). An increase of K/S was observed when milk was homogenised ($P < 0.05$). However, no differences in K/S values were found between homogenisation pressures of 10 and 20 MPa. These results suggest that K/S is a useful tool to determine changes in the translucency of Cheddar cheese. Addition of titanium dioxide and homogenisation reduced translucency. On the other hand, the use of annatto increased translucency in experimental cheeses.

Key Words: translucency, L* value, Kubelka-Munk

GRADUATE STUDENT COMPETITION: ADSA PRODUCTION, MS

1139 (M122) Effects of supplemental garlic (*Allium sativum*) powder and probiotics on diarrhea and immunoglobulin response in pre-weaned dairy calves. T. W. Kekana*, *University of Venda, Thohoyandou, South Africa.*

This study was carried out to investigate the effects of feeding Garlic powder or Probiotics or both on diarrhoeal incidence and immunoglobulin response of pre-weaned Holstein calves. Sixteen Holstein calves (BW = 34.5 ± 1.65 kg) were randomly assigned at birth to 4 treatments to evaluate the effects of garlic powder or probiotics, or both on feed intake, diarrhea, serum glucose and immunoglobulin (IgG) in Holstein calves. The treatments were: C (control, no additive); G: supplemented with 5g/d garlic powder; P: supplemented with 4 g/d probiotics (total viable count: 1.3 x 107 cfu/g) and G+P: supplemented with 5 g/d garlic powder and 4 g/d probiotic. Calves were given colostrum for the first 3 d of life followed by a standard whole milk feeding until weaning at 42 days. A commercial calf starter was offered ad libitum starting at 4 d of age until the end of the study. Fresh water was available throughout the study. Intake of whole milk and starter feed were measured daily and body weights were taken weekly. Blood samples were collected to determine glucose and IgG concentrations. Garlic and probiotics were diluted in milk and fed daily from day 4. Starter DMI tended to be higher ($P < 0.10$) in G+P calves compared to Control calves. Calves fed G and G+P had higher ($P < 0.05$) IgG than C and P calves (28.0 and 27.5 vs. 23.5 and 25.5 g/l: respectively). Calves fed C and G had lower ($P < 0.05$) final BW (56.0 kg) compared to G+P (60.3 kg). Garlic, P and their combination (G+P) did not affect ($P > 0.05$) serum glucose and body temperature. Calves in G+P and P groups had lower ($P < 0.05$) fecal score, days of diarrhea and days fed electrolytes compared to C and G calves. The results suggest complementary effects of the combined garlic powder and probiotics when fed to calves during the first 42 days of life. Improved starter feed intake and final body weight in group G+P suggest high concentrations of ruminal volatile fatty acid for a stimulated rumen development. Additionally, higher serum IgG in G+P may indicate an improved intake of nutrients responsible of immunity modulation and regulation.

Key Words: garlic powder, probiotics, IgG, Holstein calves

1140 (M123) Development of an application for touch-screen devises to capture defined calving-related events in dairy herds. A. A. Barragan*, J. D. Workman, and G. M. Schuenemann, *Dep. of Veterinary Preventive Medicine, Ohio State University, Columbus.*

Calving-related losses (survival, health, and productivity) and welfare practices have become known challenges for the dairy industry worldwide. Furthermore, management practices have been associated with this problem. It is common to observe large within- and between-herd variation in recording calving-related events and personnel performance (*P*P) over time. Successful identification of factors affecting stillbirth and personnel performance at the herd level can be challenging due to their multi-factorial nature. The objective was to assess a user-friendly mobile application (APP) for touch screen devises to aid in decision-making about calving-related events in dairy herds. The APP was developed to capture, identify, and rank risk factors (e.g., dystocia, PP, work shift transition, BCS, colostrum management) affecting stillbirth according to their contribution weights. Novel components of the APP included: 1) Login screen for individual herds, 2) Capture of selected calving-related events for both dam and calf (e.g., parity, breed, BCS, hygiene of perineum, calving ease, sex of calf, presentation, personnel), 3) Rolling list of active cows with an alarm to monitor calving progress and time in labor, 4) Rolling list of active calves (single or multiple) within 24 h after birth, 5) Colostrum management practices (quality, quantity, time of administration, calf vigor, birth weights, and personnel), and 6) Connectivity to dashboard to process data in real time. Using data from dairy herds, the APP accurately captured (100%) and integrated multiple calving-related events with PP (accounting for the effect of work shift transition), and ranked within-herd risk factors for stillbirth due to herd management. Dairymen, consultants, and veterinarians often trouble-shoot stillbirth within-herd; however, the lack of meaningful records using defined events makes it difficult to implement corrective practices. Comprehensive assessment of several events occurring in real time around-the-clock will likely reduce calving-related losses (stillbirth) while improving herd productivity and welfare.

Key Words: app, calving management, dairy

1141 (M124) Effects of dietary crude protein levels during a twelve-week period on late-lactation dairy cow performance. M. A. Quaassdorff*[1], T. Barros[1], J. J. Olmos Colmenero[2], M. J. Aguerre[1], S. J. Bertics[1], and M. A. Wattiaux[1], *[1]University of Wisconsin–Madison, Madison, [2]University of Guadalajara, Tepatilan, México.*

The objectives were to determine the effects of feeding four dietary CP levels on late-lactation dairy cow performance, and whether there were any treatment by week interactions. One

hundred twenty-eight late-lactation Holstein cows (736 ± 18 kg BW; 224 ± 54 DIM) were used in a 16-pen study with 8 cows per pen, and fed a TMR once per day for 12 weeks (*P*en = experimental unit). Treatments which included diets characterized by 11.8, 13.1, 14.6, or 16.2% CP (DM basis) were randomly allocated to pen for the entirety of the experiment. Rations consisted of approximately 67% forage (half corn silage; half alfalfa silage); and soy hulls (SH) replaced soybean meal (SBM) to achieve the desired dietary CP levels for each treatment. Pen-level data presented were covariate-adjusted and included DMI, milk yield (MY) and composition (biweekly), BW (final minus initial), and body condition score (BCS); (every 3 wk). There was no treatment by week interaction for any variables except MY ($P < 0.01$) and true protein % ($P < 0.01$), but there was a linear effect on DMI, MY, true protein %, fat yield (FY) and true protein yield (PY). No measured variables differed between treatments 14.6 and 16.2% CP except for true protein %. DMI, MY, FY and PY were lower on treatment 11.8% than other treatments. There was a quadratic effect ($P < 0.01$) for BW change, with the highest BW gain observed on the 14.6% CP treatment, but there was no difference in BCS. Results suggest that there was essentially no difference in late-lactation cow performance when diets of 14.6 or 16.2% CP were fed.

Key Words: soy hulls, soybean meal, protein nutrition

Table 1141.

	Dietary CP% (DM basis)					*P*-value[1]	
Item	11.8	13.1	14.6	16.2	SEM	L	Q
DM intake, kg/d	22.7[b]	24.0[a]	24.0[a]	24.4[a]	0.28	<0.01	0.09
Milk, kg/d	25.2[c]	28.6[b]	31.0[a]	31.3[a]	0.76	<0.01	0.06
Milk composition							
Fat, %		4.32	4.11	4.27	0.07	0.23	0.24
True protein, %	3.34[c]	3.51[ab]	3.45[b]	3.57[a]	0.03	<0.01	0.22
Milk components yield							
Fat, kg/d	1.09[b]	1.24[a]	1.28[a]	1.31[a]	0.04	<0.01	0.17
True protein, kg/d	0.82[c]	0.98[b]	1.06[a]	1.12[a]	0.02	<0.01	0.07
BW change, kg/d	0.07[cb]	0.37[ab]	0.44[a]	0.27[ab]	0.08	0.10	0.01
BCS[2]	3.17	3.31	3.28	3.27	0.05	0.15	0.07

[a-c] Least squares means within the same row with different superscripts differ ($P \leq 0.05$).
[1] Linear (L) or quadratic (Q) effect of CP% level in the diet.
[2] BCS on scale of 1 (emaciated) to 5 (obese).

1142 (M125) Patterns of circulating serotonin (5-HT), calcium, and glucose in lactating Jersey and Holstein dairy cows. S. A. E. Moore*, J. Laporta, and L. L. Hernandez, *University of Wisconsin-Madison, Madison.*

Dairy cows are challenged to maintain calcium (Ca) and glucose homeostasis during the transition period. Serotonin (5-HT) is a monoamine, which modulates Ca and glucose homeostasis in rodents. Serotonin was positively correlated with Ca and glucose status in dairy cows on d1 of lactation. However, the pattern of circulating concentrations of 5-HT over the course of a 305-d lactation is unknown. In this longitudinal study, we examined the metabolite patterns of 5-HT, Ca, and glucose on two commercial dairy farms in southcentral, Wisconsin. Cows sampled on farm 1 were multiparous Jersey cows ($n = 30$, avg lact = 3.2), which calved within a 23d period and on farm 2 were multiparous Holstein cows ($n = 35$, avg lact = 2.8), which calved within a 20-d period. Blood samples were collected daily during the transition period (d-5 through d10 relative to parturition) and on d30, 60, 90, 150, and 300. Data was analyzed using PROC MIXED and correlations were estimated using PROC CORR in SAS. Overall, there was a time effect ($P < 0.0001$) and a farm and time interaction ($P < 0.0003$). Near parturition, 5-HT decreased as compared to pre-partum by 57.8% ($P < 0.0001$) and 29.6% ($P = 0.056$) on farm 1 and farm 2, respectively. Transition period 5-HT nadir was observed at d2 on farm 1 (879 ± 215 ng/ml), and d1 on farm 2 (1064 ± 186 ng/ml). Serotonin was recovered to 1637 ± 211 ng/ml by d5 on farm 1, with a second decrease of 25.8% ($P = 0.11$) on d7. Farm 2 showed a 5-HT recovery to 1577 ± 184 ng/ml by d5 and subsequent decrease of 34.7% ($P = 0.02$) by d9. Furthermore, 5-HT increased markedly on both farms near peak lactation (d60, 90, 150) and decreased at d300. Calcium decreased compared to pre-partum levels by 35.3% ($P < 0.0001$) and 10.9% ($P < 0.0001$) on farm 1 and 2, respectively. Calcium nadir was observed at d1 on farm 1 (1.79 ± 0.06 mmol) and farm 2 (2.29 ± 0.06 mmol). Serotonin and Ca were positively correlated on farm 1 ($r = 0.24$; $P < 0.0001$) and farm 2 ($r=0.15$; $P = 0.0003$). No significant correlation was detected between 5-HT and glucose. These results show that 5-HT concentrations change dynamically through the transition period and this change is positively correlated with circulating Ca patterns. Further research should be aimed at discerning how 5-HT affects Ca in different dairy breeds.

Key Words: calcium, serotonin, transition period

1143 (M126) Ruminal degradability and intestinal digestibility of protein and amino acids in canola meal. N. Jayasinghe*, K. F. Kalscheur, J. L. Anderson, and D. P. Casper, *Dairy Science Dep., South Dakota State University, Brookings.*

Differences in processing by different plants may result in canola meal (CM) with varying nutritional composition. The Dairy NRC (2001) estimated CM to be 35.7% rumen undegradable protein (RUP) with an intestinal digestibility of 75% when DMI was set at 4% of BW. Seven CM samples were obtained from different processing plants and 1 soybean meal (SBM) to evaluate the variability in ruminal degradability and intestinal digestibility of CP. Dacron bags containing 5 g of each feed were incubated in the rumen in duplicate for 0, 2, 4, 8, 12, 16, 24 and 48 h using three ruminally cannulated lactating cows. The rate of passage was calculated at 6.6%/h. The A fraction (rapidly degradable CP) varied from 26.6% to

Table 1143.

Item[2]	Feeds[1]								SEM
	SBM	CM5	CM6	CM7	CM9	CM10	CM11	CM12	
A, %	23.0^{c}	17.8^{b}	21.7^{bc}	26.4^{c}	24.8^{c}	26.6^{a}	25.1^{a}	23.1^{ab}	1.18
B, %	76.5^{ab}	79.9^{a}	76.8^{ab}	66.3^{cd}	69.8^{bcd}	69.6^{bcd}	72.6^{abc}	62.4^{d}	1.84
C, %	0.6^{b}	2.3^{b}	1.5^{b}	7.4^{b}	5.4^{b}	3.8^{b}	2.3^{b}	14.6^{a}	1.42
Kd, % h	11.1^{a}	5.6^{bc}	5.2^{c}	9.1^{ab}	4.6^{c}	9.7^{ab}	6.2^{bc}	4.0^{c}	1.32
RUP, % of CP	31.0^{d}	46.1^{b}	44.8^{b}	35.4^{cd}	46.6^{b}	32.3^{d}	40.8^{bc}	53.8^{a}	2.05
IDP, %	94.5^{a}	76.8^{bc}	75.8^{bcd}	72.0^{de}	77.4^{b}	71.6^{e}	75.3^{bcde}	73.0^{cde}	2.50
TDP, %	98.2^{a}	89.3^{bc}	89.1^{c}	90.1^{bc}	89.4^{bc}	90.8^{b}	89.3^{bc}	85.1^{d}	0.73

[a-c] Means in rows with different superscripts differ significantly ($P < 0.05$)

17.8%, respectively, for CM10 and CM5 ($P < 0.05$). The B fraction (slowly degradable CP) was highest for CM5 (79.9%) and lowest for CM12 (62.4%), whereas the C fraction (undegradable CP) was highest for CM12 (14.6%) and lowest for SBM (0.6%). The rate of degradation of B fraction, Kd (%/h) was highest for SBM (11.1%/h) and lowest for CM12 (4.0%/h). The RUP (% of CP) was highest for CM12 (53.8%), whereas lowest for SBM (31.0%), while the IDP (measured by pepsin-pancreatin digestion) ranged from 94.5% for SBM to 71.6% for CM10. The total digestible protein (TDP) was highest for SBM (98.2%) and CM ranged from 85.1% to 90.8% for CM12 and CM10 ($P < 0.01$), respectively. The mean ruminal and intestinal digestibilities of CM are in agreement with NRC, however considerable variation exists between CM processing plants.

Key Words: canola meal, rumen degradability, intestinal digestibility

1144 (M127) Estimate of serum immunoglobulin G concentration in Jersey calves using refractometry. M. M. Spring*[1], K. M. Morrill[2], A. L. Robinson[1], and H. D. Tyler[1], *[1]Iowa State University, Ames, [2]Cornell University, Ithaca, NY.*

Previous data from our lab demonstrated that refractometry could be used to estimate serum IgG in Holstein calves; data suggested that a % Brix cut-point of 7.8 should be used to identify failure of passive transfer in 1 day old Holstein calves. The objective of the present study was to validate the use of refractometry to determine serum IgG concentrations and evaluate failure of passive transfer in Jersey calves. Blood samples (n = 108) were obtained from 1-3 day old Jersey calves and centrifuged at 3,300 x g for 20 minutes at 25°C. The serum was analyzed for %Brix and refractive index (nD) using a digital refractometer and IgG concentration was determined by radial immunodiffusion. The mean serum IgG concentration for all calves was 23.7 mg/ml (SD = 12.2), with a range of 2.2 to 65.0 mg/ml. Mean serum %Brix for all calves was 8.8 (SD = 1.1), with a range of 6.5 to 12.0. Mean serum nD for all calves was 1.34596 (SD = 0.00173), with a range of 1.34280 to 1.35110. Serum %Brix and nD were positively correlated with IgG concentration (r = 0.74 and 0.73 respectively; n = 107). Regression analysis was used to determine cut points for 10, 12, and 14 mg IgG/mL and diagnostic characteristic test characteristics were calculated to determine the sensitivity and specificity of refractometry to identify failure of passive transfer (serum IgG < 10mg/mL at 24 h old). The % Brix were 7.1, 7.3, and 7.6 and the nD cut-points were 1.24332, 1.34271 and 1.3448, respectively. The 7.3% Brix and 1.34271 nD cut-point resulted in the greatest percentage of samples being correctly classified (92.59 and 93.52%, respectively) and the best combination of diagnostic test characteristics. Our data suggest that a digital refractometer is an acceptable, rapid and low cost method to estimate immunoglobulin G in Jersey calf serum but that breed-specific cut points may need to be utilized.

Key Words: passive transfer, refractometer, jersey, validate

1145 (M128) Examination of pre-milking teat disinfectant contact times using the excised teat model. B. D. Enger*, L. K. Fox, J. M. Gay, and K. A. Johnson, *Washington State University, Pullman.*

Use of pre-milking teat disinfectants is a common practice used to aid in the control of mastitis which is the most common and expensive disease in the U.S. dairy industry. Effectiveness of pre-milking teat disinfectants in reducing pathogen load on teat skin is influenced by the duration these disinfectants remain on the teat skin, although this has not been adequately investigated. The objective of this study was to determine the percentage reduction in mastitis pathogen load, four environmental and four opportunistic (n = 8), on teat skin with disinfectant contact times of 15, 30, and 45 sec. Three commercially available disinfectants were tested: 0.25% (A) and 0.5% (B) iodophor, and 1% H_2O_2 (C). Excised teats, collected from an abattoir, were washed, dried, hung from a dowel rod, dipped in 70% isopropyl alcohol and allowed to dry. Once dry, teats were dipped in challenge solution of approximately 10^7 colony forming units/ml of a pathogen. After 5 minutes, teats were dipped with desired disinfectant and rinsed with quench solution upon achieving test contact time. Rinse was serially diluted, plated, incubated for 18-48 hr, and enumerated. Main effect differences were observed within dips, contact times, and

species ($P < 0.0001$). Dip A percentage log reduction across all species was 28% at 15 sec, 35.7% at 30 sec, and 39.2% at 45 sec, SE ± 1.7%. Dip B, percentage log reduction was 36% at 15 sec, 41.2% at 30 sec, and 43.8% at 45 sec, SE ± 1.7%. Dip C, the least efficacious disinfectant, had log reductions of 26% at 15 sec, 25.5% at 30 sec, and 28% at 45 sec, SE ± 1.7%. In summary percentage log reductions across all pathogens and dips at 15, 30, and 45 sec were 30% ± 0.97%, 34% ± 0.97%, and 37% ± 0.96% respectively, all significantly different from one another ($P < 0.05$). The relationship between duration of contact time and percentage log reduction demonstrates the importance of allowing adequate contact time to maximize pathogen reduction and reduce the risk of mastitis.

Key Words: mastitis, teat disinfectant, contact time

1146 (M129) The effects of feeding an algae supplement on milk yield, milk components, and dry matter intake.

M. E. Weatherly*[1], A. M. Gehman[2], A. M. Lisembee[2], J. D. Clark[1], D. L. Ray[1], and J. M. Bewley[1], *[1]University of Kentucky, Lexington, [2]Alltech, Inc., Nicholasville, KY.*

Feeding docosahexaenoic acid (DHA) via algae supplementation could increase milk polyunsaturated fats. The objective of this study, conducted at the University of Kentucky Coldstream Dairy, was to determine the effects of feeding cows *Schizochytrium* sp. Microalgae (SP-1, Alltech, Inc., Nicholasville, KY) on milk fat and DHA content, dry matter intake, and milk yield. Eight multiparous, mid-lactation, Holstein cows were housed in a tie-stall barn and fed a basal ration 2X. Cows were blocked by milk production and DIM and assigned to 1 of 4 treatments: 0, 100, 300, or 600 g of algae per day for 28 d. Milk samples were composited by week and analyzed for fat and DHA composition. Dry matter intake and milk yield were recorded daily and averaged by week. The PROC MIXED of SAS (SAS Institute, Inc., Cary, NC) was used to evaluate fixed effects of week, treatment, and their interactions on milk fat percentage and DHA content (g/d), milk yield (kg/d), and DMI (kg/d), with block within treatment as subject repeated by week. Stepwise backward elimination was used to remove non-significant interactions ($P \geq 0.05$). All main effects were kept in each model regardless of significance level. Week affected milk yield ($P < 0.01$) but treatment did not ($P = 0.30$). Milk yield (mean ± SE) for periods 1 to 4 was 30.44, 29.10, 25.10, and 25.21 ± 4.58 kg, respectively. Treatment and week affected fat percentage ($P = 0.02$). Fat percentage was greater ($P < 0.05$) for cows on treatments 0 and 100 (4.20 and 3.54 ± 0.18%, respectively) than cows on treatments 300 and 600 (2.52 and 2.52 ± 0.18%, respectively). Treatment, week, and the interaction of treatment × week affected DMI ($P < 0.01$, $P < 0.01$, and $P = 0.02$, respectively). Dry matter intake decreased across time across treatments until wk 4. Treatment and the interaction of treatment × wk affected milk DHA ($P = 0.03$ and $P = 0.02$, respectively). DHA content in milk was greater ($P < 0.05$) for cows on treatment 300 and 600 (3.30 and 5.18 ± 0.66 g/d, respectively) than cows on treatment 0 and 100 (0.00 and 0.39 ± 0.66 g/d, respectively). This data suggests supplementing lactating dairy cows with high-DHA microalgae may allow for the incorporation of polyunsaturated fats, including DHA, into milk; however, decreases in milk fat percentage and DMI may limit on-farm application.

Key Words: algae, milk fat, DHA

1147 (M130) Rumen morphology measurements in periruminant Holstein bull calves fed a fermentation extract of *Aspergillus oryzae*.

T. T. Yohe*, E. M. Dudash, K. M. O'Diam, and K. M. Daniels, *Dep. of Animal Sciences, Ohio State University, Wooster.*

Age and diet not only affect calf BW, they can impact rumen growth and development too. A fermentation extract of *Aspergillus oryzae* has previously been utilized as a direct fed microbial (DFM) to increase rumen bacterial numbers and promote starter intake in calves. Effects of feeding an extract of *A. oryzae* on rumen morphology in periruminant calves are largely unknown. Objectives were to determine if age and dietary inclusion of an extract of *A. oryzae* affect: organ size, muscle and sub-mucosal thickness of rumen tissue, and papillae area in periruminant Holstein bull calves. Individual calves ($n = 52$) were randomly assigned to a slaughter age, 4 wk ($n = 16$) or 8 wk ($n = 36$), and treatment, control (CON**;** $n = 27$) or DFM **(**n = 25). Calves were housed and fed individually; no bedding was used. Liquid DFM was delivered in milk replacer (2 g per day) for the first 4 wk of the trial; solid DFM (2 g per day) was top-dressed on grain thereafter. Calves were fed non-medicated milk replacer twice daily (22.0% CP, 20.0% fat DM basis; 680 g/d) and had ad libitum access to texturized grain (20% CP, 2.0% fat) and water. Treatment and the interaction of treatment and age did not affect full or empty rumen weights. However, full and empty rumen weights were greater at 8wk (5.29 ± 0.21and 1.31 ± 0.04 kg, respectively) than 4 wk (1.81 ± 0.30 and 0.52 ± 0.06 kg, respectively). Muscle thickness (894.15 ± 69.50 μm, 4 wk; 1098.58 ± 47.64 μm, 8wk) and sub-mucosal thickness (247.57 ± 43.48 μm, 4 wk; 583.67 ± 29.80 μm, 8 wk) were both affected by age, but not by treatment or interaction. Lastly, within the cranial ventral region of the rumen of 8-wk-old calves (4-wk samples not measureable), treatment had no effect on papillae area (6.52 ± 0.39 mm^2, CON; 6.65 ± 0.41 mm^2 DFM). In summary, dietary inclusion (2g/d) of an extract of *A. oryzae*did not affect rumen morphological development when supplemented animals were compared to cohorts not fed DFM. It is possible that the dose used here was not high enough to elicit treatment effects. Evaluation of other measures of performance, such as calf growth, may add further information on the efficacy of this DFM in periruminant calf diets. A higher dose of DFM may yield different effects.

Key Words: dairy calf, rumen, direct fed microbial

1148 (M131) Response of dairy cows supplemented with antioxidants and/or chelated trace minerals to intra-mammary bacterial challenge.

R. O. Rodrigues*[1], M. O. Caldeira[1], G. I. Zanton[2], and M. R. Waldron[1,3], [1]*University of Missouri, Columbia,* [2]*Novus International, Inc., St. Charles, MO,* [3]*Nutrition Professionals, Inc., Chilton, WI.*

The effects of chelated trace minerals (TM) of Zn, Cu, and Mn (Minitrex, Novus International, St. Charles, MO) and dietary antioxidant (Agrado Plus, Novus International) supplementation on responses to experimental mastitis in lactating cows were evaluated. Sixty cows were blocked by parity, expected date of parturition, and initial BW. Cows were individually fed a basal diet formulated according to NRC (2001) from d -39.3 ± 4.6 prepartum until d 38 postpartum. Treatments were top-dressed as: 1) Negative control – no TM nor antioxidant (NEG), 2) TM provided with 100% sulfates without antioxidant (ITM), 3) TM provided with 100% sulfates with antioxidant (ITMAOX), 4) TM provided 50% of sulfates and 50% of chelated TM without antioxidant (OTM), and 5) TM provided 50% of sulfates and 50% of chelated TM with antioxidant (OTMAOX). Treatments were iso-mineral except NEG; all were iso-methionine. Animals were vaccinated against *Escherichia coli* (Enviracor J-5, Pfizer Animal Health) at drying-off, -27.3 ± 4.6, and 14 d from parturition, and against rabies (IMRAB, Merial) at parturition. On d28 after calving, the right front quarter of each animal was infused with 1.74 x 10^4 CFU of *E. coli* P4:O32 diluted in 5 mL of sterile PBS and the contralateral quarter with the same volume of sterile PBS. Blood and milk samples were collected regularly during the experiment. Primiparous had higher rabies titers concentrations on d14 compared to multiparous cows, but no difference between parities on d28 (parity x time, $P < 0.001$). OTMAOX showed the highest rabies titer concentrations compared to other treatments on d14 (treatment x time, $P = 0.04$). Higher milk yield was observed for the first 3 days post-infusion in primiparous compared to multiparous cows (parity x time, $P < 0.05$). *Escherichia coli* CFU were higher in infected quarters of multiparous cows (parity x quarter, $P = 0.03$). Milk SCC were higher in AOX and OTMAOX in response to challenge than in other treatments (treatment, $P = 0.01$). Additionally, SCC in primiparous peaked earlier and higher compared to multiparous cows (Parity x time, $P = 0.004$). Blood GSH:GSSG peaked at 48 h post-infusion ($P = 0.01$). Blood GSH:GSSG in OTMAOX was highest in primiparous, but lowest in multiparous cows ($P < 0.05$). Antibody titer and SCC recruitment results suggest OTMAOX may have improved some aspects of peripartal immune function. Additionally, the earlier and elevated milk SCC in primiparous cows may have limited the severity of *E. coli* infection, thereby allowing for increased DMI and milk production.

Key Words: *Escherichia coli*, mastitis, supplementation

GRADUATE STUDENT COMPETITION: **ADSA PRODUCTION, PhD**

1149 (M132) Effect of feeding diets with different type of carbohydrates on dry matter intake, rumen fermentation, and productivity of lactating dairy cows. X. Gao*, J. Mewis, and M. Oba, *University of Alberta, Edmonton, Canada.*

The objective of this study was to investigate the effect of feeding different types of carbohydrates on DMI, rumen fermentation, and milk production of lactating dairy cows. Our hypotheses were that both high sugar and high starch diets will decrease rumen pH compared to a basal diet, but a high sugar diet has higher DMI and milk fat yield than a high starch diet. Six ruminally cannulated peak-lactating dairy cows (DIM = 75 ± 12.2; BW = 630 ± 59.2 kg) were used in a replicated 3 × 3 Latin square design with 21-d periods. Cows were fed diets consisting of 35.5% barley silage and 64.5% concentrate mix on a DM basis. Control diet (CON) contained 27% starch, 4% sugar and 28% NDF, high starch diet (STA) supplemented with additional steam-rolled barley grain contained 32% starch, 4% sugar and 26% NDF, while high sugar diet (SUG) supplemented with sucrose contained 27% starch, 9% sugar and 26% NDF. All diets were formulated to contain 17% crude protein. Although DMI was not different among these three diets, mean rumen pH of STA and SUG diets was lower than CON diet (6.29 and 6.23 vs. 6.38; $P < 0.01$). However, there was no significant difference between STA and SUG diets. In addition, duration of rumen pH < 5.8 was not different between STA and SUG diets, but it tended to be longer for SUG diet than CON diet (117 vs. 30.1 min/d; $P = 0.08$). Concentrations of total VFA and NH_3-N in rumen fluid were not different among the treatments. However, compared with CON, STA and SUG diets had lower acetate proportion (62.0 vs. 59.6 and 59.4 mol / 100 mol; $P = 0.01$), but there was no difference between STA and SUG diets. Although DMI, milk yield, milk component yields and milk fat concentration did not differ among the treatments, concentrations of milk CP (3.14 vs. 3.08 and 2.97%; $P < 0.01$) and MUN (16.2 vs. 13.3 and 14.9 mg/dL; $P < 0.01$) were higher for SUG diet compared with STA and CON diets. These results suggested that feeding high sugar and high starch diets to lactating dairy cows might decrease rumen pH without affecting DMI or milk fat yield, but that high sugar diet may increase milk CP content.

Key Words: sugar, starch, milk production

1150 (M133) Propionate is a dominant inducer of bovine cytosolic phosphoenolpyruvate carboxykinase gene expression. Q. Zhang*, S. L. Koser, and S. S. Donkin, *Purdue University, West Lafayette, IN.*

Expression of cytosolic phosphoenolpyruvate carboxykinase (PCK1) is a critical control point for gluconeogenesis. Indirect evidence suggests that increased feed intake after calving and diet modification that increase rumen propionate production, the primary precursor of gluconeogenesis in ruminants, induces PCK1 mRNA. Our objective was to determine the direct effects of propionate on regulation of bovine PCK1 promoter activity and the relationship to hormones known to modulate glucose metabolism. The full length proximal promoter of bovine PCK1 from -1238 to +221 relative to transcription initiation and nested 5' truncation deletions at -815, -409, -281 and -85 to +221 were ligated to pGL3 Firefly Luciferase Reporter Vector and transfected into rat hepatoma H4IIE cells. The pGL3-Basic (*P*romoterless) and pGL3-Promoter (SV40 promoter driven) vectors served as negative and positive controls for the experiment. Renilla Luciferase Reporter Vector was cotransfected to normalize transfection efficiency. At 5 h after transfection, cells were exposed to either 2.5 mM propionate (PRO), 100 nM insulin (INS), 1 mM 8 Br-cAMP (cAMP), 5 μM dexamethasone (DEX), or the double and multiple combinations of PRO, INS, cAMP and DEX for 23 h. Promoter activity was expressed as the ratio of firefly luciferase to renilla luciferase and data were analyzed using the PROC MIXED of SAS 9.3. All bovine PCK1 promoter constructs were capable of driving firefly luciferase expression. Propionate induced ($P < 0.001$) expression of all PCK1 promoter constructs compared with no treatment control. The induction by propionate was greatest for the -1238 to +221 promoter construct (up to 6-fold) and similar for the other four PCK1 promoter constructs (about 3-fold). Activity of the -1238 to +221 PCK1 promoter was not altered by cAMP and DEX alone but was induced (3-fold) by their combination ($P < 0.01$). Induction of the -1238 to +221 PCK1 promoter construct with cAMP and DEX, was repressed by 24% in response to INS and PRO prevented this effect ($P < 0.0001$). The data demonstrate an inductive effect of propionate on bovine PCK1 promoter activity that is dominant to the repressive effect of insulin. Furthermore, the effect of propionate to induce PCK1 appears to be independent of the actions of cAMP and dexamethasone to also induce bovine PCK1 transcription.

Key Words: cytosolic phosphoenolpyruvate carboxykinase, propionate, hormones

1151 (M134) Slow-release urea, rumen-protected methionine, and histidine: Effects on expression and activation of the mTOR signaling pathway in skeletal muscle of dairy cows receiving a diet deficient in metabolizable protein. *F*. Giallongo[*1], H. Sadri[2], A. N. Hristov[1], J. Werner[3], C. Parys[4], B. Saremi[4], H. Sauerwein[2], and C. Lang[5], *[1]Dep. of Animal Science, Pennsylvania State University, University Park, [2]Institute of Animal Science, Physiology & Hygiene Unit, University of Bonn, Germany, [3]Animal Resource Program, Pennsylvania State University, University Park, [4]Evonik Industries AG, Hanau, Germany, [5]Dep. of Cellular and Molecular Physiology, Penn State College of Medicine, Hershey.*

The mammalian target of rapamycin (mTOR) signaling pathway is mediated by two functionally distinct multi-protein complexes, mTORC1 and mTORC2. The mTORC1 is a nutrient sensor, in particular of amino acids, activating protein synthesis by phosphorylation of ribosomal protein S6 kinase (S6K1) and eukaryotic initiation factor 4E-binding protein (4E-BP1). The mTORC2 responds to growth factors but is largely nutrient insensitive and phosphorylates protein kinase B (Akt) on Ser473, resulting in activation of cell growth, and survival. We hypothesized that supplementation of diets deficient in metabolizable protein (MP) with slow-release urea or rumen-protected (RP) Met and His will affect the gene expression of key factors of the mTOR pathway, in particular of mTORC1, and will alter their activation by phosphorylation in skeletal muscle of dairy cows in support of protein synthesis. Sixty Holstein cows were blocked based on DIM and milk yield and within block randomly assigned to 1 of 5 diets in a 10-wk experiment (including the first 2 wk as covariate period): MP-adequate diet (AMP); MP-deficient diet [DMP; 5% below MP requirements (NRC, 2001)]; DMP supplemented with slow-release urea as Optigen (Alltech Inc.; DMPO); DMPO supplemented with RPMet (Mepron; Evonik Industries AG; DMPOM); and DMPOM supplemented with RPHis (Balchem Corp.; DMPOMH). Muscle biopsies were collected from *Longissimus dorsi* during the last wk of the experiment. The mRNA abundance of the following target genes was quantified by qPCR: mTOR, S6K1, and 4E-BP1. Western blotting was used to assess total (t)- and phosphorylated (*P*)-S6K1 (Thr389), t-Akt and p-Akt (Ser473), p-mTOR (Ser2481), and p-S6 (Ser240/244). Data were analyzed by the PROC MIXED of SAS. The mRNA abundance of the target genes was not affected by the treatments; treatment effects were limited to p-mTOR and p-S6: p-mTOR values in DMPO were decreased when compared against DMP ($P = 0.03$) and also tended to be lower ($P = 0.07$) in DMPOMH than in DMPOM. The p-S6 values in DMPOM tended to be greater ($P = 0.07$) than in DMPO. There was also a trend ($P = 0.09$) for decreased p-S6 in DMPO versus DMPOM and DMPOMH. In conclusion, supplementation of the DMP diet with slow-release urea, or RPMet and RPHis, respectively, altered the phosphorylation status of mTOR-associated signaling proteins in muscle. No such effects were observed when comparing the AMP and DMP diets, thus indicating specific effects of the supplements.

Key Words: rumen-protected amino acid, mTOR, dairy cow

1152 (M135) Attenuation of the integrated cortisol response following administration of oral firocoxib in preweaned calves prior to cautery disbudding. M. L. Stock[*1], R. Gehring[2], S. T. Millman[1], C. Wang[1], L. W. Wulf[3], L. A. Barth[1], and J. F. Coetzee[3], *[1]Iowa State University, Ames, [2]Kansas State University, Manhattan, [3]Pharmacology Analytical Support Team, Iowa State University College of Veterinary Medicine, Ames.*

Perioperative analgesic effects of oral firocoxib following cautery disbudding were investigated in preweaned calves. Twenty Holstein calves (55.2 ± 5.8 kg) approximately 35 d old were orally administered firocoxib, a non-steroidal anti-inflammatory prostaglandin blocker, using a dose of 0.5 mg/kg ($n = 10$) or whey protein placebo ($n = 10$) in a randomized clinical trial. All animals received a cornual nerve block using a local anesthetic prior to disbudding. Pain biomarkers including ocular temperature determined by infrared thermography, pressure algometry measuring mechanical nociception threshold, and heart rate were evaluated following cautery disbudding at 2, 4, 7, 8, and 24 hr. Blood samples were collected over 96 hr and analyzed for plasma cortisol and substance P concentrations by radioimmune assay. Additionally, ex-vivo prostaglandin E_2 (PGE_2) concentrations were determined over the same 96-hr study period using an enzyme immunoassay. Data were analyzed using a linear mixed effects model with repeated measures. An attenuation of the integrated cortisol response (mean ± LSM) as calculated as area under the effect curve was greater in placebo treated calves (1611.1 ± 249 nmol.h/L vs. 1114.2 ± 181 nmol.h/L) ($P = 0.058$). A significant decrease in cortisol concentrations (mean ± LSM) was observed in firocoxib treated animals at approximately 48 hrs after disbudding (11.3 ± 1.9 nmol/L vs. 22.8 ± 2.8 nmol/L) ($P = 0.0013$). Additionally, a significant inhibition ($P < 0.01$) of ex vivo PGE_2 concentration was observed from 12 to 48 hr following disbudding in calves treated with firocoxib. These data support the potential for firocoxib to be used to provide analgesia after cautery disbudding in calves; however, further investigation of its perioperative analgesic effects is warranted.

Key Words: disbudding, welfare, NSAID

1153 (M136) Effect of storage temperature on the bacterial growth and pH levels of bovine colostrum. C. Cummins[*1,2], I. Lorenz[2], and E. Kennedy[3], *[1]Teagasc, Animal and Grassland Research and Innovation Center, Moorepark, Fermoy, County Cork, Ireland, [2]School of Agriculture, Food Science & Veterinary Medicine, University College Dublin, Belfield, Ireland, [3]Teagasc, Moorepark, Fermoy, County Cork, Ireland.*

Storage of colostrum is a convenient practice that ensures supplies are readily available should they be needed, however storage temperature may affect colostrum quality. The objective of this study was to investigate the effect of storage temperature on bacterial growth and pH levels of colostrum. The study took place at Teagasc Moorepark Research Farm, Cork, Ireland. Colostrum from six Holstein-Friesian cows (³3rd lactation) was collected from March 5 to 12, 2013, at the first scheduled milking post-calving (<9hr post-calving). Immediately after collection samples were separated into 100-ml aliquots, which were replicated and stored in separate temperature-controlled units at one of three temperatures: 4°C, 13°C and 20°C. Aliquots were removed and frozen at 0, 6, 12, 24, 36, 48, 60 and 72 hr post storage. Consequently, they were defrosted at 4°C to determine total bacterial count (TBC) using serial dilution. Dilution rate ranged from 1:10,000 (lowest expected) to 1:10,000,000 (highest expected). Diluted samples (1ml) were incubated at 32°C for 48 hr on 3M petrifilm aerobic count plates. Subsequent recordings were obtained using a 3M Petrifilm Plate Reader. Duplicate TBCs were prepared and an average was calculated. Simultaneously, aliquots were measured for pH using an OHM Delta 2105.2 datalogger (www.lennox.ie). Calibration was carried out before each test period and the probe was cleaned weekly using product guidelines. Data was tested for normality using PROC UNIVARIATE in SAS (v9.3) displaying positively-skewed data, thus a log transformation was performed. Transformed data was analysed using a mixed model (PROC MIXED; SAS v9.3). The model included treatment, time and their interactions. Significant differences between treatments were seen in TBC once colostrum was stored for ³12 hours. Storage at 20°C had significantly higher TBC from 12 hours than storage at both 13°C and 4°C ($P < 0.001$), while TBC of colostrum kept at 13°C for $\geq$ 24 hours was significantly greater than colostrum kept at 4°C ($P < 0.001$). Additionally, colostral pH was significantly lower from 24 hr in colostrum kept at 20°C compared to 13°C and 4°C ($P < 0.001$). Furthermore, from hour 60 of storage the pH of colostrum stored at 13°C was significantly lower than that kept at 4°C ($P < 0.01$). Analysis revealed that a LogTBC >7.5 cfu/ml resulted in a pH drop to < 6.5. Further research is warranted to determine if this affects passive transfer of immunity in calves. It is clear however that stored colostrum should be refrigerated ($\leq$ 4°C) to minimise bacterial proliferation and maintain pH.

Key Words: colostrum, storage, bacteria

1154 [Withdrawn]

1155 (M138) The effect of prepartum housing on metabolic and reproductive health in dairy cows. C. L. Miltenburg[*] and S. J. LeBlanc, *University of Guelph, ON, Canada.*

The determinants of metabolic and reproductive health disorders and the degree to which housing and management can influence health are only partially understood. The objective of this randomized controlled study was to determine if a prepartum housing strategy of providing non-competitive feeding and lying access improves metabolic health and immune function and reduces reproductive disease. Forty-eight Holstein cows of all parities were randomly assigned to a close up treatment group of 6 to 10 cows in 1 pen with either 80% cows to stalls and 90 cm of feeding space/cow or 120% stocking density and 45cm of feeding space/cow for 3 weeks before expected calving. Pen size and bunk space were adjusted to maintain space per cow as animals were removed for calving. Weekly coccygeal blood samples measured non-esterified fatty acids (NEFA), beta-hydroxybutyrate (BHB), calcium, glucose, albumin, aspartate aminotransferase (AST), bilirubin and haptoglobin from 3 weeks before to 5 weeks after calving. Neutrophil phagocytosis and oxidative burst were assessed at -2, -1, 1, 2, 3 and 5 weeks relative to calving. A modified glucose tolerance test to assess insulin resistance was performed 1 week before calving. Liver biopsies were performed at weeks +1 and +3 to assess liver triglyceride content and gene expression. Vaginoscopy was used to identify cows with purulent discharge (*P*VD) and uterine and cervical cytobrush samples were collected to assess endometritis and cervicitis as well as uterine gene expression at weeks +3 and +5. There were no interactions of treatment with time. Cows in the crowded treatment had significantly lower mean albumin ($P = 0.05$) and bilirubin ($P = 0.01$) but had greater BHB ($P = 0.01$) and NEFA ($P = 0.05$). At 5 weeks postpartum, 7% of cows had PVD and 33% of cows were diagnosed with endometritis based on > 5% neutrophils. There was no significant effect of treatment on endometritis. Cows that had endometritis at week 5 tended ($P < 0.1$) to have lower average glucose and bilirubin and higher albumin concentrations throughout the study period. These results indicate that metabolic and reproductive health is more complex than can be explained solely by exposure to what is understood to be optimal access to feeding and lying space.

Key Words: endometritis, transition, crowding

1156 (M139) Intake, milk production, ruminal, and feed efficiency responses to DCAD in lactating dairy cows. M. E. Iwaniuk* and R. A. Erdman, *University of Maryland, College Park.*

Previous meta-analyses (Hu and Murphy, 2004, J. Dairy Sci. 87:2222) of the effects of dietary cation anion difference (DCAD) in lactating dairy cow diets utilized studies conducted after the development of the DCAD concept. Dietary buffers such as $NaHCO_3$ and K_2CO_3 increase DCAD and have been used in lactating dairy cow diets for several decades. However, most published studies on buffer feeding were conducted prior to the development of the DCAD concept. Our objective was to determine the intake, milk production, ruminal, and feed efficiency responses to DCAD using previous studies with dietary buffer addition and more recent studies that focused on DCAD as dietary treatments. The database consisted of 44 articles that were published between 1965 and 2011. The studies included 196 dietary treatments, and 89 treatment comparisons that varied in DCAD. For studies that lacked analyses of one or more of the dietary cations (Na, K, or Cl), ion percentages were estimated from ingredient composition using the 2001 Dairy NRC Software. Two basic models were used to evaluate DCAD responses using the NLPROC MIXED in SAS 9.2: 1) A simple linear model: Y = A + B*(DCAD) where A = intercept and B = the increment (slope) in performance per unit DCAD (meq/kg diet DM); and 2) a nonlinear model: $Y = A + M(1\text{-}e^{(K \times DCAD)})$ where M = maximal increment in performance from DCAD and K = the rate constant. In both models, study was designated as the random effect. DCAD effects best described by the linear model included milk fat percent, fat yield, rumen pH, NDF digestibility, and FCM/DMI where a 100 meq/kg increase in DCAD resulted in respective increases of 0.10% ($P < 0.001$; RMPSE = 0.01), 35 g/d ($P < 0.001$; RMPSE = 5), 0.033 pH units ($P < 0.001$; RMPSE = 0.001), 1.5% NDF digestibility ($P < 0.001$; RMPSE = 0.4), and 0.0013 FCM/DMI units ($P < 0.001$; RMPSE = 0.005). DMI, milk yield, and 3.5% FCM were best described by the nonlinear model where the maximal responses were 3.05, 2.88, and 6.57 kg/d, respectively ($P < 0.001$). The DCAD concentration at which 80% of the maximal response occurred was 456, 207, and 617 for DM intake, milk yield, and 3.5% FCM, respectively. These results suggest that DCAD has significant effects on intake, milk production and composition, digestion, and feed efficiency in lactating dairy cows.

Key Words: DCAD, meta-analysis, dairy cows

1157 (M140) Hepatic metabolomics and transcriptomics in prepartal dairy cows supplemented with Smartamine M and MetaSmart during the transition period. K. Shahzad*[1], J. S. Osorio[2], D. N. Luchini[3], and J. J. Loor[1], *[1]University of Illinois, Urbana-Champaign, Urbana, [2]University of Illinois, Champaign, [3]Adisseo S.A.S., Alpharetta, GA.*

Supplementation with Smartamine M (SM) and MetaSmart (MS) during the transition period improves postpartal dry matter intake, milk production, and blood neutrophil immune function. In the current study we used metabolomics and transcriptomics to provide a more holistic view of the adaptations induced on the liver by dry period nutrition. Liver from cows fed a control high-energy diet without (OVE) or with SM or MS were used. Metabolomics was performed via LC-MS and GC-MS (Metabolon Inc.) and transcriptomics using a whole-transcriptome bovine microarray (Agilent). From a total of 313 biochemical compounds identified, metabolomics analysis ($P \leq 0.10$) revealed a total of 20, 21, and 48 compounds affected by SM vs. OVE, MS vs. OVE, and SM vs. MS, respectively. Comparing profiles in SM vs. OVE revealed that compounds up-regulated belong to the pentose, sterol, inositol, and purine metabolism pathways, while down-regulated compounds belong to secondary bile acid, arginine and proline, purine and pyrimidine, and eicosanoid metabolism pathways. In MS vs. OVE, the compounds up-regulated belong to primary bile acid, pyrimidine, and lysolipid metabolism, while compounds down-regulated were linked with glycolysis, gluconeogenesis, urea cycle, sphingolipid, and pyruvate metabolism. Liver of MS vs. OVE cows had lower hydroxybutyrate and lactate concentration. The transcriptomic analysis of these groups resulted in 922 (SM vs. OVE), 1,573 (MS vs. OVE) and 1,033 (SM vs. MS) differentially expressed genes (DEG, P £0.05). Bioinformatics analysis using the Dynamic Impact Approach (DIA) that SM vs. OVE resulted in a marked impact and activation of 'fatty acid biosynthesis', 'cyanoamino acid metabolism', 'O-glycan biosynthesis', and 'glycosaminoglycan biosynthesis'. In MS vs. OVE, however, among the top-5 most-impacted pathway there was marked inhibition of 'phenylalanine, tyrosine, and tryptophan biosynthesis' and 'phenylalanine' metabolism. 'Cyanoamino acid metabolism' and 'taurine and hypotaurine' metabolism were highly-impacted and activated pathways in MS vs. OVE. Unique responses in SM vs. MS included a marked activation of 'fatty acid biosynthesis', 'glycosphingolipid metabolism', 'valine, leucine, and isoleucine biosynthesis', and 'sulfur metabolism'. Preliminary data interpretation suggests MS and SM induce distinct changes on the metabolome and transcriptome phenotype of the prepartal liver. The functional relevance of such changes remains to be determined.

Key Words: systems biology, metabolic profiling, bovine liver

1158 (M141) Detection of subclinical milk fever and ketosis in fresh dairy cows using rumination time, lying time, reticulorumen temperature, and neck activity. A. E. Sterrett*[1], B. A. Wadsworth[1], R. J. Harmon[1], M. Arnold[1], J. D. Clark[1], E. P. Aalseth[2], D. L. Ray[1], and J. M. Bewley[1], *[1]University of Kentucky, Lexington, [2]Earl P. Aalseth, Jr. Dairy Consulting, PLLC, Lake Stevens, WA.*

The objective of this study, conducted at the University of Kentucky Coldstream Dairy, was to evaluate changes in rumination time (RU), lying time (LT), reticulorumen temperature (RT), and neck activity (NA) around subclinical hypocalcemia (SHC) and ketosis (SKET) events. Fresh cows (90 Holstein, 19 crossbred, and 11 Jersey cows) were assigned HR Tags (SCR Engineers Ltd., Netanya, Israel), IceQubes (IceRobotics, Edinburgh, Scotland), and DVM boluses (DVM Systems, LLC., Boulder, CO) ≥ 14 days pre-partum. The Milpro P4C (Milkline, Gariga di Podenzano, Italy) system measured milk yield (MY). Blood calcium was measured on 3, 7, and 14 DIM to determine SHC (≤ 1.8 mmol/L). Milk KetoTest (Elanco, Greenfield, IN) and blood Precision Xtra (Abbott Laboratories, Abbott Park, IL) beta-hydroxybuterate tests were analyzed on 3, 7, and 14 DIM to determine SKET (both tests ≥ 1.2 mmol/L). Mean RU, LT, RT, NA, and MY were recorded and summarized for each cow day for the first 7 DIM. The GLM Procedure of SAS (Cary, NC) was used to evaluate the relationship between SKET or SHC presence and RU, LT, RT, NA, and MY. LSMeans NA was less in cows with SHC than cows without SHC (210.30 ± 6.40 and 253.81 ± 3.93, respectively, $P < 0.01$). LSMeans RT was less for cows with SHC than cows without SHC (38.58 ± 0.05 and 39.01 ± 0.03 °C, respectively, $P < 0.01$). No difference was observed for RU (316.99 ± 8.35 and 299.90 ± 5.12 min/d for SHC and non- SHC cows respectively, $P = 0.08$), MY (48.57 ± 1.64 and 50.83 ± 1.14 kg/d for SHC and non- SHC cows respectively, $P = 0.26$), or LT (10.66 and 9.97 h/d for SHC and non-SHC cows, respectively, $P = 0.03$). LSMeans LT was greater for cows with SKET than cows without SKET (10.26 and 9.58 h/d, respectively, $P = 0.04$). LSMeans NA was greater for cows without SKET compared with cows with SKET (258.86 and 236.73, respectively, $P < 0.01$). No difference was observed for RT (38.91 ± 0.04 and 38.93 ± 0.04 °C, for SKET and non-SKET cows respectively, $P = 0.72$), RU (307.11 ± 4.88 and 295.84 ± 8.14 min/d, for SKET and non-SKET cows respectively, $P = 0.24$), or MY (51.64 ± 1.09 and 49.03 ± 1.65 kg/d for SKET and non-SKET cows respectively, $P = 0.19$). These parameters may be useful for identifying fresh cow diseases.

Key Words: ketosis, hypocalcemia, fresh cow

1159 (M142) Effects of stage of gestation and feeding regime on intake and apparent total tract digestibility in Holstein × Gyr dairy cows. P. P. Rotta*[1], S. C. Valadares Filho[2], T. E. Engle[1], L. F. Costa e Silva[1], M. I. Marcondes[3], F. S. Machado[4], T. R. Gionbelli[5], B. C. Silva[5], and F. A. S. Silva[3], *[1]Colorado State University, Fort Collins, [2]Universidade Federal de Viçosa, Dep. of Animal Science, Minas Gerais, Brazil, [3]Universidade Federal de Viçosa, Brazil, [4]EMBRAPA, Juiz de Fora, Brazil, [5]Universidade Federal de Viçosa, Minas Gerais, Brazil.*

Two experiments were conducted to determine the effects of stage of gestation (SG) and feeding regime (FR) on DMI and apparent total tract digestibility (ATTD) in Holstein × Gyr dairy cows. Exp. 1: 20 multiparous Holstein × Gyr cows with average initial BW of 495 ± 10.4 kg and age 5 ± 0.3 of yr were used in this experiment. Cows were individually fed a corn silage-concentrate based diet (93% and 7% DMB, respectively). In order to allow cows ad libitum access to feed, feed delivery was adjusted to allow approximately 5% orts daily. Dry matter intake was evaluated at 122, 150, 178, 206, 234 and 262 d of gestation. Overall, DMI decreased ($P < 0.05$) as days in gestation increased. The decrease in DMI may be associated with reduction in ruminal volume caused by the rapid increase in fetal size during late gestation. Exp. 2: 44 multiparous Holstein × Gyr cows with average initial BW of 480 ± 10.1 kg and age of 5 ± 0.5 of yr were allocated to 1 of 2 FR. Feeding regimes consisted of: 1) ad libitum intake (ADLIB; $n = 20$) and maintenance intake (MAIN; $n = 24$). Maintenance intake was considered as 1.15% of BW. Cows were individually fed a corn silage-concentrate based diet (93% and 7% DMB, respectively) as a total mixed ration, twice a daily. Apparent total tract digestibility was evaluated every 28 d beginning at 122 d of gestation through day 262 by collecting 24 h fecal excretion for the last 5 d of each 28 d period. Within feeding regime, DM digestibility decreased ($P < 0.05$) as days in gestation increased. An interaction ($P < 0.05$) existed for DMI and OM apparent digestibility between FR and SG on days 150 and 178 of gestation. Cows fed at MAIN had greater ($P < 0.05$) DM and OM apparent digestibility than cows fed ADLIB. However, DM and OM apparent digestibility were similar ($P > 0.05$) for FR at 122, 206, 234 and 262 d of gestation. These data indicate that FR and days in gestation can influence ATTD.

Key Words: dairy cattle, digestibility, pregnancy

1160 (M143) Description of high cow premix recipes in California dairies. Y. Trillo*[1], A. Lago[2], and N. Silva-del-Rio[1], *[1]VMTRC, University of California, Tulare, [2]DairyExperts, Tulare, CA.*

The objective of this study was to describe high cow premix (HCP) recipes prepared in 13 California dairies ranging in size

from 1,000 to 6,000 cows. Records from a consecutive twelve month period, starting from Jan-June 2012, were extracted from the feeding management software FeedWatch 7.0. The variables included were: date, drop number, recipe, ingredient, loading sequence, target weight, as-fed weight, tolerance level, and mixer wagon capacity. Descriptive statistics were conducted with SAS 9.3. Throughout the study period, HCP recipes were prepared on farm at least 90% of the days (n = 3) or less than 70% of the days (n = 5). The median number of HCP recipe prepared per day were one (n = 5), two (n = 7) or four (n = 1). The median number of ingredients included daily in the HCP recipe was four to six (n = 7) and seven to nine (n = 6). The number of ingredients included in HCP recipe varied over time within dairy in three (n = 3), two (n = 5), one (n = 4) or zero (n = 1) ingredients. The most commonly used ingredients in HCP recipes were canola meal (n = 13), whole cotton seed (n = 11), dry distillers grains (n = 8), corn gluten meal (n = 8), almond hulls (n = 6), wheat middlings (n = 6), molasses (n = 5) and rolled corn (n = 5). Forages were also included in the HCP [straw (n = 5), alfalfa hay (n = 1)]. Other ingredients used less frequently were slow release non-protein nitrogen (n = 3), beet pulp (n = 2), rice grain (n = 2), cotton meal (n = 2), safflower (n = 2), whey (n = 2), soybean meal (n = 2), bypass fat (n = 1), ground wheat (n = 1), and soyhulls (n = 1). All dairies but one added the mineral-vitamin mix in the HCP. The ingredients most frequently added first were straw (n = 4), cotton seed (n = 3), canola meal (n = 3), almond hulls (n = 1), mineral-vitamin mix (n = 1) and wheat middlings (n = 1). The ingredients added most frequently last were molasses (n = 5), whey (n = 2), mineral-vitamin mix (n = 4), beet pulp (n = 2), soybean (n = 1) or corn gluten meal (n = 1). Ingredients with assigned tolerance level >10% of admissible deviation from target were mineral-vitamin mix, molasses, and straw (n = 1) and mineral-vitamin mix (n = 1). The frequency of HCP recipes prepared over 10% of the mixer wagon capacity (based on weight) was over 90% in four dairies. There is a large variation in HCP ingredients and preparation across dairies in California.

Key Words: dairy cattle, high cow premix, feeding management software

GROWTH & DEVELOPMENT I

1161 (T117) Body weight adjustments for feeding status and pregnant or non-pregnant condition in beef cows.

M. P. Gionbelli*[1,2], M. S. Duarte[1], S. C. Valadares Filho[1,2], E. Detmann[1,2], M. L. Chizzotti[1,2], T. R. Gionbelli[1], F. C. Rodrigues[1], D. Zanetti[1], and M. G. Machado[1], [1]*Universidade Federal de Viçosa, Minas Gerais, Brazil,* [2]*Instituto Nacional de Ciência e Tecnologia– Ciência Animal, Viçosa, Minas Gerais, Brazil.*

Dataset from 49 multiparous Nellore cows (32 pregnant and 17 non-pregnant) averaging 451 ± 10 kg was used to develop a set of equations and relations for body weight (BW) adjustments in pregnant or not pregnant cows. Cows were fed a corn silage based diet and weighed every 28 days (0700 h, before feeding) to obtain BW, and reweighed at the same time following day after 16 h fasting to obtain shrunk body weight (SBW). Pregnant cows were separated into four groups of 8 cows and harvested at 136, 189, 239 and 269 days of pregnancy (DOP) to obtain the empty body weight (EBW) and the weight of components related to pregnancy. A set of linear and non-linear equations was tested, based on theoretical suppositions, to establish the relationships between the BW, SBW and EBW of pregnant and non-pregnant cows as function of DOP. The pregnant compound (PREG) was defined as the weight genuinely related to pregnancy, that includes the gravid uterus minus the non-pregnant uterus plus the accretion in udder related to pregnancy. The PREG was deducted from the SBW or EBW of a pregnant cow to estimate the non-pregnant weights (SBW_{np} and EBW_{np}). Results are shown in Table 1161. There was no accretion in udder weight up to 238 days of pregnancy. We conclude that the weight related to the pregnancy can be estimated in a live cow allowing estimate non-pregnant EBW and SBW of a pregnant cow and calculates the body gain of only maternal tissues. *Funded by INCT-CA, CNPq, FAPEMIG.*

Key Words: *Bos indicus*, gestation, gravid uterus

1162 (T118) Changes in performance and immune response in dairy calves offered milk replacer or raw milk.

C. Yunta[1], A. Bach[2,3], and M. Terré*[1], [1]*IRTA, Caldes de Montbui, Spain,* [2]*Dep. of Ruminant Production, IRTA, Caldes de Montbui, Spain,* [3]*ICREA, Barcelona, Spain.*

The objective of the present study was to compare intake, growth performance, and immune response in dairy calves fed milk replacer (MR) or raw milk (RM). Seventy dairy female Holstein calves were randomly assigned to either MR or RM treatments and were offered 750 g/d of MR or RM respectively from days 15 to 56 and 375 g/d from 56 to 63 d of life. All the calves were weaned at d 63 and starter feed was offered ad libitum throughout the study. Daily milk and feed intake was recorded from d 2 to 63. Animals were weighed weekly and blood samples were collected at d 14, 28, 42 and 56 to determine glucose and insulin concentrations. Immune response was evaluated in blood samples collected at 35 d of age by measuring TNFa after an in vitro lipopolysaccharide (LPS) challenge in blood. Also, at d 7, 21 and 35, 1-ml of ovoalbumin was injected to calves and blood samples were collected at day 7 and 56 to measure antibody titers against

Table 1161. Summary of equations used to adjust BW of pregnant and non-pregnant cows

Estimated variable	Predictors	Relation
Non-pregnant cows		
SBW_{np}	BW	$SBW=0.8084\times BW^{1.0303}$
EBW_{np}	SBW_{np}	$EBW_{nP=}0.8424\times SBW_{np}^{1.0122}$
Pregnant cows		
SBW	BW	$SBW = 0.8084\times BW^{1.0303}$
SBW_{np}	SBW and PREG	$SBW_{nP=}SBW–PREG$
PREG	If DOP ≤ 238: GU_{dp} If DOP > 238: GU_{dp} and UD_{dp}	If DOP ≤ 238: $PREG = GU_{dp}$ If DOP > 238: $PREG = GU_{dp} + UD_{dp}$
Gravid uterus accretion due to pregnancy (GU_{dp})	GU and UT_{np}	$GU_{dp} = GU–UT_{np}$
Gravid uterus (GU)	DOP or DOP and body condition score (BCS)	$GU = 0.2243\times BCS^{0.3225}\times e^{((0.02544–0.0000286\times DOP)\times DOP)}$, or $GU = 0.2106\times e^{((0.03119–0.00004117\times DOP)\times DOP)}$
Non-pregnant uterus (UT_{np})	SBW_p and GU	If DOP≤238: $UT_{nP=}0.0012\times(SBW–GU+0.6)$ If DOP > 238: $UT_{nP=}0.0012\times(SBW–GU+0.6–2)$
Udder accretion due to pregnancy (UD_{dp})	UD_{np} and DOP	$UD_{dP=}UD_{np}\times e^{((DOP–238)\times 0.0109)}–UD_{np}$
Non-pregnant udder (UD_{np})	SBW_p and BCS	$UD_{nP=}SBW_{np}\times 0.00589\times BCS^{0.2043}$, or If DOP ≤ 238: $UD_{nP=}(SBW–GU_{dp})\times 0.00589\times BCS^{0.2043}$ If DOP > 238: $UD_{nP=}(SBW–GU_{dp}–2)\times 0.00589\times BCS^{0.2043}$
EBW	EBW_{np} and PREG	$EBW = EBW_{np}+PREG$
EBW_{np}	SBW_{np}	$EBW_{nP}= 0.8424\times SBW_{np}^{1.0122}$

ovoalbumin. Data were analyzed using a mixed-effects model with repeated measures. Data from insulin and insulin to glucose ratio were previously transformed to reach a normal distribution. No differences were found in milk or feed intake, ADG or gain to feed ratio between treatments. Plasma glucose concentrations did not differ between treatments but, plasma insulin concentration was greater ($P < 0.05$) in MR compared with RM calves (1.36 vs 0.78 ± 0.053 μg/L) as it also was the ratio insulin to glucose (0.12 vs 0.07 ± 0.535). Immune response to the in vitro LPS and the in vivo ovoalbumin challenges were similar in both groups. However, RM calves needed to receive antibiotic treatments (24%) fewer times ($P < 0.05$) than those fed MR (37%). In conclusion, even no significant differences were found in intake or growth performance, the lower insulin to glucose ratio and the decrease in the number of antibiotic treatments in RM calves compared with those fed MR, suggested an improvement on glucose metabolism, and a potential benefit on calf health when feeding RM to calves compared with feeding MR.

Key Words: calves, performance, raw milk

1163 (T119) Comparison of albumin depleted and whole serum samples for biomarker identification.

J. K. Grubbs*, C. K. Tuggle, J. C. M. Dekkers, and S. M. Lonergan, *Iowa State University, Ames.*

Serum is a highly complex mixture of proteins with a vast range in concentrations. Ease and accessibility make serum an ideal fluid for biomarker identification. Eight proteins represent over 90% of the protein content of serum. Albumin alone often comprises over 50% of total protein content in serum. Presence of high abundance proteins like albumin has long been a hurdle to proteomic researchers in establishing suitable biomarkers for disease states and other biological statuses. Historically, albumin and other high abundance proteins have been removed from serum prior to biomarker studies. The purpose of this project was to investigate the impact of albumin removal on porcine serum protein profiles and protein spot abundance variation across samples. Serum samples from eight pigs were used; half of each sample was kept as whole serum while the other half was depleted of albumin using a commercially available kit designed to remove 95% of the albumin. Depleted and whole serum samples, for a single pig, were then compared using two dimensional difference in gel electrophoresis for a total of eight comparisons run in duplicate. Among the 236 protein spots identified, 167 were changed in abundance ($P \leq 0.05$) between depleted and whole serum. Of these differences, 87 protein spots were increased in the albumin depleted serum while 76 spots were increased in the whole serum. The 87 spots found to be increased are a result of a shift in protein profile due to the removal of albumin. While some of these changes in protein profile could be linked directly to the location of albumin on the gel, most spots were not co-localized with albumin. Albumin is known to interact with many proteins, thus albumin depletion procedures may alter abundance of such proteins and increase the overall variation within the serum. These data indicate that for serum protein biomarker discovery in animal production, it may be prudent to investigate technologies and methods that allow use of whole serum over depleted serum. These data also show that using gel based proteomic approaches may be one of the technologies that ameliorates the need to deplete high abundance proteins from serum. *This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011-68004-30336 from the USDA National Institute of Food and Agriculture.*

Key Words: residual feed effciency, serum, albumin

1164 (T120) Comparison of radial immunodiffusion and enzyme-linked immunosorbant assay for quantification of bovine IgG in colostrum and plasma.

A. M. Smith, S. L. Gelsinger*, C. M. Jones, and A. J. Heinrichs*, Pennsylvania State University, University Park.*

Radial immunodiffusion (RID) is the standard quantification method for bovine IgG in colostrum and plasma. Recent studies have published ELISA IgG values; however, RID and ELISA measurements have not been compared. Heating colostrum to 60°C for 30 min does not decrease IgG concentration measured by RID; use of ELISA has not been tested. This study's objective was to compare ELISA and RID values in plasma and in colostrum before and after heating. Colostrum ($n = 58$) and plasma ($n = 99$) were collected from individual cows and calves and frozen prior to IgG assessment. Colostrum was diluted 1:10 for RID and 1:1,000,000 for ELISA. Two dilution series were created for each sample and duplicated within each assay. Values were accepted when coefficients of variation (CV) were ≤ 10.5% among duplicates from a single dilution series and < 15% among 2 series from the same sample. Samples were retested until acceptable CV were acquired. The effect of heat-treatment was tested by heating 20 mL aliquots of each colostrum to 60° C for 30 min, then cooling, freezing, and retesting using the same dilution factors. Plasma samples were tested by RID without dilution and by ELISA at 1:500,000. Requirements for CV were identical to those used for colostrum. Proc Corr and Proc Mixed in SAS were used to determine correlation coefficients and effect of heat on colostrum IgG quantification, respectively. Mean (± SD) IgG concentration of colostrum before heating was 39.7 mg/mL (± 22.7) and 81.2 mg/mL (± 29.7) by ELISA and RID, respectively; and 19.2 mg/mL (± 12.8) and 76.8 mg/mL (± 34.6) after heating. Heat treatment reduced colostral IgG concentration when measured by ELISA ($P < 0.01$) but not by RID ($P = 0.73$). Correlation coefficients (P - value) were 0.20 (0.14) and 0.27 (0.03) for unheated and heat-treated colostrum, respectively. Fat and non-IgG protein in colostrum may interfere with assays and may be a cause for low correlation. Mean (± SD) plasma IgG concentration was 11.4 mg/mL (± 7.9) by

ELISA and 15.2 mg/mL (± 9.1) by RID. Relative to colostrum, plasma results were more strongly correlated (r = 0.55; $P < 0.01$); however, direct comparisons of ELISA and RID values merit caution. Results from ELISA were < RID for colostrum and plasma, and colostrum IgG decreased during heat-treatment when measured with ELISA. Further research is needed to determine effects of heat-treatment on colostrum IgG.

Key Words: IgG

1165 (T121) Effect of fish oil and thyme on nutrient digestibility, chewing activity, and rumen metabolites of Mahabadi goat kids. A. Hozhabri[1], M. Ganjkhanlou[1], A. Zali[1], A. Emami[2], A. Akbari-Afjani[3], and M. Dehghan-Banadaky[*1], *[1]University of Tehran, Iran, [2]University of Birjand, Iran, [3]University of Zanjan, Iran.*

This study was carried out to determine the effects of supplementing fish oil and thyme on nutrient digestibility, chewing activity and rumen metabolites in Mahabadi goat kids. Twenty-eight goat kids (BW = 17.8 ± 2.8 kg, 4 to 5 mo of age) were randomly assigned to 4 treatments: (1) basal diet (BD), (2) BD + 0.2% thyme essence, (3) BD +2% fish oil, and (4) BD + 2% fish oil and 0.2% thyme essence (DM basis of concentrate). Diets were formulated to meet the requirements recommended by NRC with forage (alfalfa and corn silage): concentrate ratio of 30:70 in TMR form. Animals were kept in individual pens with self-mangers for 94 d. Chewing activity in two 24-h periods was evaluated. During the last 7 d of the experiment, fecal samples were collected every morning around feeding time and acid insoluble ash (AIA) content was used as an internal marker to determine the apparent digestibility of nutrient digestibility. Ruminal fluid samples were taken from the rumen at 3 h after the morning meal the last day of the experiment to determine rumen concentration of ammonia nitrogen (NH_3-N) and VFA. Rumen contents were sampled 5 times during the trial to measure ruminal protozoa and pH. Protozoa counts were determined using light microscopic numeration with a hemocytometer. Protozoa and pH data were analyzed by MIXED model procedure and rumen nutrient digestibility, chewing activity, NH_3-N and VFA with GLM model procedure and adjusted Tukey-Kramer. Addition of fish oil decreased NDF digestibility, and increased ether extract digestibility versus the control ($P < 0.05$). Rumen liquor pH was not affected by treatments (6.11, 6.33, 6.20. and 6.23 respectively for treatments 1-4). Ruminal ammonia concentration decreased by 0.2% thyme essence ($P < 0.05$). Addition of thyme increased acetate concentration and acetate to propionate ratio ($P < 0.1$). It was also found that diets 2 and 3 significantly decreased protozoa count compared with diet 1 ($P < 0.05$). Time to eat (minutes per day) was not affected by treatments ($P > 0.05$), but chewing time significantly decreased by with diet 2 ($P < 0.05$). The results of this experiment indicate that supplementation of goat kid diet with fish oil and thyme changed nutrient digestibility and rumen metabolites.

Key Words: fish oil, nutrient digestibility, thyme essence

1166 (T122) Effect of heat treatment and bacterial population of colostrum on passive transfer of IgG. S. L. Gelsinger[*], and A. J. Heinrichs, *Pennsylvania State University, University Park.*

Heat treatment of colostrum has been shown to increase apparent efficiency of IgG absorption (AEA) in newborn dairy calves. It has been hypothesized that this may be partially due to reduction in bacteria that occurs during heat treatment. This study's objective was to test the effect of bacteria concentration in unheated and heat-treated colostrum on IgG absorption. Colostrum treatments were created by pooling colostrum from individual cows to create a single batch. Half of the colostrum was heated to 60° C and held for 30 min before cooling and rebottling (heat-treated). The remaining half of the colostrum was rebottled without heating (unheated). Half of each treatment was frozen immediately after bottling. Remaining heat-treated colostrum was inoculated with 20 mL of unheated colostrum. Remaining unheated and inoculated heat-treated colostrum were stored at 20° C for 60 and 72 h, respectively, to achieve similar final bacteria populations and subsequently frozen until needed for feeding. Samples were collected from each colostrum treatment for IgG and bacteria analysis prior to freezing. Bull calves ($n = 104$) were randomly assigned to treatment at birth. Plasma samples were collected 48 h after birth and assessed for IgG concentration. Data were analyzed using the PROC MIXED in SAS. Initial SPC was 4.59 log cfu/mL and reduced to 2.79 log cfu/mL following heat treatment. High bacteria treatments of unheated and heat-treated colostrum contained 8.65 and 8.56 log cfu/mL, respectively. Mean AEA (48-h plasma IgG concentration) was 31.25% (20.7 mg/mL) and 15.86% (10.4 mg/mL) in calves fed unheated colostrum of low and high bacteria concentration, respectively; and 37.27% (24.0 mg/mL) and 13.94% (9.3 mg/mL) in calves fed heat-treated colostrum of low and high bacteria concentration, respectively. Bacteria level significantly reduced AEA and 48-h plasma IgG concentration ($P < 0.01$). No effect of heat treatment was observed for 48-h IgG concentration or AEA ($P = 0.42$ and 0.36, respectively); however, there tended to be an interaction between bacterial population and heat treatment for AEA ($P = 0.08$). Slicing the interaction indicated a tendency of heat-treatment to increase 48-h IgG concentration and AEA in low bacteria colostrum treatments ($P = 0.10$ and 0.07, respectively). In this study, concentration of bacteria in colostrum had greater effect on calves' ability to absorb IgG than heat treatment of colostrum.

Key Words: IgG, calf, colostrum

1167 (T123) Effect of omega-3 fatty acids and thyme essence on carcass traits of Mahabadi kids.

A. Hozhabri[1], A. Zali[1], M. Ganjkhanlou[1], A. Emami[2], A. Akbari-Afjani[3], and M. Dehghan-Banadaky[*1], *[1]University of Tehran, Iran, [2]University of Birjand, Iran, [3]University of Zanjan, Iran.*

This study was carried out to determine the effects of supplementing long-chain fatty acids of fish oil and thyme on carcass traits in Mahabadi goat kids. For this aim, twenty-eight Mahabadi goat kids (average initial BW of 17/8 ± 2/8 kg, 4-5mo) were randomly assigned to four treatments: 1) control (basal diet), 2) 0.2% thyme essence, 3) 2% fish oil and 4) 2% fish oil +0.2% thyme essence.Animals were kept in individual pens with self-mangers for 94 d. Diet was formulated to met the requirements recommended by NRC with forage (alfalfa and corn silage): concentrate ratio of 30:70 in TMR form. Kids were weighed after 10 d of adaptation and at 21 d intervals after feed restriction and slaughtered at the end of the trial by Iranian traditional procedure . The area of the 9, 10, 11, 12 and 13 ribs together with the adjoined section of spinal column was used to estimate the amount of bone-free meat, fat and bone in the carcass. The meat, fat and bone were weighed after separation and the bone-free meat component stored at -20 °C for the chemical analysis. Data were analized by GLM procedure of SAS 9.1 and tukey test ($P \leq 0.05$). Addition of 2% fish oil increased fat depth over 12 rib ($P < 0.05$). Dressing percentage, eye muscle area, carcass length, liver and kidney weight, abdominal and kidney fat were not affected by treatments ($P > 0.05$). Percentages or weights ribs dissected muscle, fat and bone, and percentages of wholesale cuts of the carcass were not affected by fish oil and thyme essence ($P > 0.05$). The results of this experiment indicate that supplementation of goat kid diet with fish oil and thyme did not influence carcass traits but, fish oil increased back fat thickness.

Key Words: thyme essence, fish oil, carcass traits

1168 (T124) Effect of stage of pregnancy, maternal feeding level and fetal sex on fetal gut length in Holstein×Zebu cows.

T. R. Gionbelli[*1], P. P. Rotta[1], C. M. Veloso[1,2], M. P. Gionbelli[1,2], S. de Campos Valadares Filho[1,2], M. A. Novaes[1], J. V. Souza[1], J. S. Santos[1], L. C. Lacerda[1], and C. S. Cunha[1], *[1]Universidade Federal de Viçosa, Minas Gerais, Brazil, [2]Instituto Nacional de Ciência e Tecnologia–Ciência Animal, Viçosa, Minas Gerais, Brazil.*

Lower gut development at birth is suggested as one hypothesis for explain the lower development during the whole life of calves from cows that were low fed throughout gestation. These calves can have lower absorption of immunoglobulin right after birth and consequently lower immune capacity and be more susceptible to diseases that can impair the normal development. Forty-one nonlactating multiparous Holstein × Gyr cows, pregnant from the same Gyr bull, were used in an experiment to assess the effect of stage of pregnancy, maternal feeding level and fetal sex on fetal gut length. Cows were fed either HIGH (ad libitum, $n = 18$) or LOW(DMI restricted to 1.15% of BW in DM basis, $n = 23$) feeding level of the same diet (93% corn silage and 7% concentrate). Fetal sex was confirmed by ultrasonography at 55 days of gestation. Cows were separated at random into four groups, which were harvested at 100, 200, 240 and 270 days of gestation ($n = 4/5$, 5/6, 5/6 and 4/6 for HIGH/LOW fed cows at 100, 200, 240 and 270 days, respectively) with at least two cows gestating same sex fetuses being harvested at each time. At harvest, fetuses were collected and dissected and gut was emptied and separated into small and large intestine, which were measured. Data were analyzed in a 2×2×4 factorial with two feeding level, two fetal sex and four stages of pregnancy. There were no significant interactions ($P > 0.19$) among feeding level, fetal sex and days of pregnancy on gut length. Small intestine and total gut length were not affected by feeding level ($P = 0.86$ and 0.75, respectively) and fetal sex ($P = 0.87$ and 0.71, respectively). Large intestine was longer ($P = 0.049$) in female (134.9 cm) than in male fetuses (123.4 cm) but was not affected by feeding level ($P = 0.16$). Fetal small and large intestine and total gut length increased ($P < 0.001$) as the pregnancy age increased but were not different between 240 and 270 days of gestation ($P = 0.64$, 0.78 and 0.62, respectively). The average fetal gut length was 431, 976, 1272 and 1361 cm at 100, 200, 240 and 270 days of gestation, respectively. The results suggest that female fetuses have longer large intestine than male fetuses, although the explanation for this finding is still inconclusive and requires further studies.
Funded by INCT-CA, CNPq and FAPEMIG.

Key Words: fetal programming, gut development, maternal nutrition

1169 (T125) Intrauterine position affects fetal weight and crown-rump length throughout gestation.

Y. D. Jang[*], Y. L. Ma, and M. D. Lindemann, *University of Kentucky, Lexington.*

To investigate the effect of intrauterine position on fetal growth throughout gestation, data from 64 gilts ($n = 784$ fetuses) that were slaughtered at assigned days of gestation (d 43, 58, 73, 91, 101, and 108; $n = 8$, 11, 11, 12, 11, and 11, respectively) on a project to evaluate fetal mineral deposition were used. Placental units were removed from the uterus, and position, sex, weight, and crown-rump length (CRL) of each fetus were recorded. Fetuses were classified into 5 categories for absolute intrauterine position: the ovarian end (OE) of the uterine horn, next to the ovarian end (NOE), the middle (M), next to the cervical end (NCE), and the cervical end (CE). Fetuses at the OE and NOE of the uterine horn were heavier (108.6, 109.3, 101.9, 103.6, and 105.0 g for OE, NOE, M, NCE, and CE, respectively; $P = 0.06$) and longer (12.8, 12.6, 12.2, 12.1, and 12.3 cm; $P < 0.01$) than those in the M at d

58 of gestation. Fetuses at the OE of the uterine horn were also heavier and longer than those at M and NCE at d 101 (1078.9, 1015.6, 945.5, 890.6, and 956.2 g, and 28.4, 27.4, 26.8, 26.3, and 26.8 cm; $P < 0.01$) and 108 (1410.3, 1453.4, 1318.0, 1254.1, and 1407.9 g, and 31.6, 31.4, 30.6, 30.1, and 31.1 cm; $P < 0.01$) of gestation. Fetuses at the CE were intermediate in weight and length. Male fetuses were heavier than female fetuses at d 43 (16.9 vs. 15.9 g), 58 (109.4 vs. 101.1 g), 73 (350.9 vs. 331.7 g), and 108 (1410.6 vs. 1298.6 g) of gestation ($P < 0.05$) and longer than female fetuses at d 58 (12.5 vs. 12.3 cm; $P = 0.06$), 73 (18.9 vs. 18.5 cm; $P < 0.05$), 101 (27.4 vs. 26.8 cm; $P = 0.07$), and 108 (31.1 vs. 30.5 cm; $P < 0.05$) of gestation. Fetal weight was highly correlated with CRL at all gestational ages (r = 0.778 to 0.955; $P < 0.01$). These results indicate that the absolute intrauterine position affects fetal growth such that each end of the uterine horn has heavier fetuses than the middle, and that male pigs grow faster than female pigs even prior to birth.

Key Words: fetal growth, gestation age, intrauterine position

---

1170 (T126) Milk diet but not quercetin intake affects postprandial glucose metabolism in neonatal calves. J. Gruse[1], S. Görs[1], W. Otten[1], J. M. Weitzel[1], S. Wolffram[2], C. C. Metges[1], and H. M. Hammon[*1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]Institute of Animal Nutrition and Physiology, University of Kiel, Germany.*

The hypothesis was tested that the flavonoid quercetin, which exerts effects on glucose metabolism in several species, influences postprandial glucose uptake in neonatal calves and that this effect depends on milk diet. Twenty-seven new-born male German Holstein calves were randomly assigned to two feeding groups receiving same amounts of either colostrum (C; $n = 14$) or a milk-based formula (F; n = 13) with same nutrient density as C, but no biologically active factors during the first two d of life. From d 3 to d 7, all calves were fed milk replacer at 12% of BW (150 g powder/L). From d 2 on, groups were subdivided each into a treatment group receiving 150 µmol/(kg BW × d) quercetin as quercetin aglycon with milk and a control group without additional quercetin. On d 7, calves were tube-fed their morning meal (4% of BW) mixed with 10 mg/kg BW [$^{13}C_6$]-glucose and the daily quercetin dose. Immediately afterwards, an intravenous bolus dose of [6.6-$^2H_2$]-glucose (5 mg/kg BW) was applied through a jugular vein catheter. Blood samples were taken to measure plasma ^{13}C and ^2H glucose enrichments and to calculate rates of glucose appearance ($Ra_{i.v.}$ resp. Ra_{oral}) and fractional first pass splanchnic uptake (FPU) of glucose. Additional blood samples were taken to determine plasma concentrations of glucose, insulin, glucagon, noradrenaline and adrenaline. Data were analysed either by General Linear Model or by PROC MIXED of SAS with feeding, quercetin, and time as fixed effects. Plasma concentrations of glucose, insulin, glucagon, and adrenaline were greater ($P < 0.05$) in C- than in F-fed calves. Recovery of decreased adrenaline to basal concentrations was faster ($P < 0.05$) when quercetin was fed. Glucose FPU and Ra_{oral} were greater ($P < 0.05$) in F- than in C-fed calves, but were not affected by quercetin. Results underline the importance of colostrum feeding during the first days of life on postprandial glucose metabolism and indicate that quercetin does not have a major effect on glucose metabolism neither in C- nor in F-fed neonatal calves.

Key Words: quercetin, glucose first-pass uptake, calf

1171 (T127) Ontogenic gene expression profiles in pig hepatogenesis. J. Kwintkiewicz[*1], T. J. Caperna[1], T. G. Ramsay[1], H. D. Guthrie[1], C. C. Talbot[2], L. L. Schreier[1], and L. A. Blomberg[1], *[1]USDA-ARS-BARC, Beltsville, MD, [2] Johns Hopkins School of Medicine, Baltimore, MD.*

Liver is a key organ required for development and growth, whether fetal or post partum. Selection for greater litter size in swine has resulted in increased variability in piglet weight/litter, and greater weight piglets thrive better postnatally. To better understand hepatogenesis, comprehensive ontogenic gene expression profiling was performed to determine baseline expression patterns associated with liver development. Liver was collected from the greatest weight fetus of four distinct unilaterally hysterectomized:ovariectimized gilts at prenatal day (PND) 37, 50, 70, and 110. Total RNA was isolated, mRNA amplified and subjected to microarray analysis (Agilent). Three comparisons were performed: PND50 vs. PND37, PND70 vs. PND50 and PND110 vs. PND70; only genes whose expression, between at least two time points, was ± 1.5 fold with $P < 0.05$ were characterized further. A total of 6061 annotated genes exhibited altered expression: 648 down- and 341 up-regulated at PND37 vs. PND50; 666 down- and 1399 up-regulated at PND70 vs. PND50; and 1564 down- and 1443 up-regulated at PND110 vs. PND70. Thirty-five transcripts were selected for validation by absolute quantitative PCR; they clustered into five functional categories: 1) hematopoietic and early liver function, 2) extracellular matrix, 3) hepatocyte function, 4) biliary function, and 5) transcription factors. To examine changes elicited following parturition, liver was collected from greatest weight piglets at post partum day (*P*PD) 1 ($n = 3$) and 2 ($n = 4$) and analyzed along with fetal samples. The expression of hematopoietic genes (e.g. coproporphyrinogen oxidase) was high at PND37 and declined by mid-gestation. Similarly, the expression of markers of undifferentiated hepatoblasts (e.g. Cbp/P300-Interacting Transactivator 1) was high in early gestation and decreased below the detection threshold post partum. In contrast, the abundance of extracellular matrix genes (e.g. hevin) peaked perinatally. Hepatocyte serum or enzyme transcripts increased gradually with a maximum induction at PPD2 vs. PND37 (e.g alcohol

dehydrogenase, a 2,266-fold increase). Likewise, the expression of inhibin beta B, involved in biliary duct morphogenesis, increased 188-fold. Transcription factors (e.g. hepatocyte nuclear factors) exhibited small variation during gestation but were significantly elevated perinatally. More impressive was the up-regulation (79-fold) of Kruppel-like factor 9 at and beyond PND 110 vs. earlier time points. The study identified commonalities and differences of expression profiles to those observed in other species; this should help scientists navigate new routes of investigation in liver cell function in swine. Future studies will examine dysregulation of these genes in runt or slow growing pigs.

Key Words: liver, development, pig

1172 (T128) Production of bioactive porcine mutant myostatin propeptide/Fc fusion protein in *Escherichia coli*. S. B. Lee*[1], S. K. Park[2], and Y. S. Kim[1], *[1]University of Hawaii, Honolulu, [2]National Institute of Animal Science, RDA, Suwon, South Korea.*

Skeletal muscle mass is negatively regulated by myostatin (MSTN), implying that MSTN inhibition would be a potential approach to increase skeletal muscle mass of meat producing animals. The activity of MSTN is suppressed by MSTN propeptide (MSTNPro), the N-terminal region of unprocessed MSTN that is cleaved off during post-translational MSTN processing. The objective of current study was to produce a mutant form of porcine MSTNPro fused to the Fc region of pig immunoglobulin G (*P*MSTNProM-Fc) in *E. coli* in order to examine its potential as an agent to enhance muscle mass in pigs. The *pMSTNProM-Fc* cDNA was constructed and cloned into pMAL-c5x vector downstream of the maltose-binding protein (MBP) gene, then was transformed and expressed in soluble forms in *E. coli*. For each L of cell culture at 4°C for 7 days, about 13 mg of soluble MBP-pMSTNProM-Fc protein was purified by amylose-resin affinity chromatography. Further purification by protein A agarose affinity chromatography yielded about 0.64 mg/L culture of MBP-pMSTNProM-Fc protein. MBP-pMSTNProM-Fc inhibited MSTN bioactivity in a dosage-dependent manner in an in vitro gene reporter assay. The capacity of MBP-pMSTNProM-Fc to inhibit MSTN was comparable to those of MBP-pMSTNPro produced in *E. coli* and commercially-available murine MSTNPro produced in an eukaryotic system. Results from the current study show that Fc fusion to MBP-pMSTNPro does not affect the bioactivity of MBP-pMSTNPro, and the production of bioactive, mutant form of pig MSTN propeptide/Fc fusion protein is possible in *E. coli*.

Key Words: myostatin propeptide, pig, Fc fusion protein

1173 (T129) Short- and medium-term changes in performance and metabolism of dairy calves offered different amounts of milk replacer. C. Yunta[1], M. Terré[1], and A. Bach*[2,3], *[1]IRTA, Caldes de Montbui, Spain, [2]ICREA, Barcelona, Spain, [3]Dep. of Ruminant Production, IRTA, Caldes de Montbui, Spain.*

The objective of the present study was to compare the intake, growth, and glucose metabolism of dairy calves fed 4, 6 or 8 L/d of milk replacer (MR). One hundred and twenty female calves were randomly assigned to one of the 3 groups (4L, 6L, and 8L) differing only in the quantity of MR offered. Daily MR and feed intakes were recorded. Calves were weighed at days 0, 35 and 63. Average daily gain (ADG) at day 35 (ADG35) and at day 63 (ADG63) as well as gain to feed (GtoF) were calculated. A glucose tolerance test (GTT), consisting of 180 mg of glucose per kg of BW infused into the jugular vein of 15 heifers per group, was performed at days 42 and 86 of life. Blood samples were collected at -5, 0, 4, 8, 12, 18, 25, 35, 35 and 60 min relative to glucose infusion and glucose and insulin levels were analyzed. Area under the curve (AUC), clearance rate (CR), insulin to glucose rate (ItoG) and insulin sensitivity were calculated. Data were analyzed using a mixed effects model with repeated measures. Total DMI was greatest ($P < 0.05$) for 8L calves (1,010 ± 22 vs 950 ± 23 g/d), but 6L and 8L calves consumed less starter feed ($P < 0.05$; 205 ± 21 g/d) than 4L calves (400 ± 22 g/d). Calves on 8L had the greatest ($P < 0.01$) ADG35 (757 ± 20.1 g/d) followed by 6L (566 ± 19.8 g/d) and 4L calves (476 ± 20.4 g/d); but ADG63 did not differ among treatments. Allowance of MR did not affect GtoF ratio. Glucose AUC or CR did not differ between treatments. However, calves on 8L produced more ($P < 0.005$) insulin (2,365 ± 211 µU/mL x 60min) than 6L (1,353 ± 219) or 4L (1,300 ± 219) calves. Calves on 8L, had an ItoG (177.5 ± 20.76 µU/mg) that was almost 2-fold greater ($P < 0.05$) than in 4L (93.1 ± 21.17) and 1.5-fold greater ($P < 0.05$) than in 6L (113.6 ± 21.17) calves. Insulin sensitivity tended ($P = 0.07$) to be less in 8L (3.38 ± 0.30 mL/min x µU/mL per kg of BW) than in 4L or 6L calves (3.43 ± 0.30). We concluded that offering 8 L/d of MR elicits a decrease in starter feed intake and tends to decrease insulin sensitivity of calves.

Key Words: calves, enhanced-feeding, metabolism

1174 (T130) Stabilization of intestinal mast cells at weaning improves performance of early-weaned pigs. A. Mereu[1], M. G. Tedo[1], J. Charve[1], A. J. Moeser[2], and I. R. Ipharraguerre*[1], *[1]Lucta S.A., Montornés del Vallés, Spain, [2]North Carolina State University, Raleigh.*

Previous work showed that weaning stress causes gut barrier dysfunction partly by triggering the release of corticotropin releasing factor (CRF) and thereby inducing the degranulation of intestinal mast cell (MC). This study investigated the

hypothesis that attenuating the weaning-induced activation of the CRF-MC axis via administration of a MC stabilizing agent (cromolyn) may improve gut permeability and piglet performance after weaning. Twenty piglets (Large White x Landrace x Pietrain) were weaned (20 ± 1 d of age; 6.4 ± 0.4 kg of BW) and injected intraperitoneally with saline (control, n = 10) or 20 mg/kg BW of sodium cromolyn (CR, n = 10) at – 0.5, 8 and 16 h relative to weaning. Piglets were housed individually and fed *ad libitum* a pre-starter diet from 0 to 14 d postweaning followed by a starter diet until the end of the study on d 35. Body weight and feed intake were measured weekly; the plasma concentration of CRF and MC tryptase (MCT) was measured on d 2; and the plasma recovery of lactulose and Co-EDTA (*P*ermeability markers) was assessed 1 h after intragastric infusion on d 2 and 35. On d 35, 8 pigs/treatment were sacrificed and their intestines were collected for later analyses. Performance data were analyzed with a mixed-effects model with repeated measures in time in which pig was treated as random effect and treatment, week, and their interaction as fixed effects. All other variables were analyzed with the same model without repeated measures. Plasma concentration of CRF, MCT, and permeability markers and mucosal morphology of the ileum were not affected by treatments. Although not significant, CR pigs had 15% more granulated MC in the ileum than control pigs (66.3 vs. 51.7 ± 0.10 cells/mm^2; $P < 0.20$). On average, CR pigs consumed more feed (369 vs. 313 ± 13.6 g/d; $P < 0.01$), gained more BW (283 vs. 234 ± 11.7 g/d; $P < 0.01$), and grew more efficiently (0.60 vs. 0.40 ± 0.07; $P < 0.05$) than their control counterparts. As a result, pigs on the CR group were 1.4 kg heavier than those in the control group by d 35 (16.5 vs. 17.9 ± 0.17 kg; $P < 0.01$). In conclusion, interventions capable of moderating the weaning-induced activation of the CRF-MC axis may contribute greatly to improve pig performance after weaning.

Key Words: stress, gut permeability, growth

1175 (T131) The effect of essential oil/botanical product on growth and performance of calves fed milk replacer.

B. L. Miller[*1], T. Earleywine[2], W. S. Bowen Yoho[3], and T. E. Johnson[3], *[1]Land O'Lakes–Purina Feed LLC, Gray Summit, MO, [2]Land O'Lakes Animal Milk Products, Shoreview, MN, [3]Land O' Lakes, Inc., Webster City, IA.*

In two separate trials, the growth and performance of calves fed milk replacer (MR) containing an essential oil/botanical product were examined. Eighteen (18) and thirty-two (32) 3 – 10 d old Holstein bull calves with average initial weights of 43.3 kg (SD = 1.62 kg) and 47.6 kg (SD = 2.50 kg) were shipped from Wisconsin to the Land O' Lakes Research Facility for trials 1 and 2, respectively. Calves were randomly assigned according to body weight (BW) and blood gamma globulin to either a control or experimental milk replacer. The experimental MR in both trials was the same as the control with an essential oil/botanical product (Digestarom, Micro-Plus Konzentrate; Stadtoldendorf, Germany) included at 0.05% active ingredient. Calves on trial 1 were fed to provide 680 g DM/d of a 22% protein/20% fat MR during d 1 to 35 in 2 feedings at 0600 and 1515h. Days 36 to 42, calves were offered 340 g DM/d in one feeding at 0600h. Calf starter (20% CP, as fed basis) was fed ad libitum. Calves on trial 2 were fed a 27% all milk protein/10% fat MR to provide 816 g DM/d during d 1 to 7, and 1135 g DM/d during days 8 – 42, in 2 feedings. Calves were offered 567.5 g in one feeding at 0600 h during days 43 - 49. Calf starter (22% CP, as fed basis) was fed ad libitum. Data were analyzed by PROC MIXEDs of SAS. For trial 1, calves offered no essential oil/botanical product tended to be inferior in total weight gain ($P = 0.12$) and MR consumption ($P = 0.11$) when compared to calves offered an essential oil/botanical product. Calves receiving an essential oil/botanical product were numerically higher ($P > 0.05$) in total starter consumption when compared to calves receiving no essential oil/botanical product. For trial 2, while there was no statistical difference ($P > 0.05$) in total body weight gain, calves fed an essential oil/botanical product were numerically higher in total body weight gain when compared to calves fed no essential oil/botanical product. Calves offered an essential oil/botanical product were superior in feed efficiency ($P = 0.07$), hip height gain ($P \leq 0.01$), and heart girth gain ($P < 0.05$), when compared to calves offered no essential oil/botanical product. Essential oil/botanical product improved calf growth and performance.

Key Words: calf, milk replacer, essential oil

1176 (T132) The effects of feeding strategy and housing management on intake and growth performance of Holstein calves from birth through weaning.

H. M. Gauthier[1], S. E. Williams[*1], D. M. Shenk[1], C. S. Ballard[1], K. M. Morrill[2], and H. M. Dann[1], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Cornell University, Ithaca, NY.*

Forty-eight Holstein calves with an average birth weight of 42.5 ± 0.4 kg were used in a randomized block design to evaluate feeding strategy and housing management from birth through weaning (wk 8). Calves were fed 675 g of colostrum replacer (≥ 180 g IgG; The Saskatoon Colostrum Co. Ltd.) within 2 h of birth. Serum total protein averaged 5.6 ± 0.1 g/dL at 2 d of age. Treatments were: 1) fixed feeding of milk replacer at 770 g DM/d from birth through 15 d of age and 900 g DM/d thereafter split into 2 feedings with calves housed in individual hutches (FI; n = 16), 2) ad libitum feeding of milk replacer with calves housed in individual hutches (AI; n = 16), and 3) ad libitum feeding of milk replacer with calves housed as a group of 4 in group hutches (AG; n = 16). Milk replacer was 24% CP and 20% fat and fed at 14% solids. Calves received water and a 23% CP starter concentrate ad libitum. Weaning occurred over a 6-d period with FI calves fed 450 g DM/d and AI and AG calves fed 900 g DM/d for 3 d

followed by 450 g DM/d for 3 d. Intake was measured daily. Body weight was measured weekly. Data were analyzed with the PROC MIXED of SAS with the experimental unit defined as a group of 4 calves with data expressed on a per calf basis. When calves were individually housed, ad libitum feeding resulted in greater intake, average daily gain, and feed efficiency than fixed feeding. Intake and body weight gain were not affected by housing when calves were fed ad libitum. However, the AG calves had a better feed efficiency than AI calves suggesting that there may be benefits to group housing and the social interaction it provides the calves although the mechanism is unclear.

Key Words: calves, growth performance, milk replacer

Table 1176.

	Treatment				*P*-value	
	FI	AI	AG	SE	FI vs. AI	AI vs. AG
Milk replacer intake, kg DM	40.6	59.7	54.8	3.4	<0.01	0.35
Starter intake, kg DM	11.2	4.5	2.2	1.8	0.04	0.41
Total intake, kg DM	51.7	64.2	57.0	3.5	0.05	0.20
Body weight gain, kg	28.0	39.3	40.3	3.4	0.06	0.84
Average daily gain, kg	0.56	0.75	0.81	0.05	0.04	0.43
Gain:Feed	0.54	0.61	0.70	0.02	0.04	0.01

1177 (T133) The impact of in utero heat stress and nutrient restriction on progeny body composition.

J. S. Johnson[*1], M. Abuajamieh[1], M. Sanz Fernandez[1], J. T. Seibert[1], S. K. Stoakes[1], A. F. Keating[1], J. W. Ross[1], J. T. Selsby[1], R. P. Rhoads[2], and L. H. Baumgard[1], *[1]Iowa State University, Ames, [2]Virginia Tech, Blacksburg.*

We demonstrated that in utero heat stress (IUHS) alters future tissue accretion in pig progeny. Whether this results from reduced maternal feed intake (FI) or the direct effect of heat stress (HS) is not clear. Study objectives were to compare the rate and quantity of tissue accretion in growing rats exposed to differing in utero environments. On gestation d 3, pregnant Sprague Dawley rats were exposed to either thermoneutral (TN; constant 22°C; $n = 4$), HS (cyclical 34ºC nighttime and 30°C daytime; $n = 4$), or pair-fed to HS-counterparts in TN conditions (*P*FTN; constant 22ºC; $n = 4$) until d 19 of gestation. HS increased ($P < 0.01$) dam rectal temperature (1.3ºC) compared to TN and PFTN conditions, and reduced FI ($P < 0.01$; 14.1 vs. 21.0 g/d) compared to TN controls. Litter size was similar ($P > 0.96$; 10.9 pups/litter) for all treatments and pup birth weight was reduced ($P < 0.04$; 29.7%) in HS dams versus TN controls. At d 26 of life, two male pups per dam [n = 8 in utero TN (IUTN); $n = 8$ IUHS; $n = 8$ in utero PFTN (IUPFTN)] were selected, and initial body composition was determined using dual-energy x-ray absorptiometry (DXA). Following the initial scan, all offspring were individually housed in TN conditions (21.8 ± 0.1°C) and DXA analyses were repeated on d 46 and 66 of life. In utero treatment did not alter ($P > 0.81$) offspring BW, FI (18.6 g/d) or ADG (5.8 g/d) from d 26 to 66. Body fat content and total adipose tissue were increased ($P < 0.01$) in IUPFTN (19.8% and 39.6 g, respectively) compared to IUTN and IUHS offspring (17.9% and 35.9 g, and 17.6% and 34.1 g, respectively). IUPFTN offspring had reduced ($P < 0.01$) body lean tissue compared to IUTN and IUHS counterparts (77.9 vs. 79.8 and 80.1%, respectively). Body composition did not differ between IUHS and IUTN offspring. In utero treatment did not alter body ash content. From d 26 to 66 the adipose to lean tissue accretion ratio was greater ($P < 0.01$; 19.2%) for IUPFTN compared to IUHS offspring. Epididymal fat pad weight was increased ($P < 0.04$; 21.6%) in IUPFTN versus IUHS offspring. In summary and in contrast to pigs, IUHS did not appear to impact body composition; however, IUPFTN rats likely experienced prenatal imprinting that altered the future hierarchy of tissue accretion.

Key Words: in utero heat stress, rat, tissue accretion

1178 (T134) Weight, height and relative accuracy indicators as a management tool for reducing age at first breeding and calving of dairy heifers.

M. Duplessis[*1,2], R. Lacroix[2], R. I. Cue[3], D. E. Santschi[2], and D. M. Lefebvre[2], *[1]Université Laval, Département des Sciences Animales, Québec, Canada, [2]Valacta, Ste-Anne-de-Bellevue, QC, Canada, [3]McGill University, Dep. of Animal Science, Ste-Anne-de-Bellevue, QC, Canada.*

In Québec, Canada, age at first calving occurs on average at 27 mo, whereas the target is 22 to 24 mo to maximize herd profitability. The aim of this study was to generate indicators (such as heifer weight and height at 15 and 24 mo, and age at which optimal weight for breeding is attained i.e. 55% of mature weight) and their respective relative accuracy (RA) using a growth predicting model based on random regression. Weight and height data records from 1995 to 2012, respectively measured by chest girth, and height at the withers on Holstein (HO), Jersey (JE), and Brown Swiss (BS) dairy heifers were obtained from Valacta database (DHI agency, Ste-Anne-de-Bellevue, QC, Canada). Heifers with less than two records were excluded from the analysis. For each heifer, weight at 15 and 24 mo were computed using a second degree polynomial equation for which individual parameters were obtained from random regression using R (v1.15.2) and nlme package. For height, a non-linear mono-molecular random regression model was used. Age at optimal breeding weight was calculated by the square root of the second degree polynomial equation. Relative accuracy was calculated as the prediction error variance, relative to an RA of 99% when a heifer was measured routinely every 3 mo, starting at 2 mo of age. Table 1178 shows the mean, standard deviation (SD) of the five indicators described above, RA and mature weight. It is possible to observe that,

Table 1178. Indicators with their respective relative accuracy (RA, %)

Indicators	Holstein			Jersey			Brown Swiss		
	Mean	SD	RA	Mean	SD	RA	Mean	SD	RA
Weight at 15 mo (kg)	425	34	87	297	26	92	379	36	87
Weight at 24 mo (kg)	627	39	43	429	27	60	560	43	67
Height at 15 mo (cm)	134	4.8		122	4.0		130	5.3	
Height at 24 mo (cm)	143	5.9		131	4.0		140	6.2	
Age at optimal breeding weight (mo)	13.6	1.4		12.7	1.4		14.5	1.7	
Mature weight	710	65		470	64		670	61	

on average, dairy heifers in Québec, Canada could be bred at 13.6 mo, the optimal age for a first calving at 24 mo. These indicators could be calculated on an individual-heifer and on a herd-level basis, and used on farm as a management tool for reducing age at first breeding and at first calving.

Key Words: dairy heifers, age at first breeding, age at first calving

1179 (T135) Growth and health of pre-weaned Holstein dairy heifers fed Proternative SF in combination with Levucell. S. D. L. Gadeken[*1], A. D. Garcia[2], F. Díaz-Royón[2], T. Erickson[1], and A. Aguilar[3], *[1]South Dakota State University, Brookings, [2]Dairy Science Dep., South Dakota State University, Brookings, [3]Lallemand, Martinsville, IN.*

The objective of this experiment was to evaluate the effects of grain starter supplemented with two live yeast-cell products on health and growth of pre-weaned Holstein heifers. In July 2013, sixty newborn heifers from a local dairy were blocked by weight and serum protein concentration (SPC). A texturized calf starter was prepared with half of the batch used as control (NS). The other half was yeast-supplemented (YS), to contain in each 1.14 kg of starter, 10 billion colony forming units (CFU) of Proternative SF (*Saccharomyces cerevisiae boulardii),* and 10 billion CFU of Levucell SC (*Saccharomyces cerevisiae*I-1077), both from Lallemand Animal Nutrition (Milwaukee, WI). The starter was formulated with cracked corn, whole oats, protein pellets, liquid fat, molasses, corn gluten feed, Bio-Mos (Alltech Inc., Nicholasville, KY), and Deccox (Zoetis, Inc. Kalamazoo, MI). Blood SPC was measured at birth with a refractometer (Misco #PA202X, Cleveland, OH). Growth was assessed on d 0, 30 and 60 d using an electronic scale, measuring tapes, and a hipometer. Calves were individually housed in polypropylene hutches until weaned at d 60. Two liters of farm-pasteurized milk (UV Pure) were bottle-fed twice daily. Starter was fed daily to 6d old calves at d1. Starter intake and individual orts were measured. Drinking water was constantly available. An SPC of 6.5 g/dL observed in both NS and YS calves suggested high passive immunity transfer, as it is strongly correlated with IgG concentrations. This exceeded the concentrations of 5.5 g/dL SPC considered excellent by the dairy industry. There was a trend for higher starter DMI (11%) in calves fed YS(1.14 kg vs. 1.01 kg for YS and NS, respectively) (P = 0.09). Weight gains (70.3 kg vs. 69.6 kg, P = 0.68), whither heights (86.4 vs. 86.9cm, P = 0.77), hip heights (91.9cm vs. 91.4cm, P = 0.59), and hip widths (27.5cm vs. 27.4cm, P = 0.58) were not different between YS and NS, respectively. Three animals were removed from the experiment due to hernias or reduced motility; no significant respiratory problems or diarrhea were observed. Under the conditions of this experiment, calf growth was not different between treatments. This can be attributed in great part to the very high SPC result of excellent colostrum feeding program which may have negated the beneficial impact of yeast supplementation.

Key Words: heifers, calves, growth, *Saccharomyces*

GROWTH & DEVELOPMENT II

1180 (W116) Effect of incubation temperature on the proliferation and differentiation of pig preadipocytes in primary culture. A. E. Bohan*, J. Bartosh, and T. D. Brandebourg, *Auburn University, Auburn.*

Better understanding molecular mechanisms governing the proliferation and differentiation of pig preadipocytes may provide insight into the regulation of adipose tissue development in vivo. Primary cultures of pig preadipocytes have served as a useful tool for investigating these mechanisms. However, to date, such cultures have generally been maintained at 37°C while normal body temperature in pigs is 39.2°C. This raises questions concerning the physiological relevance of culturing primary pig preadipocytes at 37°C. The objective of this study was to investigate the effect of culture temperature, 37 vs. 39°C, on the proliferation and differentiation of pig preadipocytes in primary culture. The effect of temperature on preadipocyte proliferation was determined using the MTT, resazurin, and cell count assays as markers for proliferation. Preadipocyte number was increased 30 to 50% when cultures were incubated at 39 vs. 37°C based upon cleavage of the tetrazolium salt, MTT ($P < 0.001$), reduction of resazurin ($P < 0.001$), and daily cell counts ($P < 0.001$). Differentiation was monitored on d 8 after induction morphologically, enzymatically, and by measuring the mRNA abundance of key adipogenic transcription factors via real-time PCR. Glycerol-3-phosphate dehydrogenase (GPDH) activity was higher in differentiating cultures maintained at 39°C than in cultures differentiated at 37°C ($P < 0.01$) in agreement with increased lipid accumulation observed in these cultures as measured by Oil Red O staining suggesting that cultures maintained at 39°C differentiated to a greater degree than those maintained at 37°C. Finally, the effect of temperature on gene expression was investigated. Expression of peroxisome proliferator-activated receptor gamma (*P*PARγ; $P < 0.01$), CCAAT/enhancer binding protein α (C/EBPα; $P < 0.01$), bone morphogenic protein 2 (BMP2; $P < 0.05$), bone morphogenic protein 4 (BMP4; $P < 0.05$), and adiponectin ($P < 0.001$) were higher while mRNA expression of CCAAT/enhancer binding protein beta (C/EBPβ; $P < 0.01$) was lower in cultures differentiated at 39°C versus those differentiated at 37°C. Collectively these data indicate that culturing primary preadipocytes at 37 rather than 39°C decreases their proliferation rates and suppresses their adipogenic potential. Furthermore the observation that incubation temperature influences gene expression in primary cultures of pig preadipocytes raises the possibility that studying porcine adipocyte hyperplasia at temperatures below physiological body temperatures may confound the ability to extrapolate observations concerning the underlying mechanisms regulating proliferation and differentiation of primary cultures of pig preadipocytes to the live animal.

Key Words: adipocyte, primary culture, pig

1181 (W117) Effects of maternal nutrient restriction on muscle satellite cell activity. J. S. Raja*, M. L. Hoffman, K. N. Peck, K. E. Govoni, S. A. Zinn, and S. A. Reed, *Dep. of Animal Science, University of Connecticut, Storrs.*

Postnatal muscle growth is altered by poor maternal nutrition during gestation. Satellite cells are myogenic precursor cells that contribute to postnatal muscle growth. Satellite cell activity can be evaluated by the expression of several transcription factors that are critical for proper myogenesis. Pax7 is expressed in quiescent and active satellite cells. Expression of MyoD is increased in active and proliferating satellite cells and terminal differentiation is marked by expression of myogenin. We hypothesized that poor maternal nutrition during gestation would alter the temporal expression of Pax7, MyoD and myogenin in satellite cells in vitro. Multiparous ewes ($n = 23$) were housed individually and fed 100% or 60% NRC requirements beginning at d 31 ± 1.3 of gestation. Lambs from control-fed (CON) or restricted-fed (RES) ewes were euthanized within 24 h of birth (d 1; $n = 12$) or were maintained on a control diet until 3 mo of age ($n = 11$). Satellite cells were isolated from the semitendinosus muscle at necropsy and cryopreserved until further use. Satellite cells were cultured in growth media for 24, 48 or 72 h before immunostaining for Pax7, MyoD and myogenin. Hoechst dye was used to visualize nuclei. The percent of immunopositive cells was calculated as the number of immunopositive cells divided by total nuclei. Data were analyzed by PROC PROC MIXED of SAS. After 24 h of culture, the percent of cells expressing MyoD was 5-fold greater in RES lambs at birth (58.40 ± 12.08%) than cells of CON lambs (11.68 ± 17.08%; $P = 0.03$). After 48 h of culture, there was a greater percentage of cells expressing myogenin in RES lambs at birth (63.25 ± 14.00%) compared with cells from CON lambs (17.57 ± 17.08%; $P = 0.04$). However, after 72 h of culture the percent of satellite cells expressing myogenin in RES lambs at birth (40.07 ± 14.00%) was approximately 50% less than cells from CON lambs (83.98 ± 17.08%; $P = 0.05$). There were no differences in the percent of Pax7 immunopostive cells at birth, or any factors in cells from lambs at 3 mo of age ($P > 0.05$). In conclusion, restricted nutrient availability during gestation alters the temporal expression of myogenic regulatory factors in the offspring and is suggestive of precocious differentiation.

Key Words: muscle, satellite cells, poor maternal nutrition

1182 (W118) Effects of milk replacer and multivitamin-mineral supplementation on performance of heat stressed dairy calves. S. Blair*[1], C. C. Williams[1], B. F. Jenny[1], M. Thomas[1], V. Morgan[1], and T. Earleywine[2], [1]*Louisiana State University AgCenter, Baton Rouge,* [2]*Land O'Lakes Animal Milk Products, Shoreview, MN.*

Seventy-one neonatal Holstein calves (40 female; 30 male) were used in a randomized block design with a 2x2 factorial arrangement of treatments to evaluate the effects of milk replacer (MR) alone or in combination with a multivitamin and electrolyte supplement on growth performance and mitigation of heat stress in southeast Louisiana. Milk replacer treatments consisted of Land O'Lakes Herdmaker Supreme (20% CP, 20% fat; CON) and Land O'Lakes Warm Front (27% CP, 10% fat; WF). Supplemented calves received either 0 or 20 ml Palamountains Calf Boost (CB) in MR once daily in the morning feeding. Calves were offered MR treatments beginning on day 2, and all milk replacer was mixed at 15% solids. Calves consuming CON were fed 2.28kg MR twice daily. Calves on WF were fed 2.72kg MR twice daily for the first three wk of life, and 3.86kg twice daily until weaning. Water and calf starter (20%CP) were offered ad libitum beginning on d 2. Beginning on d 42, MR feeding was reduced to 1 time per day for all treatment groups to decrease MR intake by 50%. On d 49 calves were weaned. Calves remained in their hutches until d 56 to determine immediate post weaning performance. Body weight, hip height, wither height, hip width, and body length were recorded weekly, and grain and water intakes were measured twice daily. Average rectal temperature, respiration rates, and fecal scores were recorded three times weekly at both 0800 h and 1600 h. All data were analyzed using the PROC MIXED of SAS. There was a main effect of MR, with calves fed WF showing greater body weights and increased hip height, wither height, and body length ($P < 0.05$). There was no significant effect of CB on growth or intake measurements. Calves fed WF consumed less grain than CON calves ($P < 0.05$) until the end of wk 7, but showed no difference at wk 8. Calves consuming WF also showed higher fecal scores ($P < 0.05$), but well within normal ranges for healthy calves. All calves consumed more water as age increased ($P < 0.05$), with no interactions of sex or treatment. There was no significant effect of MR or CB on temperature or respiration rates ($P > 0.05$). These data indicate that MR feeding management may improve growth performance in neonatal dairy calves, but multivitamin mineral supplements may not provide any additional benefit.

Key Words: calf milk replacer, multivitamin-mineral supplement, heat stress

1183 (W119) Effects of milk replacer feeding frequency on growth and performance of neonatal Holstein calves. M. Thomas*, C. C. Williams, B. F. Jenny, S. Blair, C. F. Hutchison, C. Burke, E. L. Chartier, M. Orellana, and A. H. Dolejsiova, *Louisiana State University AgCenter, Baton Rouge.*

Fifty-seven neonatal Holstein calves (40 female; 17 male) were assigned to one of three treatments at day 2 of age to study effects of milk replacer feeding frequency on growth, performance, and health. Treatments consisted of 1X, with total amount of reconstituted milk replacer fed at 0600 h; 2X, with total amount of reconstituted milk replacer divided into 2 equal amounts and fed at 0600 h and 1700 h; and 3X, with total amount of reconstituted milk replacer divided into three equal amounts and fed at 0600 h, 1200 h, and 1700 hp Calves were housed in individual hutches and fed milk replacer until abrupt weaning at 42 d of age. Total daily amount of milk replacer offered was equal to 1.5% of birth weight and reconstituted to a total volume of 10% birth weight. Water and an 18% crude protein calf starter were offered ad libitum beginning on d 3 throughout the duration of the trial. Calves remained in their hutches until day 56 to determine immediate post weaning performance. BW was determined at birth and weekly throughout the trial. Wither height (WH), hip height (HH) and hip width (HW) were measured on d 7, 14, 28, 42, and 56 of age. Feed intake, water intake, and fecal scores were recorded daily. Effects of treatment, week, and their interactions were analyzed using the PROC MIXED of SAS (Cary, NC). There was no effect ($P > 0.05$) of treatment on BW, HH, HW, or WH. There was a week effect ($P < 0.01$) for BW, HH, HW, and WH as well as grain and water intake, with all calves increasing intake and growth throughout the duration of the study. There was no effect ($P > 0.05$) of treatment on fecal scores, with scores being similar and within the normal ranges for healthy calves throughout the project. Overall, milk replacer feeding frequency did not show any significant effects on growth or performance of these Holstein dairy calves.

Key Words: dairy calves, milk replacer, feeding frequency

1184 (W120) High energy diet enhances intramuscular adipogenesis in Hanwoo steers distributed to breeding value for meat quality. K. Y. Chung*, S. W. Lee, U. H. Kim, S. C. Jang, Y. M. Cho, E. M. Lee, S. M. Lee, and H. S. Kang, *Hanwoo Experiment Station, NIAS, RDA, Pyeongchang, South Korea.*

High energy diet has been used for enhancing intramuscular adipose tissue in high quality beef cattle. Estimated breeding value (EBV) was used as a selection method to determine high quality beef group. The aim of this experiment was to determine the effect of high energy diet on the high and low

beef group distributed by EBV for carcass quality grade. We hypothesized that adipogenic gene expressions and adipose carcass traits are increased in high EBV groups when fed a high energy diet. A 2 x 2 factorial arrangement (High EBV, Low EBV, and High energy diet, control diet) in a completely random design was used to feed 26 Hanwoo steers. Two steers were fed in same pen and 13 pens were used for treatment. Blood sample was drawn once a month at the beginning from 11 to 28 month. Longissimus Dorsi (LD) muscle was collected within 10 min of harvest for analysis of mRNA SCD, PPARγ, GLUT4, MHC1, MHC2X abundance. Overall ADG and DMI were not different between high energy diet and control diet ($P > 0.05$). Serum glucose and triglyceride concentrations were increased ($P < 0.05$) by high EBV group from 22 to 28 month old. Serum NEFA levels were greater ($P < 0.05$) in 24 mo old at high EBV group and steady decreased at 28 mo old. Marbling score and yield grade were not affected by high energy diet and EBV ($P > 0.05$). Real-time quantitative PCR revealed that the mRNA content of PPARγ and SCD of high EBV group increased ($P < 0.05$) as compared to low EBV group. The mRNA level of GLUT4 and MHC1 tend to increase ($P = 0.08$, 0.09) when control diet fed at high EBV group. These data indicate that high energy diets increased serum glucose and triglyceride concentrations of high EBV-steers at final fattening period. Although there are no interaction between diet and EBV levels, adipogenic gene expressions in high EBV-steers were greater than those in low EBV-steers. The selection of EBV for meat quality affected serum glucose level and adipogenic gene expression of feedlot Hanwoo steers.

Key Words: Hanwoo, EBV, adipogenesis

1185 (W121) Impact of the sires on puberty onset in Nellore heifers.
M. V. C. Ferraz Jr.*[1], A. V. Pires[2], D. D. Nepomuceno[2], A. D. B. Ribeiro[1], M. V. Biehl[2], J. P. C. Thieme[2], E. M. Moreira[1], J. A. Faleiro Neto[1], and J. R. S. Gonçalves[3], *[1]University of São Paulo– FMVZ/USP, Pirassununga, Brazil, [2]University of São Paulo– ESALQ/USP, Piracicaba, Brazil, [3]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, Brazil.*

In Brazil the main breed of beef cattle is Nellore, where it represents 70% of the national herd. Since the late onset of puberty one of the principal problems associated with this breed. The aim of this study was to evaluate the expected progeny differences (EPDs for scrotal circumference) of sires and its effect on puberty in Nellore heifers. The daughters of 12 sires (143 calf heifers) were used. After weaning at 210 days of age, the animals were mantained in cultivated pasture of Brachiaria ssp. with mineral supplement and water ad libitum. The heifers were weighed, and the puberty onset was assessed monthly from 12 to 30 mo (by ultrasonography - corpus luteum detection). The sires were classified in precocious and non-precocious groups according to the positive (PEPD, $n = 8$) or negative (NEPD, $n = 4$) EPD to scrotal circumference. Continuous variables were analyzed by PROC MIXED, and variables with binomial distribution were analyzed by GLIMMIX procedure, both through SAS 9.3. Heifers that were NEPD daughters had the puberty onset heavier ($P = 0.009$) and older ($P = 0.013$) than the PEPD daughters (weight: 317.0 ± 10.6 vs 294.8 ± 8.7 Kg; age: 644.7 ± 59.3 vs 593.5 ± 62.7 days; for NEPD and PEPD, respectively). The percentage of pubertal heifers at 14, 18, 26 and 30 months of age, not were different between NEPD and PEPD (14 months of age: 11.1 vs 8.2%; 18 months of age: 26.7 vs 30.6%; 26 months of age –66.7 vs 73.5%; 30 months of age: 93.3 vs 92.8%, for NEPD and PEPD, respectively). We can conclude that there is genetic heterogeneity to onset puberty in Nellore breed. Furthermore, the results reveal the importance of the use of proven sires for sexual precocity. Financial support: FAPESP.

Key Words: sexual precocity, Nellore, sire

1186 (W122) Microarray studies in high and low rfi cattle reveal a potential role for gonadotropin releasing hormone (GnRH) in regulating feed efficiency.
S. D. Perkins*[1], C. Foradori[1], A. K. McNeel[2], L. A. Kriese-Anderson[1], and T. D. Brandebourg[1], *[1]Auburn University, Auburn, [2]USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Residual feed intake (RFI) is a heritable feed efficiency measure. Mechanisms underlying variation in feed efficiency are currently poorly understood. To address this issue, two divergent cohorts consisting of High (H) and Low (L) RFI individuals were created by assessing RFI in forty-eight Angus-sired steers during a 70 d feeding trial to identify steers with divergent RFI. Microarray studies using the Affymetrix Bovine Genome Array were then conducted on hypothalamic tissue (HT) RNA samples harvested from H and L RFI steers. The test diet was 50% sorghum-sudan silage, 50% grain (2.9 Mcal ME/kg DM). While on test, feed intake was recorded daily with BW and hip heights recorded at 14 day intervals. Ultrasound measurements of rib eye area (REA) and backfat (BF) were recorded initially and prior to harvest. Carcass and growth data were analyzed using a mixed model with RFI level (L, H) as the independent variable. The lsmeans for RFI were -1.25 and 1.51 for the L and H cohorts ($P < .0001$). Dry matter intake was higher for the H individuals versus the L steers ($P < .0001$) while on test BW gain was not different between the two groups ($P < 0.73$). Of the 24,000+ probes included on the Affymetrix Bovine Genome Array, 891 were found to be significantly different ($P < 0.05$) with 149 of these being highly different ($P < 0.01$) between high and low RFI. Pathway analysis of the data set using Ingenuity Pathway Analysis software revealed that the pathways most heavily represented in the differentially expressed genes were consistent with the known functions of the central nervous

system, specifically; increased cellular movement (important for synapse formation and neuronal communication), cell-to-cell communication and cellular development ($P = 1.34x10^{-24}$, $9.54x10^{-20}$,$3.14x10^{-17}$, respectively). In terms of canonical pathways, dendritic cell maturation and interleukin signaling ($P = 3.56x10^{-6}$ and $5.24x10^{-6}$, respectively) were identified as differentially activated by RFI status of particular interest and warrant further investigation. Furthermore, GnRH signaling (including GnRH agonist and GnRH signaling) was predicted to be to be greater in H steers. These findings are consistent with targeted gene expression assays using real-time PCR where GnRH mRNA abundance was lower in the arcuate nucleus of L steers**.** These data support the hypothesis that differences in hypothalamic neuropeptide gene expression underlie variation in feed efficiency in steers while the gonadotropin axis may also influence feed efficiency.

Key Words: RFI, steer, feed efficiency

1187 (W123) Microbiota diversity is inversely related to adiposity in Mangalica pigs. J. W. Broady, L. Wang, A. G. Moss, T. D. Brandebourg, and E. Schwartz*, *Auburn University, Auburn.*

Alabama is at the epicenter of an obesity epidemic representing a critical threat to public health by precipitating increased risk to stakeholders for diabetes, heart disease, stroke, arthritis, and certain cancers. Several studies in humans and in mice have demonstrated a strong interaction between the composition and diversity of gut microbiota, inflammation, and obesity. To address the connection between these parameters, we used the Mangalica pig as a model organism given the extreme, early onset, hyperphagic obesity displayed by this breed. A growth trial was conducted where obese and lean groups were created by either allowing ad libitum access to feed or restricting energy intake to 65% of ad libitum levels. Throughout the trial longitudinal analyses of the bacterial composition of the fecal microbiota was performed using denaturing gradient gel electrophoresis (DGGE). Circulating glucose was measured in whole blood samples taken from pigs following fasting or administration of an oral glucose dose. Body composition was determined at regular intervals using ultrasound and subcutaneous adipose tissues (SC) harvested at the end of the trial to facilitate gene expression studies. As animals aged and increased in adiposity, a general reduction in the overall diversity in the gut bacteria was observed with several other changes in specific bacterial taxa as indicated by DGGE analysis. At mature weight, obese pigs exhibited 2.5-fold greater SC mass ($P < 0.001$) but no differences in muscle mass ($P < 0.39$) compared to lean counterparts. Obese pigs exhibited severe fasting hypoglycemia and impaired glucose tolerance following oral glucose challenge suggesting development of insulin resistance. The mRNA expression of interleukin-6 (IL6) and tumor necrosis factor-α (TNF-α) were 4.72- and 3.74-fold higher respectively in the SC of obese versus lean Mangalica as measured by real-time PCR ($P < 0.01$). These data provide evidence that obese Mangalica pigs indeed develop a metabolic phenotype consistent with insulin resistance and this is associated with a proinflammatory shift in gene expression in SC. Furthermore, these data suggest that obesity is inversely correlated with diversity in gut microbiota. These findings will inform the design of therapies aimed at manipulating gut microbiota and/or inflammation in the treatment of obesity.

Key Words: microbiota, obesity, mangalica

1188 (W124) Muscle hypertrophy induced by myostatin inhibition is suppressed by rapamycin administration. D. Choi*[1], J. Yang[1], S. K. Park[2], and Y. S. Kim[1], *[1]University of Hawaii, Honolulu, [2]National Institute of Animal Science, RDA, Suwon, South Korea.*

Recent studies have shown that myostatin (MSTN), a skeletal muscle specific negative growth factor, may regulate skeletal muscle mass through the mTOR pathway. The mTOR pathway is known to be blocked by rapamycin (RAP), thus it was hypothesized that muscle hypertrophy induced by MSTN inhibition would be blocked by RAP treatment. This study was designed to examine the effect of RAP administration on muscle growth in MSTN-propeptide transgenic mice, a hypermuscular phenotype by MSTN inhibition. 5 wk old male heterozygous MSTN-propeptide transgenic mice and wild-type littermates were administered with 0 or 3 mg/kg body weight of RAP intraperitoneally every other day for 4 wk. At the end of RAP treatment, animals were sacrificed, and gastrocnemius, plantaris, and soleus muscles were dissected, weighed, and snap-frozen for later analysis. Body weight gain of transgenic mice was greater ($P < 0.01$) than that of wild-type mice. RAP suppressed ($P < 0.05$) body weight gain about 40% in both genotypes. Soleus, plantaris, and gastrocnemius muscle weights of transgenic mice were greater ($P < 0.05$) than those of wild-type mice. RAP suppressed ($P < 0.05$) muscle growth in both genotypes, but the extent of suppression was greater in transgenic mice than in wild-type mice (6.6% vs. 18.6% in plantaris, and 20.7% vs. 24.8% in gastrocnemius). When the expressions of MyoD and myogenin were analyzed by real time PCR, expressions of these myogenic regulatory factors were not affected by either genotype or RAP administration. The current result of suppressing muscle growth by RAP in MSTN-propeptide transgenic mice supports that the mTOR pathway is involved in the regulation of muscle growth by MSTN.

Key Words: myostatin, rapamycin, mTOR pathway

1189 (W125) Poor maternal nutrition during gestation reduces mesenchymal stem cell (MSC) proliferation in offspring. S. M Pillai[*1], M. L. Hoffman[1], K. N. Peck[1], E. V. Valley[1], T. D. Crenshaw[2], S. A. Zinn[1], and K. E. Govoni[1], *[1]Dep. of Animal Science, University of Connecticut, Storrs, [2]University of Wisconsin, Madison.*

Poor maternal nutrition may alter bone and adipose development in offspring by diverting MSC from osteoblast to adipocyte lineage. To determine if poor maternal nutrition during gestation alters bone and adipose development and function of MSC in offspring, 36 ewes were fed 100%, 60%, or 140% of requirements (NRC, 1985) beginning at d 31 ± 1.3 of gestation. Lambs from ewes fed 100% (CON), 60% (RES) and 140% (OVER) were euthanized within 24 h of birth (d 1; n = 18) or at 3 mo of age (n = 15). At necropsy, the left tibia and femur were collected for MSC culture and mineral analysis, and backfat thickness and BW were measured. The MSC were isolated from bone marrow at d 1 and cultured (α- MEM + 10% fetal bovine serum + 0.5% penicillin streptomycin + 0.25% Amphotericin-B). Proliferation of MSC was determined by bromodeoxyuridine assay. Gene expression was quantified using real-time RT-PCR. Data were analyzed using PROC MIXED in SAS. As previously reported, BW were 13% greater in OVER than CON at 1 d and 3 mo ($P \leq 0.05$), but not different in RES ($P > 0.1$). Maternal diet did not affect ($P > 0.2$) bone length, area, mineral content and mineral density at d 1 or at 3 mo. Backfat thickness was reduced 50% in RES compared with CON at 3 mo ($P = 0.01$). Compared with CON, MSC proliferation was reduced 51% and 58% in RES ($P = 0.07$) and OVER ($P = 0.03$), respectively in the presence of serum and reduced 27% and 44% in RES ($P = 0.11$) and OVER ($P = 0.05$), respectively without serum. Expression of markers of MSC commitment to adipocyte and osteoblast cell lineages were evaluated. *P2Y purinoceptor 14* was reduced 1.7 ± 0.1-fold in OVER ($P = 0.09$) and *P2Y purinoceptor 1* was reduced 1.7 ± 0.1-fold in OVER ($P = 0.09$) vs. CON. Whereas *C/EBPβ, Msh homeobox 1, Protein delta homolog 1, P2Y purinoceptor 2* were not affected by maternal diet ($P >$ 0.3). Studies are in progress to determine if maternal diet alters differentiation of MSC into osteoblasts and adipocytes. In conclusion, poor maternal nutrition reduces the proliferation of MSC in offspring which may contribute to altered bone and adipose tissue development.

Key Words: mesenchymal stem cells, proliferation, sheep

1190 (W126) Regulation of key markers of lipid metabolism by short chain fatty acids in differentiated pig adipocytes. H. Yan[*1], and K. M. Ajuwon[2], *[1]Purdue University, West Lafayette, IN, [2]Dep. of Animal Sciences, Purdue University, West Lafayette, IN.*

Short chain fatty acids (SCFA), primarily acetate, propionate and butyrate, are the major carbohydrate fermentation end products of in the gut. Previously, we had demonstrated that inulin, a fermentable fiber, alleviated high fat diet induced fat mass accumulation, and that this was accompanied by increased expression of acyl CoA oxidase (ACO), a marker of peroxisomal fatty acid oxidation, decreased expression of fatty acid synthase (FAS) and alteration in the gut microbial community structure to favor increased level of butyrate-producing bacteria. Although gut microbial structure is highly associated with SCFAs production, direct effect of SCFAs on lipid metabolism is still unclear. Therefore, we examined, by RT-PCR, the effect of SCFAs administration on markers of lipid metabolism in differentiated pig adipocytes. Increasing concentrations of SCFAs (μM to low mM) led to an upregulation of expression of acyl CoA oxidase (ACO) and sterol regulatory element binding protein 1c (SREBP-1c), which play a key role in fatty acid synthesis. Furthermore, butyrate, but not propionate and acetate, significantly reduced ($P < 0.05$) the expression of fatty acids synthase (FAS) and carnitine palmitoyl transferase 1α (CPT1α). Butyrate, but not propionate and acetate, significantly increased ($P < 0.05$) adiponectin and glucose transporter type 4 (GLUT4) expression and led to decreased leptin expression. This study showed that SCFAs, especially butyrate, may exert direct influence on lipid metabolism and adipokine expression profile in adipocytes. Results are consistent with previously observed in vivo effects of fermentable fiber on metabolic markers in pig adipose tissue and suggest that in vivo fiber effects may be partly mediated by SCFA produced during fiber fermentation.

Key Words: SCFA, adipocyte, metabolism

1191 (W127) Relationship among efficiency measures, economic value and feedlot performance assessed in growing phase of Nellore cattle. A. M. Castilhos[1], C. L. Francisco[*1], A. M. Jorge[1], R. H. Branco[2], M. E. Z. Mercadante[2], S. F. M. Bonilha[2], C. M. Pariz[1], and D. C. Rivaroli[1], *[1]Universidade Estadual Paulista–FMVZ, Botucatu, Brazil, [2]Centro APTA Bovinos de Corte, Instituto de Zootecnia, Sertãozinho-SP, Brazil*.

Data from 6 yr of studies (2007–2012) were compiled using 357 Nellore bulls (212 + 38 kg BW; 279 + 29 d of age) to evaluate the relationship among efficiency measures, current economic value and feedlot performance. Dry matter intake (DMI) was recorded for two different ways: using a GrowSafe automated feeding system (GrowSafe Systems Ltd., Air-

Table 1191.

	RFI		RIG		RG		
Variable	Low	High	Low	High	Low	High	SEM
Profit, $/steer·d^{-1}	0.72^{b}	0.56^{c}	0.48^{d}	0.77^{a}	0.38^{e}	0.77^{a}	0.03
ADG, kg/d	1.04^{bc}	1.05^{b}	1.00^{c}	1.08^{ab}	0.89^{d}	1.10^{a}	0.02
DMI, kg/d	6.40 ^{c}	7.46^{a}	7.49^{a}	6.46^{c}	7.00^{b}	6.75 ^{b}	0.12
Final BW, kg	330.39^{a}	333.88^{a}	335.63^{a}	329.91^{a}	334.66^{a}	328.39^{a}	59,39

^{ab} $P < 0.05$

drie, Alberta, Canada) or individual pens. Efficiency measures evaluated were: residual feed intake (RFI), residual intake and BW gain (RIG) and residual BW gain (RG). Residual feed intake was calculated as the residuals from the regression of total DMI on $BW^{0.75}$ and ADG. Residual gain was calculated as the residuals from the regression of total ADG on $BW^{0.75}$ and DMI. Residual intake and BW gain was determined from linear combination into RFI and RG. Animals were classified for each efficiency measure as Low (< 0.5 SD mean), Medium (within ± 0.5 SD), and High (> 0.5 SD mean) groups. Economic value included was profit ($/steer.d^{-1}), calculated from the economic data from 2006 to 2012. Feedlot performance variables were ADG (kg/d), DMI (kg/d), and final BW (kg). Profit for all groups differed ($P < 0.05$), with the exception between $High_{RIG}$ and $High_{RG}$ groups ($P = 0.98$) which had the highest profitability (Table 1191). When the groups were analyzed separately, within each of efficiency measures, the profit increased ($P < 0.0001$). Final BW was similar among all groups of efficiency measures ($P = 0.78$). Body weight gain was not different between groups $High_{RFI}$ and Low_{RFI} ($P = 0.64$), Residual feed intake groups had lower gain only compare to $High_{RG}$ group ($P = 0.01$). The $High_{RIG}$ and $High_{RG}$ increased approximately 8% and 23% ($P < 0.0001$) compared to Low_{RIG} and Low_{RG}, respectively. Among all the groups Low_{RFI} and $High_{RIG}$ had lower DMI ($P < 0.01$) and reduced by approximately 14% compared to $High_{RFI}$ and Low_{RIG}, respectively. Therefore, residual intake and body weight gain is a recommended measure to increase profitability and reduce dry matter intake of Nellore cattle.

Key Words: efficiency measures, Nellore cattle, profit

1192 (W128) Retinoic acid alters expression of key genes during differentiation of bovine intramuscular preadipocytes. J. Kim*[1], K. Chung[2], S. Chang[2], and B. J. Johnson[1], *[1]Texas Tech University, Lubbock, [2]Hanwoo Experiment Station, NIAS, RDA, Pyeongchang, South Korea.*

Retinoic acid has been shown to be important in regulating mammalian tissue development, such as, proper bone formation, growth, energy metabolism, and cell differentiation. Retinoic acid has been reported to be a potent inhibitor of adipocyte differentiation by binding to the retinoic acid receptor (RAR) or retinoid X receptor (RXR). The objective was to determine the effect of RAR agonist (retinoic acid) and RAR antagonist (LE540) on gene expression during differentiation of bovine intramuscular preadipocytes. Intramuscular (IM) adipose tissue was collected between the 10th and 13th from longissimus muscle and cultured in growth media consisting of DMEM, 10% fetal bovine serum, and antibiotics at 37°C under a humidified atmosphere of 95% O_2 and 5% CO_2. Upon reaching confluence, the growth medium was replaced by a differentiation medium consisting of DMEM and 10 μg/mL insulin, 25 nM hydrocortisone, 10 μM oleic acid, 5 μM ciglitizone, and antibiotics with treatments The treatments were: 1)control, 2)10 μM all-trans retinoic acid (RA), and 3)10 μM LE540 (synthetic RA antagonist; Waco Co.). Real-Time RT-PCR was used to measure the quantity of C/EBPβ, PPARγ, SCD, and SMAD3 mRNA relative to the quantity of ribosomal protein subunit 9 (RPS9) mRNA in total RNA isolated from cultured bovine IM adipocyte cultures. Addition of RA reduced ($P < 0.05$) PPARγ and SCD mRNA levels compared to control IM adipocytes. However, addition of LE 540 increased expression of PPARγ and SCD mRNA ($P < 0.05$) levels in bovine IM adipocytes. Relative level of C/EBPβ mRNA was inhibited ($P < 0.05$) by LE540 during differentiation. Results of this study indicated that retinoic acid inhibits bovine IM preadipocyte differentiation by downregulation of PPARγ or SCD. However, treatment of RAR antagonist induces adiopogenic gene expressions during IM preadipocyte differentiation.

Key Words: bovine intramuscular adipose cell, marbling, retinoic acid

1193 (W129) Role of G protein-coupled estrogen receptor-1 and matrix metalloproteinases 2 and 9 in the effects of Estradiol-17β on proliferation, protein synthesis and protein degradation in bovine satellite cell cultures. E. Kamanga-Sollo, B. C. Reiter, K. J. Thornton*, M. E. White, and W. R. Dayton, *University of Minnesota, St. Paul.*

In feedlot steers, Estrogen (E2) and combined E2 and trenbolone acetate (TBA) (a testosterone analog) implants enhance rate and efficiency of muscle growth; and, consequently, these compounds are widely used as growth promoters. Although the positive effects of E2 are well established, the mechanism(s) involved is not well understood. Combined E2/TBA implants result in significantly increased muscle satellite cell number in feedlot steers. Additionally, E2 treatment stimulates proliferation of cultured bovine satellite cells (BSC). The ability of

E2 to stimulate satellite cell proliferation is significant because satellite cells provide nuclei needed to support postnatal muscle fiber hypertrophy and are crucial in determining the rate and extent of muscle growth. To identify the mechanism(s) involved in E2-stimulated muscle growth, we have focused on identifying the receptors involved in the effects of E2 on BSC proliferation, protein synthesis and protein degradation. Our previous studies have shown that silencing expression of estrogen receptor 1 (ESR1) or epidermal growth factor receptor (EGFR) suppresses E2-stimulated BSC proliferation. Studies in nonmuscle cells have shown that binding of E2 to G protein-coupled estrogen receptor (GPER)-1 results in activation of matrix metalloproteinases 2 and 9 (MMP2/9) resulting in proteolytic release of heparin binding epidermal growth factor-like growth factor (hbEGF) from the cell surface. Released hbEGF binds to and activates EGFR resulting in increased proliferation. To determine if GPER-1 and MMP2/9 are involved in the ability of E2 or IGF-1 to affect BSC, we have utilized specific inhibitors to inhibit the activity of GPER-1 and MMP2/9 and assessed the impact of this inhibition on the effects of E2 on proliferation, protein synthesis and protein degradation rates in BSC cultures. Treatment of BSC cultures with G36, a GPER-1 specific inhibitor, or with an inhibitor of MMP2/9 activity completely suppressed E2-stimulated proliferation and protein synthesis ($P < 0.05$) but had no effect on the ability of E2 to suppress protein degradation. Our results show that both GPER-1 and MMP2/9 are necessary for E2-stimulated proliferation and protein synthesis in BSC cultures.

Key Words: bovine, satellite cell, muscle, estradiol-17β

1194 (W130) The effect of pre-weaning feeding and housing strategy on calf growth performance and behavior following post-weaning housing transition.

H. M. Gauthier[*1], H. A. Tucker[1], S. E. Williams[1], D. M. Shenk[1], C. S. Ballard[1], K. M. Morrill[2], and H. M. Dann[1], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Cornell University, Ithaca, NY.*

The objective was to compare the effects of pre-weaning housing and feeding strategy on post-weaning growth performance and behavior after housing transition. Forty-eight Holstein calves were fed 770 g DM/d from birth through 15 d of age and 900 g DM/d thereafter split into 2 feedings and housed in individual hutches ($n = 16$; FI), or fed ad libitum acidified milk replacer and housed in either individual hutches ($n = 16$; AI) or group hutches with 4 calves/hutch ($n = 16$; AG). Milk replacer was 24% CP and 20% fat, fed at 14% solids. Following weaning (wk 8), calves were moved to a separate housing area (wk 10) and housed in 3.05 × 3.66 m pens with 4 calves/pen. Calves were weighed before transit (FI = 79.2 ± 3.4 kg; AI = 89.7 ± 4.2 kg; AG = 88.1 ± 4.2 kg) and weekly thereafter. Behavior of individual calves ($n = 36$) for the first 5 h following transit and pen introduction was observed using 5-min scan sampling and averaged across pen. Calves were offered free choice chopped hay (16.1% CP; 58.7% NDF) and pelleted grain (25.7% CP; 29.8% NDF) daily. Dry matter intake was measured daily. Data were analyzed as a randomized block design using the PROC MIXED of SAS. Total DMI was greater ($P = 0.02$) for AI (mean ± SE; 5.85 ± 0.12 kg DM/d) compared to AG (5.29 ± 0.12 kg DM/d) and tended ($P = 0.06$) to be greater than FI (5.40 ± 0.12 kg DM/d). Average daily gain over the 2 wk period tended ($P = 0.08$) to be greater for FI (1.20 ± 0.08 kg BW/d) than AI (0.97 ± 0.08 kg BW/d) or AG (0.90 ± 0.08 kg BW/d). Feed efficiency was not altered ($P = 0.12$) by pre-weaning housing and feeding strategies averaging 6.16 ± 0.53 kg DMI/kg gain for AI, 5.67 ± 0.53 kg DMI/kg gain for AG, and 4.38 ± 0.53 kg DMI/kg gain for FI. Time spent in contact with another calf was greater ($P = 0.02$) for AG (85.4 ± 8.8 min) compared to AI (27.1 ± 8.8 min) and FI (40.0 ± 8.8 min). Housing and feeding strategy pre-weaning did not alter time spent standing ($P = 0.55$) or lying ($P = 0.55$) post-weaning. These data suggest post-weaning compensatory gain occurs with fixed intake feeding when compared to ad-libitum feeding.

Key Words: post-weaned calves, performance, behavior

1195 (W131) The effect of two sources of soy protein concentrate and hydrolyzed soy protein modified on growth and performance of calves fed milk replacer.

*B. L. Miller[*1], T. Earleywine[2], W. S. Bowen Yoho[3], and T. E. Johnson[3], [1]Land O'Lakes–Purina Feed LLC, Gray Summit, MO, [2]Land O'Lakes Animal Milk Products, Shoreview, MN, [3]Land O' Lakes, Inc., Webster City, IA.*

Fifty-one (51) 3- 10 d old Holstein bull calves with an average initial BW of 50.1 kg (SD = 1.63 kg) were shipped from Wisconsin to the Land O' Lakes Research Facility. Calves were randomly assigned according to BW and blood γ globulin to one of three 20% protein/20% fat non-medicated milk replacer (MR) diets offered in a 17.6% solution. The objective of this study was to evaluate calf performance and growth when fed MR containing one of two sources of soy protein concentrate or hydrolyzed soy protein modified as a protein source. Treatments were as follows: soy protein concentrate source 1 (SPC 1; Solae Profine F, Solae, Aarhus, Denmark); soy protein concentrate source 2 (SPC 2, Solae Danpro A, Solae, Aarhus, Denmark); hydrolyzed soy protein modified (HSPM). Calves were fed to provide 680 g DM/d during Days 1– 7, 907 g DM/d during Days 8– 14, 1134 g DM/d during Days 15– 21, and 1361 g DM/d during Days 22– 28, in 2 feedings at 0600 and 1515 h. Calf starter was not offered during this 28 d trial. Data were analyzed by PROC MIXEDs of SAS. Total weight gain, MR consumption, feed:gain, and scour scores did not differ ($P > 0.05$) among treatments. The three soy protein sources fed in this study can be interchangeably employed in calf milk replacers as all support calf growth and performance equally.

Key Words: calf, milk replacer, hydrolyzed soy protein modified

Table 1195.

Item[1]	MR Diet			
	SPC 1	SPC 2	HSPM	SE
BW Gain, kg, 4 wk total	8.69	8.58	9.36	0.710
MR Intake (DM), kg, 4 wk total	25.7	25.4	26.2	0.640
Scour Score*, 2 wk avg	1.51	1.47	1.60	0.070
Feed:Gain	3.47	3.28	3.06	0.330

* 1- 4 scale: 1 = normal, 2 = loose, 3 = water separation, 4 = 3 with severe dehydration.

1196 (W132) The effect of various fat levels and fat sources on growth and performance of calves fed milk replacer.

T. Earleywine*[1], B. L. Miller[2], W. S. Bowen Yoho[3], and T. E. Johnson[3], *[1]Land O'Lakes Animal Milk Products, Shoreview, MN, [2]Land O'Lakes–Purina Feed LLC, Gray Summit, MO, [3]Land O' Lakes, Inc., Webster City, IA.*

Seventy-one (71) 3- to 10-d-old Holstein bull calves with average initial BW of 45.6 kg (SD = 1.95 kg) were shipped from Wisconsin to the Land O' Lakes Research Facility. The objective of this study was to examine the growth and performance of calves fed milk replacer (MR) varying in fat level and fat source. Calves were randomly assigned according to BW and blood γ globulin to their respective MR diet offered in a 15.0% solids solution. Calves were assigned to 1 of 3 diets: 22% crude protein (CP), 20% fat with lard as the primary fat source; 22% CP, 15% fat with medium-chain triglycerides (MCT) as the primary fat source; 22% CP, 15% fat with lard as the primary fat source and supplemented with 8 g essential fatty acids per calf daily (EFA; Neotec4™, Provimi North America, Inc., Brookville, OH). Calves were fed to provide 680 g DM/d in 2 feedings at 0600 and 1515 h. Calves were offered 340 g DM/d in one feeding during the last week. Calf starter (20% CP, as fed basis) was fed ad libitum throughout this 42 d trial. Data were analyzed by PROC MIXEDs of SAS. There were no statistical differences ($P > 0.05$) in total BW gain, starter feed intake, or feed:gain among treatments. Calves fed a 22:20 MR with lard as the primary fat source consumed less ($P < 0.05$) MR compared to calves fed a 22:15 MR with lard as the primary fat source and supplemented with EFA. Milk replacers with MCT as the primary fat source may allow for a reduction in fat levels while supporting equal calf performance and growth.

Key Words: calf, milk replacer, medium-chain triglyceride

Table 1196.

Item[1]	MR Diet			
	22:20 w/Lard	22:15 w/MCT	22:15 w/lard, EFA	SE
BW Gain, kg	22.9	26.0	24.4	1.51
MR Intake (DM), kg	24.3[a]	24.8[ab]	25.3[b]	0.280
Starter Intake (DM), kg	20.2	23.2	20.8	1.56
Feed:Gain	1.98	1.89	1.97	0.070
Scour Score*, 2 wk avg	1.43	1.33	1.45	0.060

[1] Means in the same row not followed by a common letter differ ($P < 0.05$).
* 1- 4 scale: 1 = normal, 2 = loose, 3 = water separation, 4 = 3 with severe dehydration.

1197 (W133) Use of biometric measurements to predict age and body weight of bovine fetus.

T. R. Gionbelli*[1], M. P. Gionbelli[1,2], M. S. Duarte[1], S. C. Valadares Filho[1,2], F. C. Rodrigues[1], M. G. Machado[1], D. Zanetti[1], B. C. Silva[1], and F. A. Villadiego[1], *[1]Universidade Federal de Viçosa, Minas Gerais, Brazil, [2]Instituto Nacional de Ciência e Tecnologia–Ciência Animal, Viçosa, Minas Gerais, Brazil.*

Fetal biometric measurements that can be achieved by ultrasonography were used to develop equations to predict fetal age and fetus body weight in *Bos indicus* cattle. Dataset from 32 purebred Nellore fetuses from 130 to 272 d of gestation, obtained from cows fed corn silage based diet at various feeding levels, was used. Cows were hand mated, with day of mating considered as day zero of pregnancy. Fetal weight and biometric measurements were taken at slaughter and biometrics measurements were (all in cm): body length (BL), thoracic circumference (TC), height at shoulder (HS), height at rump (HR), cranial eyes circumference (CEC) and cranial neck circumference (CNC). Nonlinear equations ($y = ax^b$) were fitted to the data and results are shown in Table 1197. Generated functions were evaluated regressing observed values in function of predicted. The joint hypothesis that $\beta_0 = 0$ and $\beta_1 = 1$ was tested and the results shown good fit for all functions generated ($P > 0.70$). However, these regressions do not predict fetal ages accurately in early gestation, thus should not be extrapolated beyond the scope of these data (130 to 272 d of gestation). The results suggest that the gestational age and fetal body weight can be estimated from biometric measurements of fetus using ultrasonography in live cows or directly in fetuses from cows that were slaughtered without specified gestational age. *Funded by INCT-CA, CNPq and FAPEMIG.*

Key Words: biometric measurements, fetal growth, gestation

Table 1197. Functions to predict fetus body weight and fetal age from biometric measures of fetus[1]

	Predicting fetal age (days)			Predicting fetus body weight		
Biometric predictor measure	Function	r^2_{xy}	*P*-value	Function	r^2_{xy}	*P*-value
Body length, cm	$y = 14.3 \times BL^{0.6516}$	0.960	0.998	$y = 0.000155 \times BL^{2.701}$	0.981	0.708
Thoracic circumference, cm	$y = 16.89 \times TC^{0.6588}$	0.964	0.999	$y = 0.000263 \times TC^{2.769}$	0.974	0.864
Height at shoulder, cm	$y = 24.21 \times HS^{0.5536}$	0.975	0.999	$y = 0.001 \times HS^{2.367}$	0.975	0.985
Height at rump, cm	$y = 26.42 \times HR^{0.5322}$	0.983	0.999	$y = 0.00192 \times HR^{2.209}$	0.958	0.944
Cranial eyes circumference, cm	$y = 10.45 \times CEC^{0.8215}$	0.953	0.999	$y = 0.000041 \times CEC^{3.412}$	0.946	0.884
Cranial neck circumference, cm	$y = 9.97 \times CNC^{0.8478}$	0.970	0.995	$y = 0.000073 \times CNC^{3.314}$	0.962	0.689

[1] The r^2_{xy} value is for observed values regressed in function of predicted. *P*-value is the significance value for testing the joint hypothesis that $\beta_0 = 0$ and $\beta_1 = 1$, wherein *P*-values greater than 0.05 means that the H_0hypothesis was accepted.

HORSE SPECIES I

1198 (T136) Glucose-insulin homeostasis and characterization of proteins involved in glucose uptake signaling in equine skeletal muscle. R. C. Avenatti*, K. Malinowski, and K. H. McKeever, *Rutgers Equine Science Center, New Brunswick, NJ.*

The objective of this study was to test the hypothesis that glucose-insulin homeostasis, and activation of AMP-activated protein kinase (AMPK), the protein kinase Akt, and the Akt substrate protein of 160 kDa (AS160) in equine skeletal muscle are altered by acute, exhaustive exercise and by aging. Unconditioned aged (n = 6; 22.6 ± 2.25 yr) and young (n = 6; 5.5 ± 2.8 yr) Standardbred mares were assessed for glucose-insulin homeostasis via frequently sampled intravenous glucose tolerance test (FSIGTT). All mares underwent a single bout of submaximal exercise. Plasma insulin and glucose concentrations were measured via radioimmunoassay and enzyme-electrode interface, respectively. Mid-gluteal muscle biopsies were taken pre-exercise, and at 0, 4, 24, and 48 h post-exercise. Muscle samples were analyzed via western immunoblotting for changes in activation of AMPK, Akt and AS160. Minimal model analysis of FSIGTT and repeated measures ANOVA were utilized to analyze data. Null hypothesis was rejected when $P < 0.05$. FSIGTT results indicated that there was no difference between young and aged mares for insulin sensitivity (SI), glucose effectiveness (SG), acute insulin response to glucose (AIRg) or disposition index (AIRg x SI) ($P > 0.05$). Area under the curve for both insulin (AUCi) and glucose (AUCg) were not different between young and aged mares ($P > 0.05$). In response to acute exercise, young mares displayed elevated insulin concentrations at 2 ($P = 0.009$) and 4 ($P = 0.007$) h while aged mares displayed elevated insulin at 30 ($P < 0.001$) and 60 ($P = 0.001$) minutes post-exercise. Neither age nor exercise caused a significant change in AUCi ($P > 0.05$). Glucose concentration was elevated at 2 h post-exercise in young mares ($P < 0.001$), while in aged mares glucose remained elevated only until 60 min post-exercise ($P = 0.037$). Exercise caused an increase in AUCg in young ($P = 0.007$) and aged ($P = 0.031$) mares, however there was no age effect on AUCg ($P > 0.05$). Neither age nor exercise altered total protein concentrations or phosphorylated protein concentrations of AMPK, Akt or AS160 ($P > 0.05$). In conclusion, age alone is not sufficient to alter insulin sensitivity in horses, but does alter glucose-insulin dynamics in response to exercise. Also, a single bout of submaximal exercise was not sufficient to alter activation of proteins believed to be involved in glucose uptake in skeletal muscle at the time points measured. The comparative literature suggests that these proteins are important for endocrine- and exercise-related glucose uptake and energy homeostasis.

Key Words: aging, exercise, muscle

1199 (T137) Splanchnic extraction of phenylalanine in adult thoroughbred mares fed two different levels of threonine. S. Tanner, T. Barnes, K. Cybulak, and K. L. Urschel*, *University of Kentucky, Lexington.*

Previous studies in horses examining the effects of amino acid (AA) intake on whole-body protein synthesis have used intravenous phenylalanine isotope infusion and the resulting calculations required estimates of splanchnic phenylalanine extraction that were derived from other species. Threonine is believed to be the second limiting AA in some equine diets. The objectives of the study were to determine splanchnic extraction of phenylalanine, validate an oral infusion of [1-^{13}C]phenylalanine, and test the effects of threonine supplementation on whole-body protein synthesis in horses. Six thoroughbred mares were fed timothy hay and a low threonine concentrate supplemented with isonitrogenous amounts of either threonine (+THR) or glutamate (+GLU), which were top dressed on the concentrate portion of the diet. Threonine intakes were 119 (+THR) and 58 mg/kg/d (+GLU) and diets exceeded NRC recommendations for all nutrients, including threonine (33 mg/kg/d). Each horse received each diet twice for 7d; studied once with an oral infusion and once with an intravenous infusion of [1-^{13}C]phenylalanine, for a total of four study periods per horse. On d 6 of receiving each diet, blood samples were taken before and 90 min after the AA supplemented concentrate meal. The next day, a 2-h primed, constant intravenous infusion of [^{13}C]sodium bicarbonate and a 4-h primed, constant infusion of [1-^{13}C]phenylalanine, either oral or intravenous, were used with blood and breath sampling to measure blood [^{13}C]phenylalanine and breath $^{13}CO_2$ enrichment. Data were analyzed in the PROC MIXED of SAS with threonine intake, route of infusion and the interaction as the fixed effects. Baseline and post-feeding plasma concentrations of glutamate, serine, glycine, threonine, and methionine were affected by diet ($P < 0.05$). Phenylalanine flux, intake, from protein breakdown, oxidation, and non-oxidative disposal were not affected by diet ($P < 0.05$). Splanchnic extraction was 26 ± 5% and 27 ± 3% for the +THR and +GLU diets, respectively. This was the first study to use oral administration of [1-^{13}C]phenylalanine in horses and this technique offers a less invasive alternative to the intravenous infusion method. Threonine does not appear to be a limiting AA in our diet, as phenylalanine kinetics were not affected by supplementation; however differences in plasma AA concentrations in response to threonine supplementation suggest that this AA can affect the metabolism of other AA. *This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2012–67015–19448 from the USDA National Institute of Food and Agriculture.*

Key Words: splanchnic extraction, equine, amino acids

1200 (T138) Effects of a docosahexaenoic acid-rich algae supplement on plasma amino acid levels in healthy, mature horses after prolonged treatment with dexamethasone. R. A. Williams[1], K. L. Urschel[2], R. E. Schaeffer[1], and K. M. Brennan*[1], *[1]Alltech Inc., Nicholasville, KY, [2]University of Kentucky, Lexington.*

Dexamethasone (DEX) is used to treat inflammation and off-label as a calming agent in performance horses. Long-term treatment with DEX reduces insulin sensitivity (SI) and can impair other insulin-activated pathways such as protein synthesis. We previously reported that supplementation with docosahexaenoic acid (DHA)-rich algae increased SI during prolonged DEX treatment in healthy horses. The objective of this study was to determine the effect of a DHA-rich algae supplement on plasma amino acid levels in healthy, mature horses after prolonged treatment with DEX. Eight healthy, mature horses were used in a balanced, crossover design of two 56-d periods. In each period, horses were fed a basal diet (CON), or diet + 152 g/d of a DHA-rich algae (15% CP; Algae SP-1, Alltech Inc., (ALG)) providing 21.1 g/d DHA for 28 d, after which blood was sampled (*P*re-DEX) and 0.04 mg DEX/kg BW/d administered orally; treatment continued for 21 d, then blood was sampled (*P*ost-DEX). Plasma AA concentrations were determined every 30 min during a 2-h insulin infusion. Plasma amino acid concentrations were analyzed using PROC MIXED using repeated measures analysis, with pre-DEX baseline as a covariate. Diet had no effect on plasma amino acid concentrations with the exceptions of Lys, Met, Ala and Gln ($P < 0.05$). A treatment by DEX interaction ($P < 0.01$) occurred for Glu, Ser, Asn, Gly, Gln, His, Thr, Ala, Pro, Tyr, Val, Met, Leu, Phe and Lys. Within each of the CON and ALG treatments, all horses received the same diet during both the pre- and post-DEX periods and therefore the increase in plasma amino acid concentrations in response to DEX in the CON horses suggests either an increase in rates of protein degradation or a decrease in rates of protein synthesis in response to prolonged DEX administration. Daily ALG feeding appeared to mitigate these changes in plasma amino acid concentrations. Additional research is necessary to identify the mechanism of this algae effect, although we hypothesize this is due to the previously reported increased SI with ALG.

Key Words: horse, amino acid, dexamethasone, docosahexaenoic acid

1201 (T139) Evaluating the expression of microRNA miR-1 and miR-133 in the muscle of horses fed a docosahexaenoic acid-rich algae supplement after prolonged dexamethasone treatment. M. L. Spry, A. C. Smith, D. E. Graugnard, R. E. Schaeffer, and K. M. Brennan*, *Alltech Inc., Nicholasville, KY.*

MicroRNAs (miRNAs) are small noncoding RNAs that bind to the 3' untranslated (3'UTR) region of genes and are responsible for inhibiting translation or promoting mRNA degradation. Two well characterized muscle-specific miRNAs are miR-1, and miR-133. MiR-1 decreases myoblast proliferation and increases differentiation, whereas miR-133 has an opposing effect promoting myoblast proliferation while decreasing differentiation. It is known that skeletal muscle breakdown and an increase in circulating amino acids are associated with the decreased insulin sensitivity after prolonged dexamethasone (DEX) treatment. In horses there is an association between an increase in miR-1 and miR-133 levels and diseases involving muscle breakdown. Supplementing diets with DHA-rich algae (Algae SP-1, Alltech Inc., (ALG)) improves insulin sensitivity and decreases plasma amino acid levels in horses after prolonged DEX treatment. The objective of this study was to determine the effect of Algae SP-1 supplementation on miR-1 and miR-133 expression in healthy, mature horses ($n = 5$) before and after DEX treatment using a balanced, crossover design of two 56-d periods. In each period, horses were fed a basal diet (CON), or diet + 152 g/d of ALG for 28 d and muscle was sampled (*P*re-DEX). DEX was then administered (0.04 mg/kg BW/d, orally) for 21 d while dietary treatments continued. On d 49 of dietary treatments (*P*ost-DEX), muscle was sampled and microRNA was measured using TaqMan MicroRNA Assays (Applied Biosystems). The relative quantification (RQ) was expressed as a ratio of the target microRNA to control microRNA normalized to a pooled control (CON, pre-DEX) using the delta-delta Ct ($^{\Delta\Delta}$Ct) method. There was no effect of diet, DEX or diet*DEX interaction on skeletal muscle miR-1 and miR-133 expression. Novel techniques used for miRNA evaluation could be useful to help relate changes in gene expression to physiological status, however further studies are needed.

Key Words: microRNA, horse, dexamethasone, docosahexaenoic acid

1202 (T140) The effects of abrupt dietary alterations on equine cecal pH. A. Reeg*[1], T. Douthit[1], K. M. DeLano[1], M. E. Gordon[2], M. M. Raghavendra Rao[2], and K. Williamson[2], *[1]Kansas State University, Manhattan, [2]Purina Animal Nutrition, LLC, Gray Summit, MO.*

Feeding starch in quantities exceeding 3.4 g/kg BW to the equine has been shown to exceed small intestinal capacity for digestion (Potter et al., 1992). This leads to fermentation of starch in the cecum resulting in a buildup of acidic products and decline in pH. Two consecutive 22-d experiments separated by 2 d of rest were conducted to identify whether abruptly feeding 1% (3.1 g starch/kg BW) and 1.25% (3.88 g starch/kg BW) BW concentrate during experiments 1 and 2, respectively, without hay would elicit a more profound decrease in cecal pH, as compared to the baseline diet. Nine cecally cannulated 8- to 10-yr-old quarter horses, 5 geldings and 4 mares, ranging in BW from 455 to 591 kg, were utilized. Baseline diets

for both expt. consisted of 0.5% BW concentrate (Omolene 200, Purina Animal Nutrition, LLC, Gray Summit, MO; 1.55 g starch/kg BW) fed at 0700 and 1.5% BW native prairie grass hay divided into two feedings (0700 and 1930) for 21 d. On d 22 of both experiments the concentrate meal was increased to 1% (Exp. 1) and 1.25% (expt. 2) BW and fed without hay. Cecal pH was measured from d 19 to 22 of both experiments at -1, +1, +4, +8, +12, +16, +20, and +24 h relative to feeding concentrate. ANOVA was performed with mixed models (SAS 9.3, 2011) and least square means compared using Fisher's LSD ($P < 0.05$, LSM ± SE). Complete randomization with either repeated measures (Exp. 1) or a split-plot design (expt. 2) was utilized. In both experiments, there was a time effect ($P < 0.0001$) on cecal pH. Exp. 1 cecal pH at +1 (7.2 ± 0.046) and +12 (6.8 ± 0.046) h on d 22 was decreased ($P < 0.05$) when compared to mean responses at +1 and +12 h during baseline feeding (7.4 ± 0.046 and 7.02 ± 0.046, respectively). In Exp. 2 cecal pH was decreased ($P < 0.05$) only at +12 h (6.8 ± 0.041) on d 22 when compared to mean values at +12 h during baseline feeding (7.0 ± 0.041). Throughout both experiments, post-prandial cecal pH was characterized by a decline at +4 h, reached a minimum value at +8 h, and increased by +12 h. However, the primary variation between baseline and d 22 was a more rapid rise in pH from +8 to +12 h.

Key Words: equine, starch, cecal pH

1203 (T141) Utilizing fecal pH to predict cecal pH in the equine. C. J. Douthit*[1], T. Douthit[1], A. Reeg[1], N. M. Bello[1], M. E. Gordon[2], and K. Williamson[2], *[1]Kansas State University, Manhattan, [2]Purina Animal Nutrition, LLC, Gray Summit, MO.*

Cecal cannulation is commonly used for direct assessment of dietary manipulation on cecal pH in equines. However, analysis of fecal material is considered one of few viable methods for monitoring digestive health in intact horses. In this retrospective study, we assessed the association between fecal pH and cecal pH in an attempt to develop a predictive equation for cecal pH. Nine cecally cannulated quarter horses were utilized. The group was comprised of 5 geldings and 4 mares, between the ages of 8 to 10 yr and body weight ranging from 455 and 590 kg. Horses were housed in heated individual stalls with ad libitum access to water and white salt blocks. Horses were fed 1.5% BW prairie grass hay split into twice daily feedings (0700 and 1830) and 0.5% BW concentrate (Omolene 200, Purina Animal Nutrition, LLC, Gray Summit, MO) which was fed in the mornings only (0700). Horses were maintained on this diet for 3 separate 21-d periods. Cecal and fecal pH were measured on d 19 to 21 of each period at -1, +1, +4, +8, +12, +16, +20, and +24 h relative to feeding the concentrate meal. Given inherent animal-to-animal variability in the pH dynamics of the cecum and rectum over time, the minimum cecal pH after feeding was collected for each animal-day combination and modeled as a function of the corresponding minimum fecal pH using a general linear mixed model. Analysis revealed evidence for an association ($P = 0.03$) between minimal cecal pH and minimal fecal pH. The estimated rate of change for minimum cecal pH per unit increase in minimum fecal pH was 0.131 with 95% confidence interval [0.011, 0.251]. The prediction equation for estimated cecal pH was $Y = 0.131*X + 5.8969$, where X is the observed fecal pH. However, the amount of predictive variability was considerable, likely due to multiple factors contributing to cecal pH, including feed composition, animal weight, and physiological state, which can alter the transit time of digesta from cecum to rectum. Our data indicates that fecal pH appears to have limited usefulness in predicting cecal pH.

Key Words: cecal pH, equine, fecal pH

1204 (T142) Comparison of ultrasound transducers to determine rump fat thickness in mature horses at maintenance. K. J. Stutts*, J. L. Lucia, M. J. Anderson, M. M. Beverly, and S. F. Kelley, *Sam Houston State University, Huntsville, TX.*

Rump fat measurements are utilized to assess changes in subcutaneous fat thickness when conducting feeding trials in horses. Commonly, these measurements are taken using a transducer that is designed for use in the rectum to evaluate the reproductive tract. This study was conducted to determine if measurements obtained using a rectal transducer were comparable to measurements obtained using a transducer designed to measure carcass characteristics. Rump fat measurements were obtained from 30 mature horses (368 to 552 kg and 5 to 10 yr) that were part of a feeding trial. Measurements were taken at 28-d intervals for a period of 154 d at a point half way between the points of the hip (Tuber coxae and Tuber ischiadicum) and 6 cm from the midline of the horse with the transducer positioned perpendicular to the midline of the horse. Images were taken with an Aloka SSD 500V real-time ultrasound machine (Corometrics Medical Systems, Wallingford, CT) equipped with a 17.2-cm, 3.5-MHz linear transducer (carcass probe) and a 6-cm, 5-MHz linear transducer (rectal probe). All measurements using the carcass probe were conducted by a certified technician who captured images that were analyzed at the Centralized Ultrasound Processing Lab (Ames). All measurements using the rectal probe were conducted by a non-certified employee using on-screen diagnostic tools on the scanner. Longissimus muscle (LM) area between the 17th and 18th ribs and fat thickness three-quarters the length ventrally over the LM were also obtained using the carcass probe. Least squares means for rump fat thickness (RFT) and LM fat thickness (LMFT) were calculated using the GLM procedure of SAS. Pearson correlation coefficients were used to determine the relationship between RFT and LMFT. Mean RFT was greater ($P < 0.01$) using the rectal probe (1.27 ± 0.39 cm) compared to the carcass probe (1.00 ± 0.36 cm); however, there was a strong, positive relationship between the two measurements

(r = 0.76, P < 0.01). Measurements using both the rectal (r = 0.48) and the carcass (r = 0.33) probes also had a positive relationship (P < 0.01) with LMFT with a greater correlation observed between LMFT and RFT measurements using the rectal probe. These data validate the utility of the rectal probe to measure RFT in horses. Although measurements were different between the rectal and carcass probes, measurements obtained using the rectal probe accurately assessed changes in RFT and exhibited a greater correlation to changes in fat thickness over the *longissimus* muscle.

Key Words: horses, ultrasound, rump fat

1205 (T143) On-farm tapeworm testing in horses.

N. C. Whitley*[1], R. Kaplan[2], K. Moulton[1], S. B. Routh[1], R. Franco[1], and R. K. Splan[3], *[1]North Carolina A&T State University, Greensboro, [2]University of Georgia, Athens, [3]Virginia Tech, Middleburg.*

The incidence of tapeworm infection in horses was investigated on nine farms in North Carolina and one in Virginia. Two of the North Carolina farms were used in three replicates. A total of 602 horses at least 1 yr of age were used (321 individuals, 281 were replicates; 157 females, 164 males) in the summer, fall, and winter seasons. Individuals averaged 12.1 ± 0.4 yr of age and 541.8 ± 7.0 kg body weight. Animals were treated with commercial horse anthelmintics containing ivermectin and praziquantel (Zimecterin Gold; n = 412; eight farms including those replicated; and Equimax™; n = 190; four farms) as labeled for BW measured by equine weight tape plus 15% with doses rounded up to the nearest 22.7 kg (50 lb). At treatment (d 0) and 24 hlater (d 1), fecal samples were collected after defecation for tapeworm fecal egg count (FEC) using the Modified McMasters technique with a sensitivity of eight eggs per gram (epg). Descriptive statistics were used to report data. On d 0, 1.4 ± 0.01% of horses were positive for tapeworm eggs, whereas on d 1, 20.6 ± 1.7% were positive. Positive horses were found on 30% of farms on d 0 and 60% of farms on d 1. This data suggests that tapeworm infections are common on horse farms, but that most horses do not have infections or have undetectable infections. Furthermore, these data demonstrate that sensitivity of detection for tapeworms via fecal exam is greatly increased by testing 1 d after treatment.

Key Words: tapeworms, horses, FEC

HORSE SPECIES II

1206 (W134) Trotting stride variables of the North American Akhal-Teke Horse. M. C. Nicodemus[*1] and J. Beranger[2], [1]*Mississippi State University, Starkville,* [2]*American Livestock Breeds Conservancy, Pittsboro, NC.*

Although the population is less than 350 horses placing it on the threatened breed list of the American Livestock Breed Conservancy (ALBC), the Akhal-Teke Horse of North America is as a source and a reservoir for genetic diversity for the ancient breed as it includes bloodlines that are unique. Preservation of the breed and its distinctive characteristics such as its smooth and elastic gaits is of top priority to the ALBC and the Akhal-Teke Association of America, and to accomplish this, a better understanding of the breed is needed. Therefore, the objectives of this study were to measure and describe the stride timing found in the trot of the Akhal-Teke Horse of North America. Subjects (n = 6) were selected through the direction of the ALBC and the Akhal-Teke Association of America based on bloodlines and performance history. Each horse was filmed at 60 Hz being ridden under saddle by a rider familiar with the horse at a trot with hoof contact and lift-off documented using frame-by-frame analysis. Means (SD) were determined for 10 strides for each horse with variables given as % of stride and variability of measurements indicated using the coefficient of variation (CV) expressed as a % of mean. The trot was performed in a diagonal footfall pattern that alternated between periods of unipedal (Hind: 10 ± 1%, CV 6%; Fore: 10 ± 2%, CV 19%) and bipedal (Diagonal: 80 ± 2%, CV 3%) supports. The trotting velocity (4.34 ± 0.15 m/s, CV 3%) was achieved using a stride length of 2.96 ± 0.25 m (CV 8%), rate of 1.47 ± 0.11 strides/s (CV 7%), and duration of 683 ± 49 ms (CV 7%) with the limbs spending the majority of the stride in the swing phase (Fore: 55 ± 2%, CV 6%; Hind: 54 ± 2%, CV 4%). The diagonal limbs moved as couplets, both at hoof contact (Advanced Placement: 5 ± 1%, CV 15%) and lift-off (Advanced Lift-Off: 5 ± 1%, CV 19%), creating a 4-beat rhythm. Coupling, rather than pairing of limbs, was similar to the stride timing reported in previous research for Dutch Warmblood and Standardbred horses, but the unpairing of diagonal limbs occurred at dissimilar velocities. In addition, the absence of suspension that has been reported for other trotting breeds such as the Dutch Warmblood and Morgan horse was also produced at a velocity distinctive from the other breeds suggesting velocity may account for the uniqueness of the trot of the Akhal-Teke Horse of North America.

Key Words: Akhal-Teke

1207 (W135) Development of an objective on-farm equine temperament scoring system. J. N. Foley[*1], J. L. Lucia[2], and K. W. Walter[1], [1]*Truman State University, Kirksville, MO,* [2]*Sam Houston State University, Huntsville, TX.*

To evaluate interest in development of an objective equine temperament scoring system (TSS), an online survey was distributed via hyperlink to faculty at three public universities and their equine interest groups and social media pages. Of 123 respondents, 71.4% were familiar with existing TSS, 81.1% of those familiar with existing TSS felt they did not accurately represent the horse's temperament, and 70.5% were interested in an improved TSS to replace subjective scales currently used on equine websites (equinenow.com and horsetopia.com most frequently cited). Existing TSS rank the horse from 1 to 10 (1 = calm, 10 = spirited), however no further clarification is provided. To assess equine temperament more objectively, 27 horses were utilized in a two phase test. Phase 1 incorporated 10 min of isolation while tied. Frequency of vocalization, defecation, urination, lateral movements, forelimb pawing, and blatant pulling on lead were recorded and used to develop a 0 to 6 scoring system (score assigned based on frequency of aforementioned behaviors). Phase 2 tested willingness to cross an unfamiliar obstacle. Horses were allowed 1 min to cross the obstacle. If the obstacle was refused, horses were trotted in a 5 m circle for 1 min. This procedure was repeated up to 5 times, and horses were assigned a score from 0 to 6 based on time required to cross with little resistance or fear. For both phases, vital signs of heart rate (HR), respiration rate (RR), and rectal temperature (RT) were evaluated immediately before and after each test. Blood samples were taken via jugular venipuncture and later analyzed for cortisol concentration utilizing a commercially available ELISA kit. Pre-test values of HR, RR, RT and cortisol concentrations were subtracted from post-test values to calculate the difference. Pearson's correlations were analyzed for all variables within phase, and Spearman's rank test performed to compare phases. Strong positive correlation existed between difference in cortisol and assigned score in both phase 1 and 2 ($r \geq 0.61$; $P < 0.001$). A strong positive correlation between assigned score in both phases and difference in vital signs (HR, RR, RT; $r \geq 0.4387$, $P \leq 0.02$) was noted. However, there was no correlation between phase 1 and phase 2 scores ($r = 0.25$, $P = 0.20$). This suggests each phase successfully evaluated different aspects of equine behavior using clearly defined 0 to 6 point scales, and both phases could be used together to evaluate equine temperament.

Key Words: behavior evaluation, equine, temperament scoring

1208 (W136) Cooling of equine semen at 16°C for 36 h with the addition of cysteine in different concentrations. R. A. De Oliveira[1], L. S. Murata[*1], M. A. D. O. Viu[2], and M. L. Gambarini[2], *[1]University of Brasilia, Brazil, [2]Federal University of Goiás, Goiânia, Brazil.*

Equine semen manipulation during the cooling process reduces sperm viability and fertility in consequence to, among others, membrane lipid peroxidation, because of the high content of polyunsaturated fatty acids, which makes cells highly susceptible to free radicals and reactive oxygen species. The objective of the present study was to evaluate the effect of in vitro addition of cysteine in four concentrations (0, 1, 1.5, and 2.5 mM) for cooling spermatozoa of 12 stallions at 16°C for 36 h. Evaluated variables were motility, vigor, viability and plasmatic and acrosomal membrane integrity in four different moments (0, 12, 24, and 36 h). With the exception of acrosomal integrity, it was verified a reduction in motility, vigor and plasmatic membrane integrity in all samples, during cooling. In the evaluations at 36 h of cold storage, motility (mot) and viability (viab) were greater in groups treated with 1 mM (mot:46,5 ± 6,1/viab:76,5 ± 6,9) and 1.5 mM (mot:46,0 ± 4,6/viab:76,9 ± 3,7) cysteine, respectively, compared to control (mot:35,5 ± 18,4/viab:68,1 ± 13,4) and 2.5 mM (mot:39,7 ± 12,4/viab:66,0 ± 17,2) ($P < 0.05$). As for vigor (vig) and plasmatic membrane integrity (plasm), 1 mM cysteine (vig:3.6 ± 0.5/plasm: 57.2 ± 9.5) showed greater results compared to control (vig:3.2 ± 1.1/plasm:54.1 ± 11.8), 1.5 mM (vig:3.5 ± 0.6/plasm:52.2 ± 13.3) and 2.5 mM (vig:3.2 ± 1.1/plasm:55.8 ± 12.5) ($P < 0.05$). Regarding acrosomal membrane integrity, in general, there was no loss of integrity (70.5 ± 10.4; 69.4 ± 4.4; 68.0 ± 7.2 and 70.3 ± 0.5), control, 1 mM, 1.5 mM and 2.5 mM, respectively. The concentration of 1 mM cysteine was more effective for the protection of sperm cells in the commercial system of passive cooling at 16°C for 36 h, with greater values for motility, vigor, viability and plasmatic membrane integrity.

Key Words: antioxidant, cooled semen, stallion

1209 (W137) Administration of bioactive proteins to mature horses improves gait kinematics. J. Coverdale*, and J. M. Campbell[2], *[1]Texas A&M University, College Station, [2]APC, Inc., Ankeny, IA.*

Thirty mature quarter horses (439 to 684 kg and 5 to 22 yr) were utilized in a randomized complete block design to evaluate the effect of a supplement consisting of a proprietary blend of bioactive proteins on gait kinematics. These bioactive proteins are isolated from plasma. Horses were blocked by age and BW and randomly assigned to treatment within block for the 28-d trial. Treatments consisted of a commercial pelleted concentrate administered with no supplement (CON), 240 g/d of a pelleted supplement containing 66 g of bioactive proteins (Low; Lifeline, APC, Inc.), or 240 g of a pelleted supplement containing 132 g of bioactive proteins (High; Lifeline, APC, Inc.). Concentrate was fed at 0.5% BW (as-fed) daily in addition to ad libitum coastal bermudagrass hay. Each horse was exercised by a single assigned student 5 d/wk focusing on horsemanship skills at the walk, trot, and canter approximately 60 min/d. Gait kinematic analysis was performed on d 0, 14, and 28 with video footage collected and analyzed using gait analysis software (EquineTec). Horses were trotted in hand for three passes over a 10 m flight path while wearing reflective markers at each joint of the right limbs. Stride length was measured as distance the right foreleg traveled during the swing phase. Additionally, range of motion (ROM) of the knee was determined using the difference between the maximum and minimum angles observed during each frame of the swing phase. All data were analyzed using PROC GLM of SAS. Mean stride length of the front limb tended to increase linearly at d 14 as increasing levels of bioactive proteins were added to the diet ($P = 0.07$). Similarly, at d 28 stride length of the front limb increased linearly with increasing inclusions of bioactive proteins ($P = 0.05$). Stride length at the trot of the hind limb tended to increase at d 14 ($P = 0.10$) and increased linearly at d 28 ($P = 0.02$) with increasing levels of bioactive proteins. When evaluated at the trot, knee range of motion increased linearly at d 14 and d 28 with increasing levels of bioactive proteins in the diet ($P < 0.01$). In conclusion, supplementation of bioactive proteins in mature, exercising horses resulted in improved gait kinematics.

Key Words: bioactive proteins, gait, horse, stride, supplement

1210 (W138) The effect of skim milk as an equine semen extender. M. L. Freitas, C. S. Bouéres, F. J. G. De Oliveira, L. S. Murata*, and R. A. De Oliveira, *University of Brasilia, Brazil.*

Cryopreservation constitutes the best method to conserve the genetic material of great zootechnic value stallions. However, the expenses of this procedure are high, becoming an obstacle to the spread of this biotechnology. One possible way to reduce spending on the process of cryopreservation is to search for alternative and less onerous extender media. The current study aimed at comparing the commercial semen extender (control group) to UHT skim milk (treatment group) used during centrifuging for subsequent cryopreservation of equine semen. After thawing of semen, parameters such as computerized spermatic kinetics and acrosome and plasmatic membrane integrity using fluorescent dyes were assessed. No differences ($P > 0.05$) were observed in what concerns to total sperm motility (42.71 × 38.29%); progressive sperm motility (12.29 × 7.86%); plasmatic membrane integrity (53.43 × 60.14%) and acrosomal membrane integrity (93.29 × 93.71%) between the control and the treatment groups. Considering that UHT skim milk has a much lower cost than the commercial semen extender, this may henceforth skim milk is an

option for extending equine semen, which decreases the expenses of the equine semen cryopreservation process.

Key Words: equine, sperm, UHT skim milk

1211 (W139) Reproductive activity in quarter horse mares with artificial light. J. A. Ramírez-Godínez*, J. Delgado-Laphond, A. Flores-Mariñelarena, and E. Santellano-Estrada, *Universidad Autónoma de Chihuahua, México.*

The objective was to determine the effect of artificial light during the winter on the reproductive activity in quarter horse (QH) mares in México. Sixty seven QH mares, 5 to 12 yr old with an average weight of 480 ± 20 kg, and body condition between 5 and 7 were randomly divided into a control group (G0, n = 15), exposed to natural light and an artificial light group 1 (G1, n = 52), exposed to artificial light to complete 16 h light from November 15 to February 15. Both groups were alternately monitored (every other day) with a teaser stallion to assess the presence of estrus, and the reproductive tract ultrasounded to monitor follicular growth and ovulation. Means for days to estrus, ovulation, pregnancy, services per conception and size of the ovulatory follicle were compared between treatments using the GLM procedure of SAS. The effect of treatments on ovulation rate per month was analyzed by Chi Square ($\chi 2$ test) using the FREQ procedure of SAS. The use of artificial light accelerated ($P < 0.001$) the onset of estrus, ovulation and gestation considerably. The average time from exposure of artificial light to onset of estrus was 47 ± 3.21 d ($P < 0.001$) in G1 and 105 ± 6.13 d in G0, and to ovulation 81.6 ± 3.7 d with artificial light (G1) and 134.5 ± 7.0 d control group (G0). The highest rate of ovulations ($P < 0.1$) occurred in February (0.46) in G1 and in April (0.66) in G0, respectively. Diameter of the ovulatory follicle was similar ($P > 0.05$) in mares in the control group (40.7 ± 1.11 mm) than under artificial photoperiod (41.7 ± 0.58 mm). The interval from the onset of artificial light to pregnancy was 96.54 ± 4.46 d (G1) and 141.28 ± 8.53 d with natural light (G0; $P < 0.001$). The services per conception (SPC) were similar ($P < 0.05$) between treatments (1.6 ± 0.123 SPC for artificial photoperiod and 1.7 ± 0.236 SPC for controls, respectively). The use of artificial light from November to February in QH mares accelerated the presence of estrus and the ovarian activity (ovulation) which resulted in a higher proportion of earlier gestations in the year.

Key Words: estrus, ovulation, mares

1212 (W140) Composition of follicular fluid and serum, ovarian dynamics, and IGF-1 concentrations following n-3 fatty acid supplementation in mares. S. E. Buist*[1], M. J. Schmidt[1], D. M. Grieger[1], C. A. Blevins[1], S. K. Webel[2], T. L. Douthit[1], L. Murray[1], and J. M. Kouba[1], *[1]Kansas State University, Manhattan, [2]JBS United, Baylis, IL.*

The effects of a marine-derived n-3 fatty acid supplement on ovarian dynamics and follicular fluid and serum composition were evaluated during the estrous cycle in mares. Fifteen mares were assigned to a control diet (CONT, n = 7) or a fish oil-enriched diet (FO, n = 8) providing 18.48 g eicosapentaenoic acid (EPA) and 10.08 g docosahexaenoic acid (DHA) daily. Follicular activity was determined via transrectal ultrasonography at the initiation of the treatment diet. Estrous cycles were synchronized in all mares concurrently with initiation of treatment diets using a progesterone and estradiol protocol. Following ovulation post-synchronization, mare monitoring continued through the second estrous cycle. Ovarian activity, timing of ovulation, and presence of a corpus luteum were recorded. Mares were scanned during the third estrous cycle until a 35-mm follicle was detected, at which time hCG was administered. A transvaginal ultrasound-guided follicular aspiration (TUGA) was performed on the largest preovulatory follicle 14 to 16 h post-hCG. Follicular fluid was analyzed for fatty acids, estradiol 17-β, LH, progesterone, $PGF_{2\alpha}$, PGE_2, and IGF-1 concentrations. Serum samples were collected at the onset of treatment diet and every 2 wk until termination of the study to determine fatty acid concentrations. Additional serum samples were obtained before hCG administration and before TUGA procedure for measurement of IGF-1. Arachidonic acid (ARA), EPA, docosapentaenoic acid (DPA), and DHA in mare serum and EPA, DPA, and DHA in follicular fluid were increased ($P < 0.01$) in the FO group. Serum IGF-1 was decreased ($P < 0.05$) in the FO group immediately before aspiration. Concentrations of IGF-1 were decreased ($P < 0.05$) in follicular fluid in the FO group compared with controls. No other differences in follicular fluid hormone concentrations were detected. Follicular growth rate, ovulation interval, and timing of ovulation were similar between groups. These data indicate that in addition to incorporation into serum, dietary n-3 fatty acids can also be incorporated into follicular fluid, and may have an inhibitory effect on serum and follicular fluid IGF-1 concentrations in the cycling mare.

Key Words: mare, n-3, follicular fluid

INTERNATIONAL ANIMAL AGRICULTURE: **INTERNATIONAL ANIMAL PRODUCTION**

1213 (T144) Handbook for livestock research on smallholder farms in developing countries.

A. L. Goetsch*, *American Institute for Goat Research, Langston University, Langston, OK.*

Resources for on-station livestock research in many developing countries are limited, and it is common for researchers to have little direct interaction with smallholders. On-farm research offers considerable attributes, which include attention to most significant production constraints, opportunities for meaningful studies, and greater adoption by smallholders of advantageous technologies. However, few researchers perform on-farm livestock research, at least partially because of inadequate training and knowledge of the design and conduct of on-farm experiments, statistical analyses and interpretation of resultant data, and preparation of reports suitable for peer-reviewed journals. Thus, a publication has been developed as a resource for training in methods of applied livestock research, with special attention to treatments, design, implementation, analysis, interpretation, and peer-reviewed articles. The target audience is junior to mid-level professionals (e.g., MSc) and graduate students in developing countries. In addition to US participants in the publication project, there are foreign collaborators and evaluators from Ethiopia, India, China, Jordan, México, Israel, and Japan. Major sections of the publication include: introduction; on-station vs. on-farm research; topic identification; protocols; experimental design; treatment considerations; experiment implementation; statistical analyses; dissemination with an emphasis on preparation, review, and revision of scientific manuscripts; and literature cited. Furthermore, a key component is the design and analysis of numerous example study scenarios, such as: farmer research groups– missing data, nature of the data; individual smallholder households– household animals on one treatment, household animals on each treatment, missing data and household animals on one vs. each treatment, households with subplots; group or village as fixed vs. random; studies in different seasons or years; year-round performance monitoring– continuous and categorical variables; and crossovers, switchbacks, and Latin squares. There are also comparisons of P values from different analyses (e.g., SAS GLM and MIXED and GenStat). Appendices contain the relevant statistical analysis statements and inputs, results, and simulated data sets. Workshops based on the publication were held during 2013 and 2014 in Kenya, Ethiopia, China (two sites), Jordan, Malawi, México, and India (two sites) to create awareness of the resource, train junior researchers, and receive feedback for publication enhancement, with well over 200 attendees. After external peer-review in fall 2014, hardcopies will be distributed and the publication made available free on the Institute's website (www2.luresext.edu).

The project was supported by the USDA Foreign Agricultural Service (grant/agreement no. 58–3148–2-175).

Key Words: applied research, livestock, small holders

1214 (T145) Reproductive performance in United Kingdom Holstein dairies by geographic region.

J. Hildon[1], C. Vergara*[2], and H. Lopez[2], *[1]Genus ABS, Stapeley, UK, [2]ABS Global, DeForest, WI.*

Our objectives were to compare reproductive indicators from Holstein dairies in three regions of The United Kingdom and establish benchmarks for the 20% most efficient herds. Data from 30,112 cows and 95,326 inseminations recorded on Dairy Comp 305 software were evaluated from January to December 2014 from 111 dairies in Region 1 (R1[North; n = 16 herds]), Region 2 (R2[West; n = 52]), and Region 3 (R3[South; n = 43]). Analyses were conducted with the PROC MIXED using herd as the experimental unit. Mean herd size (R1 = 252 ± 126; R2 = 267 ± 119; R3 = 284 ± 156), mean daily milk production in kilograms (R1 = 27 ± 3; R2 = 27 ± 4; R3 = 28 ± 5), days for voluntary waiting period (R1 = 40 ± 5; R2 = 42 ± 4; R3 = 40 ± 4), days for pregnancy diagnosis (R1 = 37 ± 5; R2 = 37 ± 4; R3 = 35 ± 5), days to reenrollment (R1 = 15 ± 4; R2 = 15 ± 4; R3 = 14 ± 4), conception rate for inseminations after natural estrus (R1 = 37%; R2 = 36%; R3 = 34%), insemination risk (R1 = 53%; R2 = 56%; R3 = 56%), pregnancy rate (R1 = 19%; R2 = 19%; R3 = 20%), and percentage of cows pregnant by 100 DIM (R1 = 49%; R2 = 50%; R3 = 53%), by 150 DIM (R1 = 69%; R2 = 72%; R3 = 75%) and by 300 DIM (R1 = 88%; R2 = 91%; R3 = 89%) did not differ among regions. The percentage of cows bred after synchronization was lower ($P < 0.05$) for R3 (7%) than R1 (12%), and R2 (10%) but conception rate did not differ (R1 = 29%; R2 = 28%; R3 = 28%). The 20% most efficient operations had mean pregnancy rate of 24%, mean daily milk production of 27 ± 4 kg, days to pregnancy diagnosis of 33 ± 5, days to re-enrollment of 12 ± 3, insemination risk of 61%, conception rate for inseminations after natural estrus of 39%, percentage of cows bred after synchronization of 7%, conception rate for inseminations after synchronization of 33%, and percentage of cows pregnant by 100 DIM of 61%, by 150 DIM of 83%, and by 300 DIM of 96%. The percentage of cows bred after synchronization was lower for the South region but no other regional differences were detected in reproductive parameters in United Kingdom dairies.

Key Words: fertility, reproduction, estrus

1215 (T146) Crossbreeding effects for body weight and carcass characteristics in a three-breed diallel cross. D. Norris[*1], L. Tyasi[2], and J. Ng'ambi[1], *[1]University of Limpopo, Polokwane, South Africa, [2]University of Limpopo, Sovenga, South Africa.*

A 3 × 3 complete diallel mating system involving three chicken breeds, namely Potchefstroom Koekoek (P), Venda (V) and Ovambo (O), was used to estimate crossbreeding genetic effects (heterosis, maternal effects and combining abilities) for growth and carcass characteristics. Nine genetic groups consisting of 25 chickens per group were produced which were reared from hatch to 10 wk of age. Body weights were recorded at hatch, 4, 8, and 10 wk of age while meat quality analysis (color, pH and tenderness) of the breast meat was done at slaughter age (10 wk). Meat tenderness was determined using the Instron-Warner-Bratzler Shear Force (WBSF). Potchefstroom Koekoek (P) was heavier at all different growth stages among the purebreds, while the Venda had the lowest weights at all different growth stages. The highest level of heterosis (30 and 21%) was observed in the V X P cross at 8 and 10 wk, respectively. The P x V cross showed positive estimates of maternal effects except at 10 wk of age. High and positive general combining ability (GCA) was observed in the Potchefstroom Koekoek (P) breed. The P x V showed positive effects of specific combining ability (SCA) at hatch, 4, 8, and 10 wk of age. With respect to meat characteristics, the Pochefstroom Koekoek breed had higher values of a* (redness) and b* (yellowness) color indicators in comparison to the other chicken breeds. Potchefstroom Koekoek and P x O breed had higher values of pH at 2 h and 24 h after slaughter. The pH declined in all the nine genetic groups at 2 h to 24 h, except for the P x O, which increased. The O x P had the highest shear value (74.80) while the lowest shear force (43.62) was observed in the P X V genotype. The P X V and its reciprocal cross, V X P could be further evaluated for other characteristics such as egg production and used as base for improved indigenous chicken production. It may be worthwhile to also consider developing a composite chicken breed based on these two breeds.

Key Words: crossbreeding, heterosis

1216 (T147) Total bacteria counting profile of raw milk in minas gerais state according to the storage system. A. G. Fernandes[1], L. M. Fonseca[*2,3], M. P. Cerqueira[2], M. O. Leite[2], M. C. P. P. Oliveira[2], R. M. Longo[2], G. C. Ribeiro[2], C. F. A. M. Penna[2], and M. R. Souza[2], *[1]Ministry of Agriculture, Belo Horizonte, Brazil, [2]Universidade Federal de Minas Gerais* (*School of Veterinary Medicine), Belo Horizonte, Brazil, [3]University of Wisconsin–Madison/CAPES Est. Senior 18183–12–3, Madison.*

The microbial contamination of milk is influenced by several factors and it is one of the major hindering problems for milk quality improvement in Brazil. The objective of the present work was to evaluate total bacteria counting of milk collected in different storage systems. A total of 1080 samples of milk from three regions of Minas Gerais State (Triângulo Mineiro, Sul, and Leste) were analyzed for total bacteria counting, during a 12-mo period. The samples were randomly selected from three storage systems, individual bulk tank milk, collective bulk tank milk, and cans. The last two storage systems are exceptionally allowed in Brazil under specific conditions. Each storage system was represented by 360 samples, which were preserved with azidiol, and sent to the laboratory for analysis in up to 72 h, using insulated boxes with reusable ice. All samples were evaluated by flow cytometry in the official federal net of laboratories for milk quality analysis in Brazil. Data were analyzed using general linear model and Tukey test for pairwise comparison. Collection system was the major factor correlated to the milk quality, with average countings of 5.38, 5.89, and 5.75 log CFU/mL for milk stored in bulk tank milk, collective bulk tank milk, and can, respectively. Non -compliance to the current standard of 600,000 CFU/mL was found in 47.6% of the samples, with 32.2, 61.1, and 49.7% non-compliant samples from bulk tank milk, collective bulk tank milk, and can, respectively. Considering recommended international standards, only 18.1% of the samples were in the range of up to 100,000 CFU/mL, comprising 28.6, 8.3, and 17.2% for, respectively bulk tank milk, collective bulk tank milk, and can storage. Milk quality was correlated to the seasonal variation ($P < 0.05$), with 53% of the samples above the limit of 600,000 CFU/mL during the rainy season. Regional differences were also observed. It is concluded that collecting systems, and regional and seasonal differences must be considered for strategic action by the dairy industries towards microbial quality improvement of raw milk.

Key Words: Brazil, microbial contamination, milk quality

1217 (T148) Reproductive performance in Chilean holstein dairies by geographic region. F. Arias[1], H. Lopez[2], R. Krauss[1], and C. F. Vergara[*1,2], *[1]ABS Chile Ltda, Santiago, Chile, [2]ABS Global Inc., DeForest, WI.*

Our objectives were to compare reproductive indicators from Holstein dairies in the three main productive areas of the Chilean Valley and establish benchmarks for the 20% most efficient herds. Data from 24,319 cows and over 70,000 inseminations recorded in DC305, Afi-farm, and Dairy Plan were evaluated from January to December 2013. Data included 30 dairies located in: Central Area (C [fifth, sixth, and Metro Regions]; n = 12 herds]) in dry lots and free-stall housing; South-Central Area (SC [seventh and eighth Regions]; n = 6 herds]) with free-stall and grazing systems; and South Area (S [ninth and 10th Regions]; n = 12]) with free-stall and grazing systems. Analyses were conducted with the PROC MIXED of SAS using herd as the experimental unit. The regions did not differ ($P > 0.05$) by mean (SD) herd size (C = 592 ± 315; SC = 940 ± 1612; S = 989 ± 815), days open in pregnant cows (C = 137 ± 19; SC = 135 ± 19; S = 144 ± 15), days in milk (C = 203 ± 17; SC = 209 ± 39; S = 210 ± 31), and days to first breeding (C = 71 ± 5; SC = 73 ± 10; S = 79 ± 4). Similarly, pregnancy risk (C = 19%; SC = 17%; S = 16%), insemination risk (C = 53%; SC = 48%; S = 46%), all services conception rate (C = 37%; SC = 37%; S = 38%), and removal rate by 60 d in milk (C = 7%; SC = 7%; S = 5%) were not different among regions. The S region had lower ($P < 0.05$) mean (SD) daily milk production in kilograms (25 ± 4) in comparison to the SC (34 ± 5) and C region (36 ± 5). The C region had more ($P < 0.05$) days of voluntary waiting period (51 ± 3) than regions SC and S (48 ± 4 and 47 ± 3, respectively). The 20% most efficient operations based on pregnancy risk ranking had a voluntary waiting period of 52 ± 3 d, mean pregnancy risk of 21%, insemination risk of 56%, and all services conception rate of 40%. They achieved 50% pregnant by Day 100 in milk, and mean (SD) days open and days in milk of 126 ± 8 and 184 ± 16, respectively. Conception rates for first insemination (40% vs. 35%) and for the first lactation (44% vs. 37%) were higher ($P < 0.05$) for the 20% most efficient herds. The 3 regions evaluated differed only in milk production level and voluntary waiting period. The most efficient herds had higher pregnancy risk, insemination risk, and conception rates; especially for first insemination and first lactation cows.

Key Words: fertility, reproduction, estrus

1218 (T149) In vitro fermentation and digestion characteristics of shrubs *Leucophyllum frutescens* and *Zanthoxylum fagara* browsed by white-tailed deer (*Odocoileus virginianum Texanus*). A. MS.[1], C. S. MA*[1], G. C. M.[1], G. R. H.[2], and R. L. RG.[3], *[1]Universidad Juárez del Estado de Durango, México, [2]Universidad Autónoma de Nuevo León, Linares, México, [3]Universidad Autónoma de Nuevo León, San Nicolás de los Garza, México.*

Native vegetation in northeastern México is mainly composed by shrubs and small trees, which are browsed by white-tailed deer. The aim of the study was to determine, seasonally, the in vitro fermentation profiles of *Leucophyllum frutescens* and *Zanthoxylum fagara.* Foliage was sampled from summer 2005 to spring 2006 for a total of four consecutive seasons in two country sites: Linares and Los Ramones in the state of Nuevo Leon, México. In vitro gas production was recorded at 3, 6, 9, 12, 24, 48, 72, and 96 h. As inoculum, rumen fluid from fistulated sheep was utilized. Microbial protein, ME content and in vitro organic matter digestibility (IVOMD) were also evaluated. Data were analyzed according to a multi-factorial arrangement being sites (2), shrubs (2) and seasons (4) the factors. Kinetic parameters significantly varied among shrubs, sites and seasons. The asymptotic gas production (B) ranged from 149 mL of gas/g DM in *L. frutescens* in summer 2005 in Los Ramones to 273 mL of gas/g DM in *Z. fagara* in winter 2006 in Linares country. The rate of gas production (c) was the lowest in *L. frutescens* in spring 2006 (0.028%/h) while the highest (0.104%/h) in *Z. fagara* collected in summer 2005 in Los Ramones. Values regarding lag phase (L) ranged from 0.64 to 2.07 h; in general, this variable was superior during spring seasons in both sites. Interactions sites x shrub species x seasons were significant ($P < 0.001$) for all kinetic parameters except for L. Microbial protein synthesis measured as purines varied significantly among sites, shrubs and seasons. Mean values ranged from 2.76 to 10.91 µmol, the latter was registered in *L. frutescens* collected in spring 2006 in Linares. The same scenario was registered with the ME content where values varied from 0.66 to 2.60 Mcal/kg DM. Estimates of IVOMD ranged from 56.8 to 93.1%. In general, highest digestibility values were registered in *Z. fagara*. Significant interactions related to IVOMD were registered as well. Data suggested that regardless spatiotemporal variations, variables such as constant rate of gas production, ME and microbial protein synthesis support the nutritive potential of the studied shrub species specially during the summer and autumn seasons for white-tailed deer.

Key Words: gas production, semiarid regions, white-tailed deer

1219 (T150) Characterization of goat foraging and body condition in Jhadol Block, Udaipur, India.
M. Valentine*, *Cornell University, Ithaca, NY.*

India contains 125.7 million goats, 14.6% of the global goat population. Smallholder farmers own the majority of Indian goats, and animal productivity ranks far below goats' genetic potential. Our objective was to characterize the feeding practices of goat owners and the nutrition of goats in the Jhadol Block of the Udaipur District in Rajasthan, India. Sixty-four goat owners were surveyed in 10 villages of the Jhadol Block. The questionnaire focused on various aspects of the livestock system including socio–economic characteristics, livestock management, goat consumption and physical assessment of goat condition. The survey was broken into general household data, goat husbandry practices, goat diet composition, feeding habits, feed shortage mitigation, crop residue use and lactation. Most interviewees received the majority of their income as wage laborers and subsisted on their own land. Mean household landholdings were 0.52 ha with SD ± 0.248. Households owned from 1 to 22 goats with an average of 6.59 ± 4.12 goats. The highest level of education averaged 7.03 ± 3.75 yr, and 65.6% of households had electricity. Linear regression models and bivariate tables were used to compare data. Goat health was assessed using body condition scoring, which was measured by applying a five-point palpation and observation-based scale. Body condition was related to socio–economic factors, geographic location, and management practices. Body condition was significantly correlated with the household and village, in addition to whether the household cultivated forages (P = 0.0076) or lopped tree branches in the rainy season (P = 0.0385). The target population was also stratified by how many of the three local seasons (rainy, winter and summer) households took goats foraging outside of the home as a way to characterize goats' feeding regiment. Number of seasons foraged was compared to household parameters such as number of persons, number of goats, education and land. Seasons foraged was correlated with the total number of goats (P = 0.0105) and total number of other livestock owned (P = 0.0196). Aspects of the semi-extensive goat system in the Udaipur district were characterized to better understand household characteristics and practices that contribute to sound nutritional management practices and healthier goats. Information generated from these analyses advances knowledge of goat farming systems in rural Rajasthan, where there is currently limited published information to support caprine management or direct future caprine research initiatives.

Key Words: India, goat systems, semi-extensive farming

1220 (T151) Characterization of cattle manure value chains in South-Central Vietnam.
K. C. McRoberts[1], D. Parsons[2], C. F. Nicholson[3], L. V. Nam[4], and D. J. R. Cherney*[1], *[1]Cornell University, Ithaca, NY, [2]University of Tasmania, Hobart, Australia, [3]Pennsylvania State University, University Park, [4]Hue University of Agriculture and Forestry, Vietnam.*

Cattle manure value chains play an important role in smallholder crop-livestock systems in south-central Vietnam. Lowland cattle farmers sell manure through a network of chain participants to pepper, coffee, dragon fruit, and rubber farms in the Central Highlands and south coast. This study describes cattle manure value chains originating in two representative lowland communes, Nhõn Khánh (NK) and An Chấn (AC). Semi-structured interviews with value-chain participants between April and September 2013 collected information from lowland farmers (n = 101), manure collectors and traders (n = 27), rubber companies (n = 2), highland farmers (n = 50), and dragon fruit farmers (n = 20) about cattle management, manure-related labor, manure transactions, and fertilizer and manure use. Lowland cattle owners were selected using stratified random sampling. Farmer interviews identified subsequent value chain participants. Most farmers interviewed reported manure sales (AC = 78%, NK = 92%), and reported sales of 62% of farm manure with SD ± 26%. Farmers prepared manure for sale by drying it on the ground or in cakes for approximately 4 d. Dry manure (89 ± 3% DM, 18.7 ± 5.6% OM, 1.27 ± 0.37% N, and 0.59 ± 0.27% P_2O_5) was bagged and sold to local manure collectors who arranged transfer to highland farmers, south coast farmers, or traders. Manure was sold by the bag (bag volume in AC = 20.4 L, NK = 46.6 L). Sale price in farmer-reported transactions was \$34.19 ± 4.95/m^3 in AC and \$24.31 ± 3.88/m^{3}in NK. Preliminary analyses suggest annual farmer revenue of \$116 ± 102 in AC and \$120 ± 93 in NK, thus providing an important source of supplementary income. Manure not sold was composted and used for crop fertilization. Farmers reported most manure sales between February and August (during NK and AC dry season) when demand exists for organic amendments in the highlands. From NK, approximately 80% of manure sold flowed to Gia Lai Province and 20% to Đắk Lắk Province in the Central Highlands. From AC, 70% flowed to Gia Lai, 10% to Đắk Lắk, and 5% to Đắk Nông. 15% flowed to dragon fruit farmers in Bình Thuận Province late in the year. Before application, highland farmers purchasing manure often prepared a 45-d compost with manure and other amendments including potassium, urea, coffee pulp, and a commercial probiotic. This study generated descriptive information about manure value chains in Vietnam that can inform analysis of value chain dynamics via simulation modeling.

Key Words: cattle manure, value chain, Vietnam

1221 (T152) Selenium concentration in blood, milk and urine in grazing jersey herds in Costa Rica.

A. Saborío-Montero*[1], M. Alfaro-Cascante[1], F. Granados-Chinchilla[2], and A. Molina-Alvarado[1], *[1]Centro de Investigaciones en Nutrición Animal y Escuela de Zootecnia, Universidad de Costa Rica, San José, [2]Centro de Investigaciones en Nutrición Animal, Universidad de Costa Rica, San José.*

The aim of this study was to determine the concentration of selenium (Se) in blood, milk and urine in grazing Jersey cows. The study was conducted on four commercial dairy herds in the highlands (≈ 2250 m of altitude) of Cartago, Costa Rica. Cows were intensively grazing kikuyu grass (*Kikuyuocloa clandestina*) and daily supplementation consisted of concentrate according to milk yield (1 kg concentrate:3 kg of milk). Blood samples were taken from the coccygeal vessels, milk samples were collected during milking from the milk yield measure container and urine was obtained using rubbing stimulation. A total of 102, 139, and 87 samples of blood, milk and urine respectively were collected and analyzed. Atomic absorption spectrophotometry was used to determine Se concentration. Soil was sampled in each farm to determine Se and sulfur (S) concentration and their associations with average Se in blood, milk and urine. A soil borer was used to obtain 20 subsamples per sample; those subsamples were collected drilling the soil surface to a depth of 10 cm. Se an S concentration in soils was analyzed using atomic absorption spectrophotometry and $Ca(H_2PO_4)_2 \cdot H_2O$ 0.008M 10:25 extraction, respectively. Average blood, milk and urine Se concentration are shown in Table 1221. Se in soils of farms 1, 2, 3, and 4 were 98, 78, 144, and 345 µg/kg respectively, S concentration in soil was 74, 35, 57, and 32 mg/L in the same order. No association was obtained between average Se concentration in the animal fluids and the soil Se or S concentration. Se concentration in blood was correlated to Se concentration in milk ($r = 0.31$, $P < 0.01$). Differences between Se concentrations in milk among herds suggest that it could be related to supplementation on each farm. Results also indicate that high values of selenium in urine in some of the farms could imply a poor utilization or excessive supplementation of this mineral with associated economic costs. More research should be done in a wider population to support these findings.

Key Words: Jersey cows, selenium, soil

Table 1221. Selenium concentration in blood, milk and urine in four grazing Jersey herds

Herd	Se in blood (µg/L)	Se in milk (µg/L)	Se in urine (µg/L)
1	41.12	32.61[a]	200.27[ab]
2	108.11	66.57[b]	263.05[a]
3	69.44	32.94[a]	47.48b[c]
4	41.44	22.35[a]	28.35[c]

[a, b] Means in the same column not sharing a common superscript are different ($P < 0.05$)

LACTATION BIOLOGY I

1222 (M144) relationship between dry period length and production and reproduction in grazing Jersey and Holstein cows in Costa Rica. J. M. Sánchez*[1], A. Saborío-Montero[1], and A. Córdoba-Roldán[2], [1]*Centro de Investigaciones en Nutrición Animal y Escuela de Zootecnia, Universidad de Costa Rica, San José, Costa Rica,* [2]*Programa de Transferencia Tecnológica, Cooperativa de Productores de Leche Dos Pinos, San José, Costa Rica.*

The aim of this study was to evaluate relationships between dry period length (DPL) of Jersey and Holstein grazing cows and succeeding productive and reproductive performance. The study was conducted on 29 dairy herds in the highlands of Cartago, Costa Rica. The predominant pasture grass on the farms was kikuyu (*Kikuyuocloa clandestina*) and cows were supplemented with 1 kg of a grain mixture/2.5 to 3 kg of milk. A total of 4792 completed lactations (Jersey n = 3000, Holstein n = 1792) were registered from 2009 to 2012. DPL in Jersey (mean = 75.6 d, 95% CI: 74.1–77.0 d) differed (P < 0.001) from Holstein (mean = 80.7 d, 95% CI: 78.2 to 83.2 d). In Jersey cows the DPL was inversely correlated with actual milk yield (-0.23, P < 0.001) and 305-d milk yield (-0.27, P < 0.001). Open period length in Jersey cows (mean = 120 d, 95% CI: 117 to 123 d) differed (P < 0.001) from Holstein (mean = 150 d, 95% CI: 145 to 154 d). Jersey cows with DPL less than 58 d produced more 305-d milk (mean = 5583 kg, 95% CI: 5480 to 5687 kg, P < 0.001) than cows with a DPL greater than 73 d (mean = 5208 kg, 95% CI: 5086 to 5331 kg). Cows in both those dry groups produced less (P < 0.01) milk than cows with a DPL of 58 to 73 d DPL (mean = 5949 kg, 95% CI: 5885 to 6012). Jersey cows with DPL greater than 73 d had shorter (P < 0.001) lactation length (mean = 305 d, 95% CI: 299 to 310 d) than those below that threshold (mean = 324 d, 95% CI: 321 to 327 d). Calving interval for Jersey cows with DPL less than 58 d (mean = 403 d, 95% CI: 398 to 409 d) was greater (P < 0.05) than those with DPL between 58 and 63 d (mean = 392 d, 95% CI: 388 to 397 d). 305-d milk yield was greater (P < 0.01) in Holstein cows with DPL between 55 and 63 d (mean = 7620kg, 95% CI: 7434 to 7807 kg) than those with DPL less than 55 d (mean = 7162kg, 95% CI: 6964 to 7361kg) or higher than 86 d (mean = 7066kg, 95% CI: 6830 to 7301kg). Open period in Holstein cows was greater (P < 0.01) in those with DPL greater than 86 d (mean = 163d, 95% CI: 153 to 173d) compared to those cows with DPL between 55 and 86 d (mean = 144d, 95% CI: 138 to 150d). These results suggest that in grazing Jersey and Holstein cow herds milk yield and reproduction performance could be influenced by DPL.

Key Words: dry period length, grazing cows, dairy cows

1223 (M145) Effect of insulin on mRNA expression of genes related to milk synthesis in primary bovine mammary epithelial cells cultured in vitro. T. Qin[1], H. Y. Wang[1], D. P. Bu*[2], and H. B. Zhu[1], [1]*Embryo Biotechnology and Reproduction Laboratory, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China,* [2]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

The crucial role for mTOR in the regulation of milk protein synthesis in the bovine mammary gland has been reported, but the molecular events associated with regulation of milk fat synthesis remain unknown. This study was conducted to examine the potential role of insulin in the presence of two lactogenic hormones, hydrocortisone and prolactin, on milk protein and fat synthesis. Primary bovine mammary epithelial cells cultured in vitro were treated in three different ways (no hormones (NH, control), 50 ng/mL hydrocortisone and 200 ng/mL prolactin (FP), or 100 ng/mL insulin, 50 ng/mL hydrocortisone and 200 ng/mL prolactin (IFP)). Expression of 17 key genes involved in four pathways were detected by real-time PCR. Statistical significance was evaluated by unpaired t test analysis with SAS 9.0 software. Significance was declared at P < 0.05. Results showed that IFP group significantly increased the mRNA level of β-casein (CSN2), κ-casein (CSN3), Acetyl-CoA carboxylase (ACACA), fatty acid synthase (FASN) and Sterol Regulatory Element Binding Protein1 (SREBP1) compared to NH and FP groups (P < 0.05). Relative to the other groups, IFP group significantly up-regulated the expression of signal transducers and activators of transcription 5B (STAT5B) and E74-like factor 5 (ELF5) in JAK-STAT5 pathway, as well as Phosphatidylinositol 3-kinase (*P*I3K), Protein Kinase B (AKT1) and Eukaryotic initiation factor 4E (EIF4E) in PI3K/Akt/mTOR signaling pathway (P < 0.05). But the IFP hormone combinations had no effect on TSC1, TSC2 or RHEB transcription in AMPK signal pathway (P > 0.05). The results demonstrated that insulin may stimulate milk protein synthesis by JAK-STAT5 and PI3K/Akt/mTOR signaling pathways, and stimulate milk fat synthesis by PI3K/Akt/mTOR and SREBP signaling pathways in bovine mammary epithelial cells cultured in vitro. This research indicated insulin has an important role in milk protein and fat synthesis as the other two lactogenic hormones, hydrocortisone and prolactin.

Key Words: insulin, bovine mammary epithelial cells, real-time PCR

1224 (M146) Conjugated linoleic acid (CLA) trans-10, cis-12 decreases ACC-α gene expression in lactating mammary gland by decreasing specific transcripts from different promoters. D. E. Oliveira[*1], D. E. Bauman[2], and K. J. Harvatine[3], *[1]Santa Catarina State University, Lages, Brazil, [2]Cornell University, Ithaca, NY, [3]Penn State University, State College.*

Transcription of acetyl-CoA carboxylase α (ACC-α) is initiated from multiple promoters in a tissue-specific fashion and mammary expression of ACC-α is decreased during CLA-induced and diet-induced MFD. The effect of *trans*-10, *cis*-12 CLA and a low forage and high oil diet on regulation of the different ACC-α isoforms in mammary tissue was investigated. Nine mid-lactation cows were arranged in a 3 × 3 latin square design with 14-d experimental periods. Treatments were Control, 3 d i.v. infusion of *trans*-10, *cis*-12 CLA (CLA-MFD), and feeding a low forage, high oil diet (Diet-induced MFD). Milk fat yield was decreased 38% percent by the low forage and high oil diet and by 24% percent by CLA. Mammary biopsies at the end of each treatment were taken. Quantitative real-time reverse transcriptase PCR assays were developed for ACC-α specific promoters of interest. Data were analyzed using the PROC MIXED of SAS to test expression of individual ACC-α promoters I, II, III (exon 5A) and a well described splice variant (-24NT). The geometric mean of 3 housekeeping genes was calculated and used as a covariant in the model. Differences in expression of individual ACC-α promoters was declared significant at $P < 0.05$ and trends at $P < 0.1$. There was no treatment effect on expression of ACC-α transcript from promoter I. Compared to Control, ACC-α promoter II transcript were reduced 32.9% with diet-induced MFD treatment ($P = 0.005$) and tended to be decreased 18.5% by CLA treatment ($P = 0.06$). Transcript from promoter III (exon 5A) was reduced 26.4 and 35% for CLA-induced and diet-induced MFD treatments ($P = 0.0001$), respectively, compared to Control. Transcript for the -24NT splice variant was reduced by 25.8% during det-induced MFD in comparison to control ($P = 0.03$), but CLA treatment was not different from control. Promoters II, III, and -24NT splice variant transcript of ACC-α are decreased during diet induced milk fat depression demonstrating a promoter specific role of bioactive fatty acids in ACC-α gene expression.

Key Words: acetyl-CoA carboxylase promoters, gene expression, conjugated linoleic acid

1225 (M147) Conjugated linoleic acid (CLA) affects in different ways acetyl-CoA carboxylase α (ACC-α) transcripts from different promoters in mammary and adipose tissue from lactating ewes. E. Ticiani[1], M. Urio[1], A. P. Povaluk[1], M. V. Camera[1], R. Ferreira[2], L. C. Miletti[1], K. J. Harvatine[3], and D. E. Oliveira[*1], *[1]Santa Catarina State University, Lages, Brazil, [2]Santa Catarina State University, Chapecó, Brazil, [3]Penn State University, State College.*

Feeding *trans*-10, *cis*-12 CLA to lactating ewes reduces milk fat by down-regulating gene expression of enzymes involved in lipid synthesis in mammary gland. An example is acetyl-CoA carboxylase α (ACC-α), a key enzyme in the de novo fatty acid synthesis pathway. ACC-α is encoded by mRNAs transcribed from three promoters, PI, PII and PIII, characterized as tissue-specific in the ovine genome. This study evaluated the effects of a rumen-unprotected *trans*-10, *cis*-12 CLA supplement fed to crossbred Lacaune/Texel lactating ewes, on gene expression of different mRNA transcripts of ACC-α. Twelve ewes arranged in a completely randomized design received for 15 d one of the following treatments: Control (forage + 1 kg of concentrate) and CLA [forage + 1 kg of concentrate + 28 g/d of CLA (29.9% *trans*-10, *cis*-12)]. The CLA supplement (an oil mixture) was orally dosed. Mammary gland and adipose tissue biopsies were taken on Day 15. Subsequently RNA was extracted, cDNA synthesized and quantitative real-time reverse transcriptase PCR analysis conducted. Data were analyzed by PROC MIXED using ribosomal protein S18 housekeeping gene as a covariate in the model. Compared to Control, in the mammary gland CLA reduced by 29.1% ($P = 0.037$) transcript from PIII with no changes on transcripts from PI and PII ($P > 0.05$). In the adipose tissue, transcript from PI was increased by 379.8% ($P = 0.028$) in the CLA treated group when compared to Control. There was no treatment effect on transcripts from promoters II and III in the adipose tissue. Overall, our results suggest that *trans*-10, *cis*-12 CLA downregulates ACC-α gene expression by decreasing expression from promoter III in mammary tissue and increases ACC-α gene expression by increasing expression promoter I in adipose tissue.

Key Words: adipose tissue, gene expression, mammary gland

1226 (M148) Effect of different hormones on â-casein and lactoferrin expression in mammary epithelial cells. *W. Q. Li[1,2], J. Q. Wang[*1], D. P. Bu[1], and X. M. Nan[1], [1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Life Science, Henan Agricultural University, ZhengZhou, China.*

An inverse relationship in expression patterns for lactoferrin (LTF) and caseins occurs throughout the lactation cycle: when LTF expression is high, casein expression is low and vice versa. The objective of this study was to investigate the effect of different hormones on β-casein (CSN2) and LTF expression in mammary epithelial cells. Primary bovine mammary epithelial cells were treated with eight kinds of induction mediums to induce expression of CSN2 and LTF, including group A dexamethasone&prolactin&insulin (1 μg/mL, 5 μg/mL, 5 μg/mL), group B dexamethasone&prolactin&insulin (1 μg/mL, 10 μg/mL, 5 μg/mL), group C β estradiol (5 μg/mL), group D 10 ng IGF-I, group E 100 ng IGF-I, group F 200 ng IGF-I, group G 400 ng IGF-I, group H 1000 ng IGF-I. Materials administered in groups C-H did not include dexamethasone&prolactin&insulin. Relative mRNA expression of CSN2 and LTF was detected at 24h after induction by qPCR. Data was analyzed by One-way ANOVA and pearson correlation procedure of SAS 9.0. The results showed that 100ng IGF-I was the most suitable inducing material for β-casein ($P < 0.05$) and no significant difference of LTF expression among groups was observed ($P > 0.05$). Correlation coefficient of CSN2 and LTF expression was -0.277. It was concluded that CSN2 expression in bovine mammary epithelial cells depended on hormone and IGF-I, but not LTF. More research is needed to explore the relationship between β-casein and lactoferrin.

Key Words: β-casein, lactoferrin, mammary epithelial cell

1227 (M149) Effects of methionyl-methionine on milk protein synthesis in bovine mammary gland. J. X. Yang[1], H. Y. Liu[1], C. H. Wang[1], Q. B. Xu[*1], and J. X. Liu[2], [1]*Institute of Dairy Science, Zhejiang University, Hangzhou, China,* [2]*Zhejiang University, Hangzhou, China.*

This study was conducted to evaluate effect of methionyl-methionine (Met-Met) on milk protein synthesis in cultured lactating bovine mammary tissues. Mammary tissues were obtained from three lactating Holstein dairy cows and incubated in DMEM/F12 for 72 h. Triplicate isolated cultured mammary tissues were treated with conditional medium containing certain essential amino acid (AA) for 3 h before treatment exposure. The concentration of Met-Met was adjusted through replacing the medium Met with Met-Met at ratios of 0, 5, 10, 15, 20, and 25%, respectively. After incubation with experimental medium, tissues were collected for determination of α_{s1} casein expression by RT-qPCR and western blot. The AA absorption was determined by the change of free AA concentration in the medium. The mRNA abundance of AA transporters, mTOR and JAK2-STAT5 signaling pathway were measured for the control and optimal ratio of Met-Met treatment. Replacement of Met-Met for single Met significantly increased α_{s1} casein expression, with the highest expression at 15% of Met-Met substitution. Compared with the control, mRNA abundance of AA transporters including ATB (0, +) and CAT1 was increased, and AA absorption were significantly improved in 15% Met-Met group ($P < 0.05$), in which the mRNA abundance of mTOR, S6K1, 4E-BP1, JAK2 and STAT5 ($P < 0.05$) was also increased. From these results, it is indicated that Met-Met promoted milk protein synthesis and AA absorption in cultured bovine mammary tissues, and mTOR and JAK2-STAT5 signaling pathways may be involved in the Met-Met-stimulated milk protein synthesis.

Key Words: αs1 casein, bovine mammary gland, methionyl-methionine

1228 (M150) Effect of bta-miR-145 overexpression and down-expression on the other microRNA expression in primary bovine mammary epithelial cells. W. Q. Li[1], D. P. Bu[*1], J. Q. Wang[2], and X. M. Nan[1], [1]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China,* [2]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijng, China.*

MicroRNA research has made great progress. MicroRNA overexpression by mimic or down-expression by inhibitor is a common method to study the function of microRNA. However, it is unknown that whether overexpression or inhibition of a certain microRNA affects other microRNAs expression or not. This study was performed to evaluate the effect of bta-miR-145 overexpression or down-expression on other microRNAs expression. Bta-miR-145 mimic (150pmol/well) or inhibitor (300pmol/well) was transfected in primary bovine mammary epithelial cells in 6-well plates. After 24h transfection, expressions of bta-miR-145, bta-miR-214, bta-miR-181a, bta-miR-21 were detected by RT-qPCR method. Relative quantification (ΔΔCt) method was used to analyze the data. The geometric mean of 5SrRNA and U6 was used to normalize the expression of microRNAs. All data were tested by one-way ANOVA program of SAS 9.1. The results showed that the overexpression effect of bta-miR-145 was achieved in cells by its mimic, and inhibiting effect of bta-miR-145 was achieved by its inhibitor. In addition, bta-miR-181a and bta-miR-145 had the same expression trend, while bta-miR-214 and bta-miR-145 had the opposite expression trend. And bta-miR-21 expression was almost not affected by bta-miR-145

overexpression and down-expression. It was concluded that one kind of microRNA overexpression or inhibition would cause expression change of other microRNAs. It is suggested that system biology views should be take to explain the related biological problems.

Key Words: bta-miR-145, overexpression, down-expression

1229 (M151) Stearic acid alters microRNA profiles in bovine mammary gland epithelial cells. Y. G. Chai[1], X. M. Nan[1], D. P. Bu[*2], J. J. Loor[3], and J. Q. Wang[2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [3]University of Illinois, Urbana.*

MicroRNAs (miRNA) are important regulators of cellular processes. The objective was to study whether the addition of stearic acid would alter the microRNA profile of bovine mammary epithelial cells. Cells were cultured and passaged in DMEM/F12 basic medium with 10% fetal bovine serum. For experimental assays, cells at 80% confluence were cultured in lactation medium (containing insulin, epidermal growth factor, transferring, hydrocortisone, progesterone and fatty acid free bovine serum albumin) with or without stearic acid (SA) for 24 h. A customized microarray containing 672 bovine miRNA was used to investigate their functional roles in bovine mammary gland epithelial cells in response to supplemental stearic acid (SA). Total miRNA expressed in the control and SA incubations was 157 and 165. Seventeen of 165 miRNA were differentially expressed with SA, and 12 (bta-miR-452, bta-miR-30c, bta-miR-362–5p, bta-miR-181a, bta-miR-194, bta-miR-2368, bta-miR-2893, bta-miR-2888, bta-miR-2374, bta-miR-29c, bta-miR-19a, and bta-miR-2411) were verified by real-time PCR. Using TargetScan, PicTar, GO and KEGG for functional analyses revealed that gene targets of miRNAs affected by SA are associated with regulation of transcription and mTOR signaling. This study provides novel data on miRNAs responsive to fatty acid in vitro.

Key Words: stearic acid, microRNA, lactational response

1230 (M152) The peroxisome proliferator-activated receptor γ (PPARγ) agonist thiazolidinedione (TZD) does not overcome *trans*-10, *cis*-12 conjugated linoleic acid (CLA) inhibition of milk fat synthesis in lactating dairy ewes. E. C. Sandri[1], E. M. Sandri[2], M. V. Camera[1], A. P. Povaluk[1], M. Urio[1], E. Ticiani[1], K. J. Harvatine[3], and D. E. Oliveira[*1], *[1]Santa Catarina State University, Lages, Brazil, [2]Santa Catarina State University, Chapecó, Brazil, [3]Penn State University, State College.*

Peroxisome proliferator-activated receptor γ (PPARγ) is regulated by ligand activation and regulates lipid synthesis pathways, but a functional role for PPARγ in diet-induced MFD in vivo has not been established. This study evaluated the effect of PPARγ agonist thiazolidinedione (TZD) on milk fat synthesis and its interaction with *trans*-10, *cis*-12 CLA. Twenty-four lactating ewes (60 ± 0.45 kg of BW) were randomly assigned one of the four treatments (n = 6/treatment) for 7 d: Control (100 mL/d of saline); TZD (IV 4 mg of TZD/kg of BW per d in 100 mL of saline); CLA (oral dose of 27 g/d of rumen-unprotected CLA (oil mixture: 29.9% *trans*-10, *cis*-12), and TZD+CLA (TZD infusion initiated 1 d before CLA dosing). Milk was sampled and analyzed for fat, protein and lactose concentration. Compared to control, fat content was 22.3% lower in CLA (6.14 vs. 4.77%, P = 0.05), tended to be 20.7% lower in TZD+CLA (6.14 vs. 4.87, P = 0.06), and did not differ between control and TZD (6.14 vs. 6.70%, P = 0.39). Compared to TZD, fat content was 28.8% lower in CLA (6.70 vs. 4.77%, P = 0.008) and 27.3% in TZD+CLA (6.70 vs. 4.87%, P = 0.01). Fat content did not differ between TZD+CLA and CLA (4.87 vs. 4.77%, P = 0.87). Treatments did not affect the concentration of milk protein and lactose (P > 0.05). In conclusion, TZD did not stimulate milk fat synthesis and was not able to overcome CLA inhibition of milk fat synthesis, indicating that PPARγ does not mediate CLA-induced MFD

Key Words: milk fat depression, lipid synthesis pathway, peroxisome proliferator-activated receptor γ

1231 (M153) Fatty acid synthase is essential for milk fat formation in goat mammary gland. J. Zhu[1], J. Luo[*2], Y. Sun[1], and H. Shi[1], *[1]Northwest A&F University, Yangling, China, [2]Northwest A & F University, Yangling, China.*

The inevitable role of fatty acid synthase (FASN) on fatty acid metabolism has been a validated concept for a quite long period of time. However, the details of its effect on milk fat formation remain to be unclear. This study explored the potential role of FASN in regulating milk fat accumulation and secretion in lactating goat mammary gland epithelial cells (GMECs). Using quantitative real-time PCR, we detected that FASN was predominantly expressed in fat, small intestine and mammary

gland tissues among 10 different tissues (subcutaneous fat, small intestine, mammary gland, lungs, rumen, muscle, spleen, liver, kidney and heart) collected from three Xinong Saanen dairy goats at mid-lactation period. In addition, we also found a much higher expression level of FASN gene at mid-lactation mammary gland compared with dry-off period (17.9-fold) from three Xinong Saanen dairy goats. These results indicated the potential role of FASN in lactation. Using designed shRNA targeting FASN sequence to construct adenovirus vector with BLOCK-IT system, the effect of shRNA on mRNA expression of GMECs were determined after 48-h incubation of infected GMECs. Inhibition of FASN by C75 (10 ng/uL) and shRNA mediated interference, with the adenovirus as infection vector, markedly reduced cellular triglyceride (TAG) content by decreasing the expression of genes related to TAG synthesis (glycerol-3-phosphate acyltransferase, GPAT; 1-acylglycerol-3-phosphate O-acyltransferase, AGPAT6; diacylglycerol acyltransferase 2, DGAT2) and enhancing the expression of lipolysis related genes (adipose triglyceride lipase ATGL; hormone-sensitive lipase, HSL) (except ATGL response to shRNA treatment) in GMECs. Consistent with the markedly decreased expression of the genes related to lipid droplets formation and secretion (tail-interacting protein 47 gene, TIP47; adipose differentiation-related protein, ADRP; butyrophilin 1a1, BTN1A1; xanthine oxidoreductase, XOR), cellular lipid droplets were also reduced sharply after incubation with C75 or Ad-shRNA investigated by Oil red O staining method. The results provided evidence of FASN's essential role in TAG synthesis and secretion in GMECs. Hence, FASN may be future essential for goat milk fat formation.

Key Words: fatty acid synthase, milk fat, mammary gland epithelial cells, dairy goat

LACTATION BIOLOGY II

1232 (W141) Daylength affects simultaneously mammary epithelium integrity and mammary epithelial cell exfoliation in milk. M. Boutinaud[*1], A. Bondon[1], P. Debournoux[1], J. Couedon[1], M. Johan[1], A. Narcy[2], and C. Hurtaud[1], *[1]INRA, Saint Gilles, France, [2]INRA, Nouzilly, France.*

Some of the mammary epithelial cells (MEC) responsible for milk synthesis are exfoliated into milk during the lactation process. MEC exfoliation into milk could play a role in mammary epithelium integrity. A trial was performed to study the effects of daylength and type of diet on milk calcium content. Calcium is known to play a role of cement for tight junction closure between epithelial cells. The aim of this study was to identify a potential effect of daylength and dietary anion-cation differences on mammary epithelium integrity and MEC exfoliation in milk. A trial was performed according to a Latin square design using 8 dairy cows averaging 103 ± 44 DIM with two treatments in a factorial arrangement with 4 periods of 14 d. The cows received 2 levels of dietary anion-cation differences (DCAD; 0 mEq/kg DM for D0 and 400 mEq/kg for D400) and 2 d lengths (8 h of light/d for short days and 16 h/d for long days). The cows were only exposed to solarium lights providing UVA and UVB. Once per period, milk was collected to purify MEC from milk after centrifugation and immunocytochemical sorting. MEC exfoliation was evaluated using the determination of MEC concentration in milk. The percentage of apoptotic MEC was determined by flow cytometry after TUNEL labeling. Epithelium integrity was monitored using the determination of blood lactose sampled 1 hbefore morning milking, and the ratio Na:K in milk. Blood prolactin concentrations from samples collected at 0700 h and 1400 h were determined by RIA. Data were analyzed using PROC MIXED. There was no significant interaction between daylength and DCAD level. Milk yield did not vary with any treatments averaging 32.7 kg. d^{-1}. DCAD treatment did not affect any of the parameters. Blood lactose and Na:K ratio were higher with short compared with long days ($P < 0.05$) indicating that mammary epithelium integrity was more disrupted with short days. More MEC and more apoptotic MEC were exfoliated in milk with short days compared to long days (338 vs. 227 · 10^6 exfoliated MEC per day, for respectively short and long days; $P < 0.05$). As expected blood prolactin concentration was lower with short days ($P < 0.05$). Taken together these results suggest that MEC exfoliation could be induced by low prolactin concentration during short days.

Key Words: mammary epithelial cell, mammary epithelium integrity, photoperiod, feeding

1233 (W142) Serotonin receptors expression in caprine and ovine mammary gland by real time PCR-RT. A. Suárez-Trujillo[*1], A. Argüello[1], M. A. Rivero[2], J. Capote[3], and N. Castro[1], *[1]Dep. of Animal Science, Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain, [2]Dep. of Morphology, Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain, [3]Canarian Agronomic Science Institute, La Laguna, Tenerife, Spain.*

The role of serotonin (5-HT) as a feedback inhibitor of lactation in humans, mice and cows has been previously reported. This action is mediated by 5-HT receptors, which are expressed in the mammary tissue. The 5-HTR subtype 7 is expressed in the three quoted species, but in bovine, subtypes 1B, 2A, 2B and 4 have been also found. The aim of this study was to identify the 5-HTR (subtypes 1A, 1B, 1D, 1E, 1F, 2A, 2B, 2C, 3A, 4, 5a, 6 and 7) expression in the goat and sheep mammary gland using Real Time PCR-RT. Lactating Holstein cows, Majorera dairy goats and Canarian dairy ewes were used to obtain hypothalamus and mammary gland samples. The sampling was performed immediately after slaughter. Samples were kept in RNA later, and subsequent RNA extraction was performed using a combination between TriPure reagent (Roche, Barcelona, Spain) and E.N.Z.A. total RNA kit (Omega, Nordic Naturals, inc) protocols. cDNA synthesis was conducted using iScript cDNA synthesis kit (BioRad, Madrid, Spain). The primers used in this study were obtained from published data (1B, 1F, 2A, 2B, 2C, 4, 5a and 7) or were designed using bovine CD sequences from GeneBank (1A, 1D, 1E, 3A and 6). Hypoxanthine phosphosibosyltransferase I (HPTR1), Ribosomal Protein (S18), β-Actin and Glyceraldehyde 3-Phosphate Dehydrogenase (GAPDH) genes were utilized as internal control. Hypothalamus samples were used as positive control to evaluate the primers in the three studied species. Real Time PCR was performed at 57.5°C of annealing temperature for all primers. The receptors found in bovine mammary gland were in agreement with previous studies. Receptors 1B, 1E, 2A, 2B, 4 and 7 were found in the three species. Additionally, receptors 1D and 5a were observed in goats and sheep. Moreover, 1A and 1F subtypes were only detected in ovine mammary gland. Nevertheless, subtypes 2C, 3A and 6 were found neither bovine, nor caprine or ovine mammary gland. In conclusion, the same 5-HTR subtypes previously described in cows are expressed in caprine and ovine mammary gland. In addition, in caprine mammary gland were identified two more (5-HTR_{1D} and 5-HTR_{5a}), and the most number of 5-HTR were found in ovine mammary gland. Further studies will be necessary to study more in deep the role of serotonin as inhibitor of lactation in small ruminants.

Key Words: serotonin receptors, goat, sheep

1234 (W143) Immortalization of a primary bovine mammary epithelial cell line by the SV40 large T-antigen gene. H. Hu[1,2,3], N. Zheng[1,2,3], W. Dai[1,2,3], H. Gao[1,2,3], and J. Wang[*1,2,3], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Ministry of Agriculture–Milk and Dairy Product Inspection Center, Beijing, China, [3]Ministry of Agriculture–Laboratory of Quality & Safety Risk Assessment for Dairy Products, Beijing, China.*

In this study, we report an immortalized cell line expression of SV40 large T-antigen established from a Chinese Holstein primary mammary epithelial cell (CMECs) cultured in vitro. The plasmid that carried the SV40 large T-antigen sequence was introduced into mammary epithelial cells by retroviral mediation. Following injection, cells were cultured under puromycin for selection and 10% resistant cells remained after two wk. Four immortalized bovine mammary epithelial cell colonies were obtained, but only a single colony was surpassed over 50-passage and was designated CMEC-H. The obtained clone was characterized with respect to their morphogenetic behavior, long-term proliferative potential, and differentiation characteristics. The immortalized mammary epithelial cells grew in close contact with each other and exhibited the typical "cobblestone" morphology characteristic with obvious boundary that were more homogeneous than in the primary mammary epithelial cells. And the homogenously polygonal of immortalized cell was maintained from passage 1 to 50. The population growth rate between immortalized cells at passage 5 or 50, doubled in number within 36 h, was not significantly different but was faster than in the primary cells. The typical and representative karyotype of CMEC-H was counted at 100 chromosomes, which was more than the normal diploid chromosome number 60. The telomerase expression of CMEC-H had consistently demonstrated the presence of telomerase activity as an immortalized cell line, but the cell line failed to induce tumor formation in nude mice. The immortalized epithelial cell expressed epithelial cell markers, including cytokeratins CK7, CK8, CK18, and CK19. The gene and protein expressions of caseins (α_{S1}-casein, β-casein, and κ-casein) indicated that the immortalized CMEC-H maintained the milk protein synthesis function of epithelial cells. We conclude that CMEC-H may become a valuable reagent for studying the secretion mechanism of mammary gland.

Key Words: bovine mammary epithelial cell, immortalization, SV-40 large T-antigen

1235 (W144) Color measurement as potential tool for determination of colostrum quality in primiparous and multiparous dairy cows. J. J. Gross[*], E. C. Kessler, and R. M. Bruckmaier, *Veterinary Physiology, Vetsuisse Faculty University of Bern, Switzerland*

Instruments for on-farm determination of colostrum quality like refractometers and densimeters are increasingly used in dairy farms. The colostrum color is also supposed to reflect its quality. A pale or mature milk like color is associated with a lower colostrum value compared to a more yellowish and darker color. The objective of this study was to elucidate the relationships between color measurements (CIE L* = from white to black, a* = from red to green, b* = from yellow to blue) and colostrum quality as assessed by two common on-farm instruments and composition in colostrum in cows and heifers. Thirteen primiparous and twelve multiparous cows were milked for the first time exactly 4 h post-calving. Colostrum was analyzed for total IgG by ELISA and for fat, protein and lactose by a FTS Infrared Milk Analyzer (Bentley Instruments Inc., Chaska, MN, USA) (Previously validated for use with colostrum). A Brix sugar refractometer (BRIX) and a Kruuse colostrum densimeter (DENS) were used to assess colostrum quality at 20°C. For color measurements of colostrum samples, a calibrated spectrophotometer (Microflash 200d, Data-color International) was used. In primiparous cows, the total IgG concentration was poorly correlated with L*, a*, and b* (r = -0.13, 0.02, and 0.12; $P > 0.05$), while in multiparous cows correlations were higher (-0.40, 0.32, and 0.06, resp., $P > 0.05$). While DENS did not correlate with color measurements, BRIX was closely correlated with L* (r = -0.68, $P < 0.01$), and b* (r = 0.55, $P < 0.0001$) in primiparous and for b* in multiparous cows (r = 0.52, $P < 0.001$). Milk fat concentration was correlated with a* (r = 0.42, $P < 0.001$, and r = 0.44, $P < 0.001$, for primi- and multiparous cows) and b* (r = 0.27, $P < 0.05$, and r = 0.43, $P < 0.01$), while milk protein concentration was more correlated to b* (r = 0.53, $P < 0.0001$, and r = 0.30, $P < 0.05$). Highest correlations were found between milk lactose percentage and b* in primiparous (r = -0.59, $P < 0.0001$) and multiparous cows (r = 0.56, $P < 0.0001$). In conclusion, the color measurements via spectrophotometer were closest correlated with milk fat, protein and lactose concentrations in colostrum but only to a lesser extent with total IgG concentration colostrum of primiparous cows. An implementation of color measuring devices in automatic milking systems might be a potential instrument also to access colostrum quality besides detecting abnormal milk.

Key Words: colostrum, color, quality

1236 (W145) Effect of milk yield genotype on gene expression in liver and adipose tissue from periparturient Holsteins. W. J. Weber[1], M. Carriquiry[2], S. C. Fahrenkrug[1], and B. A. Crooker[*1], *[1]University of Minnesota, St. Paul, [2]Universidad de la República, Montevideo, Uruguay.*

Multiparous cows from unselected (stable milk yield since 1964; UH; $n = 5$) and contemporary CH; $n = 6$) Holsteins that differed in milk yield (6200 and 11,100 kg milk/305 d) were fed the same diet ad lib, milked 2x/d, and exposed to the same management and environmental conditions. Liver and adipose biopsies were collected at -14, 3, 14, and 35 d in milk (DIM). RNA was extracted and expression of 38 genes (focused on the somatotropic axis, glucose and lipid metabolism) and 12 possible internal control genes determined by digital multiplexed analysis (nanoString nCounter). Expression was normalized to the positive control and the geometric mean of 5 internal control genes. Data were transformed (square root) and analyzed by repeated measures using PROC MIXED (SAS) with DIM as the repeated effect. Means differed when $P < 0.05$. Expression of 23 genes in liver and 20 in adipose was altered by DIM. Liver and adipose expression of 6 and 8 genes was greater in CH and of 8 and 7 genes was greater in UH, respectively. There were line by day interactions for IGFBP2 and IGF-ALS in liver and DGAT2, HNF4a, IGF2 in adipose. Hepatic GHRtot and GHR-1A were greater in UH than CH. GHR-1A decreased at 3 but recovered by 14 DIM. Adipose GHRtot was greater in CH. Hepatic IGFBP2 was greater in CH than UH, increased at 3 DIM and although decreasing, remained increased through 35 DIM. Hepatic IGF-ALS was greater in UH, decreased at 3 DIM in both lines and returned to prepartum values by 14 and 35 DIM in UH and CH, respectively. Hepatic FGF21 was greater in CH than UH and peaked at 3 DIM in both lines. FGF21 was not detected in adipose. DGAT1 was similar in UH and CH liver and greater in CH adipose. Liver DGAT1 increased at 3 DIM but was not altered by DIM in adipose. DGAT2 was similar in UH and CH liver and greater in UH adipose. Liver DGAT2 decreased through 35 DIM in both lines. Adipose DGAT2 decreased at 3 DIM and recovered by 35 DIM in UH but not in CH cows. Results are consistent with a prolonged postpartum reduction in hepatic sensitivity to somatotropin and in triglyceride synthesis from de novo fatty acids in adipose of contemporary Holsteins.

Key Words: gene expression, liver, adipose

1237 (W146) Comparative glycolysis and Krebs cycle metabolism of the bovine and murine mammary gland determined with [$^{13}C_6$]glucose and mass spectrometry. L. J. Juengst[*1], E. E. Connor[2], R. L. Baldwin, VI[2], and B. J. Bequette[1], *[1]Dep. of Animal and Avian Sciences, University of Maryland, College Park, [2]USDA-ARS, Bovine Functional Genomics Laboratory, Beltsville, MD.*

The compositions of bovine and murine milk differ significantly with respect to the proportions of lactose, protein, and fat. To better understand the metabolic origins of this difference, we interrogated the crossroads of glycolysis and the Krebs cycle in the mammary gland of cows and mice using a glucose stable isotope (^{13}C) tracer approach in vitro. Mammary tissue was collected from mid-lactation dairy cows ($n = 4$) and Day 15 of lactation mice ($n = 6$) then sliced to form explants (0.5 mm thick, 100 to 150 mg). Explants were incubated for 3 h (5% CO_2) at 37°C in DMEM containing a 50:50 mix of unlabeled and [$^{13}C_6$] labeled glucose at 2.5, 5, 7.5 or 10 mM concentrations. Following incubation, explants were rinsed in PBS and stored at −80°C. Intracellular metabolites were extracted and derivatized for determination of ^{13}C-isotopomer enrichments employing gas chromatography-mass spectrometry. Alanine, glutamate, and aspartate ^{13}C-isotopomer enrichments were monitored as representative surrogates of their Krebs cycle counterparts pyruvate, α-ketoglutarate, and oxaloacetate, respectively. These data provided the inputs to calculate glycolytic and Krebs cycle fluxes. In bovine mammary tissue, increasing media glucose concentration increased glycolytic flux as represented by an increasing contribution of glucose to pyruvate flux. However, the proportion of pyruvate derived from glucose catabolism reached a plateau (44 to 46%) at 7.5 mM glucose. Similarly, in murine mammary tissue, glycolytic rate increased with increasing media glucose concentration, though no plateau was attained and glucose contributed to 43% of pyruvate flux at the highest glucose concentration. Krebs cycle flux was assessed by the relative activities of pyruvate dehydrogenase (PDH) vs. pyruvate carboxylase (PC) based on [^{13}C] tracer kinetics. For bovine mammary explants, PDH flux activity increased to a maximum at 5.0 mM glucose whereas PDH vs. PC activities of murine mammary tissue was not responsive to glucose concentration. The current study suggests that the dairy cow mammary gland shifts from high anapleurotic flux rates into the Krebs cycle to energy-producing (oxidative) fluxes with increasing glucose concentration whereas the murine mammary gland maintains a more rigid metabolic balance, and thus is less adaptive to glucose availability.

Key Words: bovine, murine, mammary metabolism

1238 (W147) Is there a core microbiome in bovine milk samples from healthy quarters with somatic cell counts of less than 200,000 cells/mL?. S. L. Brooker*[1], J. E. Williams[1], S. M. Reynolds[1], K. M. Yahvah[1], L. K. Fox[2], and M. A. McGuire[1], *[1]University of Idaho, Moscow, [2]Washington State University, Pullman.*

Recent analysis has shown that healthy bovine milk contains a commensal bacterial community. Rigorous data are not available on the bacterial community structure in bovine milk, thus it is unknown whether there is a 'core' microbiome within healthy bovine milk. Quarter milk samples were collected from nine Holstein cows that had at least two low SCC quarters (< 200,000 cells/mL). Characterization of the microbial community was performed by culture independent 454 pyrosequencing of amplicons from the V1-V3 region of the 16S rRNA gene to determine relative abundance. Cows were selected only if milk from at least two quarters was below 200,000 SCC. The relative abundance data show that most healthy quarters have bacterial communities that include *Clostridium* spp. (5 to 75% relative abundance), *Pelomonas* spp. (10 to 35% relative abundance), *Duganella* spp. (< 5% relative abundance), *Turicibacter* spp. (0 to 10% relative abundance), and *Sporacetigenium* spp. (0 to 45% relative abundance), with all samples having a large influence from unclassified bacterial spp. (5 to 55% relative abundance). The Shannon and Chao diversity indices of the bacterial communities between cows were not different ($P > 0.1$) suggesting similar distribution of community membership. Analysis by PCoA using the Bray dissimilarity matrix showed strong clustering based on the relative abundance of *Clostridium* spp., which was a major contributor in all healthy quarter samples. No clustering based on SCC was apparent among the samples. Clustering of healthy quarters within cow was also not discernable suggesting a high variation in the bacterial community even between quarters of the same cow. These results propose a highly variable bacterial community exists in bovine milk even between healthy quarters within a cow. Though there appears to be no obvious 'core' set of bacterial members, the variation present could account for similar functional roles within quarter milk bacterial community. This work was supported by the Idaho Agricultural Experiment Station, NIH grants P20 RR15587 and P20 RR016454 and the Institute for Bioinformatics and Evolutionary Studies (IBEST) at the University of Idaho.

Key Words: milk, bacteria, microbiome

1239 (W148) Impact of machine milking on teat dimensions. J. F. Guarin*[1,2], D. J. Reinemann[3], and P. L. Ruegg[1], *[1]Dep. of Dairy Science, University of Wisconsin–Madison Madison, [2]Grupo de Investigación Biogénesis, Facultad de Ciencias Agrarias, Universidad de Antioquia, Medellin, Colombia, [3]Dep. of Biological Systems Engineering, University of Wisconsin–Madison, Madison.*

The objective of this study was to determine associations between machine milking and changes in teat dimensions. A total of 1751 teats from 445 cows from the University of Wisconsin dairy herd were measured pre and immediately post-milking. The difference in teat length (Length), barrel width (Barrel) and teat tip diameter (Tip) before (PRE) and after (POST) machine milking was determined. Absolute change (Delta) on teat dimensions was calculated as POST-PRE measurements. Relative change (DeltaMeasureREL) was calculated as POST-PRE/PRE and expressed as percentage. Additional covariates included: Milk flow peak (PeakFlow), and parity (1, 2 or $\geq$ 3). Descriptive statistics were determined using PROC UNIVARIATE, FREC, GLM, and LOGISTIC of SAS version 9.3. Means and SD for Pre-milking Length, Barrel, and Tip were 44.3 ± 8.3, 23.9 ± 3.7, and 19.6 ± 2.3 mm, respectively. Means for PRELength were different for parity ≥ 3 (46.6 mm) when compared with 1 (42.8 mm) and 2 (43.6 mm) ($P < .0001$). Means for PREBarrel were significantly different among parities ($P < .0001$). Means for PRETip increased significantly with parity and were 19.3, 19.6, and 20.0 mm for parities 1, 2, and ≥ 3, respectively ($P < 0.001$). A positive association was found between PREBarrel and PeakFlow ($P < .0001$) for primiparous cows only. Teat dimensions were affected by milking. During milking, teat length increased by 1.3 mm, teat barrel decreased by 2.2 mm and teat tip decreased by 0.7 mm. Changes in teat dimensions on length, barrel, and tip were not influenced by parity. Out of the 1751 teats, 163 (9.3%) became congested at the barrel. Out of the 1751 teats, 163 (9.3%) teat barrels became congested. Congestion was defined as PREBarrel measurements that were smaller than PostTeatBarrel measurements, implying congestion of the tissue during milking. There was a strong association between pre-milking teat barrel dimension and peak milk flow for primiparous cows. Further research on teat dimensions changes and its influence on mastitis is required.

Key Words: dairy cow, induced changes, teat dimension

Table 1239. Descriptive statistics for the impact of machine milking on teat dimensions

Teat dimension (n = 1751 quarters from 445 cows)	Mean ± SD	Range
Pre-milking (mm)		
PRELength	44.3 ± 8.3	26.0–80.0
PREBarrel	23.9 ± 3.7	14.0–50.0
PRETip	19.6 ± 2.3	10.0–30.0
Post-milking (mm)		
PostLength	45.6 ± 8.5	24.0–100.0
PostTeatBarrel	21.7 ± 2.8	12.0–40.0
PostTeatTip	19.0 ± 2.2	10.0–30.0
Absolute change[1] (mm)		
DeltaLength	1.3 ± 5.5	-20.0–26.0
DeltaBarrel	-2.2 ± 3.0	-20.0–10.0
DeltaTip	-0.7 ± 2.3	-10.0–8.0
Relative change[2] (%)		
DeltaLengthREL	5.5 ± 23.4	−83.3–118.2
DeltaBarrelREL	−8.3 ± 11.2	−50.0–50.0
DeltaTipREL	-2.5 ± 12.4	−50.0–66.7

[1] Postmilking value– premilking value.
[2] (Postmilking value– premilking value)/premilking value x 100.

1240 (W149) Comparison of ecological indices of bacterial communities in bovine milk varying in somatic cell count. J. E. Williams*[1], S. M. Reynolds[1], K. M. Yahvah[1], S. L. Brooker[1], L. K. Fox[2], B. Shafii[1], and M. A. McGuire[1], [1]*University of Idaho, Moscow,* [2]*Washington State University, Pullman.*

Somatic cell count (SCC) of milk is often used to determine the health status of the mammary gland. However, little is known about the bacterial community structure within milk of varying SCC. Next generation sequencing technology has provided researchers the opportunity to characterize the bacterial diversity and community structure within bovine milk. We hypothesized that the bacterial diversity and community structure would be different among milk with low (< 200,000 cells/mL), medium (200,000 to 400,000 cells/mL), and high (> 400,000 cells/mL) SCC. Utilizing ecological indices that describe bacterial diversity, we analyzed 16S rRNA (V1-V3 region) sequencing data from quarter milk samples collected from 15 Holstein cows. Comparisons among quarter milk samples with different SCC were performed using analysis of variance and mixed model procedures of SAS (v9.3) and significance was declared at $p \leq 0.05$. Additionally effects of SCC status were compared using predetermined contrasts of milk with low versus medium and high, as well as medium versus high levels of SCC. Based on richness estimators (Chao1 and abundance-based coverage estimators [ACE]), milk with high SCC had a bacterial community less rich and diverse than milk with low or medium SCC. Also, according to Shannon's and Simpson's diversity indices when SCC is medium and high, there is a decrease in number of bacterial genera present as well as a decrease in the evenness of the bacterial community membership compared to milk with low SCC. While milk categorized as high SCC is different from milk with low and medium SCC, the bacterial diversity and community structure in low SCC milk is not different from milk with medium SCC. Future studies are needed to explore how bacterial community membership among milk samples differs with varying SCC. *This work was supported by the Idaho Agricultural Experiment Station, NIH grants P20 RR15587 and P20 RR016454 and the Institute for Bioinformatics and Evolutionary Studies (IBEST) at the University of Idaho.*

Key Words: milk, microbiome, diversity

1241 (W150) Effects of arginase inhibition on casein expression and proliferation of bovine mammary epithelial cells. *L. Ding[1], M. Wang*[1], L. Chen[1], H. Wang[1], and J. J. Loor[2], [1]Yangzhou University, China, [2]University of Illinois, Urbana-Champaign, Urbana.*

Reviews of the ruminant literature concluded that the uptake of Arg by the mammary gland greatly exceeds its output in milk. Furthermore, milk protein yield was increased by post-ruminal infusion of Arg compared with a control treatment that included infusion of water and a mixture of essential amino acids (AA) excluding Arg. Those results indicated that Arg might have an important role on casein synthesis regulation. Our previous research subsequently revealed that excess Arg has a regulatory function on the casein synthesis via effects on transcription of the casein gene. Whether Arg regulates the synthesis of casein by the metabolism of enzymes is not very clear. The specific objective of this work was to elucidate the effect of arginase on the regulation of casein expression using an arginase inhibitor in vitro. Primary bovine mammary epithelial cells (The mammary epithelial cell were isolated from three healthy multiparous dairy cow at lactation stage) were cultured with different concentrations (0, 0.5, 1, 2 μmol/L) of the arginase inhibitor nor-NOHA. The casein expression and the proliferation of mammary epithelial cells were determined after 24-h of in vitro culture triplicate/treatment). Statistical analysis was done using the OneWay Analysis of Variance (ANOVA) with multiple comparison test of Duncan using SPSS v16.0. And the P values less than 0.05 were declared to be significant ($P < 0.05$). The results showed that the concentration of arginase-1 in different groups dropped ($P < 0.05$) when the concentrations of nor-NOHA increased, and was quite small in the cells incubated with 1 and 2 μmol nor-NOHA/L. The different concentrations of nor-NOHA had no effect ($P > 0.05$) on the proliferation of mammary epithelial cells. Compared with the control group (0 μmol/L), the expression of casein was lower ($P < 0.05$) in other groups and was lowest in the group with the nor-NOHA concentration of 2 μmol/L. Additionally, in cells incubated with 0.5 μmol/L nor-NOHA the expression

level of OTC and ODC was significantly lower ($P < 0.05$) than other treatments. The expression of eNOS was lowest ($P < 0.05$) in the group with the nor-NOHA concentration of 1 μmol/L. In conclusion, the activity of arginase can be inhibited by nor-NOHA. Furthermore, nor-NOHA affected expression of casein and some arginine metabolism-related enzymes. With the increase of nor-NOHA concentration, the inhibitory effects on casein increased.

Key Words: arginine, casei expression

1242 (M154) Proximate composition and physic-chemical characteristics of broiler fed varying levels of honey in their diet. F. Patience Olusola[*1], A. Victor O.[2], O. Bayonle O.[2], and O. Olumuyiwa Jacob[2], *[1]Osun State University, Osogbo, Nigeria, [2]Osun State University, College of Agriculture, Osogbo, Nigeria.*

Heat stress is a major limiting factor in poultry production especially in hot–humid zones of the world. It could cause suffering, death, reduction in feed consumption, could reduces production and growth rate of broiler chicken. To combat this limitation, different anti-stress is used containing vitamins like honey, which is a natural energy booster, with antioxidant, antibacterial properties and act as anti-stress due to it mineral and vitamins composition, e.g, it has about 20.3 mg of calcium, 13.6 mg of phosphorus, 176 mg of potassium, etc. This study evaluate the effect varied level of honey at 0 mL of honey inclusion/kg of feed as treatment 1 (T1), 10 mL of honey/kg of feed as treatment 2 (T2), 20 mL of honey/kg as treatment 3 (T3) and 30 mL of honey/kg of feed as treatment 4 (T4), arranged in a completely randomized design. One hundred and fifty-six d old Gallus domesticus were used and fed with formulated broiler starter and finisher feed for 8 wk and mixed with honey at varied level, while water was given ad libitum. Results shows that for physicochemical parameters, T1 had significant higher ($P < 0.05$) values for Cold shortening, Thermal shortening, Cooking loss and Water-holding capacity than, T2, T3, and T4, respectively. For fresh broiler meat, T2 had the lowest protein content but highest significant values for moisture, ether extract and ash content than T1, T2, and T4, respectively. For boiled broiler meat, T2 (48.75 ± 0.56) had the lower protein content ($P < 0.05$) than T1 (50.60 ± 0.56), T3 (51.00 ± 0.56), and T4 (51.23 ± 0.56), with T4 having same significant value as T1. For grilled broiler meat, T3 had the highest protein content 57.15 ± 0.83 than T2 having the least value of 52.70 ± 0.83. Broiler fed with 20 mLs (T3) and 30 mLs (T4) of honey inclusion in their diet, performed better than T1 (0 mL) and T2 (10 mLs). While Ti proved to have the best physio-chemical parameter compared to other treatments.

Key Words: grilled, boiled, physicochemical, honey and broiler

1243 (M155) Carcass and organ characteristics of broilers fed varying levels of honey. A. Victor Olabisi*, F. Patience Olusola, O. Olumuyiwa Jacob, and O. Kehinde O., *Osun State University, Osogbo, Nigeria.*

The synergestic relationship between Broiler Production and Animal Protein cannot be over emphasised as the later does better by converting feed into the final product, meat. This study has looked in manuvering the kind of feed which is readily available to the birds so as to foster a good feed conversion ratio. The results obtained for carcass characteristics are as presented below. The results showed that there were variation in the figures recorded for the live weight, dead weight, de-feathered weight, full gizzard, flat weight, lungs weight, kidney weight, breast weight among all the treatments. From the study, it was observed that liver weight was highly significant ($P > 0.05$) but numerically birds fed with 20 mL of honey had the highest liver weight followed by birds fed 30 mL of honey and the least weight was in the birds fed 10 mL of honey. The heart weight was significantly ($P > 0.05$) affected by honey, though 20 mLs of honey fed birds had the largest heart weight, but it was not significantly different ($P < 0.05$) from birds fed 30 mLs of honey while birds fed 10 mL of honey had the least heart weight and testis weight has no significant difference ($P < 0.05$) among the treatments. However, birds fed with 20 mL of honey had the highest weight, live weight, dead weight, neck weight, back weight, liver weight, heart weight and trachea weight. The empty crop weight appeared same for all the inclusion at different meals of honey.

Key Words: meat, honey, weight gain

1244 (M156) Ractopamine and immunocastration: Effects on enhanced pork loin. A. F. S. I. de Freitas[*1,2], D. S. Lucas[3], D. A. Fausto[4], S. F. N. Pertile[4], E. F. Delgado[4], N. S. Janzantti[5], and E. T. F. Silveira[6], *[1]UNESP, São José do Rio Preto, São Paulo, Brazil, [2]IFMT, Campo Novo do Parecis, Mato Grosso, Brazil, [3]UFF, Rio de Janeiro, Brazil, [4]ESALQ/USP, Piracicaba, São Paulo, Brazil, [5]UNESP, São José do Rio Preto– São Paulo, Brazil, [6]ITAL, Campinas, São Paulo, Brazil.*

The consumer is increasingly demanding high quality meat produced under the criteria of respect for the environment and animal welfare. The aim of this study was to evaluate the influence of ractopamine (RAC) in pig diets as well as castration method, physical or immunocastration, on the quality of pork loin. Male pigs were commercial selected Agroceres, AGPIC 337 (initially with $n = 120$ males). In maternity phase (0 to 21 d old) half of the piglets were physically castrated at 5 d postpartum. The males underwent immunocastration (Vivax, Pfizer Animal Health) in two doses of 2 mL, 8 and 4 wk before slaughter. For half of the pigs physically- and immunocastrated, ractopamine was included (RAC, 7.5ppm, Ractosuin, Ourofino Agribusiness) in feed for 21 d (± 2 d) before slaughter. After the slaughter were randomly selected five carcasses of each treatment and removed the *Longissimus dorsi* (LM). The experiment was completely randomized designer ranged in a 2 × 2 factorial with five repetitions. There was no difference ($P > 0.75$) for the meat water content; however, RAC in the diet resulted in more protein ($P < 0.05$) and less ether extract fat ($P < 0.05$) in the muscle, even though there was

no effect on carcass yield. The addition of RAC also resulted in less tender meat ($P < 0.01$) at 24 h postmortem. The meat from the animals fed RAC had higher meat yield by the injection process (enhancement). However, there was no influence of RAC in weight loss by exudation (purge loss) ($P \geq 0.78$) indicating an improvement pork loin juiciness. Immunocastration and RAC had a negative impact while physically castrated males with RAC a positive impact on cooking loss, which favor higher income by providing greater juiciness.

Key Words: swine, castration method, meat quality

1245 (M157) Analysis of porcine myosin heavy chain isoforms by liquid chromatography and mass spectrometry.

G. D. Kim*[1], E. Y. Jung[2], H. W. Seo[2], J. Y. Jeong[3], S. T. Joo[4], and H. S. Yang[2], *[1]Dep. of Food Science and Biotechnology, Kyungnam University, Changwon, South Korea, [2]Division of Applied Life Science, Gyeongsang National University, Jinju, South Korea, [3]Institute of Agriculture and Life Science, Gyeongsang National University, Jinju, South Korea, [4]Dep. of Animal Science, Gyeongsang National University, Jinju, South Korea.*

Myosin, a myofibrillar protein in the skeletal muscle, consists of two heavy chains (MHC) and four light chains. Nine MHC isoforms have been observed in muscles of mammalian species, and four MHC isoforms (I/slow, 2a, 2x, and 2b) were recognized in porcine skeletal muscle. MHC is a critical component that determines the metabolic and contractile properties of muscle fibers, which in turn related to meat quality. Therefore, analysis of MHC isoforms expression is important in animal muscles such as porcine and bovine skeletal muscle. However, MHC isoforms from porcine skeletal muscle is complicated due to the similarity in molecular weights among the MHC isoforms (i.e., 223.743, 223.924, 223947, and 224.010 kDa for MHC I/slow, 2a, 2x, and 2b, respectively). We analyzed the porcine MHC isoforms by LC-MS/MS system following SDS-PAGE electrophoresis. The *longissimus dorsi* muscle was taken from each of three commercial pigs (Landrace×Yorkshire×Duroc) for SDS-PAGE electrophoresis and LC-MS/MS analysis (Tempo nano-LC system, Applied Biosystems, CA). A total of 525 unique peptides were identified and compared to each amino acid sequence of the porcine MHC isoforms. We selected four representative peptides that were identical to MHC I/slow, 2a, 2x, and 2b. The peptide identified as TLEDQLSEVKTKEEEHQR corresponds to residues 1253–1270 of MHC 2b, and differs from the other MHC isoforms (TLEDQLSELKSKEEEQQR, TLEDQLSELKTKEEEQQR, and TLEDQMNEHRSKAEETQR for MHC 2a, 2x, and I/slow). MHC 2x was confirmed by the peptide ELEGEVESEQKRNVETVK, which corresponds to residues 1925–1942. MHC I/slow and 2a were also confirmed by the unique peptides DIGTKGLNEE (residues 1926–1935) and TNAACAALDKK (residues 1539–1549), respectively. These types of unique peptides are useful for confirmation of MHC isoforms and could be used as MHC-specific markers for porcine skeletal muscle.

Key Words: myosin heavy chain, porcine skeletal muscle, LC-MS/MS

1246 (M158) Occurrence of dietary unsaturated fatty acids and their biohydrogenation products in muscles of non-ruminating foregut fermenters.

A. Schwarm*[1], M. Kreuzer[2], F. Leiber[3], S. Ortmann[4], and M. Clauss[5], *[1]ETH Zurich, Institute of Agricultural Sciences, Switzerland, [2]ETH Zurich, Switzerland, [3]Research Institute of Organic Agriculture (FiBL), Frick, Switzerland, [4]Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany, [5]University of Zurich, Clinic for Zoo Animals, Exotic Pets and Wildlife, Switzerland.*

Muscles of ruminants contain higher proportions of saturated fatty acids (SFA) and monounsatured FA, but lower proportions of polyunsaturated FA (PUFA), than those of monogastric herbivores, which is considered unfavourable for human health. This is explained by an almost complete microbial biohydrogenation (saturation) of dietary PUFA in the rumen before reaching the site of FA absorption, the small intestine. The objective was to investigate whether the muscles of non-ruminating foregut fermenter contain more PUFA and more biohydrogenation products than those of ruminants, due to their shorter passage times and thus incomplete biohydrogenation of C18 PUFA in the forestomach. The studied intermediates formed during biohydrogenation were *cis*-9, *trans*-11 C18:2 conjugated linoleic acid (CLA) and *trans*-11 C18:1 vaccenic acid (TVA). The study species included Bennett wallabies (*Macropus rufogriseus*, $n = 12$) and collared peccaries (*Pecari tajacu*, $n = 10$). Wallabies were free-ranging on grass pastures. Peccaries were maintained on a zoo diet (75% apples, carrots; 25% hay, bread). *Biceps femoris* muscles were sampled from carcasses. Fatty acid methyl esters were separated on a Supelcowax–10 column and the isomers of C18:1 on a Varian column after split injection in a HP 6890 gas chromatograph. The ratio of SFA:PUFA in muscles of wallaby and peccary was with 0.6 and 1.6, respectively, lower than in domestic ruminants (> 4) and in domestic pigs (2.6). In wallaby muscles, the concentration of TVA plus CLA was with 8% of total fatty acids (tFA) higher than in ruminants (2.6% tFA), with a TVA:-CLA ratio of 3.7 (ruminants: 2.1). In peccary muscles, CLA and TVA were not detectable (< 0.1% tFA), which therefore resembled the domestic pig. In conclusion, the results indicate that muscles of non-ruminating foregut fermenters are less saturated than those of ruminants and pigs. However, occurrence of *trans*-fatty acids was not uniform for the studied non-ruminating foregut fermenters, which may be related to differences in diet, microbial population and endogenous desaturation.

Key Words: *trans*-fatty acids, wallaby, peccary

1247 (M159) Effects of amino acid supplementation of reduced crude protein (RCP) diets on fatty acid compositions of subcutaneous fat and muscle. A. N. Young*, J. K. Apple, J. W. Yancey, T. M. Johnson, T. C. Tsai, and C. V. Maxwell, *Dep. of Animal Science, University of Arkansas Division of Agriculture, Fayetteville.*

Barrows and gilts ($n = 210$/gender) were used to test the effects of crystalline AA supplementation of reduced CP diets on fatty acid composition of the LM and s.c. fat from the jowl from growing-finishing swine. Pigs were blocked by BW, and pens (6 pigs/pen) within each block and gender were assigned randomly to either corn-SBM diets (C) devoid of crystalline LYS and formulated to 95% SID AA requirements or 1 of 4 RCP diets (CP and crystalline LYS levels for the dietary treatments during each are presented in the accompanying table, 1247). During the last 3-wk feeding phase, 10 mg/kg of Paylean were included in all diets. Jowls and a subsample of whole pork loins (2 loins/pen) were captured during carcass fabrication, and the LM and s.c. fat from each jowl was freeze-dried for determination of fatty acid composition. The LM from barrows had greater ($P < 0.001$) proportions of SFA than the LM from gilts, whereas LM MUFA content increased in the LM of barrows but decreased in the LM of gilts with decreasing dietary CP (linear RCP × gender, $P = 0.037$). Conversely, LM PUFA composition increased in gilts and decreased in barrows with decreasing dietary CP (linear RCP × gender, $P = 0.056$). Jowl fat from barrows had more ($P = 0.008$) SFA and less ($P < 0.001$) PUFA than jowl fat from gilts, whereas the proportions of SFA– particularly palmitic and stearic acids– and PUFA– specifically linoleic acid– in jowl s.c. fat decreased (linear, $P \leq 0.019$) with decreasing dietary CP. Also, weight percentages of all MUFA, especially oleic acid, increased (linear, $P < 0.001$) as dietary CP was reduced in the diet. Results indicate that the fatty acid composition of pork lean and fat were altered by reducing dietary CP, and the pattern of increased MUFA composition of jowl s.c. fat may imply enhanced de novo synthesis in pigs fed RCP diets supplemented with crystalline AA.

Key Words: fatty acid composition, reduced CP, swine

Table 1247. CP (added LYS) of experimental diets for each feeding phase (% as fed)

Phase	C	RCP1	RCP2	RCP3	RCP4
1	23.70	21.61 (0.19)	19.58 (0.37)	17.61 (0.56)	15.72 (0.75)
2	21.53	19.46 (0.18)	17.44 (0.36)	15.49 (0.54)	13.61 (0.71)
3	18.97	17.34 (0.15)	15.75 (0.29)	14.16 (0.44)	12.68 (0.59)
4	17.66	16.30 (0.13)	14.96 (0.24)	13.64 (0.36)	12.37 (0.48)
5	20.24	18.60 (0.15)	17.01 (0.30)	15.44 (0.45)	13.93 (0.60)

1248 (M160) Postmortem pH evolution in four muscles and onset, state and resolution of rigor mortis of guinea pigs (*Cavia porcellus*) carcass. D. Núñez-Valle[1], L. P. Cevallos-Velastegui[1], A. Morales-delaNuez[2], N. Castro[3], A. Argüello[3], and D. Sánchez Macías[*1], *[1]Agroindustrial Engineering, Universidad Nacional de Chimborazo, Riobamba, Ecuador, [2]Facultad de Ciencia Pecuarias, Escuela Superior Politécnica de Chimborazo, Riobamba, Ecuador, [3]Dep. of Animal Science, Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain.*

The effect of pH on meat quality is a subject that has been deeply investigated extensively in meat science, and there is a wealth of qualitative knowledge. In the same way, rigor mortis is one of the most important physicochemical changes in skeletal muscles occurring at a relatively earlier postmortem period and then maintaining for a certain period, which results in an increasing toughness of meat. No information exists in the literature about the pH evolution or instauration and resolution of rigor mortis in guinea pig. The objective of this work was to determine the postmortem evolution of pH in four different muscles of guinea pig, as well as to establish the rigor mortis instauration, rigor state and its resolution. Forty-eight guinea pigs, randomly selected from the same production system were divided into four groups of 12 animals as follows: 3-mo-old female, 3-mo-old male, 12-mo-old female, and 12-mo-old male. Four muscles, *longissimus dorsii* (LD*), quadriceps femoris* (QF), *triceps braquii* (TB), and *psoas major* (PM), were used to measure pH at 15, 30, 45 min, each hour from 1 to 12, 15, 18, 21, and 24 h postmortem. These muscles were selected because of energy metabolism described in other species, which PM displays the lowest and LD the highest anaerobic capacity. Analysis of variance with repeated measures was conducted to test the significance of the two variables muscle and time postmortem. Splitting the data was used to check the effect of age or sex. Least squares means were calculated and considered significantly different if $P < 0.05$. pH started near 7 in LD and TB, followed by QF, and PM had the lower pH value at 15 min postmortem. pH decreased during the experimental time until 5 h in TB and QF, and 6 h in LD and PM. However, pH decline rate was slower for PM, being higher after 6 h than the other muscles. After 12 to 15 h postmortem, pH values increased slightly. Rigor mortis was onset after 5 to 6 h postmortem. After rigor onset, the muscle undergoes a longer period of rigor state, which was resolved after 13 to 15 h postmortem. No differences were found regardless sex or age. In conclusion, authors recommend at least 15 h of chilling for guinea pigs carcass, until the rigor mortis was resolved.

Key Words: guinea pig, pH, rigor mortis

1249 (M161) Water holding capacity and cooking losses of different muscles of guinea pigs (Cavia porcellus). L. P. Cevallos-Velastegui[1], D. Núñez Valle[1], A. Morales-delaNuez[2], N. Castro[3], A. Argüello[3], and D. Sánchez Macías[*1], *[1]Agroindustrial Engineering, Universidad Nacional de Chimborazo, Riobamba, Ecuador, [2]Facultad de Ciencia Pecuarias, Escuela Superior Politécnica de Chimborazo, Riobamba, Ecuador, [3]Dep. of Animal Science, Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain.*

It is well-known that aging produces changes in meat characteristics. Meat quality depends on organoleptic properties (color, texture, flavor and juiciness) which are related to zootechnical characteristics (breed, age, sex) or anatomical characteristics such as type of muscle. The main objetive of this study was to describe the water holding capacity and cooking losses of ten different muscles of guinea pig after chilling for 12 h at 4°C. Forty eight guinea pigs randomly selected from the same production system were divided into four groups of 12 animals as follows: 3-mo-old female, 3-mo-old male, 12-mo-old female, and 12-mo-old male. Ten muscles were excised after 12 h postmortem: *longissimus dorsii, quadriceps femoris, triceps braquii, psoas major, biceps femoris, semimembranosus, semitendinosus, gracilis, gluteal,* and *gastrocnemio*. Water-holding capacity (WHC) was measure using 0.3 g of muscle between two papers with 1 kg of weight during 10 min. Vacuum packaged muscle was introduced in a 70°C water bath for 30 min, and cooking losses (CL) were measured. A two-way analysis of variance was conducted to test the significance of the two fixed variables muscle and age or sex. Least squares means were calculated and considered significantly different if $P < 0.05$. With regard to WHC, *triceps braquii, psoas major,* and *gracilis* showed the lower values, while *gastrocnemio* had the higher values. *Quadriceps femoris* displayed similar values than *longissimus dorsii*. The 12-mo-old animals had lower WHC than 3-mo-old guinea pigs. However, when we compare data splitting male and female, it is possible to observe that female guinea pigs lost more water than males at 3 mo of age. With regard to CL, *longissimus dorsi*, *gastrocnemio, quadriceps femoris* and *biceps femoris* had similar CL values, while the higher values corresponded to *triceps braquii* and *gracilis*. It was also observed that male guinea pigs had higher values of CL than female animals; these differences were more clearly observed in 3-mo-old animals.

Key Words: guinea pig, water holding capacity, cooking losses

MEAT SCIENCE & MUSCLE BIOLOGY II

1250 (T153) Effect of the inclusion of plant extracts, vitamins and their association on biological efficiency, carcass length, total beef cuts, tissue composition and carcass muscularity of Nellore cattle.
M. B. Silva[*1], A. M. Jorge[2], F. D. Resende[3], G. R. Siqueira[4], G. F. Berti[5], J. M. B. Benatti[6], C. L. Francisco[1], and D. C. M. Silva[1], *[1]Universidade Estadual Paulista-FMVZ, Botucatu, Brazil, [2]Faculdade de Medicina Veterinária e Zootecnia, Universidade Estadual Paulista, Botucatu-SP, Brazil, [3]Agência Paulista de Tecnologia dos Agronegócios-APTA, Colina, Brazil, [4]APTA-Polo Regional Alta Mogiana, Colina, Brazil, [5]Centro Universitário da Fundação Educacional de Barretos, Barretos, Brazil, [6]Universidade Estadual Paulista-FCAV, Jaboticabal, Brazil*.

This study evaluated the effects of four treatments [(C) Control diet including A, D and E vitamin; (V) Control diet plus 50% A, D and E vitamin; (E) Diet including plant extracts; (A)Diet with an association of these two additives (50% A,D and E vitamin + plant extract)] on biological efficiency, carcass length, tissue composition, carcass muscularity and total beef cuts of 56 Nellore (*Bos indicus*) young bulls (+360 kg initial weight and +20 mo of age). The treatments provided the same diet for all animals (85 and 15%, for concentrate and forage, respectively), varying only the inclusion of the different additives. All treatments received monensin (30 mg/kg of concentrate). Animals were individually weighed, blocked by initial body weight, and maintained in individual pens for 105 d (finishing phase; 21 and 84 d, for adaptation and trial period, respectively). At the slaughterhouse, carcasses were identified, cooled for 24 h, and weighed to determine the biological efficiency. Right carcass half was used to calculate total beef cuts. Sample from ninth to 11th ribs (HH section; left carcass half) was obtained to determine tissue composition and carcass muscularity. There was no effect of treatments for carcass traits ($P > 0.10$), and total beef cuts ($P > 0.10$). In conclusion, the inclusion in the diet of plant extracts, vitamins and their associations not affected the carcass characteristics and total beef cuts of Nellore cattle. *Supported by CNPQ/NUTRON.*

Key Words: plant extracts, tissue composition, beef cattle, Nellore

1251 (T154) Pearson's correlation between fatty acid profile and gene expression of transcription factors and lipogenic enzymes in the muscle of young bulls fed soybean or cottonseed, with or without vitamin
E. M. M. Ladeira[*1], D. M. Oliveira[1], A. Chalfun Junior[1], M. L. Chizzotti[2], P. D. Teixeira[1], and T. C. Coelho[1], *[1]Universidade Federal de Lavras, Brazil, [2]Universidade Federal de Viçosa, Brazil.*

This study had the objective to evaluate the correlations between mRNA expression of peroxisome proliferator-activated receptor-α (PPAR-α), sterol regulatory element binding protein-1c (SREBP-1c); stearoyl-CoA desaturase-1 (SCD1), acetyl CoA carboxylase (ACC) and fatty acid profile in the muscle of young bulls fed diets containing soybean grain or cottonseed, with or without vitamin E supplementation. Twenty-eight Red North young bulls with an average age of 20 mo and initial average live weight of 339 +15 kg were allotted in a completely randomized design using a 2 × 2 factorial arrangement. The animals were slaughtered at an average weight of 456 ± 15.1 kg ($P > 0.05$), and two samples were then taken from the longissimus dorsi (LD) muscle of each animal between the 12th and 13th ribs. The first sample was stored at -20°C for subsequent lipid extraction and fatty acid analysis using gas chromatography; and the second sample was stored at −80°C for quantitative gene expression analysis by RT-qPCR. After analyzes of fatty acid content and relative gene expression according to the diets, data of all treatments were used to carry out the Pearson's correlation study using the PROC CORR tool of SAS 9.3. Linoleic acid content was negatively (-0.38; $P < 0.05$) and positively (0.38; $P < 0.05$) correlated with expression of PPAR-α and SREBP-1c, respectively. On the other hand, α-linolenic and oleic acids were positively (0.55; $P < 0.01$ and 0.46; $P < 0.05$, respectively) correlated with PPAR-α, showing an agonistic effect of these fatty acids on the nuclear receptor. In addition, correlations between linoleic acid content and expression of SCD1 (0.39; $P < 0.05$) and ACC (-0.38; $P < 0.05$) were observed in the LD muscle. No correlations ($P > 0.05$) between arachidonic acid and the expression of PPAR-α and SREBP-1c were observed. Oleic and palmitoleic acids had positive correlations with ACC mRNA (0.47; $P < 0.05$ and 0.41; $P < 0.05$, respectively), but a negative correlation between stearic acid content and ACC gene expression was observed (-0.38; $P < 0.05$). In conclusion, linoleic acid was the main fatty acid that influenced expressions of PPAR-α, SREBP-1c, SCD1 and ACC. Furthermore, unsaturated fatty acids affect in different ways gene expression of these genes. *Funded by Fapemig, CNPq, Capes, and INCT-CA.*

Key Words: PPAR, SCD, SREBP-1c

1252 (T155) Effect of functional oils and high levels of glycerine in the diet of Purunã bulls finished in a feedlot on fatty acid composition in the Longissimus muscle grilled. F. Zawadzki*[1], D. C. Rivaroli[2], A. Guerrero[1], J. A. Torrecilhas[1], C. A. Fugita[1], J. Torrent[3], and I. N. D. Prado[1], *[1]State University of Maringá, Maringá, Brazil, [2]Universidade Estadual Paulista-FMVZ, Botucatu, Brazil, [3]Oligo Basics USA LLC., Chanhassen, MN.*

Bulls were distributed in a complete randomized design by a factorial scheme 2 × 2 to evaluate the effects of the addition of a commercial mixture of functional oils– cashew and castor oil (Essential, Oligo Basics, Paraná, Brazil) and the effects of corn replace by glycerine (800 g of glycerol kg^{-1}) in the diet of Purunã bulls on fatty acids of the *Longissimus* muscle grilled. Thirty-three bulls (206.1 ± 20.0 kg BW, 8 mo old) were allocated in individual pens and distributed into 4 treatments: CON, without glycerine or functional oils); FOL, functional oil (3 g $animal^{-1}$ d^{-1}); GLY, 203 g kg^{-1} of glycerine of dry matter; and GFO, 203 g kg^{-1} of glycerine of dry matter and 3 g $animal^{-1}$ d^{-1} of functional oils. The bulls were fed during 252 d a diet with 420 g corn silage, 477 g ground corn, and 103 g soybean meal d^{-1}; or a diet with 420 g corn silage, 203 g glycerol and 150 g soybean meal. All diets were kept isonitrogenous and isoenergetic. The bulls were slaughtered at commercial slaughterhouse with BW of 468 kg (SD 31.53) ± 19 mo old. The carcasses were labeled and chilled for 24 h at 4°C. *Longissimus* muscle samples were taken by complete cross-section between the 12th and 13th ribs and taken to the laboratory and was frozen at -20°C. *Longissimus* muscle samples were sliced into 1-cm-thick steaks 2 h before grilling. Industrial grill was used to samples grilling at 200°C until reaching 75°C internal temperature. Total lipids were extracted using method with a chloroform/methanol mixture. Fatty acid methyl esters (FAME) were prepared by triacylglycerol methylation according ISO-R-5509 (1978). Then, the esters were extracted with 2 mL of n-heptane and stored at -18°C for later chromatographic analysis (Thermo 3300 gas chromatograph). Retention times and peak area percentages were automatically computed with Chronquest 5.0 software. The fatty acids composition in the *Longissimus* muscle grilled were similar ($P > 0.05$) for bulls fed with functional oils addition. On the other hand in the diet with high level of glycerine the fatty acids ($P < 0.05$) pentadecanoic, margaric, *cis*-10-heptadecaenoic, oleic, *cis*-vaccenic, and ∑-monounsaturated increase in the *Longissimus* muscle grilled. Whereas the fatty acids 15:1 *n*-9, stearic, docosapentaenoic, ∑-saturated fatty acid and ratio ∑-Omega-6:∑-Omega-3 had reduction in the *Longissimus* muscle grilled of bulls feed with glycerine.

Key Words: cashew nutshell liquid; castor oil; meat quality

1253 (T156) Effects of dietary rolled barley grain processed by lactic and citric acid on meat quality in feedlot cattle. M. Nematpoor*[1], K. Rezayazdi[2], and M. Dehghan-Banadaky[3], *[1]University of Tehran, Karaj, Iran, [2]Dep. of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran, [3]University of Tehran, Iran.*

The objectives of the present study were to evaluate the effects of feeding barley grain steeped in lactic acid and citric acid on meat quality in feedlot cattle. Thirty Holstein male calves (initial BW = 308 ± 22 Kg) were used in a completely randomized design. Data were analyzed by the GLM procedure of SAS and Tukey test used considering 5% probability. Feedlot cattle fed twice daily a total mixed ration containing rolled barley grain (51% in DM) steeped for 48 h in an equal quantity of top water, in 0.5% lactic acid or 1% citric acid. The experiment was conducted with 3 rations and 10 animals in each group. Rations were: 1) Control (with rolled barley), 2) rolled barley treated with citric acid, and 3) rolled barley treated with lactic acid. Calves were stunned and dressed at the abattoir. All samples were collected from the *M. longissimus lumborum* (LL) on the day after slaughter. Measurements were performed on fresh (24 h post mortem) and a steak was sampled from the right LL between the 12th and 13th vertebrae (Canadian grade side). The used of treatments had no effect on yellowness (6.85, 6.08 and 6.50, respectively), cook loss (36.79, 34.80 and 35.77, respectively), WB shear force (5.07, 5.29 and 5.12, respectively), water-holding capacity (2.10, 1.94 and 1.82, respectively) and pH (5.50, 5.41 and 5.33, respectively) in steaks from calves ($P > 0.05$). The lightness (34.79, 35.23 and 35.94, respectively) and the redness (14.13, 15.51 and 15.96 kg respectively) of LL muscle were significantly affected by treatments ($P < 0.05$). Moreover, feeding feedlot cattle barley grain steeped in 0.5% LA was improved meat quality, but was not observed any effect from CAB diets.

Key Words: meat quality, lactic acid, citric acid

1254 (T157) Natural additives in the diet of bulls (Angus vs. Nellore) finished in feedlot: Fatty acids composition. C. A. Fugita*, R. Prado, I. N. D. Prado, F. Zawadzki, C. Eiras, M. Valero, and R. Passetti, *State University of Maringá, Brazil.*

Natural extracts could be an alternative for the use of antibiotics as growth promoters in animal feed. The objective of this study was to evaluate the effects of the inclusion of natural additives in the diet of bulls finished in feedlots on *Longissimus* muscle fatty acids composition. Forty-eight bulls (Angus vs. Nellore) finished in feedlot during 94 d were used. The experiment was completely randomized and animals were distributed into four treatments: control (CON); essential oils (EOL– addition of 4 g/animal/day of a mix of essential oils from castor bean- *Ricinus communis*- and ca-

shew- *Anacardium occidentale*); Confimax (MAX– addition of 10 g/animal/day of mix of essential oils from oregano- *Origanum vulgare*, castor bean and cashew, and yeast); and yeast (YST– addition of 5 g/animal/day of yeast- *Saccharomyces cerevisiae*). Bulls were an average of 22 mo old and 318 ± 30 kg at the beginning of the trial and were slaughtered with an average of 468 ± 45kg. Roughage:concentrate ratio was 50:50. A variance analysis was performed and a comparison of means was performed using Tukey test at 10% of significance. Most fatty acids in the *Longissimus* muscle were not altered by the inclusion of additives. The myristic acid was higher ($P < 0.10$) in the CON (3.27%) treatment compared to the EOL (2.83%). Palmitic acid was lower ($P < 0.10$) for the YST. Oleic acid was higher ($P < 0.10$) for the YST (41.4%) and lower for MAX (39.0%) treatment. Natural additives had no effect on SFA, MUFA, PUFA, *n*-3, *n*-6, and the ratio between PUFA/SFA and *n*-6/*n*-3. When fatty acids were analysed individually, some differences were found for YST, indicating a healthier meat fatty acid composition profile for this treatment. The used natural additives had mild effects on fatty acid composition of bulls finished in feedlot.

Key Words: animal nutrition, essential oils, meat quality

1255 (T158) Effects of tannins extract addition in to the diet on physicochemical characteristics of meat from finishing bulls. B. O. Lopez[*1], M. A. Mariezcurrena[1], M. D. Mariezcurrena[1], and R. Barajas[2], *[1]Universidad Autónoma del Estado fde México, Toluca, México, [2]FMVZ-Universidad Autónoma de Sinaloa, Culiacan, México.*

Meat samples of *Longisimus dorsi* obtained from sixteen finishing bulls (*Bos Taurus x Bos indicus*) were used to determine the effects of effects of tannins extract addition in to the diet on physicochemical characteristics of meat from finishing bulls. Animals were fed during last 70 d in finishing period diets supplemented or not with 0.3% DM of a condensed and hydrolyzable tannins blend. After harvested and 24-h chilling period, loin of left carcass side was cross-sectioned at 12th rib level, and four 2.5-cm thickness steaks were removed from each carcass. Steaks sample were immediately placed in identified plastic bags and were vacuum-sealed and transported to laboratory. One subsample bag was open and used for water retention determinations. The remainder of the bag samples were frozen at -20°C and kept frozen until used for laboratory determination. Samples were slowly defrosted, then bags were opened, and aliquots were taken by duplicate and subjected to next measurements: dry matter (forced-air oven), crude protein (N x 6.25 Kjeldhal), ether extract content, ash (550°C; 3 h), and shear force. Results were analyzed by ANOVA for a completely randomly design, with eight replicates by treatment, carcass was consider as the experimental unit. Water retention capacity was similar ($P = 0.48$) between treatments (86.7 ± 114%); dry matter content was not affected ($P = 0.39$) by treatments (25.6 ± 308%), crude protein was not altered ($P = 0.48$) by TE addition (20.15 ± 304%), ether extract was similar ($P = 0.19$) across treatments (5.24 ± 1.22%), ash (2.0 ± 114%) was not altered by TE level ($P = 0.20$), shear force tended to increase ($P = 0.07$) in meat samples from TE supplemented cattle (8.88 and 10.21 kg/cm^2). Loss by cooking was not different ($P = 0.30$). It is concluded that tannin extract supplementation did not alter substantially physicochemical characteristics of frozen meat from finishing bulls.

Key Words: finishing-bulls, meat, tannin

1256 (T159) Effect of polymorphsims in the DECR1 and LDHB genes on beef color stability. J. D. Neal*, J. W. Buchanan, and R. G. Mateescu, *Oklahoma State University, Stillwater.*

The mitochondrial 2,4-dienoyl CoA reductatse gene (DECR1) encodes an enzyme that is associated with the β-oxidation of polyunsaturated fatty enoyl-CoA esters. The lactate dehydrogenase B gene (LDHB) encodes an enzyme that catalyzes the interconversion of muscle lactate to pyruvate. These enzymes affect the oxidative capacity of muscles and potentially influences meat color stability. Meat color plays a crucial role in customer preference of retail beef cuts, and losses of $1 billion annually can be attributed to discolored products. This experiment was created to evaluate the influence of polymorphisms in the DECR1 and LDHB genes on beef color stability. A population of 140 beef cattle finished on grain and grass based diets was harvested, and steaks from these animals were evaluated by panel and instrumental means. Measurements were taken every 12 h for 156 h to evaluate the overall appearance of the steaks. Steaks were separated into high, moderate, or low color stability groups. DNA was extracted from individual tissue samples and SNPs within the DECR1 and LDHB genes were identified. Real time polymerase chain reaction (RT-PCR) and High Resolution Melt curve analysis were run on the extracted DNA samples to determine the genotypes of the cattle. A regression analysis was used to test the association between the new SNPs in the DECR1 and LDHB genes and the beef color stability.

Key Words: beef, meat, quality

1257 (T160) Meat quality in yearling bulls fattened in three production systems from Mexican dry tropic. G. Corral-Flores[1], C. Rodríguez-Muela[1], A. Flores-Mariñelarena[1], J. A. Ramírez-Godínez[1], F. S. Solorio[2], and C. R. Duran[*2], *[1]Universidad Autónoma de Chihuahua, México, [2]Universidad Autónoma de Yucatán, Merida, México.*

The objective was to evaluate the effect of the production system and genetic group in carcass measurements in yearling bulls from mexican dry tropic. Forty-eight animals of

two genetic groups (Brahman*Charolais Bh*CH and Brahman*Brown Swiss Bh*BS) were randomly asigned to Intensive Silvopastoral (ISP, $n = 19$), Silvopastoral + Suplementation (ISP+S, $n = 15$) and Feedlot (F, $n = 14$). Animals were harvested in a commercial abattoir when they target 450 ± kg live weight, to evaluate hot carcass weight (HCW), yield (Y), rib eye area (REA), fat thickness (FT), and marblilng score. As well as bromatological (humidity, ash, crude protein, ether extract) and physicochemical characteristics (*P*H, meat and fat color for L, a*b*). PROC MIXED of SAS was used. Difference was found ($P < 0.05$) for systems, marbling score was higher in F (446.36 ± 31.77), followed by ISP+S (245.7 ± 26.2) and ISP (167.6 ± 26.9). Genetic group was different ($P < 0.05$), in yield better response was in Bh*CH (58.9 ± 0.7%) than Bh*BS (57.7 ± 0.6%), as well as REA (74.0 ± 2.7 cm^2 *vs* 66.2 ± 2.5 cm^2. Cattle fattened in F had DFD meat with highiest pH at 48 h postmortem (6.7 ± 0.06), while bulls in ISP+S and ISP were similar ($P > 0.05$) because they were near to normal pH value. In meat color F had lower L, higher a* and b* 36.9 ± 1.1, 15.9 ± 0.8 and 20.1 ± 0.9), respectively; while ISP+S and ISP had similar values ($P > 0.05$) for fat color as well as protein and humidity. In ash, ISP and ISP+S were similar ($P > 0.05$; 4.0 ± 0.07% y 4.0 ± 0.07), but they were higher than F (3.4 ± 0.08%). Ether extract was high in F (5.76 ± 0.5%) vs. 2.03 ± 0.4% in ISP+S *vs*1.5 ± 0.4% to ISP. It was concluded that cattle in ISP can produce the same carcass characteristics, nutritional facts than F; however, they have the advantage to produce lean meat. Also, carcass characteristics may be affected by genetic group. Supplementation can improve beef quality related with marbleing score.

Key Words: silvopastoral, feedlot, marbling, cattle

1258 (T161) Effect of diet without forage on beef quality in *Bos taurus* and *Bos indicus* young bulls.

M. L. Chizzotti*[1], P. D. Teixeira[2], M. M. Ladeira[2], J. R. R. Carvalho[2], K. C. Busato[2], R. A. Gomes[2], A. C. Rodrigues[2], and M. C. L. Alves[2], *[1]Universidade Federal de Viçosa, Brazil, [2]Universidade Federal de Lavras, Brazil.*

The objective was to evaluate beef quality of finishing young bulls Nellore or Aberdeen Angus fed a whole grain corn diet without roughage (WR, 85% of whole corn and 15% of commercial pellet) or a traditional diet containing 30% of corn silage and 70% of concentrate (30:70). Thirty-six animals with average initial body weight of 381.2 ± 11.87 kg were used in a 2 × 2 factorial design (2 breeds and 2 diets). Both diets had 12.5% crude protein and 2.88 Mcal/kg of ME. Animals were fed for 82 d after a 28-d adaptation period and slaughtered at the end. Samples were taken from the *Longissimus dorsi* muscle between the 12th and 13th ribs for centesimal composition analyses, color (L*, a*, b*), cooking weight loss (CWL) and shear force (SF). The model included the effects of breed, diet, and their interaction and was analyzed using PROC GLM in SAS 9.1. The moisture, ashes, protein, CWL, a*, and b* were not affected by breed and diet. However, Angus bulls showed higher muscle ether extract in WR than Nellore animals. Angus animals showed greater tenderness when compared to Nellore, and WR had a tendency to increase tenderness. Nellore presented a higher brightness (L*) when compared to Angus animals. Angus animals and diet with whole grain corn increased the levels of ether extract, and the use of Angus animals improved meat tenderness.

Key Words: color, shear force, beef

Table 1258. Centesimal composition (%), color (L*, a*, b*), cooking weight loss (CWL), and shear force (SF) of beef from young bulls Nellore and Angus receiving diets with or without roughage

	Nellore		Angus			*P* Value		
Attributes	30:70[1]	WR[2]	30:70	WR	SEM	Breed	Diet	B*D
Moisture (%)	73.7	74.4	73.9	73.51	1.08	0.77	0.88	0.56
Ashes (%)	1.2	1.2	1.2	1.3	0.15	0.81	0.61	0.87
Protein (%)	17.1	16.7	17.0	17.2	0.20	0.82	0.88	0.67
Ether extract (%)	4.9	4.1	4.1	6.2	0.04	0.04	0.05	< .0001
CWL(%)	27.4	27.4	27.7	25.6	1.58	0.30	0.11	0.14
SF (Kgf)	6.0	5.8	5.8	5.2	0.47	0.05	0.07	0.41
L*	49.2	48.7	48.3	47.7	0.51	0.02	0.97	0.56
a*	7.3	7.5	7.7	7.8	0.48	0.16	0.44	0.92
b*	9.7	9.5	9.4	9.2	0.42	0.1003	0.2745	0.8556

[1]Diet containing 30% roughage and 70% concentrate (30:70).

[2]Diet with 85% corn grain and 15% commercial pellet (Without roughage, WR).

1259 (T162) Prediction of lamb carcass back fat thickness by skin-fold measurement.

H. A. Ricardo*[1], and R. O. Roça[2], [1]*Grande Dourados Federal University* (*UFGD), Dourados, Brazil,* [2]*São Paulo State University* (*FCA/UNESP), Botucatu, Brazil.*

Skinfold measurement is a common method for determining body fat composition and nutritional status in humans for athletic and health goals. Many subjective and objective methods are available for prediction of sheep carcass composition, with more accuracy for automated methods. The objective of this preliminary study was to start the assessment of the use of skin-fold measurement as predictor of lamb carcass composition. The first trial evaluated the use of skinfold measurement to predict carcass back-fat thickness (BF) and rib eye area (REA). Twenty market lambs (29.73 ± 3.15 kg of BW) were chosen randomly at the slaughterhouse floor. Skin-fold measurement (mm) was taken in vivo with a clinical plicometer with sensibility of 2 mm, reading range of 80 mm, and pressure of ± 10 g/mm^2, including: skin fold on sternal bone (SSF); skin fold on m. *Longissimus* between first and least lumbar vertebra (LSF); skin fold on rump back-fat thickness location (RSF), and average skin fold (ASF), with the three measurements. After slaughter, carcasses were chilled over 24 h at 4°C. Hot and cold carcass weights (HCW and CCW) were recorded. BF and REA were taken in the cold carcass on m. *Longissimus* between 12th and 13th ribs. A stepwise regression was performed with BW, skin-fold measurement, and carcass weights to predict BF and REA. A two-step model was obtained for BF prediction with SSF and HCW ($P < 0.01$). SSF and HCW were responsible for 39.97 and 48.72%, respectively, of BF variation, resulting in a model $R^2 = 0.89$ (RSD = 0.40). A stepwise model for REA used SSF and BF ($P = 0.0847$). SSF and BF had a partial R^2 of 0.34 and 0.29, respectively, which model representing 63% of REA variation. In conclusion, skin-fold measurement can be used to predict lamb carcass BF and REA, and shows potential to be used in the estimation of carcass composition.

Key Words: back-fat prediction, lamb, plicometer

1260 (T163) Carcass traits and meat quality of goat kids supplemented with chromium-methionine.

A. Emami[1], M. Ganjkhanlou[2], A. Zali[2], and M. Dehghan-Banadaky*[2], [1]*University of Birjand, Iran,* [2]*University of Tehran, Iran.*

The objective of this study was to evaluate the effects of supplementing chromium-methionine (Cr-Met) on carcass traits and meat quality in Mahanadi goat kids. Thirty-two male kids (BW = 22 ± 2 kg, 4 mo of age) were used in a completely randomized design in one of four treatments: 1) control (without Cr), 2) 0.5, 3) 1.0, and 4) 1.5 mg Cr as Cr-Met/animal/d. Diet was formulated to meet the requirements recommended by NRC with forage (alfalfa and corn silage): concentrate ratio of 30:70 in TMR form. Diets were the same, except for top-dress addition of Cr-Met fed in two equal meals (0700 and 1700 h). Animals were kept in individual pens for 84 d. Kids were slaughtered following the end of trial after 16-h fasting. The area of the ninth, 10th, 11th, 12th and 13th ribs together with the adjoined section of spinal column were used to estimate the amount of bone-free meat, fat and bone in the carcass. The meat, fat and bone were weighed after separation and the bone-free meat component stored at -20°C for the chemical analysis. Physical meat quality parameters (drip loss, DL, pH and Warner-Bratzler shear force, WBS) were investigated on longissimus thoracis (LT) at 24 h after slaughter. Data were analyzed by GLM procedure of SAS 9.1 and Tukey test ($P \leq 0.05$). The muscle, fat, and bone percentages were not affected by Cr-Met ($P > 0.05$). pH, moisture (%), intramuscular fat (%), crude protein content (%) and DL percentage were also not affected by Cr supplementation ($P > 0.05$). Supplemental Cr decreased WBS (6.89, 5.97, 5.60 and 5.83 in control to 4, respectively; $P = 0.07$). These results suggest that supplementation diet with Cr-Met did not influence the carcass traits and meat quality but improved tenderness of LT in Mahabadi goat kids.

Key Words: chromium-methionine, Mahabadi goat kid, tenderness

1261 (T164) Effect of high level of copper on meat quality in Iranian Mahabadi goat kids.

M. Ganjkhanlou[1], A. Zali[1], A. Hatefi[1], A. Emami[2], A. Akbari-Afjani[3], and M. Dehghan-Banadaky*[1], [1]*University of Tehran, Iran,* [2]*University of Birjand, Iran,* [3]*University of Zanjan, Iran.*

This study was performed to determine the effects of supplementing high level of copper (Cu) on meat quality in goat kids. Fourteen male kids (BW = 21 ± 2 kg, 4 mo of age) were used in a completely randomized design with two treatments: 1) control (without Cu), and 2) 100 mg Cu as copper sulfate/animal/d. Diet was formulated to meet the requirements recommended by NRC with forage (alfalfa and corn silage): concentrate ratio of 30:70 in TMR form. Diets were the same, except for top-dress addition of Cu-So_4 fed in two equal meals (0700 and 1700 h) and orts were collected before morning meal. Experimental period was 90 d. The end of trial following 16 h fasting kids were weighed and slaughtered. Meat samples were taken from the *Longissimus dorsi* muscle (LDM). Color [lightness (L*), redness (a*) and (b*) yellowness] and Warner-Bratzler shear force (WBS) were measured at 24 h after slaughter. Cooking loss (CL) was determined by weighing the samples before and directly after cooking in a water bath at 70°C for 1 h. Percentage of CL was calculated. Data were analyzed by GLM procedure of SAS 9.1 and adjust Tukey test ($P \leq 0.05$). Addition of Cu failed to significantly affect lightness (L*) and CL percentage ($P > 0.05$). However, Cu supplementation de-

creased WBS (41.31 and 38.00 in control to 2, respectively) but increased redness (a*: 14.90 and 16.43 for treatment 1 and 2 respectively) and yellowness (b*: 12.53 and 17.60 for treatment 1 and 2; $P < 0.05$). These results indicated that dietary supplementations of Cu did not influence CL and lightness. Although Cu supplement increased redness, yellowness, and improved tenderness of LDM in Mahabadi goat kids.

Key Words: Mahabadi goat kid, meat quality, lightness

1262 (T165) Effect of fish oil and thyme on meat quality and meat oxidative stability of Mahabadi kids.

A. Hozhabri[1], M. Ganjkhanlou[1], A. Zali[1], A. Emami[2], A. Akbari-Afjani[3], and M. Dehghan-Banadaky[*1], *[1]University of Tehran, Iran, [2]University of Birjand, Iran, [3]University of Zanjan, Iran.*

This study was performed to determine the effects of supplementing fish oil and thyme on meat quality and meat oxidative stability in Mahabadi goat kids. For this aim, 28 Mahabadi goat kids (BW = 17.8 ± 2.8 kg, 4 to 5 mo of age) were randomly assigned to four treatments: 1) basal diet (BD), 2) BD + 0.2% thyme essence, 3) BD +2% fish oil, and 4) BD + 2% fish oil and 0.2% thyme essence (DM basis of concentrate). Diets were formulated to meet the requirements recommended by NRC with forage (alfalfa and corn silage): concentrate ratio of 30:70 in TMR form. Animals were kept in individual pens with self-mangers for 94 d. Kids were weighed and slaughtered at the end of the trial. Meat samples were taken from the *Longissimus dorsi* muscle (LDM). Color [lightness (L*), redness (a*), chroma, hue angle, and yellowness (b*)], cooking loss and drip loss percentage, Warner-Bratzler shear force, and pH of LDM were measured at 24 h after slaughter. Some of the LDM were immediately stored at -20°C for assaying moisture, intermuscular fat and crude protein content. TBARS values were measured at 1 and 2 mo after slaughter. Data were analized by GLM procedure of SAS 9.1 and Tukey test ($P \leq 0.05$). Addition of fish oil and thyme failed to significantly effect on redness (a*), yellowness (b*), chroma, hue angle, lightness (L*), pH, moisture (%), intramuscular fat (%), crude protein content (%), Warner-Bratzler shear force, cooking loss, and drip loss percentage of LDM ($P > 0.05$). TBARS values of the LDM were significantly increased as the storage time increased from 1 to 2 mo ($P < 0.05$). It was also found that diets 2 and 4 significantly decreased and diet 3 significantly increased lipid oxidation and the TBARS value compared with diet 1 at during of storage ($P < 0.05$). The results of this experiment indicated that supplementation of diet with 0.2% thyme essence decreased oxidative stability and improved quality of LDM during refrigerated storage.

Key Words: fish oil, Mahabadi goat kid, thyme essence

1263 (T166) Effect of fish oil and thyme on performance, blood metabolites, meat sensory of Mahabadi kids.

A. Hozhabri[1], A. Zali[1], M. Ganjkhanlou[1], A. Emami[2], A. Akbari-Afjani[3], and M. Dehghan-Banadaky[*1], *[1]University of Tehran, Iran, [2]University of Birjand, Iran, [3]University of Zanjan, Iran.*

This study was performed to determine the effects of supplementing fish oil and thyme on performance, blood metabolites and meat sensory in Mahabadi goat kids. For this aim, 28 Mahabadi goat kids (BW = 17.8 ± 2.8 kg, 4 to 5 mo of age) were randomly assigned to four treatments: 1) control (basal diet), 2) 0.2% thyme essence, 3) 2% fish oil, and 4) 2% fish oil +0.2% thyme essence. Animals were kept in individual pens with self-mangers for 94 d. Diet was formulated to meet the requirements recommended by NRC with forage (alfalfa and corn silage):concentrate ratio of 30:70 in TMR form. For measuring blood metabolites (glucose, triglyceride, cholesterol, high and low density lipoprotein, albumin, total protein and blood urea nitrogen), blood samples were collected every 21 d before morning feeding. Kids were weighed after 14 d of adaptation and at 21-d intervals after feed restriction and slaughtered at the end of the trial. Meat samples were taken from the *Longissimus dorsi* muscle and frozen at -20°C until taste panel evaluation. Feed conversion ratio (FCR) was calculated according to FCR = DMI (kg)/average daily gain (kg). Data were analyzed using PROC MIXED of SAS 9.1. The Tukey test was used for comparison of treatment means. Dry matter intake, average daily gain and feed conversion ratio were not affected by fish oil and thyme essence ($P > 0.05$). Plasma glucose, triglyceride, cholesterol, high and low density lipoprotein, albumin, total protein and blood urea nitrogen were not affected by treatments ($P > 0.05$). Addition of fish oil and thyme failed to significantly affect sensory properties of meat ($P > 0.05$). The results of this experiment indicate that supplementation of goat kid diet with fish oil and thyme did not influence performance, blood metabolites and meat sensory.

Key Words: fish oil, thyme essence, performance

MEAT SCIENCE & MUSCLE BIOLOGY III

1264 (W151) Sun dried meat quality derived from young bulls fed licuri cake derived from biodiesel production. R. L. Oliveira*, A. A. L. Govêa, A. G. Leão, N. G. D. N. Júnior, W. F. D. Souza, S. T. Carvalho, T. M. Silva, A. D. S. Nunes, and R. R. D. Albuquerque, *Universidade Federal da Bahia, Salvador, Brazil.*

This study was conducted to determine the best level of licuri cake in the diets of young bulls based on physical-chemical evaluation and sensory sun dried meat. The experiment was conducted at the School of Veterinary Medicine and Animal Science of the Federal University of Bahia, located in São Gonçalo do Campos, Bahia, Brazil, for 99 d with 15 d for the adaptation of animals, management and diets. Thirty two Nellore bulls non castrated average age of 24 mo and initial body weight of 368 ± 32 kg. Before beginning, the animals were vaccinated against clostridia, and wormed against endo and ectoparasites. Later, they were housed in individual 8-m^2 pens, with slatted floors, and provided with food and water in a covered area. The animals were distributed into four treatment groups, constituting diets with 0, 7, 14, and 21% of licuri cake in the dry matter. The forage used was hay of Tifton with particle size of approximately 5 cm and forage:concentrate ratio of 40:60. Treatments consisted of isonitrogen diets and formulated for 1.2 kg/day for gain according to NRC (1996). For the preparation of sun dried meat, a sample of the soft round (*Semimenbranosus*) was then divided into sections 5 in thick each. We used salt in a proportion of 5% (± 150 g) in relation to the weight of natural matter (3 kg), which was manually rubbed surfaces of the pieces evenly. After this process, the pieces were kept in an ambient temperature of 25°C for better penetration of salt. At the end of 16 h curing was taken drainage of exudate and washing the pieces in water to remove excess salt. The licuri cake added to the diet quadratic effect on the shear force ($P < 0.05$). For sensory parameters was no effect on aroma where the inclusion of 7 to 14% of the licuri cake reduced of sun meat appreciation ($P < 0.05$). There was no effect for the other characteristics evaluated. Licuri cake can be added to the diet of crossbred cattle to the level of 7% without causing changes in the quality of sun dried meat.

Key Words: flavor, *semimembranosus*, shear force

1265 (W152) Processed burguer quality derived from young bulls fed licuri cake from biodiesel production. R. L. Oliveira*[1], A. A. L. Govêa[1], A. G. Leão[1], C. B. D. Pellegrini[1], N. G. D. N. Júnior[1], C. L. D. Abreu[1], T. M. Silva[1], V. B. D. Silva[1], and E. S. dos Santos[2], *[1]Universidade Federal da Bahia, Salvador, Brazil, [2]Federal University of Bahia, Salvador, Brazil.*

This study was conducted to determine the physicochemical and sensory parameters of burgers from young bulls fed diets containing licuri cake. The experiment was conducted at the School of Veterinary Medicine and Animal Science of the Federal University of Bahia, located in São Gonçalo dos Campos, Brazil, over a period from July to October 2012. Thirty-two Nellore bulls were used, with initial weight of 368 ± 32 kg. Before the beginning of the experiment, the animals were vaccinated against clostridia, wormed against endo and ectoparasites and then assigned to individual 8-m^2 pens with food and water in a covered area. The experimental period was 84 d, with 15 d added for animal adaptation, totaling 99 d. The experimental design was completely randomized. The animals were divided into four treatments consisting of diets with 0, 7, 14, and 21% of licuri cake inclusion, based on dry matter. The forage used was hay of Tifton with particle size of approximately 5 cm and forage:concentrate ratio of 40:60. Treatments consisted of isonitrogen diets and formulated for 1.2 kg/d for gain according to NRC (1996). At the end of the experiment, the animals were submitted to feed fasting and slaughtered. The portion of beef burger used in processing was *Semimenbranosus* muscle (81.3%) and pig fat (15%). Other ingredients added to the burger were salt (3%), black pepper (0.2%), garlic paste (0.3%), and sugar (0.2%). The centesimal composition of the burgers was not altered by levels of licuri cake ($P > 0.05$). However, the inclusion of licuri cake promoted increased linearly between physicochemical characteristics of brightness ($P < 0.05$) and color of meat hamburger, increasing consumer acceptability and appearance of the product. The licuri cake can be added in the diet of beef cattle to the level up to 21% without causing significant changes in the qualitative parameters of the burger.

Key Words: color, confinement, *semimenbranosus*

1266 (W153) Collagen, cooking losses and shear force of aged meat from Nellore steers fed protected or unprotected linseed oil. W. Henrique*[1], L. R. Simonetti[2], T. M. Pivaro[3], V. G. Carvalho[2], E. A. Oliveira[2], C. C. P. D. Paz[1], and A. A. M. Sampaio[2], *[1]Instituto de Zootecnia, Sertãozinho, Brazil, [2]Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil, [3]FCAV/UNESP JaboticabaL, Pradópolis, Brazil.*

This work assess the effects of aging times and the inclusion of protected or unprotected linseed oil of rumen degradation on the diet of 21 Nellore steers finished on feedlot on collagen (COL), cooking losses (CL) and shear farce (SF) of *Longissimus* muscle. At the beginning of the experiment, animals had 18 mo of age and 397.74 ± 14.07 kg of BW, and they were kept in individual pens and adapted during 21 d. The diets were composed by 40% corn silage and with no oil addition (73% TDN and 2.9% EE), with in natura linseed oil or with protected linseed oil (76% TDN and 6.1% EE). After 105 d at feedlot, the animals were slaughtered with 522.72 ± 27.99 kg of BW and carcasses were chilled for 24 h. After this period, a section of the *Longissimus* between sixth and 13th ribs was removed and separated in 2.54 cm steaks, which were individually vacuum packed and chilled to 2°C for 1, 7, or 14 d. The amino acid hydroxyproline was quantified to measure the collagen content by spectrophotometer reading at 500 nm; for CL, the steaks were roasted in an electric woven up to 71°C at its geometric center, and the weights before and after cooking were used for the calculation. After 24 h of cooling, six cylinders of 1.27 cm diameter were removed from the steaks to determine the force required to cut across each cylinder using a texturometer, and the average were used to represent the SF. The results were submitted to analysis of variance using mixed models, considering a random block one, and a 3 × 3 factorial scheme. For COL (0.70 mg/100 g muscle), no differences were found among treatments ($P = 0.5806$), and for the aging times, a quadratic effect ($P = 0.0168$) was observed. An interaction for CL was found ($P = 0.0433$), and its evaluation showed a quadratic effect ($P = 0.0134$) for unprotected linseed oil during aging periods, the remaining variables showed no differences ($P > 0.05$). SF was not influenced by the treatments ($P = 0.2718$) and aging times showed a quadratic effect ($P < 0.0001$) (5.38; 3.35 and 3.34 kgf, for 1, 7, and 14 d, respectively). Meat tenderness is not affected by the addition of linseed oil on the bovine diet, but it is improved by aging up to 14 d. On the other hand, collagen content is increased by aging.

Key Words: *Longissimus*, tenderness, Zebu

1267 (W154) Effect of aging times and inclusion of unprotected or protected linseed oil on the diet of Nellore steers over the color of *Longissimus*. W. Henrique*[1], L. R. Simonetti[2], T. M. Pivaro[3], V. G. Carvalho[2], E. A. Oliveira[2], C. C. P. D. Paz[1], and A. A. M. Sampaio[2], *[1]Instituto de Zootecnia, Sertãozinho, Brazil, [2]Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil, [3]FCAV/UNESP Jaboticabal, Pradópolis, Brazil.*

The objective was to evaluate the effects of aging time and the inclusion of unprotected or protected linseed oil from rumen degradation on the diet of 21 Nellore steers, finished at feedlot in individual pens, and their influence over the color aspects of *Longissimus* muscle. At the beginning of the experiment, animals had 18 mo of age and 397.74 ± 14.07 kg of BW and they were kept in adaptation during 21 d. The diets were composed by 40% corn silage and with no oil addition (73% TDN and 2.9% EE), with in natura linseed oil or with protected linseed oil (76% TDN and 6.1% EE). After 105 d at feedlot, the animals were slaughtered with 522.72 ± 27.99 kg of BW and carcasses were chilled for 24 h. After this period, a section of the *Longissimus* between sixth and 13th ribs was removed and separated in 2.54 cm steaks, which were individually vacuum packed and chilled to 2°C for 1, 7 or 14 d. After this processing, in different points of these steaks, we cut a cross-section of muscle for exposure of myoglobin to oxygen for 30 min. Then a colorimeter was used to determine the color of the meat by evaluating the lightness (L*), 0 = black and 100 = white; redness (a*); and yellowness (b*). The results were submitted to analysis of variance using mixed models, considering a random block one, and a 3 × 3 factorial scheme. No interactions were observed between diets and aging times ($P > 0.05$). For L* (40.84) and b* (14.85), no difference among treatments were found ($P = 0.4145$ and $P = 0.0703$, respectively), and the aging time showed a quadratic effect on both characteristics ($P = 0.0002$ and $P < 0.0001$). The values of a* (16.49) were not affected by diets ($P = 0.3116$) and aging times (linear regression- $P = 0.9565$; quadratic- $P = 0.5068$). Protected or unprotected linseed oil can be used on Nellore steers diet without changing aspects of meat color.

Key Words: cattle, luminosity, meat

1268 (W155) Aging times and inclusion of unprotected or protected linseed oil on Nellore steers diet and its influence on cholesterol and lipid oxidation of the meat.

L. R. Simonetti*[1], W. Henrique[2], T. M. Pivaro[3], V. G. Carvalho[2], E. A. Oliveira[2], C. C. P. D. Paz[2], and A. A. M. Sampaio[2], *[1]Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil, [2]Instituto de Zootecnia, Sertãozinho, Brazil, [3]FCAV/UNESP Jaboticabal, Pradópolis, Brazil.*

The objective was to assess the effects of aging time and the inclusion of unprotected or protected linseed oil from rumen degradation on the diet of 21 Nellore steers, finished at feedlot, over the cholesterol content and lipid oxidation of *Longissimus* muscle. At the beginning of the experiment, animals had 18 mo of age and 397.74 ± 14.07 kg of BW, and they were kept in individual pens and adapted during 21 d. The diets were composed by 40% corn silage and with no oil addition (73% TDN and 2.9% EE), with in natura linseed oil or with protected linseed oil (76% TDN and 6.1% EE). After 105 d of feedlot, the animals were slaughtered with 522.72 ± 27.99 kg of BW and carcasses were chilled for 24 h. After this period, a section of the *Longissimus* between sixth and 13th ribs were removed and sampled as 2.54 cm steaks, individually vacuum packed and chilled to 2°C for 1, 7 or 14 d. For cholesterol content, 10 g of fresh meat were used after each aging time, and the lipid oxidation was obtained by the method based on 2-thiobarbituric acid (TBARS), both using spectrophotometer with 538 nm. The results were submitted to analysis of variance using mixed models, considering a random block one, and a 3 × 3 factorial scheme. No interactions were observed, cholesterol content was not influenced by diet ($P = 0.5727$) or by aging times (linear regression- $P = 0.5008$, and quadratic- $P = 0.7493$), showing lower levels than those considered normal for the *Longissimus* muscle (36.5 and 33.16 mg/100 g of muscle to diets and times aging, respectively), which is important because of its influence in preventing cardiovascular disease. Lipid oxidation was also not influenced by factors evaluated ($P > 0.005$), and the average was 0.41 mg of malonaldehyde/kg of muscle. Add linseed oil on the diet of Nellore steers does not cause a loss in quality of meat for human consumption, using *in natura* or protected form.

Key Words: *Longissimus*, human health, TBARS

1269 (W156) Effect of aging times and inclusion of unprotected or protected linseed oil from ruminal degradation on the diet of Nellore steers over pH and water holding capacity of meat.

L. R. Simonetti*[1], W. Henrique[2], T. M. Pivaro[3], V. G. Carvalho[2], E. A. Oliveira[2], C. C. P. D. Paz[2], and A. A. M. Sampaio[2], *[1]Universidade Estadual Paulista Júlio de Mesquita Filho, Jaboticabal, Brazil, [2]Instituto de Zootecnia, Sertãozinho, Brazil, [3]FCAV/UNESP Jaboticabal, Pradópolis, Brazil.*

This work assess the effects of aging times and the inclusion of protected or unprotected linseed oil of rumen degradation on diet of 21 Nellore steers, finished at feedlot, over pH and water holding capacity (WHC) of *Longissimus* muscle. At the beginning of the experiment, the animals had 18 mo of age and 397.74 ± 14.07 kg of BW and they were kept in individual pens and adapted during 21 d. The diets were composed by 40% corn silage and with no oil addition (73% TDN and 2.9% EE), with in natura linseed oil or with protected linseed oil (76% TDN and 6.1% EE). After 105 d at feedlot, the animals were slaughtered with 522.72 ± 27.99 kg of BW and carcasses were chilled for 24 h. After this period, a section of the *Longissimus* between sixth and 13th ribs was removed and separated in 2.54-cm steaks, which were individually vacuum packed and chilled to 2°C for 1, 7, or 14 d. The pH was determined using a pHmeter with a penetration electrode and the WHC was obtained by the difference between the weights of the meat samples of approximately 2 g before and after being submitted to pressure of 10 kg for 5 min. The results were submitted to analysis of variance using mixed models, considering a random block one, and a 3 × 3 factorial scheme. No interactions were observed between diets and aging times ($P > 0.05$). No differences were observed for pH among treatments ($P = 0.9276$) and aging times (linear regression- $P = 0.3454$, and quadratic- $P = 0.3147$), with an average of 5.45 considered normal for beef. The diets did not influence ($P = 0.7500$) the WHC (74.61%), and for aging times, a quadratic effect ($P = 0.0286$) was observed (69.27, 75.88 and 78.68% for 1, 7, and 14 d, respectively). The addition of linseed oil in any form on Nellore steers diet does not alter pH and WHC, however, aged meat for up to 14 d is benefic because it increased the WHC, which influences many other aspects of meat quality, as juiciness.

Key Words: meat quality, *Longissimus*, Zebu

1270 (W157) Aged beef from Nellore young bulls fed crude glycerin in diets with different roughage sources. J. F. Lage*, A. F. Ribeiro, M. Machado, L. R. Simonetti, E. A. Oliveira, E. E. Dallantonia, and T. T. Berchielli, *Universidade Estadual Paulista Júlio de Mesquita Filho, Jaboticabal, Brazil.*

This trial aimed to evaluate the effects of feeding crude glycerin (CG)- 80% glycerol- included on 10% of DM diet, replacing corn with three roughage sources: corn silage (CS), sugarcane (SC) and sugarcane bagass (SCB) on pH, water holding capacity (WHC), Warner-Bratzler shear force (WBSF) and cooking losses (CKL) of aged beef from Nellore young bulls fed in feedlot. Thirty animals with 416 ± 24.68 kg initial BW were randomly assigned to three treatments, with ten replicates and fed during 90 d in feedlot. Animals were slaughtered at average BW of 550.50 kg BW and all carcasses were refrigerated at 0°C for 24 h. *Longissimus* muscle (LM) section 10 cm thick was removed from the posterior end of the wholesale rib, individually vacuum-packaged and aged for 7 and 14 d at 0 to 2°C. The WHC was measured for the difference between the weights of the sample before and after it was subjected to a pressure of 10 kg for 5 min. Steaks of 2.54 cm were removed and same samples were used to analysis of WBSF and CKL. The experiment was conducted according to a completely randomized design in a factorial arrangement 3 × 3 (three diets x three aging times). Data were analyzed by the PROC PROC MIXED of SAS, and the Tukey test used considering 5% probability. The WHC ($P = 0.68$), WBSF ($P = 0.15$) and CKL ($P = 0.88$) did not differ among diets, however, the beef from animals fed SC had a higher pH values than animals fed other diets ($P < 0.01$). The WHC was not different between beef aged in 7 or 14 d ($P = 0.72$). The pH was higher and CKL was lower ($P = 0.02$) in beef aged for 14 d. The WBSF was lower in d 14 than d 7($P < 0.01$). The use of corn silage, sugarcane or cane bagass in diets with crude glycerin replacing corn in 10% of DM did not affect the tenderness, WHC and CKL, but animals fed sugarcane had beef with higher pH values. The aging time until 14 d reduces the cooking losses and is an effective method to improve the tenderness of beef from Nellore young bulls.

Key Words: aging times, glycerol, meat quality

1271 (W158) Effect of aging times on tenderness of five muscles from carcass of Nellore young bulls. L. R. Simonetti*, J. F. Lage, E. E. Dalanttonia, E. A. Oliveira, M. B. Abra, G. M. Delamagna, L. Maneck Delevatti, and T. T. Berchielli, *Universidade Estadual Paulista Júlio de Mesquita Filho, Jaboticabal, Brazil*.

The objective of this study was to evaluate the aging effects on cooking losses (CKL) and Warner-Bratzler shear force (SF) of five muscles: *biceps femoris* (BF), *gluteus medius* (GM), *longissimus* (LD), *semitendinosus* (ST) and *trapezius thoracis* (TT) of Nellore young bulls fed in feedlot. Fourteen animals at 15 mo of age were confined in individual pens with feeders and drinkers. The diet was consisted of 40% corn silage and 60% concentrate. After 60 d of feedlot, the animals were slaughtered and the carcasses were chilled to 0°C for 24 h. The muscles were removed, cut into steaks of 2.54 cm and individually vacuum packed and chilled to 0 to 2°C for 1, 7, and 14 d postmortem. Steaks 2.54 cm thick were removed and same samples were used to analysis of WBSF and CKL. The experiment was conducted according to a completely randomized design in a 3 × 5 factorial arrangement (3 aging times × 5 muscles) with 14 replicates. The data were analyzed by PROC MIXED of the SAS and the Tukey test considering 5% probability. The interaction between muscles and aging times was significant ($P < 0.01$) to CKL and SF. The greater value for CKL was observed in muscle ST (36.73%) on d 7, being that muscles BF (33.82%) and TT (35.68%) at d 7 did not differ from the ST. Muscle LD (29.65%) on d 7, GM (28.64%, 29.60%) on d 1 and 7, BF (28.42%) on d 1 and TT (28.14%) at d 14 showed smallest values for CKL. The CKL at d 1 compared to d 14 was not different to muscles LD, ST and TT ($P > 0.05$). ST muscle (5.56 kgf) showed the highest values of SF in all aging times ($P < 0.01$). GM muscle (4.03 kgf) and BF (3.73 kgf) was not changed the SF at aging times. The LD muscle had the SH decreased with seven d of aged, not differing from d 14. The smallest SF was obtained for TT (2.96 kgf) in 14 d of aged. The ST muscle not changes the tenderness as an aging time up to 14 d. GM and BF muscles are considered tenderest on the d 1.

Key Words: beef cattle, meat quality, shear force.

1272 (W159) Color and pH of meat aged from Nellore young bulls fed crude glycerin associated with soybean grain in low or high starch diets. M. B. Abra, J. F. Lage*, L. G. Rossi, L. R. Simonetti, E. A. Oliveira, G. M. Delamagna, E. E. Dalanttonia, V. B. Carvalho, and T. T. Berchielli, *Universidade Estadual Paulista Júlio de Mesquita Filho, Jaboticabal, Brazil.*

This trial aimed to evaluate the meat quality aged in 7 or 14 d from Nellore young bulls fed crude glycerin (CG; 80% of glycerol) associated with soybean grain (SG) in low (LS) or high starch (HS) diets finished in feedlot. Twenty-eight animals that were 20 mo old and 428.57 ± 35.33 kg of initial BW were used in a randomly design in a factorial arrangement 2 × 2 x 2 (LS or HS diets, with or without oil and two aging times) with seven replicates. The diets (40:60) were: 10% of CG in DM diet replacing corn (HS); 10% of CG in DM diet replacing corn plus SG; 10% of CG in DM diet replacing soybean hulls (LS) and 10% of CG in DM diet replacing soybean hulls plus SG. After 140 d of feeding, all animals were slaughtered with a 590.21 ± 52.29 kg of BW. All carcasses were refrigerated at 0°C for approximately 24 h. A boneless *Longissimus* muscle

(LM) section 10 cm thick was removed from the posterior end of the wholesale rib. The LM was sliced into steaks of 2.54 cm, individually vacuum packaged and chilled at 0 to 2°C for 7 and 14 d. The color reading was conducted using the CIE L*a*b* system. The water holding capacity (WHC) was measured for the difference between the weights of the sample before and after it was subjected to a pressure of 10 kg for 5 min. Data were analyzed by the PROC MIXED of SAS, and the Tukey test used considering 5% probability. There was no interaction ($P > 0.05$) for any of the variables evaluated. Thus, effects were discussed independently. Similar values of lightness (L*), redness (a*), yellowness (b*), pH and WHC were observed for beef from animals fed LS or HS diets. Likewise, the inclusion of SG was not affected the meat quality traits. However, the lightness ($P < 0.01$) and yellowness ($P < 0.01$) was higher in beef aged for 14 d. The crude glycerin (10% of DM) associated with SG in LS or HS diets did not affect the meat quality traits as a pH, WHC and color of Nellore young bulls. The aging time for 14 d increases the lightness and yellowness of beef.

Key Words: glycerol, meat quality, oil

1273 (W160) Effects of excess dietary sulfur on beef carcass characteristics and quality after aging.

J. Hawley*, E. B. Kegley, J. W. Yancey, and J. K. Apple, *Dep. of Animal Science, University of Arkansas Division of Agriculture, Fayetteville.*

To test the effects of excess dietary S on beef carcass characteristics and quality (color shelf-life, oxidative stability, and sensory attributes), 20 steers (initial BW = 279 ± 60.4 kg) were blocked by BW and assigned randomly to 1) no additional S (~ 0.15% S) or 2) high S (0.40% S). Steers grazed fall pastures and were offered corn and soybean meal supplements for 114 d. Steers were moved to the feedlot, remained on prior dietary treatments, and received corn and soybean meal rations for 123 d. Steers were slaughtered at an average BW of 565 ± 38.4 kg. Boneless rib sections were obtained and aged 14 d at 4°C before fabrication into 2.54-cm-thick steaks. Steaks were overwrapped with oxygen permeable film and stored in open-topped, coffin-chest display cases (2.8°C) under continuous warm-white, fluorescent lighting (1600 lx) for 7 d of simulated retail display. Trained panelists ($n = 11$) evaluated raw LM color on d 0, 1, and 7. Instrumental (L*, a*, and b*) color was evaluated on d 0, 1, 4, and 7. Thiobarbituric acid reactive substances (TBARS) were measured on d 0 and 7 from LM cross-sections. Consumer sensory panel ($n = 151$) assessed cooked LM sensory attributes. Steer growth did not differ ($P = 0.58$) between dietary S levels. Dietary S did not affect HCW ($P = 0.50$), dressing percentage ($P = 0.44$), USDA yield grade ($P = 0.56$), LM area ($P = 0.36$), or 12th rib fat thickness ($P = 0.66$). Although TBARS were greater ($P < 0.0001$) on d 7 than 0 of simulated retail display, values did not ($P = 0.19$) differ between dietary S levels. No differences were observed in total color ($P = 0.27$) or percent discoloration ($P = 0.42$); however, LM from steers fed 0.40% S were perceived to display greater worst-point color ($P < 0.05$; treatment × day) on d 1 of simulated retail display. Dietary S did not effect a* ($P = 0.50$), b* ($P = 0.61$), or L* ($P = 0.64$). Furthermore, consumers failed to perceive a difference in tenderness ($P = 0.26$), juiciness ($P = 0.61$), overall impression ($P = 0.37$), beef flavor ($P = 0.40$), or off-flavor ($P = 0.79$) between the two dietary S levels. These results suggest that supplementing beef cattle diets with 0.40% S had no appreciable effects on steer performance or beef carcass characteristics, objective color, oxidative stability, and sensory attributes.

Key Words: beef, quality, sulfur

1274 (W161) Effect of β agonist and immunocastration on meat characteristics Nellore cattle.

M. Rezende Mazon[1], S. Luz e Silva[*2], D. Silva Antonelo[1], K. Nubiato[1], D. Juliana Brigida[1], B. Baptista[1], and P. R. Leme[2], *[1]University of Sao Paulo, Pirassununga, Brazil, [2]University of Sao Paulo/FZEA, Pirassununga, Brazil.*

Beta agonists (BAA) have been used to improve feedlot performance and carcass yielding, but some negative effects on meat quality. Immunocastration could be an alternative because increasing fat deposition. Therefore, this work was developed to evaluate the effect of BAA and immunocastration on meat quality traits of feedlot finished Nellore cattle. Ninety-six males (409 ± 50 kg LW; 20 mo old) were divided in two groups, and half of the animals received two doses of immunocastration vaccine (Bopriva) within 30-d interval. Animals were fed during 70 d a common diet containing 76% concentrate and 24% roughage (corn silage). Each of these groups were them splitted in three groups and fed during 30 d: control diet without BAA (CON); CON diet plus 80mg/day zilpaterol hydrochloride (Zilmax) (ZIL); CON diet plus 300mg/day of ractopamine hydrochloride (Optaflexx) (RAC). After 100 d of feeding, animals were slaughtered, and four samples of LM was collected between 12th and 13th ribs and aged for 0, 7, 14 or 21 d. Following aging samples were analyzed for L*, a*, b* color, cooking loss (CL), Warner-Bratzler shear force (WBSF). Data was analyzed as repeated measurements in a block (initial BW) complete randomized design with a 2 × 3 factorial arrangement, considering sex condition, treatment, ageing period and first and second order interactions as fixed effects. Immunocastrated males showed higher values ($P < 0.001$) of L* (36.4 vs. 33.3), a* (14.9 vs. 13.9) and b* (10.0 vs. 8.1) compared to non-castrated. Sex condition did not affect CL (22.2%) or WBSF (4.1 kg). There was a significant sex x aging period interaction ($P = 0.0053$) for WBSF that, different from expected, non-castrated males showed smaller WBSF than immunocastrated for non-aged (time 0) samples (5.2 vs. 6.3 kg; $P = 0.0131$). There was no sex difference for samples aged for 7, 14, or 21 d (4.4, 3.2 and 3.1 kg). Treatments had no effect on L* (34.9, but treatments

CON and RAC showed higher a* values (14.8 and 14.6) than ZIL (13.7; $P < 0.05$). CON had higher b* value than ZIL (9.5 vs. 8.6; $P = 0.0271$), but they did not differ from RAC (9.0). CL was not significantly affected by treatments. The WBSF was greater for ZIL (4.4 kg) than to RAC (4.0 kg) and CON (3.8) treatments. Sex condition affects meat color but has no impact on CL or WBSF. Use of BAA alter color attributes and WBSF of meat from Nellore cattle.

Key Words: feedlot, color, maturation

1275 (W162) The use of bioelectrical impedance analysis to predict carcass composition in calf-fed Holstein steers. N. D. May*[1], T. J. McEvers[1], L. A. J. Walter[1], J. A. Reed[1], J. P. Hutcheson[2], and T. E. Lawrence[1], *[1]West Texas A&M University, Canyon, [2]Merck Animal Health, DeSoto, KS.*

The beef industry relies heavily on subjective evaluation of beef carcasses to quantify carcass composition. Bioelectrical Impedance Analysis may offer the ability to objectively quantify carcass composition in a rapid, repeatable manner and more accurately determine composition of cattle fed growth promotants. Thus, bioelectrical impedance analysis was utilized to estimate the percentage of salable red meat yield (SRMY), fat trim (FT), and bone (BONE) within Holstein ($n = 110$) carcasses supplemented zilpaterol hydrochloride (ZH) or not supplemented (CON). Following a 36-h chilling period, bioelectrical impedance analysis was conducted by placing source and detector electrodes in the semimembranosus muscle posterior to the aitch bone and in the intercostal muscles between the first and third ribs to attain measures of electrical resistance (Rs) and electrical reactance (Xc). Additional measurements of hot carcass weight (HCW), carcass temperature (TEMP), electrode gap (EGAP) were collected to calculate measurements of impedance (I), resistive density (RsD), reactive density (XcD), resistive volume (RsVOL), and reactive volume (XcVOL). Upon completion of measurements, carcasses were subsequently fabricated into subprimal yield components reflective of industry standards (max. fat depth $\leq$ 6mm). Dependent variables of SRMY (52.26 to 67.72%), FAT (10.39 to 29.35%) and BONE (12.03 to 23.11%) were used in multiple linear regression equations. Estimates were calculated via STEPWISE regression methods in SAS (SAS 9.3, SAS Institute, Cary, NC). Predictive models for FT included variables of XcD, TEMP, RsD and EGAP accounted for 72 and 81% ($R^2 = 0.72$ and 0.81) of the variation in CON and ZH cattle, respectively. Moreover, predictive models for BONE included variables of Xc and HCW accounted for 43 and 58% ($R^2 = 0.43$ and 0.58) of the variation in CON and ZH cattle. Percentage of SRMY used variables RsD and XcD and accounted for 54 and 70% ($R^2 = 0.54$ and 0.70) of the variation in CON and ZH cattle, respectively. These results suggest that bioelectrical impedance analysis may serve as a reliable objective measure of carcass composition for concentrate fed Holstein steers.

Key Words: Holstein, impedance, composition

1276 (W163) Increasing levels of sodium benzoate affect myosin heavy chain type expression in cultured bovine satellite cells. J. O. Baggerman*, J. E. Hergenreder, and B. J. Johnson, *Texas Tech University, Lubbock.*

Sodium benzoate is used by commercial bakers to increase tolerance in yeast to calcium propionate, a mold inhibitor. Yeast cell wall is produced during the production of yeast extract from primary grown bakers yeast. While this primary grown yeast is washed before yeast cell wall is produced from the culture, some residual sodium benzoate may be retained. Due to increasing interest in feeding yeast cell wall to feedlot cattle, the present study was conducted to examine the effects of sodium benzoate on bovine muscle satellite cells (BSC). Cultured BSC were grown to confluence and treated with increasing levels of sodium benzoate added to the differentiation media, a negative control, 0.001 μ*M*, 0.01 μ*M*, 0.1 μ*M*, 1 μ*M*, 10 μ*M*, and 100 μ*M*, with four wells per dose. The cells were allowed to differentiate for 48 h and then harvested for RNA and protein analysis. The 1 μ*M* dose increased ($P < 0.05$) the gene expression of AMPKα compared with the 0.001 μ*M* dose and tended ($P < 0.10$) to be greater than the 0.01 μ*M* dose. The 0.1 μ*M* dose tended ($P < 0.10$) to have a greater expression of the AMPKα gene compared with the 0.001 μ*M* dose. Concentrations IGF-1 mRNA were greater in the 0.1 μ*M* dose compared with the control ($P < 0.05$). Among the cultures receiving sodium benzoate, there was a numerical increase of myosin heavy chain (MHC) type I gene expression as concentration of sodium benzoate increased, with the 10 μ*M* and 100 μ*M* doses having greater ($P < 0.05$) gene expression than the control, 0.001 μ*M*, and 0.01 μ*M* doses. The 0.001 μ*M* dose tended ($P < 0.10$) to have a lower abundance of MHC type I mRNA than the 0.1 μ*M* and 1 μ*M* doses. The 100 μ*M* dose had a greater expression of MHC type IIA than the control, 0.001 μ*M*, and 0.01 μ*M* doses ($P < 0.05$). The 10 μ*M* and 100 μ*M* doses had greater ($P < 0.05$) levels of MHC type IIX mRNA compared with the control, 0.001 μ*M*, and 0.01 μ*M* doses. The 0.01 μ*M* dose had a greater ($P < 0.05$) concentration of AMPKα protein than the 10 μ*M* and 100 μ*M* doses. These results indicated sodium benzoate could induce MHC type I expression in cultured BSC.

Key Words: benzoate, myosin, satellite cells

1277 (W164) Surgical castration and immunocastration improve cuts yield of high market value from animals crossbred Aberdeen Angus x Nellore. A. D. Moreira[1], F. D. Resende[2], G. R. Siqueira[3], J. M. B. Benatti[1], M. H. Moretti[4], J. A. Alves Neto[1], B. S. Lima[1], J. F. Lage[*1], G. Z. Miguel[5], P. H. Gonçalves[6], and F. D. Santos[6], *[1]Universidade Estadual Paulista, Jaboticabal, Brazil, [2]Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [3]APTA-Polo Regional Alta Mogiana, Colina, Brazil, [4]UNESP-FCAV, Jaboticabal, Brazil, [5]Universidade do Estado de Mato Grosso, Pontes e Lacerda, Brazil, [6]Centro Universitário da Fundação Educacional de Barretos, Brazil.*

This trial aimed to evaluate the effect of castration methods (surgical or immunological) on percentage of main cuts from hindquarter of beef cattle raised in pasture. Thirty animals 1/2 Angus × 1/2 Nellore with 233.0 ± 38.2 kg of initial BW and 8 mo of age were fed in pasture of *Brachiaria brizantha* cv. Marandu receiving 3 g/kg BW/day of proteic-energetic supplement (25% crude protein and 60% of total digestible nutrients). Animals were supplemented for 356 d (20 d for adaptation and 336 d of experimental period (July 21, 2011, to July 11, 2012). The treatments comprised 10 replicates: non-castrated animals (NC); surgical castrated (SC) and immuno-castrated (IC). The surgical castration was realized on last day of adaptation period and the immunocastration was realized with Bopriva (anti-GnRH) being applied on the first day, 84 and 237 d after beginning of the experiment. The animals were slaughtered and all carcasses were chilled at 0°C for 24 h. After slaughter were recorded the carcass weight (CW; hot and cold) and carcass shrink loss (CSL). Cuts from left carcass (Rib Eye, Striploin Back Chain, Rump Heart, RumpCap e Tenderloin Chain) were removed and weighed. These cuts are considered of high market value in Brazil. Data were analyzed (randomly design) by the PROC MIXED of SAS and the Fisher test used considering 10% probability. Animals NC had greater final hot CW (281.8 kg; $P < 0.001$) and cold CW (278.3 kg; $P < 0.001$) than those animals SC and IC. However, the castration methods did not affect the hot and cold DP ($P > 0.10$). Animals NC had higher CSL (1.26%; $P = 0.024$) than those animals SC (0.76%) and IC (0.87%). Animals castrated showed greater hindquarter yield (47.8%; $P = 0.003$) than animals NC (46.3%). The total weight (sum of all cuts evaluated) in relation the total weight of hindquarter was not affect by castration methods ($P > 0.10$). However, when these sum of all cuts were realized in relation to cold CW had greater percentage these cuts of hindquarter from both animals castrated than animals NC ($P = 0.049$). A greater commercial cuts yield from hindquarter in the carcass is profitable in a beef cattle market. The castration methods evaluated in the animals produces carcass with greater commercial cuts yield from hindquarter in relation to cold carcass weight.

Key Words: anti-GnRH, commercial cuts, yield carcass

MILK PROTEIN AND ENZYMES

1278 (T167) Separation and quantification of major milk proteins in different species by reversed phase high performance liquid chromatography. L. Ma, D. P. Bu*, J. Q. Wang, and J. T. Chen, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

To detect milk proteins, reversed phase high performance liquid chromatography (RP-HPLC) (Waters 2695 Series chromatograph, USA) was successfully performed to separate and quantify the major proteins from cow (n = 20), goat (n = 20), buffalo (n = 20) and yak (n = 20) milk which were collected around the fourth month of lactation for each species from February to April 2013 within 30 min. Descriptive statistics and Duncan's multiple comparison of protein contents were obtained by SAS 9.1 via GLM model (SAS Institute Inc., Cary, NC). Main protein data sets were analyzed by PCA using the Unscrambler 9.8 (CAMO software AS, Oslo, Norway). Results showed that the contents (g/L) of milk total protein were significantly different in milk from yak (62.87), buffalo (56.09), goat (42.83), and cow (37.35), respectively. Average content of major protein fractions obtained were all converted by purity of individual protein standard (Sigma-Aldrich, St. Louis, MO) to assess the real individual protein content. Composition (g/L) of yak milk contained the highest κ-CN content (9.80), and this was significantly higher than in buffalo, cow, and goat milk (7.35, 6.24 and 5.56). Content (g/L) of α-CN in yak milk (16.14) was significantly higher than those for buffalo, cow, and goat milk (11.53, 11.81, and 9.48). The β-CN content (g/L) was similar in yak and buffalo milk (23.34, 22.68), but higher than in goat and cow milk (20.53, 13.31). The β-LgB quantification (g/L) in goat and buffalo milk was similar (3.69, 3.88), significantly lower than in yak milk (9.46), but higher than in cow milk (1.19). The α-La content (g/L) was highest in buffalo milk (7.96), while significantly lower in cow, goat, and yak milk (1.45, 1.28 and 1.47). Cow milk contained highest content (g/L) of β-LgA (2.15), and this was significantly higher than that in buffalo, yak, and goat milk (0.13, 0.12 and 0.14). And different chromatographic profiles were obtained for them. The data of milk protein can be differentiated according to animal species by principal component analysis (PCA). It was concluded that major milk proteins from different animals had special profiles.

Key Words: milk protein, reversed phase high performance liquid chromatography, species

1279 (T168) Size distribution of casein micelles in milk from dairy cows with different crossbreding levels of Holstein-Zebu cattle. D. R. Freitas[1], M. M. Santoro[1], F. N. Souza[1], C. V. Ladeira[1], M. O. Leite[2], C. F. A. M. Penna[2], S. A. Diniz[1], M. X. Silva[1], J. P. Haddad[1], L. M. Fonseca[1], and M. P. Cerqueira[*2], *[1]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, [2]Universidade Federal de Minas Gerais (School of Veterinary Medicine), Belo Horizonte, Brazil.*

Over the years, there has been an increasing interest in milk casein, because of their industrial importance. Casein micelle structure is crucial for gel formation in cheese and yogurt, and it is correlated with milk stability after of heating, freezing or drying. The present study evaluated the casein micelles mean size distribution in raw milk from crossbred Holstein-Zebu dairy cows, as follows: 1/2 Holstein-Zebu (n = 41); 9/16 Holstein-Zebu (n = 21); 5/8 Holstein-Zebu (n = 31); 3/4 Holstein-Zebu (n = 29); 7/8 Holstein-Zebu (n = 51); and 15/16 Holstein-Zebu (n = 27). The milk composition (protein, lactose, fat, nonfat and total solid contents), somatic cell count score, age, d in milk, and milk production were also recorded. Size of casein micelles was determined by Photon Correlation Spectroscopy (PCS) after milk fat removal by centrifugation. The mean size of the casein micelles was 170.22 + 21.18 nm (121.8– 235.6 nm). The logistic regression analysis was adjusted ($P < 0.20$) for days in milk, crossbreeding levels of Holstein-Zebu cattle, age, milk production, somatic cell count score, urea levels, fat, protein, lactose, and nonfat milk solids. The final model of the logistic regression analysis ($P < 0.05$) showed that the mean size of the casein micelles was associated with the crossbreeding levels of Holstein-Zebu cattle (odds ratio: 0.27; $P = 0.001$), somatic cell count score (odds ratio: -1.40; $P = 0.001$) and nonfat contents (odds ratio: −6.55; $P = 0.033$). To the best of our knowledge, this is the first study that access the effect of the crossbreeding levels of Holstein-Zebu on the mean diameter of casein micelles. This fact has important implications to production of milk-based products, and thus economic output of the dairy industry.

Key Words: casein, milk quality, raw milk

1280 (T169) Comparative analysis of immunoglobulin and lactoferrin in bovine milk from different species. J. T. Chen[1,2], L. Ma[1], J. Q. Wang[1], Y. X. Yang[1], and D. P. Bu[*1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China.*

Immune active components in milk play an important role in the host defence. Bovine milk from different speices has its own character. The objective of the current study was to char-

acterize the concentrations of immunoglobulins (IgA, IgG, IgM) and lactoferrin in bovine milk samples of different species. Sandwich enzyme-linked immunosorbent assay (ELISA) was performed according to the manufacturers instructions to quantify the immunoglobulins and lactoferrin (Lf) contents in yak milk (n = 20), buffalo milk (n = 20) and Holstein cow milk (n = 20) samples, and correlation analysis was completed. The results showed that immunoglobulins and lactoferrin in yak milk, buffalo milk, and Holstein cow milk samples had linear relationsship between concentration and absorbance values, and the standard curve equation R was greater than 0.99. There were significant differences of IgA, IgG, IgM and Lf in different milk samples ($P < 0.05$). The contents of IgA, IgG, IgM and Lf in different species bovine milk samples showed remarkable individual differences. IgA and IgG concentrations in yak milk were significant higher than in the other two kinds of milk. While IgM and Lf in Holstein cow milk were higher than others. In addtion to negative correlation between IgA and IgM existed only in Holstein cow milk samples, the trends of IgA, IgG, IgM and Lf in the same kinds of bovine milk all showed a positive correlation. The results indicated that the content of immunoglobulins and lactoferrin in different species milk samples were influenced by genetic factors and had distinctive characteristics. According to the correlation of immunoglobulins and lactoferrin, forecasting the content of immunoglobulins and lactoferrin within species may be possible.

Key Words: bovine milk, immunoglobulin, lactoferrin

1281 (T170) Effect of thermal conditions on the concentration of biological active whey protein in cow milk.

J. T. Chen[1,2], L. Ma[1], D. P. Bu[1], Y. X. Yang[1], and J. Q. Wang[*1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China.*

Biological active whey protein in cow milk play an important role in the health of human, which is sensitive to thermal conditions during dairy processing. The objective of the present study was to investigate the variation of mainly immune active proteins concentration in cow milk, which was heated by reference commercial pasteurized milk processing technical specification of China dairy industry standards. The contents of the immunoglobulins (IgG, IgM, IgA), lactoferrin (Lf) and bovine serum albumin (BSA) were determined after different thermal processing by Sandwich enzyme-linked immunosorbent assay (ELISA), respectively. The results showed that pre-heat treatment and homogenizing had relatively mild effects on immune active protein concentration. From 75 to 115°C with holding times for 15 sec, immune active proteins contents were decreased significantly. The concentration of immune active proteins remained fairly constant and lightly decreased over time when heating temperature maintained at 85°C. Immune active proteins contents were extremely low and the diversity among different treatments was small at heating temperatures ranging from 125 to 145°C for 4s. When heated at 138°C for 4s, 6s and 8s, concentrations of immune active proteins had shown no significant difference. When milk heated at UHT and superheated conditions, treatment of raw milk at 140°C for 4s had a relatively higher content. These finding indicated that the appropriate condition of pasteurization heating at 75°C for 15s, and treatment at 140°C for 4s are fit for UHT processing. Moreover, there is no need for superheated which has no benefit for dairy nutritional properties.

Key Words: cow milk, biological active whey protein, heat-stability

---

1282 (T171) Effect of extraction methods on the 2-DE map of whey proteome in cow milk.

J. T. Chen[1,2], L. Ma[2], D. P. Bu[2], Y. X. Yang[2], and J. Q. Wang[*1,2], *[1]Heilongjiang Bayi Agricultural University, Daqing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

For all proteomic approaches, protein extraction and sample preparation are the most critical steps for optimal results. However, protein isolation is often complicated. The objective of this study was to investigate the effect of extraction methods on two-dimensional electrophoresis (2-DE) maps of whey proteome in cow milk and explore an optimal eatraction method. Samples were extracted from cow milk by different isoelectric precipitations and ultracentrifugation methods. SDS-PAGE and 2-DE maps were analysised by QuantityOne v4.62 and PDQuest 8.0 software, respectively. The results of 2-DE maps showed that milk whey protein could be effectively extracted by the methods above with less background, no significant strips and good repeatability. However, there were still some residual caseins appearing in each map. 2-DE maps of whey protein refined by isoelectric precipitations were relatively informative compared with the gel maps obtained by ultracentrifugation. Moreover, the richness of different whey proteins in various maps extracted by the method adjusting pH to 4.6 as isoelectric point is slightly higher than adjusting pH to 4.8. The results indicated that adjusting pH to 4.6 as isoelectric point to extract whey protein has some advantages than the other two methods. However, all the methods used in this research could effectively remove high abundant casein to improve the detection sensitivity of low abundance proteins, which could provide some useful information for the futher research on whey protein proteomic of cow milk.

Key Words: whey protein, extraction methods, two-dimensional electrophoresis maps

1283 (T172) Effect of metabolic acidosis in lactating dairy cows on concentration of milk proteins.

C. M. de Magalhães Rodrigues Martins, K. C. Welter, M. A. Arcari, C. A. Fernandes de Oliveira, J. L. Golçalves, V. L. Schvartzaid, A. Saran Neto*, and M. Veiga dos Santos, *University of São Paulo, Pirassununga, Brazil.*

Milk casein subunits (α, β and κ-casein) play a role to avoid the formation of toxic amyloid fibrils and maintain the milk thermal stability. When milk is produced by healthy cows fibrils are not formed because an alternative aggregation pathway is followed that results in formation of the casein micelle. However, nutritional disorders of lactating cows may negatively influence on composition and quality of milk. Thus, the present study aimed to evaluate the effect of the dietary cation-anion difference on concentrations of milk subunits of casein and whey proteins. Sixteen Holstein cows were distributed in four contemporary 4 × 4 Latin square, consisting of four periods of 21 d. Cows were distributed to four treatments according to the dietary cation-anion difference (DCAD): 1) +290 mEq/kg of DM; 2) +192 mEq/kg of DM; 3) +98 mEq/kg of DM; 4) −71 mEq/kg of DM. The cows were fed total mixed ration and the DCAD was calculated according to the contents of Na, K, Cl, and S of the diets. Individual milk samples were collected for determination of the concentrations of α (α-CN), β (β-CN) and κ-casein (κ-CN), α-lactalbumin (α-La) and β-lactoglobulin (β-Lg), by high performance liquid chromatography. The results were analyzed using the PROC MIXED of SAS (2001) (α = 0.05). The DCAD reduced linearly the concentration of κ-CN [κ-CN = 5.02(0.30)–0.00098(0.0004)*DCAD] as well as increased the concentration of β-LG [β-LG = 1.41(0.16) + 0.00047(0.0002)*DCAD] (Table 1283). The κ-CN and β-LG have a potential tendency to assemble into toxic amyloid fibrils. Thus, as a consequence of metabolic acidosis due to reduction of DCAD, β-LG may be associated with the κ-CN in the micelle and the milk stability during the heat treatment may be reduced.

Key Words: casein, DCAD, milk stability

Table 1283. Effect of dietary cation-anion difference (DCAD) on the milk proteins concentration (mg/ml of milk)

Milk proteins	DCAD (mEq/Kg of DM)					*P*		
	-71	98	192	290	*SEM*	*Linear*	*Quadratic*	*Cubic*
α-CN	6.38	6.36	6.52	6.17	0.12	0.404	0.165	0.118
β-CN	7.34	7.29	7.38	7.10	0.19	0.423	0.482	0.449
κ-CN	5.07	4.96	4.95	4.68	0.15	**0.031**	0.361	0.478
β-LG	1.41	1.45	1.46	1.59	0.08	**0.040**	0.330	0.539
α-LA	0.84	0.76	0.74	0.77	0.05	0.115	0.172	0.815

1284 (T173) Process optimization for production of whey protein hydrolysate from cheese whey having antioxidant property.

S. Athira*, B. Mann, R. Sharma, and R. Bajaj, *National Dairy Research Institute, Karnal, India.*

Oxidative stress, the increased production of reactive oxygen species and reactive nitrogen species combined with overtaking endogenous antioxidant defense mechanisms, is a significant causative factor for the initiation or progression of several life style mediated diseases. Dietary consumption of antioxidants appears to benefit endogenous antioxidant defense strategies in the fight against oxidative stress. Cheese whey is a rich by-product in nutritional terms: possessing high biological value components, excellent functional properties, and an inert flavour profile. In particular, biological activities of whey proteins and their hydrolysates have received more attention in recent years. Peptides generated from whey protein hydrolysis have antioxidant properties and it depends on the protease specificity as well as hydrolysis conditions. Currently, data on the hydrolysis conditions for the direct production of hydrolysate from whey is lacking. So in the present study, mozzarella cheese whey was ultrafiltrated to concentrate the protein content and the retentate after preheat treatment was hydrolyzed using commercial food grade enzyme alcalase. Response Surface Methodology (RSM) was applied to optimize the hydrolysis conditions, including incubation time, hydrolysis temperature and pH with the purpose of obtaining the most powerful antioxidant hydrolyzate from whey proteins. A central composite circumscribed (CCC) design was employed to study the effect of the experimental variables on the antioxidant activity determined by 2, 2'-azinobis (3-ethylenebenzothiazoline-6-sulphonic acid) ($ABTS^{\cdot+}$) radical scavenging activity and the parameters of the model were estimated by multiple linear regression. The highest antioxidant activity (1.18 ± 0.015μM of trolox/mg of protein) was found in retentate hydrolyzed for 8 h at pH 9 and temperature 55°C. Seven β-lactoglobulin derived peptides were identified by RP-HPLC-MS/MS in this hydrolyzate. Amino acid composition of the peptides DTDYK f(96–100) and VLDTDYK f(94–100) indicating their important contribution on antioxidant property of whey protein hydrolysate (WPH) was evaluated. Hydrolysis of ultrafiltrated retentate of whey can be an energy and cost effective method for the direct production of WPH from whey compared to the industrial production of WPH from Whey protein concentrate. This study suggests that WPH with good nutritional and biological properties can be effectively used in health promoting foods as a biofunctional ingredient.

Key Words: whey protein hydrolysate, antioxidant property, bioactive peptides

1285 (T174) The effect of heat and extraction technique on β-lactoglobulin hydrolysis. C. Kembel[*1], and R. Jimenez-Flores[2], *[1]California Polytechnic State University, San Luis Obispo, [2]Dairy Products Technology Center, California Polytechnic State University, San Luis Obispo.*

Whey proteins are an abundant source of biologically active peptides that have a diverse set of properties. One limitation in the production of novel peptides is the native folding of the proteins secondary and tertiary structure. β-Lactoglobulin is a barreled protein with a hydrophobic core capable of binding other proteins and fatty acids. Due to its prevalence in whey, it represents an important source of bioactive peptides. Presenting a method for the production of novel peptides by native whey protein change in conformation will bring value added products to market. Previous studies have shown the resistance of isolated, native, β-lactoglobulin to trypsin hydrolysis in protein-lipid emulsions. However incorporation of washed cream (40% fat) into this system (natural emulsion from cream) significantly changes the hydrolysis patterns of β-lactoglobulin. The hydrolysis patterns of β-lactoglobulin was evaluated using electrospray ionization mass spectrometry (ESI-MS) after three heat treatments (none, 50°C– 20 min, and 70°C–20 minutes) and four extraction methods (none, supercritical carbon dioxide, hexane, and Folch). Although hydrolysis was improved compared to native β-lactoglobulin, the degree of hydrolysis did not exceed 42% in any of the treatments. Substitution of purified native β-lactoglobulin with whey protein isolate (WPI) in the 40% cream solution significantly increased the number and type of β-lactoglobulin peptides released when subjected to various heat treatments and fat extraction methods. The degree of hydrolysis reached a maximum 64% and there appeared to be sequential, predictable peptide release depending on the heat treatment and extraction technique used. The heat treatment and extraction method change the absorption and spreading process of β-lactoglobulin within and along the MFGM and thus, effecting which peptides are available and released by the enzymatic action.

Key Words: β-lactoglobulin, peptides, mass spectrometry

1286 (T175) Evaluation of the viscosity profile during simulated conditions of thermal processing. A. Souza[1], L. C. Junior[2], R. Stephani[1], M. Pinto[3], A. Carvalho[*3], Perrone[3], and R. Costa[2], *[1]Gemacom Tech, Juiz de Fora, Brazil, [2]EPAMIG, Juiz de Fora, Brazil, [3]Federal University of Viçosa, Brazil.*

The understanding about milk protein interactions provides better cost/benefit ratio to food industry by using each type of protein within the desired characteristics in final product. Denaturation and interaction of different proteins occur in different way and intensity when pH value varies accordingly to the medium in which they are located. This study aimed to verify the influence of whey protein/casein interaction in the evolution of viscosity at different pH (6.0, 6.5 and 7.0) values using the Rapid Viscosity Analyzer (RVA) (model 45000, Perten Instruments, Sweden) as thermal processing simulator. Samples of commercial whey protein concentrate (WPC) and milk protein concentrate (MPC) were analyzed. Thermal denaturation and level of protein interaction were measured by RVA. Further, fat, protein, ash, lactose, pH, protein concentration and moisture were performed according to procedures described by the Association of Analytical Communities (AOAC, 2005). The solid-liquid concentration of the dispersion measured in the RVA was 0.3 gg^{-1} dry weight in water. Viscosity was as low as possible in low pH and high MPC/WPC level. At pH 7.0 and 100% whey protein concentrate results in higher final viscosity. At pH 6.0 and 100% milk protein concentrate results in lower final viscosity. High viscosity can be related with favoured κ-CN-whey protein complex formation at high pGH (Anema, 2008). Further, increased viscosity in treatments with high proportion of WPC can be explained by the difference in size of aggregates formed between whey proteins and/or κ-CN-whey proteins and by the higher degree of denaturation at higher pH values. References: (1) Anema, S.G. On heating milk κ-casein from the casein micelles can precede interactions with the denatured whey proteins. Reference: *Journal of Dairy Research,* 75, p. 415–421, 2008; (2) AOAC International. Official Methods of Analysis of AOAC International. United States, 2005.

Key Words: protein denaturation, pH, RVA

1287 (T176) Viscosity measurement of solutions composed by whey protein using a rapid viscosity analyser (RVA). M. Alves[1], M. Martins, P. H. Junior, R. Moreira, G. Mendes, M. Pinto, Perrone, and A. Carvalho[*], *Federal University of Viçosa, Brazil.*

The evaluation of the viscosity performance of protein solutions used as ingredients in food is essential for this application in the food production. The Rapid ViscoAnalyzer (RVA) is a rotational viscometer capable of continuously measuring the viscosity of a sample under controlled temperature conditions (Booth & Bason, 2007). Using a RVA, the current study aimed to evaluate the viscosity of solutions prepared from whey protein concentrates (WPCs) produced from milk whey samples initially subjected to thermal treatment 72°C for 15 s (*P*T72) or microfiltration (0.8 μm- MF0.8 or 1.4 μm- MF1.4). Each treatment was ultrafiltered and subjected to vacuum evaporation using a rotary evaporator and dried in a spray dryer. The resulting WPCs were evaluated for their content of fat, total solids, moisture, ashes, and total protein. Furthermore, water activity (Aw) of each WPC was measured. The solutions prepared from the WPCs were also evaluated for their viscosity. Data analysis was performed using Statistical Analysis System v9.2 software (SAS Institute Inc., 2006). The WPCs presented

composition compatible with the international standards, with a significant difference ($P < 0.05$) for fat concentration. Viscographic profiles indicated that WPCs produced from microfiltered whey had higher viscosities than those subjected to heat treatment. In addition, 10 min was determined to be the optimal length of time for heat treatment to maximise WPCs viscosity. The WPC solutions obtained from pasteurized whey showed lower viscosities than solutions obtained from microfiltration whey. This result demonstrates the importance of technological choices on the behavior of the WPC and further, WPC can be design for different food applications. Finally, a rapid viscosity analyzer was demonstrated to be an appropriate tool to study the application of whey proteins in food systems.

Key Words: milk protein, microfiltration, RVA

NONRUMINANT NUTRITION: AMINO ACID, MINERAL AND ENERGY NUTRITION IN MONOGASTRICS

1288 (M162) Calcium level and dEB affect the protein and mineral digestibility of lactating sows.
R. Davin[*1], S. A. Guzmán-Pino[1], D. Solà-Oriol[2], E. G. Manzanilla[1], and J. F. Pérez[1], [1]*Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain,* [2]*Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain.*

Limestone ($CaCO_3$) and sodium bicarbonate are included in pig diets to supply Ca and increase dietary electrolyte balance (dEB = Na + K– Cl, in mEq/kg diet), respectively. However, both ingredients increase the diet acid-binding capacity and may interfere with the phytate-protein and phytate-Zn complex in the digestive tract. The aim of this study was to assess if diets differing in Ca level and dEB may affect the whole-tract apparent digestibility in lactating sows fed on a typical European sow diet (25.0% corn, 20.0% barley, 20.0% wheat, 18.3% soy meal, 10.0% wheat bran, 2% rapeseed meal) containing a high phytic acid level (2.9 g phytic P/kg), and supplemented with an overdose of phytase (1260 FTU/kg). A total of 48 lactating sows (14 d of lactation) were distributed according to their parity number and number of piglets into six experimental diets (2 × 3 factorial) differing in the Ca level: 6 or 9 g/kg (lowCa or highCa, respectively), and dEB: 40, 176 or 235 mEq/kg (lEB, mEB or hEB, respectively). Calcium chloride (10 g/kg) was added to lEB diets. The rest of Ca was provided as $CaCO_3$. Sodium bicarbonate was added (5 g/kg) to hEB diets. Titanium dioxide (3 g/kg) was used as indigestible marker. Diets were offered ad libitum for 7 d. Two fecal samples were obtained in two different times on d 21 of lactation for each sow and then pooled. Blood samples from sows fed highCa diets were individually collected on Day 21 to measure acid-base status of the sows. Sows fed highCa diets showed higher ($P < 0.05$) digestibility of CP (87.4%), Ca (21.4%), P (45.2%), and Zn (20.9%) than sows fed lowCa diets (85.8, 14.3, 40.8 and 7.04%, respectively). The use of sodium bicarbonate in lowCa diets (hEB) decreased ($P < 0.05$) DM digestibility as compared to the lowCa-mEB and the three highCa diets. The lBE diet reduced blood pH, bicarbonate and base excess values as compared with mBE and hBE ($P < 0.05$). In conclusion, the results showed that low Ca diets and sodium bicarbonate may reduce nutrient whole-tract digestibility in lactating sows fed on high phytic acid diets, even when phytase was overdosed.

Key Words: calcium, dietary electrolyte balance, digestibility

1289 (M163) Early dietary amino acid restrictions and flaxseed oil supplementation on the leanness of pigs and quality of pork: growth performance, serum metabolites, and carcass traits.
C. K. Adhikari[*1], L. I. Chiba[1], S. D. Brotzge[1], M. D. S. Vieira[2], S. P. Rodning[1], W. G. Bergen[1], C. L. Bratcher[1], and E. G. Welles[1], [1]*Auburn University, Auburn, AL,* [2]*Federal University of Rio Grande do Sul, Porto Alegre, Brazil.*

A total of 64 pigs were used to assess the effect of early dietary AA restrictions [100 or 80% of the 2012 NRC standardized ileal digestible (SID) Lys requirements during the grower (G) and finisher (F)-1 phases] and lipids (0 or 3% flaxseed oil + 2% poultry fat) on G-F pig. Each phase was based on weight, and at 24.7 ± 0.5 kg, pigs were assigned to 4 G diets with 4 gilt pens and 4 barrow pens/diet, and switched to F-1 diets when they reached 51.2 ± 0.3 kg. Pigs were switched to common F-2 diets at 80.0 ± 0.4 kg, and pigs fed 0 or 5% lipids earlier were continued to receive 0 or 5% lipids until harvest at 110.5 ± 0.5 kg. There were no interactions between dietary AA restrictions and lipids. Pigs fed the AA restricted diets consumed less SID Lys and DE ($P < 0.015$) and had depressed ADG compared with unrestricted pigs during the G phase, but they grew faster ($P = 0.042$) and utilized feed ($P = 0.064$) and SID Lys ($P < 0.001$) more efficiently during the F-1 phase. Dietary AA restrictions had no effect on overall ADG or carcass traits. Overall efficiency of feed, SID Lys, and DE utilization for BW gain ($P < 0.004$) and SID Lys utilization for fat-free lean gain (FFLG; $P < 0.001$) was improved by dietary AA restrictions. Dietary AA restrictions reduced serum urea N ($P < 0.025$) at the end of the G and F-1 phases and increased glucose ($P = 0.027$) at the end of the G-phase, but had no clear effect on triglycerides (TG) and other metabolites. Dietary lipids reduced ADFI ($P < 0.064$) during the G and F-2 phases, improved G:F ($P < 0.047$) during all phases and overall, and improved ADG during the G ($P = 0.003$) and F-1 ($P = 0.066$) phases. Belly firmness was reduced ($P < 0.001$), but dietary lipids had no effect on other carcass traits. Dietary lipids increased TG ($P < 0.075$) at the end of the G and F-1 phases, but reduced urea-N ($P = 0.037$) at the end of the F-2 phase. In conclusion, pigs subjected to early dietary AA restrictions improved overall efficiency of AA and DE utilization for BW gain and FFLG. As expected, dietary lipids improved G:F but reduced belly firmness.

Key Words: early amino acid restrictions, flaxseed oil, pigs

1290 (M164) Effects of supplementation with a commercial source of selenium in a laying hens feeding system. L. Betancourt*, *Universidad de La Salle, Bogotá, Colombia.*

Selenium enriched eggs are included as functional food in the market, because the role of selenium in human health and diseases has been recognized. The objective of this study was to enrich eggs with selenium from an organic source of selenium (seleno-yeast) on production parameters, egg quality and Leukocyte differential counts. Six hundred thirty laying hens of the Babcock line were used, between 27 and 65 wk of age. Hens were kept in cage and randomly distributed into two treatments with five replicated. The control treatment (T0) based on commercial feed without addition of seleno-yeast, and T1 treatment, based on commercial feed plus 450 ppm of seleno-yeast (1000 ppm selenium Kg-1). The eggs were lyophilized and selenium was measured through a plasma spectrophotometer ICAP 6300. The egg production and classification was recorded weekly, laying percentage and the feed conversion ratio were calculated. Egg tasting and conceptual evaluations were done. The egg selenium content was higher ($P < 0.05$) for T1 group with 1.376 mg kg-1 of lyophilized egg compared with T0 with 0.173 mg kg-1of lyophilized egg. The addition of selenium did not significantly affect the egg production. The egg production percentage was 94.6 ± 3.88 and 95.2 ± 5.15; and the feed conversion ratios were 1.49 ± 0.061 and 1.48 ± 0.082 for T0 and T1, respectively. Therefore, leukocyte differential counts were not affected. The heterophile: lymphocyte ratios were 1.22 ± 0.31 and 1.58 ± 0.45 to T0 and T1 treatments, respectively. Egg organoleptic characteristics such as taste, color and texture, did not presented differences. This study confirmed that it is possible to enrich the content of selenium in eggs under an egg commercial production system without affecting the growth performance and the organoleptic characteristics. The cost of feed with selenio-yeast inclusion did not exceed the 1%, thus producing selenium enriched eggs is technically feasible to improve consumer health and competitiveness of the poultry industry.

Key Words: antioxidant, egg, glutathione

1291 (M165) Correlating molecular spectroscopy and chemometrics to explore carbohydrate utilization of co-products from bio-fuel and bio-brewing processing. L. Chen[1,2], X. Zhang[1], X. Huang[*2], and P. Yu[2], *[1]Dep. of Animal Science, Tianjin Agricultural University, China, [2]Dep. of Animal and Poultry Science, University of Saskatchewan, Saskatoon, Canada.*

Co-products from bioethanol and brewing industry are excellent resources of protein and energy. Conventional studies often focus on traditional "wet" nutritional profiles. To date, there is little research on the relationship between carbohydrate molecular structural and nutritional values of the co-products. In this study, five kinds of corn DDGS and two kinds of barley DDGS with different batches were collected from different manufacturers in the north of China. The objectives of this project were to investigate the correlation between carbohydrate molecular structure and nutritional values, in terms of the carbohydrate chemical profile, true digestible nutrient, energy values, and digestion. The result showed that acid detergent fiber content in corn DDGS and barley DDGS had negative correlation ($P < 0.05$) with structural carbohydrate peak area, cellulose compounds, and carbohydrate component peaks. The correlation between carbohydrate peak area and true digestible neutral detergent fiber (tdNDF) were negative ($P < 0.05$). Spectral peak area of cellulose compounds, carbohydrate peak area had negative correlations ($P < 0.05$) with the dry matter content. There were no correlation between carbohydrate spectral intensities and energy values, carbohydrate sub-fractions partitioned and digestion. The results indicate that carbohydrate spectral profiles are highly associated with carbohydrate utilization in co-products from bio-fuel and bio-brewing processing.

Key Words: carbohydrate nutritional values, molecular spectral features, carbohydrate molecular structure

1292 (M166) Phosphorus utilisation and sodium-dependent phosphate co-transporters gene expression in growing pigs fed low available phosphorus diets. B. B. Pokharel[*1], C. M. Nyachoti[2], and W. K. Kim[3], *[1]Dep. of Animal Science, University of Manitoba, Winnipeg, Canada, [2]University of Manitoba, Winnipeg, Canada, [3]University of Georgia, Athens.*

Type II sodium-dependent phosphate co-transporters (NaPi) encoded by the SLC34A gene family are involved in renal and intestinal phosphate (Pi) absorption to maintain plasma Pi content. However, the effects of reduced dietary phosphorus (P) content on the expression of these genes and P utilisation in growing pigs are poorly defined. Thus, an experiment was conducted with 54 growing pigs (19.5 ± 1.11 kg BW) to examine the effects of reduced dietary available phosphorus (aP) content on P utilisation and NaPi gene expression. Pigs housed in groups of three per pen were randomly allotted to three experimental diets containing 0.23 (control), 0.17, and 0.11% aP to give six observations per diet and had ad libitum access to feed and water. All diets contained 0.3% TiO_2 as an indigestible marker. After each wk, one pig per pen was housed in a metabolic crate for 24 h to collect fecal and urine sample and then sacrificed to obtain jejunal and kidney sample. Fecal and urine sample were subsampled and analysed for P content. Expression of NaPi co-transporter genes (NaPi-IIb in jejunum, NaPi-IIa and NaPi-IIc in kidney) was analysed using quantitative real-time polymerase chain reaction (qRT-PCR). The expression of the NaPi-IIb gene in the jejunum was enhanced up to 250% ($P < 0.01$) in first wk of

pigs fed diet with 0.11% level of aP compared to the other dietary treatments. During wk 1, 2, and 3, the digestibility of P was lower ($P < 0.05$) in pigs fed diet with 0.11% level of aP (28.23, 27.14 and 23.33%, respectively) compared to control (39.07, 37.71 and 41.51%, respectively). Expression of NaPi-IIa and NaPi-IIc gene in kidney was enhanced ($P < 0.05$) by up to 160 and 180%, respectively, in wk 2 in pigs fed 0.11% aP diet. Urinary P was lower ($P < 0.05$) in pigs fed 0.11% aP diet (26.03 mg/L) compared to control (85.3 mg/L) in wk 3. In conclusion, dietary P content affected NaPi gene expression and P utilisation. Enhanced expression of NaPi-IIb in jejunum was seen in earlier period of reduced aP diets followed by higher expression of NaPi-IIa and NaPi-IIc in kidney later on. NaPi-IIb was not directly associated with the jejunal P uptake suggesting either post-transcriptional regulation or very low amount of aP for intestine to be able to pick up.

Key Words: sodium-dependent phosphate co-tranporters, pigs, available phosphorus

---

1293 (M167) The impact of an inflammatory challenge and dietary omega-6 to omega-3 fatty acid ratios on protein deposition in nursery pigs. L. Eastwood* and D. Beaulieu, *Prairie Swine Centre, Inc., Saskatoon, SK, Canada.*

The objective of this experiment was to determine if decreasing the dietary omega (ω)-6 to ω-3 fatty acid ratio would affect protein deposition in nursery pigs during a prolonged *E. coli* lipopolysaccharide (LPS) inflammatory challenge. Twenty-four barrows were assigned to one of four treatment groups at 21 d of age (d 0). Treatments, arranged as a 2 × 2 factorial, were diets (10:1 and 5:1 ω-6:ω-3 plant based FA ratios) and challenge (LPS injection, *ad lib* intake; or saline injection, pair fed to match LPS injection intake levels). On d 15 and 18, pigs were injected with 15 µg/kg BW LPS in saline or saline alone. On d 21, 1.5 h post-feeding, pigs were given a flooding dose of ^2H_2O and at 2.5 h post-feeding received another LPS or saline injection. Following the final injection, pigs were slaughtered (5.5 h post-feeding). Liver, semi-tendinosus muscle and blood samples were collected, and the remaining carcass was ground and analyzed for N and DM. Whole carcass protein deposition was determined relative to an initial slaughter group of pigs. Liver, muscle and blood samples were analyzed for ^2H_2O enrichment to determine the fractional rate of protein synthesis (FSR) during final day of the LPS challenge. ADFI (d 0 to 15) was unaffected by diet ($P > 0.05$); however 5:1 fed pigs tended to have higher ADG relative to the 10:1 fed pigs (28.8 vs. 25.0 ± 1.4 g/d; $P = 0.06$). Pigs consuming the 5:1 diet, regardless of challenge group, had higher whole body protein deposition rates for the 3 wk period relative to pigs consuming the 10:1 diet (87.8 g/d vs. 61.3 g/d; $P = 0.04$). Similarly, 5:1 fed pigs tended to have increased FSR in the liver on the final day of the challenge relative to those consuming the 10:1 diet (8.55% synthesized/h vs. 6.16%/h; $P = 0.08$). There was no effect of LPS challenge on carcass composition, protein deposition rate or on liver or muscle FSR measured using ^2H_2O enrichment ($P > 0.05$). Protein deposition measured over time and on the final challenge day (FSR) provided similar results. This experiment shows that altering the FA ratio in nursery pig diets can alter the efficiency by which the animal utilizes nutrients for growth, as evidenced by similar feed intakes but improved ADG and protein deposition rates.

Key Words: Swine, omega-3, protein synthesis

1294 (M168) Phosphorus digestibility in high protein canola meals, conventional canola meal, and soybean meal fed to growing pigs. C. K. Parr*, Y. Liu, C. M. Parsons, and H. H. Stein, *University of Illinois at Urbana-Champaign, Urbana.*

An experiment was conducted to determine the digestibility of Ca and P in 2 high protein canola meals (CMA; 45.69% CP and CMB; 46.97% CP) fed to growing pigs, and to compare values obtained in high protein canola meal with digestibility of Ca and P in conventional canola meal (CM-CV; 35.10% CP) and soybean meal (SBM). The Ca and P contents of CMA, CMB, and CM-CV were 0.64 and 1.26%, 0.51 and 1.16%, and 1.25 and 1.16%, respectively. Four cornstarch-based diets were formulated using each source of canola meal or SBM as the sole source of P in the diet. Four additional diets that were similar to the initial four diets with the exception that 500 FTU/kg of microbial phytase were added to each diet were also formulated. Therefore, a total of eight diets were formulated. Forty-eight barrows were divided into two periods and randomly allotted via a randomized complete block design using a 2 × 4 factorial arrangement to the eight dietary treatments based on initial BW. There were six replicate pigs per dietary treatment. Experimental diets were provided for 12 d with the initial 5 d being the adaptation period. Indigo carmine was added as an indigestible marker to the morning meals on d 6 and 11, respectively. Fecal collections started when the first marker appeared in the feces and ceased when the second marker appeared. The endogenous loss of P was assumed to be 190 mg kg^{-1} DMI. At the conclusion of the experiment, feed intake, Ca and P intake, apparent total tract digestibility (ATTD) of Ca and P, and standardized total tract digestibility (STTD) of P were calculated. Results indicate that ATTD of Ca and P and STTD of P were not different among treatments. Apparent total tract digestibility of Ca was 62, 66, 69, and 73% for CMA, CMB, CM-CV, and SBM, respectively. Standardized total tract digestibility of P was 55, 60, 49, and 66% for CMA, CMB, CM-CV, and SBM, respectively. Inclusion of phytase to the diets reduced both Ca and P outputs ($P < 0.05$). Inclusion of phytase improved ($P < 0.05$) ATTD of Ca and P and STTD of P regardless of the ingredient in the diet and there was no interaction between diet and phytase supplementation.

Key Words: canola meal, phosphorus, pig

1295 (M169) Effect of dietary net energy concentrations on the growth performance of growing gilts housed individually. G. I. Lee[1], K. S. Kim[2], J. C. Park[2], and D. Y. Kil[*1], *[1]Chung-Ang University, Anseong-si, South Korea, [2]Rural Development Administration, Cheonan-si, South Korea.*

Dietary net energy (NE) concentrations influence pig performance, but the information for their effects on young gilts has been limited. Therefore, the objective of this experiment was to determine the effect of different NE concentrations in diets on the growth performance of growing gilts. A total of 60 growing gilts (Landrace × Yorkshire; initial BW = 15.9 ± 0.55 kg) were allotted to five dietary treatments of 9.6, 10.1, 10.6, 11.1, or 11.6 MJ NE/kg with 12 replicate pens and one pig per pen in an 28-d feeding experiment. Ratios between standardized ileal digestible AA and NE concentrations in all diets were similar. The NE and AA concentrations in diets were calculated based on the values from NRC (2012). Pigs were allowed ad libitum access to feed and water. The NE concentrations of five diets used in the growth trial were also determined based on digestible nutrients, DE, and ME measured in metabolism experiments with replicated 5 × 5 Latin square design using 10 growing pigs (initial BW = 15.9 ± 0.24 kg). Results indicated that calculated NE concentrations in diets were close to measured NE concentrations (9.5, 10.1, 10.4, 11.0, and 11.4 MJ NE/kg) in diets. The final BW, ADG, and ADFI were not affected by dietary treatments. However, there was a quadratic relationship ($P = 0.01$) between feed efficiency and dietary NE concentrations (0.51, 0.50, 0.49, 0.50, and 0.52 for 9.6, 10.1, 10.6, 11.1, and 11.6 MJ NE/kg of diets, respectively). The NE intake per BW gain (MJ NE/kg of BW gain) was increased (linear and quadratic, $P < 0.01$) with increasing NE concentrations in diets. In conclusion, dietary NE concentrations affect feed efficiency and NE intake per BW gain of growing gilts.

Key Words: growing gilts, growth performance, net energy,

1296 (M170) Gluconeogenesis and substrate utilization in chicken embryos during later development determined by *in ovo* continuous infusion of [$^{13}C_6$] glucose and [$^{13}C_3$]glycerol. Q. Hu*, U. Agarwal, and B. J. Bequette, *Dep. of Animal and Avian Sciences, University of Maryland, College Park.*

We aimed to quantify the rates of gluconeogenesis (GNG) and substrate partition to the Krebs cycle in embryonic (e) day e14 and e19 chicken embryos ($n = 5$ to 6 per group). An in ovo continuous tracer infusion approach was employed to test the hypotheses that GNG and non-essential amino acid (NEAA) synthesis increase from e14 to e19. [$^{13}C_6$]Glucose or [$^{13}C_3$] glycerol was continuously infused (8 h) into the chorio-allantoic compartment on e14 and e19. Based on [$^{13}C_6$]glucose infusion, glucose entry rate, Cori cycling and GNG were higher ($P < 0.05$) in e19 than in e14 embryos, presumably to support greater deposition of glycogen in the muscle and liver in preparation for pipping and hatching. In the liver, the contribution of glucose to alanine, aspartate, and glutamate synthesis was greater ($P < 0.05$) in e14 than in e19 embryos whereas the synthesis of NEAA from glycerol was higher ($P < 0.05$) in e19 than in e14 embryos. These patterns of glucose and glycerol utilisation by the liver suggest a metabolic shift to conserve glucose for glycogen synthesis and an increased utilisation of yolk glycerol (triacylglycerides) after e14. Although the contribution of glycerol to GNG in e19 embryos was greater ($P < 0.05$) than in e14 embryos, the contribution of glycerol to GNG (1.3−6.0%) was minor. Based on [$^{13}C_6$]glucose tracer kinetics, the activities of both pyruvate carboxylase (*P*C) and pyruvate dehydrogenase (*P*DH) in the liver were higher ($P < 0.05$) on e19; however, the higher ($P < 0.05$) relative activity of PC *vs* PDH on e14 suggests a greater anaplerotic flux into the Krebs cycle of the e14 liver. In conclusion, the in ovo continuous tracer infusion approach allowed for measurement of chicken embryo whole body and liver metabolism over a shorter window of development compared to our previous approach of dosing tracer in ovo for 3 to 4 d. Lastly, this study provided quantitative estimates of the developmental shifts in substrate utilisation, GNG and NEAA synthesis by chicken embryos, as well as qualitative estimates of the activity of enzymes central to the Krebs cycle, and glucose and fatty acid metabolism.

Key Words: chicken, embryo, metabolism

1297 (M171) Plasma vitamin concentrations are altered by fat-soluble vitamin administration in suckling pigs. Y. D. Jang[*1], J. Y. Ma[1], J. S. Monegue[1], H. J. Monegue[1], R. L. Stuart[2], and M. D. Lindemann[1], *[1]University of Kentucky, Lexington, [2]Stuart Products Inc, Bedford, TX.*

Plasma concentrations of some vitamins are purported to be low in nursing piglets raised in confinement. This experiment was conducted to investigate the effect of fat-soluble vitamin administration by different administration routes on plasma concentration of those vitamins in suckling pigs. A total of 45 pigs from five litters were allotted to three treatments at birth (three pigs/treatment within each litter). Treatments were oral and i.m. injection of 400 IU of α-tocopherol, 40,000 IU of retinyl palmitate, and 40,000 IU of vitamin D_3 at d 1 of age with the control treatment that had no vitamin administration. Blood samples were collected at d 0 (initial), 1, 2, 3, 4, 6, 9, 14, and 20 post-administration. Plasma 25-hydroxycholecalciferol (25OHD_3), α-tocopherol, retinyl palmitate, and retinol concentration were analyzed. Growth performance did not differ by vitamin administration. Effects of treatment, d, and d × treatment interaction ($P < 0.01$) were observed in which plasma concentration increased immediately regardless of administration routes to peak at d 2 (4.0, 155.4, and 235.4 ng/

mL) for $25OHD_3$ and at d 1 post-administration (3.9, 14.3, and 32.3 ug/mL) for α-tocopherol for control, oral, and injection, respectively. The injection treatment had greater plasma values than the oral treatment. Plasma retinyl palmitate concentration increased only with the injection treatment and peaked at d 1 post-administration (0.13, 0.44, and 3.10 ug/mL for control, oral, and injection, respectively). Plasma α-tocopherol and retinyl palmitate concentration in the oral and injection treatments decreased from the peak plasma values to be similar with the values in the control treatment at d 9 and 3 post-administration, respectively. Plasma $25OHD_3$ concentration in the oral and injection treatments was maintained greater than that in the control treatment until d 20 post-administration. These results demonstrate that plasma status of $25OHD_3$, α-tocopherol, and retinyl palmitate are changed after administration to newborn pigs, and that the change of plasma profiles of these vitamins is different between types of vitamins administered and between administration routes. The injection administration is more efficient to enhance plasma $25OHD_3$ level until weaning than the oral administration.

Key Words: fat-soluble vitamin administration, plasma vitamin concentration, suckling pigs

---

1298 (M172) Digestibility of amino acids in distillers dried grains with solubles produced in Europe from wheat, maize, or mixtures of wheat and maize and fed to growing pigs. S. M. Curry*[1], J. K. Htoo[2], H. V. Masey O'Neill[3], and H. H. Stein[1], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]Evonik Industries AG, Hanau-Wolfgang, Germany, [3]AB Vista Feed Ingredients, Marlborough, UK.*

European ethanol plants may use wheat or maize or combinations of wheat and maize as feedstock. The distillers dried grains with solubles (DDGS) produced, therefore, may vary in composition and nutritional attributes according to the grain that was used in the production. There are, however, limited data on how these differences influence the digestibility of AA in DDGS. Therefore, an experiment was conducted to compare the standardized ileal digestibility (SID) of AA by growing pigs in European DDGS produced from wheat, maize, or wheat-maize mixtures. Twelve barrows (average initial BW: 23.0 ± 2.2 kg) were equipped with a T-cannula in the distal ileum and allotted to a replicated 6 × 6 Latin square design with 6 diets and 6 periods. The five sources of European DDGS that were used included wheat DDGS from 2011, wheat DDGS from 2012, wheat-maize DDGS (80% wheat and 20% maize), maize-wheat DDGS (70% maize and 30% wheat), and maize DDGS. A diet containing each source of DDGS as the sole source of AA was formulated and a N-free diet was used to determine basal endogenous losses of CP and AA. Results indicated that the SID of CP was greater ($P < 0.05$) in maize DDGS compared with wheat DDGS from 2011, wheat DDGS from 2012, and maize-wheat DDGS. The SID of all indispensable AA except Trp was also greater ($P < 0.05$) in maize DDGS compared with all other DDGS sources. For Trp, the SID in wheat-maize DDGS, wheat DDGS from 2011 and wheat DDGS from 2012 was not different from that of maize DDGS, but greater ($P < 0.05$) than in maize-wheat DDGS. The SID of all indispensable AA except Leu in maize-wheat DDGS did not differ from the values calculated for wheat DDGS from 2011 and wheat DDGS from 2012, and no differences between SID values for AA in wheat DDGS from 2011 and wheat DDGS from 2012 were observed. In conclusion, the SID of AA in maize DDGS produced in Europe is greater than in European wheat DDGS and DDGS produced from mixtures of wheat and maize.

Key Words: amino acid digestibility, distillers dried grains with solubles, pigs

---

1299 (M173) The determination of the amino acid requirements of pigs in the nursery phase. E. A. Vermillion*, C. R. Dove, and M. J. Azain, *University of Georgia, Athens.*

An experiment using 202 total pigs, assigned to one of four diets was conducted to determine the essential amino acid requirements of nursery pigs. Except for lysine, diets met or exceeded 1998 NRC. Treatment 1 was slightly deficient in lysine relative to the 1998 NRC (1.40, 1.23, and 1.10% of total dietary lysine in phases I, II, and III, respectively). Treatment 2 was equivalent to the 1998 NRC recommendations (1.50, 1.33, and 1.20% of total dietary lysine in phases I, II, and III, respectively). Treatment 3 was intermediate between the 1998 recommendations and the newly revised 2012 publication (1.60, 1.43, and 1.30% of total dietary lysine in phases I, II, and III, respectively). Treatment 4 was equivalent to the 2012 NRC publication (1.70, 1.53, and 1.40% of total dietary lysine in phases I, II, and III, respectively). Crystalline amino acids (LYS, THR, MET) were used to maintain an ideal amino acid pattern (1.00, 0.62, 0.57 respectively) across treatments. Treatments were fed over three phases: Phase I, D0–7; Phase II, D7–21; and Phase III, D21–35. There were no significant differences ($P > .10$) in growth rate or feed intake, but feed efficiency improved linearly ($P < .05$) as amino acid content increased (Gain:Feed of 0.66, 0.69, 0.70, and 0.72 in treatments 1, 2, 3, and 4, respectively). Blood samples were obtained from pigs at the end of each dietary phase (d 7, 21, and 35) for determination of plasma urea concentration. There was a significant linear response to diet on d 7, 21, and 35 ($P < 0.05$), with a significant quadratic response on d 21 and 35 ($P < 0.001$). This suggests that nitrogen excretion is reduced in pigs fed higher levels of crystalline amino acids, which could potentially reduce environmental impact. In contrast to the positive linear correlation between dietary lysine levels and feed efficiency, the blood urea response indicated that the requirement for amino acids was met at 1.33% total lysine diets in Phase II, and 1.20% lysine in Phase III; these results most closely corre-

spond to the 1998 NRC guidelines. These results suggest that the decision whether to feed the higher levels of amino acids in the nursery depends on the added cost associated with those diets. Based on growth rate and feed intake, there is no evidence that the higher dietary levels are needed. However, feed efficiency and plasma urea response indicate that the higher levels may be justified.

Key Words: lysine, nursery, pigs

1300 (M174) Effect of dietary energy level and weaning weight on growth performance and digestibility in weanling piglets.

M. D. S. Vieira[1], A. M. L. Ribeiro[1], A. D. M. Kessler[1], L. I. Chiba*[2], M. L. Somensi[1], L. Bockor[1], and L. G. Teixeira[1], *[1]Federal University of Rio Grande do Sul, Porto Alegre, Brazil, [2]Auburn University, Auburn, AL.*

The experiment was conducted to determine the capacity of piglets weaned at light weight to achieve similar growth performance with those weaned at heavy weight by increasing the ME content of the diet and keeping constant Lys:ME. Thirty-two male piglets were classified according to their weaning weight (WW) as light (4.5 ± 0.4 kg) or heavy (6.7 ± 0.5 kg) and housed individually in metabolic cages for 28 d. Six treatments, 2 WW and 3 ME levels (I: 3400; II: 3600; and III: 3800 kcal/kg) in a 2 × 3 factorial arrangement, were used in pre-starter (PS, d 0 to 14) and starter (ST, d 14 to 28) period. The control diet (I) was formulated with standard energy and nutrient recommendations (Brazilian Tables for Poultry and Swine), whereas indispensable and dispensable AA, Ca, P, and lactose levels in the diets II and III were adjusted for the increased ME (e.g.,4.14 and 3.91 g Lys/Mcal ME for the PS and ST periods, respectively). Fecal and urine samples were collected to determine apparent total tract digestibility (ATTD) of energy and nutrients. Age at weaning was used as covariate in the statistical model. There were no WW x ME interactions for any of the response criteria. Overall, light WW piglets had less ADG and AFDI ($P < 0.05$), but there was no difference in the G:F. Heavy WW piglets ingested more ME, Lys, and N than light WW piglets during the entire phase ($P < 0.05$). During the PS period there was a linear effect of ME on G:F; increasing ME improved G:F ($P < 0.05$). Also in this period, the increment in ME increased ATTD of GE, and DE and ME values ($P < 0.05$). During the ST and total period, there was no effect of increased ME levels on ME and Lys intake, but increasing ME levels increased ATTD of GE, CP, and DM, N retention, and DE and ME values ($P < 0.05$). In conclusion, light piglets did not improve growth performance when fed diets with increasing ME levels. Increased ME levels improved digestibility and utilization of nutrients, but did not improve growth performance.

Key Words: energy density, nursery piglets, weaning weight

1301 (M175) Effect of dietary energy level and weaning weight on body composition and efficiency of energy utilization in weanling piglets.

M. D. S. Vieira[1], A. M. L. Ribeiro[1], A. D. M. Kessler[1], M. L. Somensi[1], L. I. Chiba*[2], L. Bockor[1], and C. S. Marcolla[1], *[1]Federal University of Rio Grande do Sul, Porto Alegre, Brazil, [2]Auburn University, Auburn, AL.*

The experiment was conducted to evaluate the effects of dietary ME and weaning weight (WW) on body composition and energy utilization in weanling piglets. Thirty-two male piglets were classified according to their WW as light (4.5 ± 0.4 kg) or heavy (6.7 ± 0.5 kg), and housed individually in metabolic cages for 28 d. Six treatments, 2 WW and 3 ME (I: 3400; II: 3600; and III: 3800 kcal/kg) with constant Lys:ME were used. The control diet (I) was formulated with standard energy and nutrient recommendations (Brazilian Tables for Poultry and Swine), whereas AA, Ca, P, and lactose levels in the diet II and III were adjusted for the increased ME. Body composition, energy and nutrient deposition rates, and energy efficiency of gain were measured through comparative slaughter technique. There were no WW x ME interactions for any of the responses. BW, ADFI, and ADG were greater ($P < 0.05$) in piglets with heavier WW than lighter WW, but there was no difference in G:F. Also, heavy WW piglets had greater fasted BW, eviscerated carcass and empty BW (EBW), compared to light WW piglets ($P < 0.05$), but there was no difference in the organ + blood (OB) fraction. When those responses were equalized per kilogram of fasted BW, light WW piglets had greater OB than heavy WW piglets. Gastrointestinal tract and kidneys were greater in heavy WW piglets, while urinary tract and blood were greater in light WW piglets when equalized per kilogram of fasted BW ($P < 0.05$). There was no effect of ME on physical body composition, and ME and WW did not affect chemical body composition. The rates of water, ash, and protein deposition in the carcass and OB were greater in heavy WW piglets ($P < 0.05$). Water and protein deposition in EBW also were greater in heavy WW piglets ($P < 0.05$). Increasing ME did not affect energy and nutrient deposition rates in any of the body fractions. Heavy WW piglets had greater intakes of ME, with higher estimates of ME for maintenance and heat production ($P < 0.05$). Energy efficiency was not affected by the WW or ME content of the diets. In conclusion, heavy WW piglets had greater protein deposition and efficiency of gain than light WW piglets. The ME level did not improve the response criteria evaluated in the current study.

Key Words: energy deposition, metabolizable energy, weaning weight

1302 (M176) Egg quality of brown laying hens fed with different Met + Cys and chelate Cu levels.

J. E. D. Moraes[1], C. C. Pizzolante[1], A. P. O. Saccomani[2], E. A. D. Oliveira[3], S. K. Kakimoto[4], J. C. Dadalt*[5], and M. A. D. T. Neto[5], *[1]APTA-Unidade de Pesquisa de Brotas-SAA-SP, Brotas, Brazil, [2]Instituto de Zootecnia-APTA-SAA-SA, Nova Odessa, Brazil, [3]Secretaria de Agricultura de Brotas, Brazil, [4]Granja Kakimoto, Bastos, Brazil, [5]University of São Paulo, Pirassununga, Brazil.*

The objective of the current study was to evaluate effects from Met + Cys levels combined with chelated Cu concentrations for brown laying hens. Nine hundred sixty brown laying hens (6 replicates/treatment, 8 birds/replicate) from 22 to 26 wk of age were allotted in a randomized bloc design under factorial scheme 5 × 4 (Met+Cys x Chelated Copper). The diets were formulated according had similar composition (2800 kcal/kg ME, 15.5% CP) and were formulated according with the lineage of the birds, except for Met + Cys and copper levels. At the final day of period two eggs/experimental unit were evaluated for weight, specific gravity-change, % shell, shell thickness, % albumen, % yolk, Haugh unit, yolk index, and yolk color. Statistical analysis was performed using ANOVA and Tukey's test 5%. In conclusion, Met + Cys and Chelate Cu did not affect external and internal quality results of eggs from brown layer hens at 26 wk of age.

Key Words: albumen, yolk, organic mineral

Table 1302. External and internal egg quality of brown laying hens fed with Met + Cys and chelated Cu levels

	Met + Cys (%)					
Variable	1.1	0.95	0.80	0.65	0.50	CV (%)
Weight (g)						
Specific Gravity -change	1.096	1.095	1.097	1.094	1.095	0.49
% shell	10.00	9.83	10.16	9.76	9.86	7.72
Shell thickness (mm)	38.80	38.75	38.79	38.69	38.48	7.13
% Albumen	68.06	68.04	67.71	67.88	67.71	3.68
% Yolk	21.94	22.13	22.59	22.36	22.43	7.69
Haugh unit	101.22	102.63	101.54	100.75	101.23	5.29
Yolk index	49.46	50.75	49.88	50.00	50.65	9.01
Yolk color						

	Chelated Cu (ppm)				
	88	43	22	0	CV (%)
Weight (g)					
Specific Gravity	1.096	1.096	1.095	1.095	0.49
% Shell	9.94	9.96	9.93	9.85	7.72
Shell thickness (mm)	38.68	39.37	38.22	38.62	7.13
% Albumen	68.34	67.99	67.85	67.35	3.68
% Yolk	22.09	22.05	22.22	22.81	7.69
Haugh unit	101.98	101.43	100.44	102.04	5.29
Yolk index	49.38	50.78	50.27	50.15	9.01
Yolk color	6.8	6.8	6.6	6.4	15.11

In line, means do not differ ($P > 0.05$) by Tukey test.

1303 (M177) Validation of net energy system of feed formulation in growing-finishing pigs fed barley based diets with alternative feed ingredients.

D. E Velayudhan*, and C. M. Nyachoti, *University of Manitoba, Winnipeg, Canada.*

The aim of this study was to determine the growth performance and carcass characteristics of growing-finishing pigs fed diets formulated on net energy (NE) basis thereby validating the NE system of feed formulation. Twenty-four pigs (12 barrows and 12 gilts) with an initial BW of 25 kg were blocked by sex and allotted one of the three treatments, resulting in 8 replicates, 4 barrows and 4 gilts per treatment. Dietary treatments were; a barley-based control diet with alternative feed ingredients (distillers dried grains with soluble, canola meal and peas) formulated on digestible energy (DE) basis (Diet A), control diet formulated on a NE basis (Diet B) and Diet B + Multi-carbohydrase enzyme (Diet C). Pigs were offered their respective diets in a three-phase feeding program for 25 to 50 kg (Phase 1), 50 to 75 kg (Phase 2), and 75 to 110 kg (Phase 3) BW. Diet A was formulated to contain 3402 kcal/kg of DE and Diet B and Diet C to contain 2475 kcal/kg of NE with 0.98, 0.85, and 0.73% SID Lys for phases 1, 2, and 3, respectively. Individual pig BW and feed disappearance were monitored biweekly during each phase to determine average daily gain (ADG), average daily feed intake (ADFI), and gain to feed ratio (G:F) ratio. Pigs were slaughtered once they reached 100 kg BW to determine carcass characteristics. During Phase 1, an improvement in ADFI ($P = 0.02$) was observed for diets formulated on NE basis with enzyme supplementation (1.78 kg/d) when compared to Diet B without enzymes (1.57 kg/d). In Phase 3, a significant difference was observed for ADG ($P = 0.01$), wherein Diet B showed a BW gain of 0.89 kg/d compared to 0.79 kg/d for the control diet. Also a trend for an increase in G:F ratio ($P = 0.072$) was observed between diets formulated on DE and NE basis. For overall performance, when compared to the control diet, pigs fed Diet B showed significant improvement in ADG (0.90 vs. 0.96 kg/d; $P = 0.02$) and G:F (0.43 vs. 0.47; $P = 0.05$). No significant differences ($P > 0.10$) were observed among dietary treatments for any of the carcass characteristics. In conclusion, the results indicate a better growth performance when diets were formulated on a NE basis when compared to the DE system. Though not significant, enzyme supplementation numerically enhanced the overall performance.

Key Words: enzyme, net energy, pig

1304 (M178) Effects of dietary tryptophan:lysine ratio and sanitary conditions on performance of weaned pigs fed antibiotic-free diets. B. Jayaraman[*1], J. K. Htoo[2], and C. M. Nyachoti[1], *[1]University of Manitoba, Winnipeg, Canada, [2]Evonik Industries AG, Hanau-Wolfgang, Germany.*

The aim of this study was to determine the optimum standardized ileal digestible (SID) Trp:Lys ratio for weaned pigs reared in clean or unclean sanitary conditions and fed antibiotic-free diets. Mixed-sex pigs (Duroc x [Yorkshire x Landrace]; average initial BW of 7.0 ± 0.5 kg) weaned at 21 ± 1 d were randomly assigned to 10 dietary treatments in a 2 × 5 factorial arrangement in a 28-d study giving 6 replicates (3 pigs per pen) per treatment. The main factors were sanitary conditions (clean, CL and unclean, UCL) and 5 dietary SID Trp:Lys (16, 18, 20, 22, and 24%) in a completely randomized design. Diets were corn-wheat-soybean meal based with a constant SID Lys of 1.18% that was set to be seconding limiting AA. For the first 14 d, CL group (n = 90) were kept in pens, followed immediately by the UCL group (n = 90) for the next 14 d in the same room. Piglets were provided ad libitum access to feed and water. Under the CL condition, the room was disinfected before arrival of piglets and the room was cleaned weekly. For the UCL pigs, the room was not disinfected and cleaned after CL group and manure from swine herd was added (5 kg per pen) to the pens on d 0 and d 7 of the experiment. Pigs BW and pen feed disappearance were recorded weekly to determine ADG, ADFI and G:F. The effect of sanitary conditions was observed (P < 0.05) for ADG and G:F throughout the study. During d 0 to 7 and d 8 to 14, the ADG for CL vs. UCL were 206 vs. 160 g and 420 vs. 364 g, respectively. During d 0 to 7 and d 8 to 14, the G:F for CL vs. UCL was 0.73 vs. 0.54 and 0.76 vs. 0.64, respectively. Increasing dietary SID Trp:Lys ratio did not affect ADG and ADFI during d 0 to 14. The highest ADG was achieved at SID Trp:Lys of 20% for CL and 24% for UCL pigs, respectively. Increasing dietary Trp:Lys had a linear trend (P < 0.10*)* towards improved G:F during d 0 to 7 in the UCL group showing that SID Trp:Lys of 24% improved G:F. In conclusion, pigs raised under unsanitary conditions had reduced ADG and G:F in piglets, and increasing the level of SID Trp:Lys 24% could improve G:F after weaning.

Key Words: tryptophan, sanitation, piglets

1305 (M179) Egg quality of brown layers fed with different levels of threonine and chelate zinc. J. E. D. Moraes[1], C. C. Pizzolante[1], A. P. O. Saccomani[2], E. A. D. Oliveira[3], S. K. Kakimoto[4], J. C. Dadalt[*5], and M. A. D. T. Neto[5], *[1]APTA-Unidade de Pesquisa de Brotas-SAA-SP, Brotas, Brazil, [2]Instituto de Zootecnia-APTA-SAA-SA, Nova Odessa, Brazil, [3]Secretaria de Agricultura de Brotas, Brazil, [4]Granja Kakimoto, Bastos, Brazil, [5]University of São Paulo, Pirassununga, Brazil.*

The objective of this study was to evaluate effects from Thr levels combined with chelated Zn concentrations for brown laying hens. Nine hundred sixty brown laying hens (6 replicates/treatment, 8 birds/replicate) from 22 to 26 wk of age were allotted in a randomized block design under factorial scheme 5 × 4 (Met+Cys x Chelated Copper). The diets were formulated according had similar composition (2800 kcal/kg ME, 15.5% CP) and were formulated according with the lineage of the birds, except for Thr and Zn levels. At the final day of period, two eggs per plot were evaluated for weight, specific gravity, Haugh unit, yolk index, and for percentages of yolk, albumen and shell. Statistical analysis was performed using ANOVA and contrast between mean for (P < 0.05) by Tukey's test. There was no interaction effect of Thr and Zn. Egg weight (56.36 ± …g), specific gravity (1.099 ±), Haugh units (126.00 ±) yolk index (27.72 ±) and shell thickness (39.61 ±) shell percentage (10.05 ±) had no significant effect under Thr and chelate Zn levels. Effects (P < 0.05) were observed for Thr on percentages of yolk and albumen (Table 1305). The lower percentages of egg yolk occurred under 1.1 and 0.80% Thr and albumen under 0.65% Thr levels.

Key Words: albumen, yolk, chelate minerals

Table 1305. Percentages of yolk and albumen of eggs from brown layers fed Thr

	Thr (%)						
	1.1	0.95	0.80	0.65	0.50	Mean	CV (%)
Yolk %	21.92^{b}	22.40^{ab}	21.79^{b}	23.08^{a}	22.36^{ab}	22.32	9.23
Albumen %	68.03^{a}	67.62^{ab}	68.14^{a}	66.77^{b}	67.66^{ab}	67.64	3.24

Means bearing different superscript letters within a row differ by Tukey (P < 0.05). In conclusion, Thr levels may affect the internal egg quality. Zn concentrations did not affect the external and internal qualities of egg.

1306 (M180) Tryptophan:lysine ratio for pigs from 15 to 30 kg of body weight. T. J. Pasquetti*[1], P. C. Pozza[2], I. Moreira[2], L. M. Diaz Huepa[2], L. D. Castilha[2], M. R. Fachinello[2], L. A. C. Esteves[2], V. R. C. Paula[2], and S. W. Kim[3], *[1]Universidade Estadual de Maringá, Bolsista CAPES, Maringá, PR, Brazil, [2]Universidade Estadual de Maringá, PR, Brazil, [3]North Carolina State University, Raleigh.*

The aim of this study was to determine the digestible Tryptophan:Lysine (Trp:Lys) ratio for starting pigs (15 to 30 kg). A previous study was performed to determine the true ileal amino acids digestibility of the diet with low Trp and Lys levels. In the growth performance study, a total of 64 individually housed barrows (15 ± 0,23 kg) were allotted in a completely randomized block design, with 16 treatments and four replicates. Treatments were arranged as a 4 × 4 factorial scheme (four levels of digestible Trp: 0.155, 0.185, 0.215, 0.245% and four levels of digestible Lys: 0.972, 1.112, 1.252 and 1.392%). Glutamic acid was used to keep the diets with the same nitrogen levels. At the end of the study, body weight (BW) and feed intake were recorded and feed:gain ratio (F:G) calculated. Ultrasonography was performed using an Aloka (SSD 500) and Sonograder (Renco) equipments, and measurements of backfat thickness and loin depth were performed using the ImageJ software. Considering the regression analysis, the BW (P = 0.03) and average daily gain (P = 0.005) increased linearly with increased levels of digestible Trp. By surface response method, the average daily feed intake (ADFI) increased linearly (P = 0.014) as the levels of digestible Trp increased in the diets, while Lys showed a quadratic effect (P = 0.004). For the ADFI the optimum Lys level was estimated at 1.195%. An interaction between digestible Trp and Lys (P = 0.056) was found on F:G. Considering the surface response method, there was a quadratic effect (P = 0.042) of digestible Trp and Lys levels on F:G, estimating on 0.210 and 1.198% the optimum levels of digestible Trp and Lys levels, respectively, which results in a Trp:Lys ratio of 0.175. No differences (P > 0.05) were observed on backfat thickness. A quadratic effect of digestible Trp (P = 0.021) and Lys (0.026) levels was observed on loin depth (measured through Aloka SSD 500), which by surface response method the optimum Trp and Lys levels were 0.208 and 1.136%, respectively, providing a Trp:Lys ratio of 0.183%. Using the regression analysis we observed a quadratic effect (P = 0.042) of digestible Trp on loin depth (Sonograder- Renco), which was estimated to be optimum at 0.210%. In conclusion, the optimum digestible Trp and Lys levels for growth performance are 0.210 and 1.198%, and for loin depth are 0.208 and 1.136%, which provide a Trp:Lys ratio of 0.175 and 0.183%, respectively.

Key Words: response surface; growth performance, requirements.

1307 (M181) Energy intake and nutrient digestibility in heavy finishing swine fed varying levels of soluble fiber. D. J. Rodrigues*[1], M. C. Thomaz[1], U. D. S. Ruiz[2], M. M. Lima[1], M. S. F. Oliveira[1], M. V. Marujo[1], F. F. Castro[1], and E. Daniel[3], *[1]Sao Paulo State University, Jaboticabal/SP, Brazil, [2]Univ. Estadual Paulista, Dracena, Brazil, [3]Dep. of Animal Science, FCAV/UNESP, Jaboticabal/SP, Brazil.*

Depending on its characteristics, dietary fiber may depress daily energy intake and utilization of dietary nutrients in growing pigs. These effects are likely lower in finishing pigs. This study was conducted to determine the effect of increasing dietary levels of soluble fiber on daily feed and energy intake, as well as apparent fecal nutrient and energy digestibility in finishing pigs. In total 36 individually housed barrows (commercial crossbred; initial BW 78.38 ± 0.32 kg), were assigned to four dietary treatments in a randomized block design: control (corn and soybean meal based; 3229 kcal/kg calculated ME, 13.9% CP, 1.5% soluble fiber) and three isonitrogenous diets with increasing levels of soluble fibers (4, 8, and 12%; from added pectin, containing 63% of soluble fiber), and consequently decreased levels of calculated ME (3095, 3017, and 2946 kcal/kg). Pigs were fed ad libitum. At a BW of 105 kg, feces were collected twice daily, during 3 d. Insoluble ash was used as marker for determining digestibility. Statistical analyses were performed using the PROC MIXED of SAS. The results showed a linear decrease for both daily feed intake (P = 0.0157) and daily DE intake (P = 0.0005) between 100.86 and 126.19 kg BW. Quadratic effects (P < 0.0001) were observed for the digestibility of DM, GE and CP; the maximum digestibility values were obtained at 0.74, 1.33 and 1.60% additional soluble fiber in diet, respectively. There was linear decrease (P < 0.0001) for the digestibility of ash. These results confirm that feedstuffs containing soluble fiber can be used to reduce daily energy intake in heavy finishing pigs through qualitative feed restriction, but its negative effect on the nutrient digestibility must be considered.

Key Words: daily energy intake, feed restriction, soluble fiber

Table 1307. Daily feed (kg/d) and DE intake (kcal/d), as well as apparent fecal digestibility (AFD, %) of energy and nutrients in finishing pigs fed diets containing different levels of soluble fiber (SF)

	Experimental diets (% SF)					
	1.5	4	8	12	SE	Effect of diet SF
Daily feed intake	1.64	1.56	1.61	1.34	0.18	Linear
Daily DE intake	6822	5792	5937	4925	317.32	Linear
AFD						
DM	89.75	89.26	87.54	85.35	0.32	Quadratic
GE	89.92	90.19	88.21	86.29	0.33	Quadratic
Ash	51.91	45.38	34.94	28.05	1.09	Linear
CP	86.64	87.63	84.99	82.90	0.69	Quadratic

1308 (M182) Amino acid digestibility in field peas, fish meal, corn, soybean meal, and soybean hulls.

J. K. Mathai*, and H. H. Stein, *University of Illinois at Urbana-Champaign, Urbana.*

An experiment was conducted to determine the standardized ileal digestibility (SID) of AA in field peas, fish meal, corn, soybean meal, and soybean hulls. Six ileal-cannulated gilts (initial BW: 26.5 ± 0.74 kg) were allotted to a 6 × 6 Latin square design with 6 diets and 6 periods. A N-free diet was formulated to determine basal endogenous losses of AA and CP and to enable the calculation of SID of AA. The remaining diets were formulated with each test ingredient as the sole source of AA, with the exception that the soybean hulls were included in a diet that also contained soybean meal to compensate for the low CP in soybean hulls. The AID and SID values were calculated in the soybean hulls diet using the difference procedure whereas AID and SID in the other ingredients were calculated using the direct procedure. The SID of Lys was greater ($P < 0.05$) in field peas, fish meal, and soybean meal than in corn and soybean hulls (Table 1308). The SID of Trp was greater ($P < 0.05$) in corn than in soybean meal, and greater ($P < 0.05$) in soybean meal than in field peas. The SID of His, Lys, and Trp was less ($P < 0.05$) in soybean hulls than in other ingredients. These data indicate that the SID of AA in most indispensable AA is not different between field peas, fish meal, and soybean meal, whereas the SID of some indispensable AA is less in soybean hulls than in other ingredients.

Key Words: amino acid digestibility, feed ingredients, pigs

Table 1308. Standardized ileal digestibility (SID; %) of AA in field peas, fish meal, corn, soybean meal (SBM), and soybean hulls fed to pigs

	Ingredients					
Item	Field Peas	Fish meal	Corn	SBM	Soybean hulls	*P*-value
His	92.7^{ab}	87.3^{c}	93.3^{a}	90.2^{b}	69.5^{d}	< 0.05
Ile	87.6^{ab}	86.7^{b}	90.7^{a}	87.7^{ab}	83.4^{c}	< 0.05
Lys	90.6^{a}	87.7^{a}	73.1^{b}	86.3^{a}	69.8^{d}	< 0.05
Met	87.9^{bc}	87.2^{c}	92.1^{b}	87.4^{c}	97.1^{a}	< 0.05
Phe	89.2^{b}	86.0^{bc}	92.9^{a}	88.4^{b}	89.2^{b}	< 0.05
Thr	86.9^{ab}	84.3^{b}	89.2^{a}	85.4^{ab}	85.9^{ab}	< 0.05
Trp	85.8^{c}	91.2^{ab}	95.0^{a}	90.6^{b}	76.4^{d}	< 0.05
Val	86.5^{bc}	84.9^{cd}	90.2^{b}	85.9^{c}	100.5^{a}	< 0.05

$^{a-d}$ Means within a row lacking a common superscript letter differ.

1309 (M183) Lysine and tryptophan levels in diets for gilts from 15 to 30 kg of body weight.

T. J. Pasquetti[*1], P. C. Pozza[2], I. Moreira[2], T. C. D. Santos[2], D. Perondi[3], C. D. L. Costa Filho[2], W. Tanamati[2], P. L. D. O. Carvalho[4], and C. F. Muniz[2], *[1]Universidade Estadual de Maringá, Bolsista CAPES, Maringá, PR, Brazil, [2]Universidade Estadual de Maringá, PR, Brazil, [3]Dep. of Animal Science-FCAV/UNESP, Jaboticabal/SP, Brazil, [4]Universidade Estadual do Oeste do Paraná, Marechal Cândido Rondon, PR, Brazil.*

The aim of this study was to determine the optimum levels of digestible lysine (Lys) and tryptophan (Trp) in diets for gilts from 15 to 30 kg of body weight. A previous study was performed to determine the true ileal digestibility of amino acids in the basal diet (low Lys and Trp levels), to verify if some deficiencies occurred with other essential amino acids. The growth performance study was performed using a total of 64 individually housed gilts (15,03 ± 0,19 kg), allotted in a completely randomized block design, with 16 treatments and four replicates. Treatments were arranged as a 4 × 4 factorial scheme (four levels of digestible Trp: 0.155, 0.185, 0.215, 0.245% and four levels of digestible Lys: 0.972, 1.112, 1.252 and 1.392%). Glutamic acid was used to keep nitrogen levels similar across diets. The body weight (BW) and feed intake were recorded and F:G was calculated. Ultrasonography was performed using an Aloka (SSD 500) and Sonograder (Renco) equipments, and backfat thickness and loin depth were measured using the ImageJ software. Considering the regression analysis, a quadratic effect of digestible levels of Trp was observed on ADG ($P = 0.038$), in which the optimum level was obtained 0.224%. The increased levels of digestible Trp improved linearly ($P = 0.005$) the ADFI. An interaction between Trp and Lys was observed for F:G ($P = 0.007$). No interaction was observed for ADG ($P = 0.247$), ADFI ($P = 0.233$), backfat measured with Sonograder ($P = 0.603$), and Aloka ($P = 0.462$) and for loin depth measured with Sonograder ($P = 0.632$) and Aloka ($P = 0.086$). By surface response method, a quadratic effect ($P = 0.034$) of digestible levels of Trp and a linear effect of Lys ($P = 0.005$) were observed on F:G, in which the optimum level of digestible Trp was obtained at 0.216%. Trough regression equation method, the backfat thickness (measured through Aloka or Sonograder) increased linearly ($P = 0.052$ and 0.021, respectively) and the loin depth (measure through Aloka) showed quadratic effect ($P = 0.034$) for Trp levels, in which the optimum level was estimated at 0.205%. The loin depth, measured through Sonograder, increased linearly ($P = 0.039$) with digestible levels of Lys. In conclusion, the optimum levels of digestible Trp, to improve average daily gain and loin depth, are 0.224 and 0.205%, respectively.

Key Words: amino acids, ileal digestibility, growth performance.

1310 (M184) Effects of mineral supplementation on the performance of nulliparous and multiparous does fed forage containing diets. L. Verjel-Trigos*[1], I. Rodriguez-Carrascal[1], and C. Ordoñez-Gomez[2], [1]*Universidad Francisco de Paula Santander-Ocaña, Colombia,* [2]*Universidad Nacional de Colombia, Bogotá.*

The effect of the mineral supplementation on the performance of nulliparous and multiparous rabbit does fed forage containing diets was evaluated in 18 rabbit does crossed New Zealand and Russian californian with an average live weight 3.65 ± 0.15 kg, placed in individual cages, distributed following a complete randomized design with factorial arrangement 2 × 3, with two levels of parity (PA), multiparous (M) and nulliparous (N), and three levels in salt supplementation (S), without salt (NS), with 6% P (S6), 11.4% Ca y 6% P, and 8% P (S8), 15.2% Ca y 8% P, with three replications. The diet consisted of 85% of commercial feed and 15% trichantera forage based in DMI (Mineral composition: 1.4% Ca and 0.56% P). Salts was formulated to keep a constant calcium:phosphorus ratio and levels of trace minerals. The salt was offered in plastic licks from 15 d before mating to weaning. Lactation period was 30 d. To rabbit does performance was evaluated farrowing weight, weaning weight and DMI. In the performance of kits the litter size at birth, at weaning and weight gain in lactation was evaluated. Data were analyzed in module GLM of SAS ver. 9.2. Analysis of covariance to the initial weight of the rabbit does and comparison of means by orthogonal contrasts was performed. The performance of kits was not affected ($P > 0.05$). In rabbit does performance no interaction between S and PA was observed ($P > 0.05$). There were no differences ($P > 0.05$) between groups for DMI, 101.1, 107.7, 109.9, 101.0, 107.8 and 103.0 g/d of DMI to N-NS, N-S6, N-S8, M-NS, M-S6 and M-S8, respectively and 0.42, 0.37, 0.38 and 0.34 g/d of salt to N-S6, N-S8, M-S6 and M-S8, respectively. The farrowing weight of rabbit does was higher ($P < 0.01$) in S8 compared to S6, 3841, and 3388 g to S8 and S6, respectively. S8 increase ($P < 0.05$) the weaning weight of the rabbit does relative to S6, 4055, and 3608 g to S8 and S6, respectively. In conclusion, supplementation with salt 8% P improves the performance of rabbit does fed forage containing diets, but not affect the performance of the litter.

Key Words: phosphorus, rabbit does, salt

1311 (M185) Amino acid digestibility in oilseed meals fed to growing pigs. C. S. Park*, A. R. Son, and B. G. Kim, *Konkuk University, Seoul, South Korea.*

An accurate determination of the standardized ileal digestibility (SID) of AA is important for swine diet formulation, especially in protein supplements. The objective of this experiment was to determine the SID of AA in 11 sources of oilseed meals fed to growing pigs. The oilseed meals used in this study were sesame meal (SM, 50.0% CP), two sources of soybean meal (SBM) produced in Korea (SBM-K1, 47.4% CP; SBM-K2, 47.1% CP), SBM produced in India (SBM-I, 39.6% CP), high-protein distillers dried grains (HPDDG, 38% CP), perilla meal (*P*M, 43.2% CP), canola meal (CNM, 37.5% CP), copra meal (CM, 21.7% CP), corn germ meal (CGM, 21.4% CP), palm kernel expeller (*P*KE, 15.3% CP), and tapioca distillers dried grains (TDDG, 18.4% CP). Experimental diets were prepared to contain each ingredient as a sole source of AA and an N-free diet was also prepared to estimate the basal endogenous losses of AA. Twelve barrows with an initial BW of 29.0 ± 3.0 kg were surgically fitted with a T-cannula at the distal ileum and were allotted to a 12 × 9 incomplete Latin square design with 12 diets and 9 periods. Following the 5-d adaptation period, ileal digesta were collected for 8 h on d 6 and 7. Values for the SID of Lys in SM, SBM-K1, SBM-K2, SBM-I, HPDDG, PM, CNM, CM, CGM, PKE, and TDDG were 16.6, 81.2, 86.9, 85.3, 66.1, 32.5, 61.6, 21.4, 51.8, 46.0, and 43.3, respectively (SEM = 4.8, $P < 0.01$). Values for the SID of Met in SM, SBM-K1, SBM-K2, SBM-I, HPDDG, PM, CNM, CM, CGM, PKE, and TDDG were 64.6, 91.5, 87.9, 85.8, 91.5, 38.3, 76.6, 55.2, 73.4, 67.4, and 20.8, respectively (SEM = 5.5, $P < 0.01$). In conclusion, values for the SID of most AA in SBM-K1, SBM-K2, SBM-I, HPDDG, and CNM were greater than those in SM, PM, CM, and TDDG.

Key Words: feedstuffs, protein supplements, swine

1312 (M186) Standardized total tract digestibility of phosphorus in oilseed meals fed to growing pigs. C. S. Park*[1], Y. D. Jeong[2], B. G. Kim[1], and S. K. Park[2], [1]*Konkuk University, Seoul, South Korea,* [2]*Rural Development Administration, Suwon, South Korea*.

We determined the standardized total tract digestibility (STTD) of P in 11 sources of oilseed meals fed to growing pigs. The test ingredients were sesame meal, two sources of soybean meal (SBM) produced in Korea (SBM-K1 and SBM-K2), SBM produced in India, high-protein distillers dried grains (HPDDG), perilla meal (PM), canola meal, copra meal (CM), corn germ meal (CGM), palm kernel expeller, and tapioca distillers dried grains. Experimental diets were formulated to contain each ingredient as a sole source of P and a P-free diet was also prepared to estimate the basal endogenous loss of P. Twelve barrows with an initial BW of 47.9 ± 2.6 kg were allotted to a 12 × 8 incomplete Latin square design with 12 diets and 8 periods. After 4 d of adaptation period, feces were collected for 4 d of collection period according to the marker-to-marker method. There was a difference ($P < 0.001$) in the STTD of P among oilseed meals (Table 1312). Values for the STTD of P in SBM-K1, HPDDG, CM, and CGM were greater ($P < 0.05$) than that in PM. In conclusion, the STTD of P in oilseed meals were in the range of 58.5 to 76.8% except HPDDG, PM, and CGM.

Key Words: feedstuffs, macromineral, swine

Table 1312. Phosphorus (P) and standardized total tract digestibility (STTD) of P in 11 sources of oilseed meals fed to growing pigs (% as-fed basis, $n = 8$

Item	P	STTD of P
Ingredient		
Sesame meal	0.63	58.5[bc]
Soybean meal-Korea 1	0.63	74.9[ab]
Soybean meal-Korea 2	0.57	58.6[bc]
Soybean meal-India	0.54	67.4[abc]
High-protein distillers dried grains	0.24	86.4[a]
Perilla meal	1.29	54.5[c]
Canola meal	0.99	61.9[bc]
Copra meal	0.56	76.9[ab]
Corn germ meal	0.53	82.6[a]
Palm kernel expeller	0.54	70.6[abc]
Tapioca distillers dried grains	0.23	70.8[abc]
SEM		4.7
P-value		< 0.001

[a,b,c] Within a column, means without a common superscript letter differ ($P < 0.05$).

1313 (M187) Standardized total tract digestibility of phosphorus in cereal grains and coproducts fed to growing pigs.

Y. D. Jeong[1], C. S. Park[*2], B. G. Kim[2], and S. K. Park[1], *[1]Rural Development Administration, Suwon, South Korea, [2]Konkuk University, Seoul, South Korea.*

The objective of this experiment was to determine the standardized total tract digestibility (STTD) of P in 2 sources of cereal grain including barley and wheat and nine sources of byproduct ingredient including almond meal, two different sources of corn gluten feed, corn gluten meal (CGM), lupin hull (LH), lupin kernel (LK), rice bran (RB), soybean meal, and wheat bran. Each ingredient was included to an experimental diet as a sole source of P. A P-free diet was formulated to estimate the basal endogenous loss of P. A total of 12 diets were assigned to a 12 × 8 incomplete Latin square design with 12 barrows and 8 periods. Pigs with an initial BW of 46.7 ± 3.2 kg were individually housed in metabolism crates. Each period lasted 8 d consisted of 4-d adaptation and 4-d collection periods. Feces were collected based on the marker-to-marker method. Despite of the greatest concentration of P in RB, the STTD of P in RB was lower ($P < 0.05$) than CGM and LK (Table 1313). Value for the STTD of P in LH was also lower ($P < 0.05$) than those in CGM and LK. In conclusion, the STTD of P in barley and wheat were not significantly different and these values were similar to values in cereal coproducts used in this experiment.

Key Words: feedstuffs, macromineral, swine

Table 1313. Phosphorus (P) and standardized total tract digestibility (STTD) of P in 11 sources of oilseed meal fed to growing pigs (% as-fed basis, $n = 8$)

Item	P	STTD of P
Cereal grain		
Barley	0.30	60.3[ab]
Wheat	0.30	63.9[ab]
Cereal coproduct		
Almond meal	0.05	62.3[ab]
Corn gluten feed source 1	0.62	68.3[ab]
Corn gluten feed source 2	0.95	63.4[ab]
Corn gluten meal	0.24	75.7[a]
Lupin hull	0.17	51.3[b]
Lupin kernel	0.36	72.3[a]
Rice bran	1.73	53.3[b]
Soybean meal	0.62	66.1[ab]
Wheat bran	0.86	69.3[ab]
SEM		4.1
P-value		< 0.001

[a,b] Within a column, means without a common superscript letter differ ($P < 0.05$).

NONRUMINANT NUTRITION: THE IMPACT OF FEED ADDITIVES ON THE HEALTH AND PERFORMANCE OF SWINE AND POULTRY

1314 (T177) Evaluating the toxicity of metabolites derived from the trichothecene biotransformation using Biomin BBSH 797 in vitro. S. Schaumberger*[1], and U. Hofstetter[2], [1]*BIOMIN Holding GmbH, Herzogenburg, Austria,* [2]*Biomin Holding GmbH, Herzogenburg, Austria.*

Biomin BBSH 797, a *Gen. nov. sp. nov*. of the family *Coriobateriaceae* isolated from bovine rumen fluid, is able to specifically detoxify trichothecenes in the intestinal tract of animals. The live strain is able to produce enzymes that reduce the epoxide group of these mycotoxins, which results in the formation of non-toxic metabolites. The objective of this trial was to prove that the metabolite de-epoxy-deoxynivalenol (DOM-1), formed during the degradation of deoxynivalenol (DON), has lower toxicity. The lymphocyte proliferation assay (LPA) was used to show the effects of DON and DOM-1 on the clonal proliferation on isolated chicken lymphocytes. Lymphocytes were cultured with DON (10–0.08 µg/mL) and DOM-1 (232–1.18 µg/mL). As a control, the mitogen Concanavaline A (ConA) was used. The number of proliferated cells was quantified with a colorimetric immunoassay after in vitro stimulation. 5-Bromo-2'-deoxyuridine (BrdU) was added and incorporated into the DNA of proliferating cells. Incorporated BrdU was measured with an ELISA-method. The absorbance values directly correlated with the amount of DNA synthesis and hence the number of proliferating cells. Results show that at a concentration of 15 µg DON/mL the proliferation of lymphocytes was lower in comparison to ConA. After adding 0.3 µg DON/mL to the cells only one-third of them could proliferate whereas at a concentration of 0.63 µg DON/mL the growth of the lymphocytes stopped. In comparison, the metabolite DOM-1 only stopped the proliferation of cells at a concentration of 113 µg DOM-1/mL. The results show that the metabolite DOM-1 is almost 500 times less toxic than DON.

Key Words: Biomin BBSH 797, trichothecene, biotransformation

1315 (T178) Effects of dietary supplementation of β-mannanase on ileal digestibility of fiber and viscosity of jejunal digesta in nursery pigs fed corn and soybean meal-based diets. I. Park*[1], T. J. Pasquetti[1,2], and S. W. Kim[1], [1]*North Carolina State University, Raleigh,* [2]*Bolsista do, CNPq, Brazil.*

This study is to determine the effects of β-mannanase (CTCZYME, CTCBIO Inc., Seoul, South Korea) on ileal digestibility of nutrients and viscosity of jejunal digesta in nursery pigs fed corn and soybean meal-based diets. Forty-eight barrows at 6 wk of age (initial BW: 15.7 ± 1.1 kg) were assigned to four dietary treatments with different levels of β-mannanase (0, 200, 400, and 600 Unit/kg feed). Experimental diets contained 56.4% corn, 30.0% soybean meal, 10.0% DDGS, and 3.7% others. Pigs were housed individually in metabolism crates and received experimental diets at a fixed amount based on BW of pigs (daily feed allowance = 0.09 x $BW^{0.75}$ kg) for 11 d. Chromium oxide (0.3%) in experimental diets as an indigestible marker was provided from d 8 to 11. Actual feed intake, any feed refusals, and BW were measured on d 7 and 12 to monitor growth. On d 12 after 8 h of last meal, pigs were euthanized to collect digesta from jejunum and ileum. Digesta from jejunum were used to measure viscosity with a viscometer (DV+, Brookfield Engineering Laboratories, Inc., MA). Digesta from ileum were used to measure apparent ileal digestibility of energy, NDF, and ADF. Tissues from jejunum were fixed for morphological evaluation. The data were analyzed using PROC MIXED of SAS based on randomized complete block design. Morphology of jejunum was not affected by dietary supplementation of β-mannanase. Viscosity of digesta in jejunum tended to decrease linearly (P = 0.076, 5.2 to 3.8 mPa·s) with increasing supplementation of β-mannanase. Dietary β-mannanase also tended to increase (P = 0.093, 53.4 to 64.7%) apparent ileal digestibility of energy in a quadratic manner at the highest digestibility at 600 Unit of β-mannanase per kg feed. There was no change in ileal digestibility of NDF and ADF by supplemental β-mannanase indicating that the increase in energy digestibility is not due to the release of monosaccharides from mannans by β-mannanase. Collectively, dietary supplementation of β-mannanase enhanced energy utilization in nursery pigs by reducing viscosity of digesta potentially enhancing digestibility of nutrients.

Key Words: ADF, β-mannanase, energy utilization, NDF, pigs, viscosity

1316 (T179) Effects of dietary supplementation of selenium-enriched probiotics on productive performance and intestinal microflora of weanling piglets raised under high ambient temperature. C. Lv[1], T. Wang*[2], S. F. Liao[2], and K. Huang[1], [1]*Nanjing Agricultural University, Nanjing, Jiangsu, China,* [2]*Mississippi State University, Starkville.*

Probiotics have been suggested as one of the most desirable alternatives to feed antibiotics for swine. The objective of this study is to evaluate the efficacy of a selenium-enriched probiotics (SeP) preparation on productive performance and intestinal microflora of piglets raised under high ambient temperature. Forty-eight crossbred weanling piglets (28 d old) randomly allotted into 12 pens (four piglets/pen) and four dietary treatments (three pens/treatment) were fed ad libitum for 42 d a basal diet (control; Con), or the basal diet supplemented with

probiotics (Pro), sodium selenite (ISe), or the SeP preparation. The basal diet contained 0.16 mg/kg-diet of total intrinsic Se, and the ISe and SeP preparations elevated the total Se level to 0.46 mg/kg-diet. The Pro and SeP preparations contained equivalent amounts of *Lactobacillus acidophilus* and *Saccharomyces cerevisiae* (approximately 10^{11} and 10^{9} CFU/mL, respectively). Blood and fecal samples were collected on d 0, 14, 28, and 42 post-initiation of the feeding trial. The SeP group had higher final BW ($P < 0.05$), greater ADG ($P < 0.05$), lower FCR ($P < 0.01$), and lower diarrhea incidence ($P < 0.01$) than the Pro, ISe or Con group. Blood Se concentration and GSH-Px activity were both higher ($P < 0.01$) in the SeP group than in the Pro, ISe or Con group. On d 28 and 42, the serum concentrations of T3 were higher ($P < 0.01$) and T4 lower ($P < 0.01$) in the SeP group than in the ISe, Pro or Con group. On d 28, the serum T3 in the ISe group was higher ($P < 0.01$) than in the Pro or Con group, and on d 28 and 42 the serum T4 were lower ($P < 0.01$) in the ISeP group than in the Pro or Con group. Also on d 28 and 42, the fecal counts of *Lactobacillus* bacteria was higher ($P < 0.01$) while *Escherichia coli* lower ($P < 0.01$) in the SeP or Pro group than in the ISe or Con group. The results of RFLP showed that the fecal microbial flora in the SeP group changed the most (numerically) as compared to the Pro or ISe group. In conclusion, the overall results of this study indicate that this SeP preparation may serve as a better alternative to antibiotics than pure probiotics for using as a growth promoter for piglets.

Key Words: probiotics, selenium, pig, productive performance, fecal microflora, glutathione peroxidase, thyroid hormone

1317 (T180) Growth performance and carcass characteristics of pigs fed high-fiber diets supplemented with *Bacillus* spp. expressing multi-enzyme activities.

A. Owusu-Asiedu[*1], R. Lizardo[2], J. Brufau[2], and A. Awati[1], [1]*DuPont Industrial Biosciences- Danisco Animal Nutrition, Marlborough, Wiltshire, United Kingdom,* [2]*IRTA-Mas de Bover, Constantí, Tarragona, Spain.*

Increasing the amount of cereal byproducts such as corn distillers-dried grain with solubles; CDDGS, and wheat bran; WB in swine diets decreases pig performance and negatively affects carcass characteristics. The current study evaluated the potential of specifically selected *Bacillus* spp. direct fed microbial product with multi-enzyme activities (BDFM) to counteract the negative effect in pigs fed diets containing 20% CDDGS and 20% WB. Ninety-six Pietrain X (Landrace X Duroc) pigs (initial BW 31.60 ± 1.30 kg) were used in a 14-wk study. Pigs were blocked by BW and sex and randomly assigned to two dietary treatments with three pigs/pen and 16 replicate pens/treatment. The basal diets were formulated to meet the nutritional requirements of the pigs and contained corn and SBM and cereal byproducts. The NE and digestible Lys in the basal starter, grower and finisher phases diets were; 9.77, 9.85, and 9.71 MJ/kg, and 1.01, 0.93, and 0.85%, respectively, and AA were adjusted on ideal protein basis. The *Bacillus* product containing 3×10^{8} CFU/g was added at 0 (Control) or 500 g/MT of feed in the test diet (BDFM). Pigs were allowed to consume the assigned experimental diet for the entire study period, and ADG, ADFI and G:F determined. Backfat and loin depth were measured at slaughter using a Fat-O-Meater device and carcass lean meat percentage determined. Data were analyzed using the Proc PROC MIXED in SAS. Overall, ADFI (1910 vs. 1887; SEM = 27.34) and ADWG (762 vs. 779 g/d; SEM = 11.20) were not affected ($P > 0.05$) by BDFM supplementation. However, compared with Control, pigs fed the BDFM supplemented diet had improved ($P < 0.05$) overall G:F ratio (0.400 vs. 0.413; SEM = 0.004). Carcass weight and killing-out percentage tended to improve ($P < 0.10$), whereas backfat depth was reduced (16.8 vs. 15.1 mm; $P = 0.01$) and lean meat percentage improved (58.9 to 61.5%; $P = 0.01$) with BDFM supplementation compared with control. In conclusion, dietary inclusion of specifically selected *Bacillus* spp. expressing multi-enzyme activities improved feed efficiency and carcass characteristics in pigs fed high fiber-based diets.

Key Words: *Bacillus* spp., dietary fiber, pigs

Table 1317.

	Control	BDFM	SEM	*P*-value
Growth Performance (d0 to 97)				
Overall ADG, g/d	761.8	778.6	11.10	0.29
Overall ADFI, g/d	1910.0	1887.2	27.34	0.56
Gain:Feed	0.400	0.413	0.004	0.04
Carcass Characteristics				
Carcass weight, kg	78.8	79.5	0.272	0.08
Kill out percent, %	74.2	74.9	0.255	0.09
Backfat depth, mm	16.8	15.1	0.462	0.01
Lean meat, %	59.8	61.5	0.453	0.01

1318 (T181) Effects of star anise (*Illicium verum*) on growing performance and antioxidant status of sows and nursing piglets.

G. Y. Wang[1], C. Yang[2], Y. X. Guo[1], Z. Yang[*3], and Y. Wang[4], [1]*College of Animal Science, Shandong Agricultural University, Tai-an, China,* [2]*College of Life Science, Shandong Agricultural University, Taian, China,* [3]*College of Animal Science, Shandong Agricultural University, Taian, China,* [4]*Agriculture and Agri-Food Canada, Lethbridge, AB*.

To investigate the effects of star anise (*Illicium verum*) that was processed to particle sizes of 300 μm on performance and antioxidant status of sows and nursing piglet**s**. Thirty sows (Landrace × Large White) at 85 d of gestation were randomly allocated into 5 treatments with 6 replicates in a complete randomized design. Pregnant sows were fed corn-soybean meal

based diets and supplemented with 0, 2.5, 5.0, 7.5 and 10.0 g/kg diet of star anise (SA) powder, respectively. After farrowing, all sows were fed a lactation diet without star anise until weaning and litter size was standardized to 10 piglets by cross-fostering within 24 h postfarrowing. ADFI, body weight loss of lactating sows, body weight and eliminating ratio of piglets of each replicate were measured weekly. Blood samples from 6 sows and 12 piglets per treatment were obtained at weaning to determine the serum antioxidant enzymatic activities. All treatments had similar body weight loss of sows, birth weight, body weight at d 7 and mortality rates of piglets. However, pregnant sows supplemented with 5 g/kg SA had higher ($P < 0.05$) average daily gain and body weight of piglets at d 14 and d 21 as compared with that of control. With pregnant sows supplemented SA at the level of 2.5 to 10 g/kg, lactating sows had higher ($P < 0.05$) activities of superoxide dismutase (SOD) than the control. In lactation period, concentration of malondialdehyde (MDA) was lower ($P < 0.05$) with dietary supplementation star anise from late pregnancy to the end of breastfeeding at the level of 5.0 g/kg. The activities of glutathione peroxidase (GSHPx) and total antioxidant capacity (T-SOD) in serum of lactating sows were increased by the addition SA at levels of 5.0 and 7.5 g/kg. As compared with that of control, all additions of star anise had lower ($P < 0.05$) MDA, however, piglets had higher ($P < 0.05$) activities of SOD, T-SOD and GSHPx in serum with pregnant sows supplemented SA at the level of 2.5 to 10 g/kg. Dietary supplementation star anise from late pregnancy to the end of breastfeeding improved growing of piglets and serum antioxidant status of lactating sows and weaning piglets. The optimum supplementation rate of SA in the pregnant sow's diet appeared to be between 2.5 and 5 g/kg diet.

Key Words: star anise, sow, piglets, growing performance, antioxidant status

---

1319 (T182) The effects of Calibrin-Z or a Calibrin-Z-based blended product on post-weaning performance of nursery pigs. S. L. Johnston*[1], F. Chi[1], S. Ching[1], R. Cravens[1], and O. Adeola[2], *[1]Amlan International, Chicago, IL, [2]Purdue University, West Lafayette, IN.*

One hundred ninety-two pigs (BW = 5.8 kg, 21 d old) were used in an experiment to evaluate the effects of two clay-mineral products on the post weaning performance of nursery pigs. The two products were a clay-mineral product, Calibrin-Z (Z), and a Calibrin-Z-based blended with a fermentable fiber and an organic acid (CBZ). There were four treatments: 1) Control (C); 2) C+Z at 0.2%; 3) C+CBZ at 0.1%; and 4) C+CBZ at 0.3%. The experiment was conducted as a randomized complete block design with weight and sex as blocking factors. There were four pens of gilts and four pens of barrows per treatment, with six pigs per pen. Pigs had ad libitum access to feed and water. The trial lasted 35 d, diets were corn and soybean meal-based complex nursery diets, all ingredients were commercially available so mycotoxins concentration would be those comonly found in commercial diets. There were decreasing amounts of whey, plasma, soy protein concentrate, fishmeal and lactose as the trial progressed. No differences ($P > 0.1$) in ADG were seen during the experiment with values for ADG for d 0 to 35 of 302 g for the C fed pigs vs. an average of 324.4 g for the pigs fed the two products. There was a significant improvement ($P < 0.05$) in the G:F ratio from diet supplementation from the two products from d 21 to 28, but there was no difference ($P > 0.1$) between products indicating that either product would increase feed efficiency. Furthermore, there was a linear ($P < 0.05$) improvement in G:F from d 21 to 28 when pigs were fed increasing concentrations of CBZ. During the last 2 wk, there was a tendency ($P < 0.10$) for improved G:F with diet supplementation from the two products, again with no difference ($P > 0.1$) between products, and a tendency ($P < 0.10$) for linear improvement in G:F with addition of CBZ. For the overall period there was a tendency ($P < 0.10$) for linear improvement in G:F from increasing concentration of CBZ and an improvement in G:F ($P < 0.05$) from dietary supplementation from Z or CBZ, with overall G:F ratios of 653 g/kg for the C pigs vs. an average of 680 g/kg for the pigs fed the C or CBZ, with no difference ($P > 0.1$) between the two products. Thus, supplementing the diet of nursery pigs with Calibrin-Z based products improved feed efficiency.

Key Words: feed efficiency, nursery, pigs

1320 (T183) Nutrient digestibility of rice bran, with or without exogen enzymes, for weaned piglets. J. C. Dadalt*, G. D. V. Polycarpo, C. Gallardo, P. D. A. P. Ribeiro, B. Alves, and M. A. D. T. Neto, *University of São Paulo, Pirassununga, Brazil.*

The objective of the current study was to evaluate the digestibility of dry matter (DM), crude protein (CP), mineral matter, apparent digestible (DE) and metabolizable (ME) energy, and nitrogen retention of rice bran (RB), with or without exogen enzymes inclusion, in weaned piglets. Twenty-five crossbred barrows with initial weight 6.86 kg ± 1.3 kg, were alloted in a completely randomized design under five treatments and five replicates. The experimental unit was represented by one pig within its respective metabolic cage. The experimental period was 10 d, 5 d of adaptation and 5d of total feces and urine collection. The treatments were: Control diet (CD); CD + 30% rice bran (CD + RB); CD + 30% RB + 200 mg/kg of carbohydrase (CD+RB+Carb); CD + 30% RB + 50 mg/kg of phytase (CD+RB+Phy); CD + 30% RB+ Carb + Phy (CD+RB+Carb+Phy). The control diet was based on corn (61.33%), skim milk powder (10%) and dried whey (15%). The enzymes used were: commercial phytase with an activity of 10,000 FTU/g; carbohydrase providing 10% of Galactomananase, 10% of Xilanase, 10% of β-glucanase, 60% of malted barley and 10% of α-galactosidase. Isolated or combined with carbohydrase,

phytase did not influence ($P > 0.05$) the digestibility of rice bran nutrients. These results would be associated with adverse factors such as animal and nutritional profile of feedstuff. The DE– 3062 kcal/kg and ME– 3029 kcal/kg were similar to Brazilian tables for poultry and pigs (2011). The apparent digestibility coefficients of DM, CP, mineral matter and nitrogen retention were 65.47%; 72.58%; 36.59% and 62.21%, respectively. These results were similar some found in the literature using growing and finishing pigs, however, there are different results. The current study suggests that the used enzymes are not effective to improve nutritional value of gross energy, DM, CP and MM of rice bran for young pigs after weaning.

Key Words: carbohydrase, metabolism, phytase

Table 1320. Digestibility coefficients of rice bran for weaned piglets

	Ingredients					
Variables	RB	RB+ Carb	RB+ Phy	RB+ Carb+ Phy	*P*-values	SEM
DM %	65.47	68.76	68.38	67.38	05730	0.866
CP %	72.58	76.13	75.45	75.26	08424	1.401
N retention %	62.21	63.69	64.12	65.40	09206	1.525
MM %	36.59	42.20	44.28	45.56	07090	2.774
DE (kcal/kg)	3062	3201	3123	3093	06105	40.677
ME (kcal/kg)	3029	3165	3089	3058	06255	40.915
ME:GE %	66.85	69.87	68.17	67.50	06271	0.813

1321 (T184) The improvements in growth, bone mineral status and nutrient digestibility in pigs following the addition of phytase is accompanied by modifications in ileal nutrient transporters.

S. Vigors*[1], T. Sweeney[2], D. N. Doyle[1], C. J. O'Shea[1], and J. V. O'Doherty[1], *[1]School of Agriculture and Food Science, University of College Dublin, Ireland, [2]College of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Ireland.*

Phytase improves growth performance, nutrient digestibility and bone structure in pigs. However, little is known about its effect on ileal nutrient transporter gene expression. Before the start of the experiment all pigs were allowed an adaption period of 14 d and were fed a standard weaning diet. Forty-eight weaner pigs (11.75kg, sem 0.75) were randomly assigned to one of three experimental diets for a period of 44 d to measure growth performance. Following this six animals per treatment were randomly selected and slaughtered to measure the coefficient of apparent ileal nutrient digestibility (CAID), coefficient of apparent total tract nutrient digestibility (CATTD) and ileal nutrient transporter gene expression. The experimental treatments were as follows, 1) a high phosphorus (HP) diet containing 5.9 g/kg total P (tP), 3.2 g/kg available P (aP) and 6.8 g/kg calcium (Ca), 2) a low phosphorus (LP) diet containing 4.5 g/kg (tP), 1.8 g/kg aP and 5.2 g/kg Ca and 3) a phytase (*P*HY) diet containing the LP diet + 1000 FTU/kg of phytase. The addition of PHY increased ADG (700 g/day vs. 610 g/day sem 0.02; $P < 0.05$), final BW (43kg vs. 37kg sem 1.02; $P < 0.01$) and decreased FCR (1.74 vs. 2.05 sem 0.09; $P < 0.05$) compared with the LP diet. Pigs offered the PHY diet had higher CAID of gross energy (748 g/kg vs. 699 g/kg vs. 700 g/kg, sem 7.0; $P < 0.001$) compared to the HP and LP diets, respectively. Pigs offered the PHY diet had a higher CAID of nitrogen (716 g/kg vs. 669 g/kg sem 14.3; $P < 0.05$) compared to the HP diet. The addition of PHY improved the CATTD of Ca (766 g/kg vs. 487 g/kg vs. 451 g/kg sem 42.96; $P < 0.001$) and P (558 g/kg vs. 220 g/kg vs. 389 g/kg sem 43.12; $P < 0.001$) compared to both LP and HP, respectively. The PHY diet had increased gene expression of PEPT1 (1.40 vs. 0.47 sem 0.29, $P < 0.05$) and a tendency towards increased gene expression of FABP2 (1.67 vs. 0.73 sem 0.37 $P < 0.10$) compared to the LP diet. The LP diet had lower gene expression of SGLT1 (1.32 vs. 0.51 sem 0.31) and GLUT2 (0.26 vs. 1.26 sem 0.29) ($P < 0.05$) compared to the HP diet. In summary, offering a diet supplemented with PHY improves growth performance and ileal and nutrient digestibility. PHY addition increases the gene expression of the peptide transporter PEPT1 and tended to increase the fatty acid transporter FABP2.

Key Words: phytase, nutrient transporter gene expression, pigs

1322 (T185) Effects of bromelain supplementation on growth performance, nutrient digestibility, blood profiles, fecal microbial shedding, fecal score, and fecal noxious gas emission in weanling pigs.

M. M. Hossain*, H. L. Li, and I. H. Kim, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

A total of 140 weanling pigs [(Yorkshire × Landrace) × Duroc] with an average BW of 6.75 ± 1.48 kg were used in a 6-wk trial. Pigs were randomly allotted to one of four experimental treatments according to their initial BW (7 pens per treatment with 5 pigs per pen). Dietary treatments were: CON, basal diet; T1, CON + 0.05% bromelain; T2, CON + 0.10% bromelain; T3, CON + 0.20% bromelain. The experiment was divided into two phases (d 1 to 14 and d 15 to 42). All diets, in mash form, were formulated to meet or exceed the nutrient requirements (NRC, 2012) for weanling pigs. Feed intake and BW were monitored at the end of each phase. T3 treatment had greater (342 vs. 305 g; 409 vs. 387 g; $P < 0.05$) ADG and ADFI than CON treatment in phase 1. In phase 2, the ADG was improved (from T1 to T3: 612, 616, 637 vs. 583 g; $P < 0.05$) in all bromelain treatments compared with CON treatment, ADFI and G:F ratio of T3 treatment was higher (833 vs. 803 g; 0.765 vs. 0.726; $P < 0.05$) compared with CON treatment. Overall, T3 treatment showed greater (539 vs. 490 g; 691 vs. 664 g; $P < 0.05$) ADG and ADFI than CON. Moreover, pigs fed bromelain diets increased (0.769, 0.770, 0.780 vs. 0.738; $P < 0.05$) G:F ratio compared with those fed CON diet. Pigs fed bromelain diets increased (2 wk: 79.06,

79.96, 79.42 vs. 77.98%; 78.51, 78.86, 78.43 vs. 75.69%; 6 wk: 74.49, 74.67, 75.02 vs. 72.70%; 69.43, 70.78, 71.32 vs. 73.39%; $P < 0.05$) the ATTD of dry matter and nitrogen compared with those fed CON diet at wk 2 and wk 6. On d 42, the blood creatinine in CON group was higher (1.30 vs. 1.04, 0.97, 0.88 mg/dL; $P < 0.05$) compared with those in bromelain treatments. The concentration of fecal *E. coli* counts were decreased (6.22 vs. 6.41 $\log_{10}$cfu/g; $P < 0.05$) in T2 treatment compared with CON treatment. The fecal NH_3 emission in T2 and T3 treatments decreased (17.72, 17.33 vs. 22.95 ppm; $P < 0.05$) compared with CON. In conclusion, dietary supplementation with 0.2% bromelain has been shown to improve the growth performance, ATTD of DM and N, and decreased *E. coli* and excreta NH_3emission in weaning pigs.

Key Words: bromelain, growth, performance, fecal microbial, weanling pigs

---

1323 (T186) Effect of nutrifen supplementation with different levels of metabolic energy on growth performance, nutrient digestibility, meat quality, blood profile, excreta microflora, and excreta gas emission of broiler chickens. H. Shin, A. Hosseindoust, and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

A total of 816 ROSS 308 both male, female 1-d old, body weight 45.2 ± 0.7 g broiler chicken were used in this 4-wk trial to evaluate the effect of nutrifen supplemented to broiler chicken diets containing different levels of metabolizable energy. Experimental diets consisted of two different levels; high energy diet (HE) and low energy diet (LE, 100kcal lower than HE diet, ME in HE diet: phase 1, 2950 kcal/kg; phase 2, 3100 kcal/kg) and the experimental treatments were: 1) LCON (low energy diet); 2) LNF (LCON + nutrifen 0.09%); 3) HCON (high energy diet); and 4) HNF (HCON + nutrifen 0.09%). There were 12 replications and 17 chickens per replication in each treatment. Results showed that HNF treatment enhanced body weight gain (431 vs. 398 g; 1523 vs. 1470 g; $P < 0.05$) compared with LCON treatment at d 14 and 28. There was no effect ($P > 0.05$) on carcass and meat quality among treatments. However, yellowness in high energy level diets was increased (HCON and HNF vs. LCON and LNF: 8.53, 8.55 vs. 7.95, 7.69; $P = 0.036$) compared with that in low energy level diets. Digestibility of dry matter in nutrifen treatments was higher (LNF and HNF vs. LCON and HCON: 77.43, 77.70 vs. 74.95, 75.47%; $P = 0.025$) than that in CON treatments. As to nitrogen digestibility, HNF treatment was higher (67.87 vs. 64.90%; $P < 0.05$) compared with that in LCON treatment. Total cholesterol in LNF treatment was decreased (106.8 vs. 117.8, 118.9mg/dL; $P < 0.05$) than that in LCON and HCON treatments. Also, total cholesterol of chickens fed with nutrifen diets was decreased (LNF and HNF vs. LCON and HCON: 106.8, 114.1 vs. 117.8, 118.9 mg/dL; $P < 0.05$) compared with those fed with CON diets. Ammonia gas emission in LNF treatment was decreased (34.8 vs. 42.9, 40.3 ppm; $P < 0.05$) than that in HCON and HNF treatments. Moreover, low energy level treatments were decreased (LCON and LNF vs. HCON and HNF: 38.8, 34.8 vs. 42.9, 40.3 ppm; $P = 0.003$) excreta ammonia gas emission compared with high energy level treatments. No interaction effect was observed in this trial. These results showed that adding nutrifen at a level of 0.09% in diet can improve the growth performance, nutrient digestibility, blood cholesterol contents of broiler chickens.

Key Words: broiler chickens, energy level, growth performance, nutrifen

---

1324 (T187) Effect of fermented organic rare earth (ORE) on growth performance, nutrient digestibility, blood profiles, meat quality, relative organ weight, excreta microflora, and noxious gas emission in broiler chickens. Y. Liu, S. D. Upadhaya, and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

This study was to evaluate the effect of fermented organic rare earth (ORE) in broiler chickens. A total of 765 ROSS 308 1-d-old broilers, BW of 48.97 ± 0.11 g, were used in this 4-wk feeding trial, 1 to 14 d for starter and 15 to 28 d for finisher. Dietary treatments included 1) NC (Basal diet, free antibiotics diet), 2) ORE1 (NC + fermented ORE 0.05%), 3) ORE2 (NC + fermented ORE 0.10%), 4) ORE3 (NC + fermented ORE 0.15%), and 5) PC (Antibiotics diet, NC + tiamulin 0.1%). All birds were allotted into one of five treatments with nine replications (17 birds per replication) in a completely randomized design. At the starter stage, feed intake (FI) was increased (1.250 vs. 1.284; $P < 0.05$) in ORE2 compared with NC. At the finisher stage, BW gain (BWG) tended to increase (NC, ORE1, ORE2, ORE3: 953, 973, 976, 992 g; linear, $P = 0.061$) as the level of fermented ORE increased in the diets. The FCR in PC was improved (1.699 vs. 1.764, $P < 0.05$) compared with the NC. At the end of the trial, DM (78.31 vs. 75.52%; $P < 0.05$; linear, $P = 0.050$) and GE (79.96 vs. 76.61%; $P < 0.05$; linear, $P = 0.010$) in treatment ORE3 increased compared with NC, and they also increased as the level of fermented ORE increased in the diets. The DM digestibility in PC was higher (78.49 vs. 75.52%; $P < 0.05$) than that in NC. The pH value of breast muscle in ORE2 increased (5.58 vs. 5.41; $P < 0.05$) compared with PC. Yellowness (NC, ORE1, ORE2, ORE3: 15.51, 15.34, 16.14, 17.17; linear, $P = 0.003$) increased with the increasing amount of fermented ORE in the diets. And the lower value of drip loss was observed in broiler chickens fed the diet with 0.15% fermented ORE (3.14 vs. 4.32%; $P < 0.05$) than PC treatment. There was a tendency to increase the weight of liver (NC, ORE1, ORE2, ORE3: 2.95, 2.86, 3.23, 3.23; $P < 0.01$) as the amount of fermented ORE increased in the diet. However, there was no influence on the relative organ weight, excreta microflora, and noxious gas emission. In conclusion, the results from this study demonstrate that feeding

0.10 or 0.15% fermented ORE improved growth performance, nutrient digestibility, and meat quality in broiler chickens.

Key Words: broiler chicken, excreta microflora, fermented organic rare earth, growth performance, meat quality, nutrient digestibility

1325 (T188) Apparent total tract digestibility and Ileal digestibility of dry matter, nitrogen, energy and amino acids in conventional, *Bacillus subtilis* fermented and enzyme treated soybean meal fed to weanling pigs. H. Yun, E. Balolong Jr., and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

This experiment was conducted to determine the apparent total tract digestibility (ATTD), apparent ileal digestibility (AID) and standardized ileal digestibility (SID) dry matter, nitrogen, energy and amino acids of six soybean products. The products were soybean meal (SBM), fermented soybean meal A (FSMA), fermented soybean meal B (FSMB), fermented soybean meal C (FSMC), enzyme treated soybean meal (ETSM) and speciality soya protein (HP300). There are six treatments: SBM, FSMA, FSMB, FSMC, HP300 and N-free dietary treatments. In the experiment, six [(Landrace × Yorkshire) × Duroc] weanling barrows with average BW 8.99 ± 0.40 kg were surgically equipped with simple T-cannulas approximately 15 cm before the ileo-cecal junction and allowed to a 6-wk feeding trial. Results of the experiment showed that FSMC and HP300 had the greatest (90.03, 89.35%; $P < 0.05$) ATTD for most AA, but the ATTD for Arg, Ile, Lys, Met and Phe in FSMB similar to FSMC. Piglet fed FSMC and HP300 had higher (89.02, 88.86 vs. 85.84%; 88.19, 87.69 vs. 84.42%; $P < 0.05$) DM and energy digestibility compared to SBM. AID of DM, N and energy and total AA in FSMB, FSMC and HP300 were higher (82.40, 82.71, 82.59 vs. 78.45%; 82.54, 83.24, 82.95 vs. 79.33%; 81.26, 82.27, 81.68 vs. 76.77%; 80.90, 81.45, 80.78 vs. 77.83%; $P < 0.05$) than SBM in which the value was highest in the FSMC diet. The AID of Isoleucine was greater in pigs fed FSMB and HP300 than in FSMA. The AID of Arg, Leu, Phy and Val in FSMC was greatest of all the other soybean meals. The AID of Lys (74.73%) and total AA (77.90%) in FSMA was the least ($P < 0.05$) among the entire soybean products, but the AID for most other AA in FSMA was not different from the value of AID of AA in SBM. The SID of His (82.28%), Lys (78.65%) and total AA (82.34%) in FSMA was the least ($P < 0.05$) among all the protein sources but SID for most other AA in FSMA was not different from the SID of AA in SBM. In conclusion, dietary supplementation of FSMC and/or HP300 can improve the ATTD, AID and SID of DM, N, energy, total AA and most of the essential amino acids in weanling pigs.

Key Words: amino acids, apparent ileal digestibility, apparent total tract digestibility, fermented soybean meal, hamlet protein, weanling pigs

1326 (T189) Effect of bromelain supplementation on growth performance, nutrient digestibility, blood profiles, fecal score, fecal microflora and noxious gas emission in sows and piglets. M. Jung, Y. Lei, and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

This study was conducted to investigate the effect of dietary bromelain on growth performance, nutrient digestibility, blood profiles, and fecal microflora of sows and piglets. Twenty sows (Landrace × Yorkshire) were randomly assigned to three dietary treatments. Dietary treatments included: 1) CON (basal diet), 2) T1 (basal diet + 0.05% Bromelain), 3) T2 (basal diet + 0.10% Bromelain), 4) T3 (basal diet + 0.20% Bromelain). Individual piglet BW was assessed on d 0, 7, 14, and 21 (weaning), and 7 d after weaning to calculate ADG. Fecal *Lactobacillus* and *E. coli* shedding were measured by using MacConkey agar plates and lactobacilli medium III agar plates. No difference ($P > 0.05$) was observed on body weight loss, parity, litter number, weanling pig number, backfat, estrus interval and ADFI in sows. The birth weight of litter from CON treatment was lower (1.343 vs. 1.510, 1.491 kg; $P < 0.05$) compared with T2 and T3 treatments and the piglets of T3 group also had higher (6.953 vs. 6.073 kg; $P < 0.05$) weanling weight compared with CON group. Moreover, T3 treatment had a higher (212 vs. 182 g; $P < 0.05$) ADG than CON treatment. However, there is no difference ($P > 0.05$) in piglet survival rate and stillbirth rate among treatments. After weaning of piglets, the ATTD of N in sows fed with T3 diet was higher (68.95 vs. 63.96, 64.55%; $P < 0.05$) compared with sows fed with CON and T1diets. The ATTD of E and DM showed no difference ($P > 0.05$) among treatments. The blood BUN of sows in T3 group was lower (12.0 vs. 15.7 mg/dL; $P < 0.05$) compared with CON group. Moreover, the BUN of piglets in T3 group was lower (12.6 vs. 15.9 mg/dL; $P < 0.05$) compared with T1 group. There was no difference ($P > 0.05$) in WBC, RBC, lymphocyte, IgG and ceatinine observed among treatments in sows and piglets. The fecal *Lactobacillus* of sows fed with T2 and T3 diets were higher (7.39, 7.40 vs. 7.28 $\log_{10}$cfu/g; $P < 0.05$) compared with sows fed with CON diet. Moreover, the fecal *E. coli* concentration of sows fed with T2 and T3 diets were lower (6.26, 6.28 vs. 6.57 $\log_{10}$cfu/g; $P < 0.05$) compared with sows fed with CON diet. In conclusion, the addition of 0.2% Bromelain in the diet can improve weaning BW in piglets and increase nutrient digestibility of sows during lactating period.

Key Words: Bromelain, performance, piglet, sow

1327 (T190) Effect of Calsporin on growth performance, nutrients digestibility, organ weight, meat quality and excreta and intestinal microflora and slurry noxious gas emission in broiler chickens. H. Beak, H. L. Li, and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

This study was conducted to determine the effect of dietary Calsporin supplementation on growth performance, nutrient digestibility, relative organ weight, meat quality, intestinal microbial flora, and slurry noxious gas emissions in broilers. A total of 816 1-d-old male ROSS 308 broilers (BW of 46.06 g ± 0.67 g; 16 pens/treatment and 17 broilers/pen) were used in a 5-wk study. Broilers were randomly allotted to 1 of 3 dietary treatments and Calsporin BBS, which contains 1×10^9 CFU/g *Bacillus subtilis* C-3102.: T1) CON, basal diet, T2) CON + 300 ppm Calsporin (3×10^5 CFU/g), and T3) CON + 600 ppm Calsporin (6×10^5 CFU/g). The T3 enhanced BW gain (BWG) (700 vs. 658 g; $P < 0.05$) compared with the CON treatment during the d 8 to 21. During d 22 to 35, T3 showed greater BWG (843 vs. 801 g; Linear, $P < 0.05$) and better feed conversion ratio (FCR) (1.665 vs. 1.792; Linear, $P < 0.05$) than those in CON. The FCR (1.686 vs. 1.792; Linear, $P < 0.05$) in T2 was linearly improved compared with CON. In the overall period, the BWG (1630, 1662 vs. 1573 g; $P < 0.05$) and the FCR (1.544, 1.534 vs. 1.624; $P < 0.05$) in T2 and T3 were higher than the control. The apparent total tract digestibility (ATTD) of dry matter (DM) (73.43 vs. 76.54, 77.20%; $P < 0.05$) and energy was linearly increased (75.34 vs. 78.83, 79.87%; $P < 0.05$) by Calsporin inclusion in the diet. Slurry NH3 emissions were linearly reduced (9.9 vs. 8.2, 7.8 ppm; $P < 0.05$) by dietary supplementation of Calsporin. The *Lactobacillus* counts in cecum and ileal were linearly (6.25, 6.59, 7.16 $\log_{10}$cfu/g; $P < 0.05$) increased by Calsporin inclusion in the diet. Dietary supplementation of Calsporin linearly reduced *E. coli* counts in cecum (6.12, 5.74, 5.43 $\log_{10}$cfu/g; $P < 0.05$) *Cl. Perfringens* counts in large intestine (3.14, 2.97, 2.86 $\log_{10}$cfu/g; $P < 0.05$) and excreta (3.31, 3.17, 3.03 $\log_{10}$cfu/g; $P < 0.05$), and *Salmonella* counts in cecum (2.66, 2.23, 2.13 $\log_{10}$cfu/g; $P < 0.05$), ileal (2.87, 2.58, 2.42 $\log_{10}$cfu/g; $P < 0.05$), large intestine (3.04, 2.59, 2.44 $\log_{10}$cfu/g; $P < 0.05$) and excreta (2.88, 2.76, 2.61 $\log_{10}$cfu/g; $P < 0.05$). In conclusion, results indicate that Calsporin inclusion can improve BWG and FCR, increase cecum *Lactobacillus* counts and reduce intestinal *E. coli, Cl. Perfringens* and *Salmonella* counts, especially at 6×10^5CFU/g.

Key Words: growth performance, probiotics, fecal microbial, broilers

1328 (T191) Evaluation of Korean aged garlic extract (AGE) by *Leukonostoc citreum* SK2556 on production achievement, meat quality, relative organ weight, targeted *Escherichia coli* colony, slurry gas emission and hematological profiles in broilers. *J. W. Park, S. D. Upadhaya, and I. H. Kim*, Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

The aim of this study was to investigate the effects of dietary supplementation of Korean aged garlic extract (AGE) fermented by *Leukonostoc citreum* SK2556 on growth performance, meat quality, excreta microbiota, slurry gas emission and blood profiles in broilers. A total of 765 broilers were randomly allotted to 5 treatments with 9 replications per treatment and 17 chicks per pen in this 5-wk trial. The experiment lasted for 5 wk and dietary treatments were as follows: 1) NC (basal diet, no antibiotics); 2) PC (NC + 5ppm enramycin); 3) AGE1(NC + 0.05% aged garlic extract); 4) AGE2 (NC + 0.1% aged garlic extract); 5) AGE3 (NC + 0.2% aged garlic extract). The broilers were weighed and feed intake were recorded on d 1, 14, 28, and 35 for calculating BW gain (BWG), feed intake (FI), and feed conversion ratio (FCR). All data were subjected to GLM procedures of SAS (1996) as a randomized complete block design, with pen as the experimental unit. Differences among treatments were separated by Duncan's multiple range test; $P < 0.05$ was considered statistically significant. Broiler fed with AGE2 treatment showed significantly higher ($P < 0.05$) disparity in BWG compared to NC treatment (910 g vs. 842 g) at the d 15 to d 28. In the same time, FCR was higher ($P = 0.0454$) in NC (1.95) treatment compared with AGE3 (1.83) and AGE2 (1.81). Growth performance was increased in AGE3 (1756 g) and AGE2 (1735 g) than NC (1638 g) diet ($P < 0.05$) though FCR value was decreased ($P = 0.012$). Liver weight was decreased in AGE3 (28.27%) and AGE2 (28.27%) compared to NC (40.60%) treatment ($P = 0.0478$). On analyzing of different profiles of breast meat, only redness (a*) was improved in NC treatment than AGE2 (15.94 vs. 12.23; $P < 0.05$). With regards to *E. coli* load ($\log_{10}$cfu/g), broiler fed NC (6.70) showed distinctly higher count than AGE2 (6.54; $P < 0.05$). The percentage of lymphocyte in blood presented higher in numeric value in AGE1 treatment which was followed by PC, AGE2, NC and AGE3 respectively ($P > 0.05$). In conclusion, our findings demonstrated that the administration of AGE at a level of 0.1 and/or 0.2% can improve body weight gain but reduce the FCR, liver weight as percentage, and *E. coli* load without significant change in other criteria in broiler.

Key Words: aged garlic extract, broilers, *Leukonostoc citreum* SK2556, enramycin, growth performance, microflora

1329 (T192) The effect of vitality mineral liquid complex on production performance, nutrient digestibility, blood characteristics, egg quality and excreta microflora in laying hens. M. Mohammadi Gheisar, J. P. Lee, and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

A total of 360 Hy-line brown laying hens (40-wk-old), were used in this 5-wk experiment to evaluate the effect of vitality mineral liquid complex on production performance, nutrient digestibility, blood characteristics, egg quality, and excreta microflora in laying hens. Laying hens were randomly allocated into 5 dietary treatment groups which consisted of: 1) CON (normal water), 2) I2 (pH 2.2, Ion water), 3) P2 (pH 2.2, polymerization water), 4) I3 (pH 3.0, Ion water), and 5) P3 (pH 3.0, polymerization water). In this study, feed intake and egg broken rate was unaffected ($P > 0.10$), but egg production was increased in I3 and P3, respectively, when compared to CON treatment (96.63, 96.45 vs. 94.55; $P < 0.05$) at wk 3, egg production in P3 was higher (96.85 vs. 94.74; $P < 0.05$) than CON treatment at wk 5. Nutrient digestibility of the Ca in P2, I3, and P3 treatment, respectively, was higher (56.50, 57.58, 55.27 vs. 51.15%; $P < 0.05$) than CON treatment. The blood profile of calcium counts was increased (26.05, 27.23, 27.70 vs. 22.45; $P < 0.05$) in P2, I3, and P3 treatments compared with CON treatment and phosphorus counts was improved (5.28 vs. 4.58; $P < 0.05$) in I3 treatments compared with CON treatment. Moreover, effect of vitality mineral liquid complex improved the eggshell thickness (40.44 vs. 39.72 mm^{-2}; 40.59 vs. 39.68 mm^{-2}; $P < 0.05$) with P3 treatment at 4 and 5 wk of trial. The inclusion of I3 and P3 diets showed a lower (2.24, 2.19 vs. 2.40 log_{10}cfu/g; 6.24, 6.20 vs. 6.50 log_{10}cfu/g; $P < 0.05$) amount of excreta *Salmonella* and *E.coli* counts compared with CON diets. Our results indicated the vitality mineral liquid complex improve the egg production, calcium, phosphorus counts in blood, and decrease the *Salmonella* and *E.coli* counts in laying hens.

Key Words: Egg production, egg quality, laying hens, mineral, nutrient digestibility

1330 (T193) Effects of nutrifen on growth performance, nutrient digestibility, blood profiles, fecal microflora, fecal gas emission, and fecal score in weanling pigs. D. Jung*, H. L. Li, and I. H. Kim, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

A total of 135 weanling pigs (7.96 ± 1.03kg; 28 d of age) were used in a 42-d feeding trial to evaluate the effect of nutrifen on growth performance, apparent total tract digestibility (ATTD), blood profiles, fecal microflora, fecal gas emission and fecal score. Pigs were randomly distributed into 1 of 3 treatments on the basis of BW (9 replicate pens per treatment with 5 pigs per pen). Dietary treatments were: CON, basal diet; NF1, basal diet + 0.1% nutrifen; NF2, basal diet + 0.2% nutrifen. The diets were fed during the experiment in 2 phases: d 0 to 14, and 15 to 42. All diets, in mash form, were formulated to meet or exceed the nutrient requirements (NRC, 2012) for weanling pigs. Feed intake, BW and incidences of diarrhea were monitored at d 14 and 42. Incidences of diarrhea were monitored using a fecal scoring system. At the end of each phase two pigs per pen were bled for serum and fresh fecal samples were collected to determine nutrient digestibility and noxious gas emission. Average daily gain (ADG) was greater (337, 338 vs. 316 g; $P < 0.05$) in nutrifen supplemented pigs during d 0 to 14. During d 14 to 42, ADG and Gain:Feed ratio (G:F) was higher in NF2 treatment compared with that of CON. ADG and G:F was greater (500, 509 vs. 481 g, $P < 0.05$; 0.699, 0.714 vs. 0.676, $P < 0.05$) in nutrifen supplemented pigs during d 0 to 42. Energy digestibility was higher (82.56, 83.13 vs. 79.05%; $P < 0.05$) in nutrifen supplemented pigs compared to CON at d 42. At d 42, pigs fed with NF2 diet had lower (4.83 vs. 6.45 $10^6/\mu\lambda$; $P < 0.05$) blood RBC concentration compared with those fed CON. IgG concentration was greater (525, 532 vs. 499 mg/dL; $P < 0.05$) in nutrifen treatments compared with that of CON. HDL-cholesterol concentration in NF2 treatment higher (40 vs. 33, 34 mg/dL; $P < 0.05$) compared with that in other treatments. The fecal *Lactobacillus* and *E. coli* counts, and fecal score showed no difference ($P > 0.05$) among treatments. The ammonia emission concentration in NF2 treatment decreased (9.7 vs. 13.6 ppm; $P < 0.05$) compared with that in CON treatment. In conclusion, nutrifen could increase growth performance, energy digestibility, IgG and HDL-cholesterol, decrease fecal gas emission without impact on fecal microflora and fecal score in weanling pigs.

Key Words: blood profiles, growth performance, nutrient digestibility, nutrifen, weanling pigs

1331 (T194) Effect of rare earth element-yeast on egg production, nutrient digestibility, egg quality, blood profiles, excreta gas emission, and excreta microbiota in laying hens. J. H. Cho*, L. Cai, and I. H. Kim, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

Rare earth elements (REE) are considered as an alternative to antibiotic because they have the similar action to antibiotic. Rare earth elements–yeast, an improved form of organic REE, may be more effective when fed to livestock because of the lower REE concentration. The objective of this study was to determine the effects of REE–yeast on egg production, nutrient digestibility, egg quality, blood profiles, excreta gas emission, and excreta microbiota in laying hens. A total of 216 ISA brown laying hens at 52 wk of age were used in this 5-wk feeding trial. Treatments consisted of soybean meal based diets supplemented with 0, 0.05, and 0.1% REE–yeast. All birds were allotted to one of three treatments with six replicates (12 hens per replication). All diets were formulated according to

recommendations of the manual of the breeder for ISA brown and to meet NRC (1994). During wk 1 and 2, laying hens fed 0.05% and 0.1% REE-yeast had a higher egg production (90.33, 92.67 vs. 87.00%; 90.33, 92.50 vs. 86.67%; $P < 0.01$) than those fed diets without REE-yeast and egg production improved (linear, $P < 0.01$) as dietary REE-yeast increased in the diet. During wk 3, 4, and 5, laying hens fed 0.1% REE–yeast had a higher egg production (92.50 vs. 86.83%; 92.33 vs. 86.33%; 92.17 vs. 85.67%; $P < 0.05$) than those fed without REE–yeast. Nitrogen digestibility (65.22, 66.31, 69.22%; linear, $P = 0.03$) increased with increasing REE–yeast levels in the diet, and the greatest value was observed in laying hens fed 0.1% REE yeast. In wk 4, laying hens fed REE–yeast had higher yolk height (9.25, 9.58, 9.72 mm; linear, $P < 0.01$) and Haugh unit (92.79, 96.63, 97.11; linear, $P = 0.01$) increased with increasing REE-yeast in diets. In wk 5, Haugh unit (94.53, 97.17, 95.60; $P < 0.05$) increased quadratically with increasing REE–yeast levels in the diet. At the end of experiment, ammonia tended to decrease linearly (15.25, 13.25, 12.75 ppm; $P < 0.1$) with increasing REE–yeast in the diet. However, effects were not observed in blood profiles and excreta microbiota. In conclusion, dietary supplementation with REE–yeast improved egg production, nutrient digestibility, and egg quality in laying hens.

Key Words: egg production, egg quality, laying hen, nutrient digestibility, rare earth elements–yeast

---

1332 (T195) Effects of *Bacillus subtilis* on growth performance, relative organ weight, meat quality, salmonella population, and blood profiles in broilers.

J. H. Cho*, M. Begum, and I. H. Kim, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

A total of 720 male and female ROSS308 broiler chicken (1 d old, initial BW 46.12 ± 0.51 g) were used in this 4-wk trial (5 treatments with 9 replications/treatment and 16 chicks/pen). Dietary treatments were: 1) CON (basal diet), 2) A (CON + 0.1% *Bacillus subtilis B2A* 1.0×10^9 cfu), 3) B (CON + 0.1% *Bacillus subtilis B2A* 1.0×10^7 cfu), 4) C (CON + 0.1% *Bacillus subtilis B2A* 1.0×10^8 cfu), and 5) D (CON + 0.1% *Bacillus subtilis B2A* 1.0×10^9 cfu). The broilers were weighed and feed intake were recorded on d 1, 8, 18, and 28 for calculating body weight gain (BWG), feed intake (FI), and feed conversion ratio (FCR). All data were subjected to GLM procedures of SAS (1996), with pen as the experimental unit. Differences among treatments were separated by Duncan's multiple range tests; $P < 0.05$ was considered statistically significant. During 1 to 8 d, BWG was higher (163 vs.149 g; $P < 0.05$) in treatments D compared with treatment A. During 19 to 28 d, FI (1359 vs. 1242 g) and FCR were higher (1.776 vs. 1.613; $P < 0.05$) in CON compared with treatment D. Overall (1 to 28 d), birds from CON treatment had higher ($P < 0.05$) FI (2286 vs. 2126 g) and FCR (1.658 vs. 1.538) than D treatment. The drip loss of birds from treatment A was lower (3.14 vs. 6.18%; $P < 0.05$) than that of treatment C on d 1. No difference ($P > 0.05$) was observed in relative organ weight and blood profiles among treatments. However, the salmonella populations in chicken fed with CON diet was higher (3.88 vs. 2.73, 2.83, 2.64, 2.75 $\log_{10}$ cfu/g; $P < 0.05$) compared with those fed with other four diets in large intestine. Moreover, the salmonella populations in CON treatment was higher (2.67 vs. 2.18 $\log_{10}$cfu/g; $P < 0.05$) than that in treatment B in small intestine. In conclusion, *Bacillus subtilis B2A* partially improved FCR, while decreasing salmonella populations in big or small intestine without any adverse effect on relative organ weight and blood profiles in broilers.

Key Words: *Bacillus subtilis*, blood profiles, broilers, growth performance, meat quality, salmonella populations

---

1333 (T196) The effect of *Salicornia herbacea* and *Dendropanax morbifera* on the growth performance, meat quality, fecal microbial population and fecal noxious gas emission in broilers.

J. P. Lee, M. M. Hossain, and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

This experiment was conducted to examine the effect of *Salicornia herbacea* and *Dendropanax morbifera* as a phytogenic additive on performance, carcass traits, fecal microbial population and fecal noxious gas emission of broiler chicks. In this study, 680 1-d-old chicks (Ross 308) were allocated to five treatments with eight replicates (17 birds/replication) based on a completely randomized design. Diet was same for all treatments, but two different liquid phytogenic additives used as these treatments: CON, basal diet; SAL1, 1cc/l *S. herbacea*; SAL2, 5cc/l *S. herbacea*; SAL3, 10cc/l *S. herbacea*; DPM, 5cc/l *D. morbifera*.All broilers were fed maize-soybean meal-based diets that were formulated to meet or exceed the National Research Council (1994)nutrient recommendations. The broilers were weighed and feed intake were recorded on d 1, 7, 21, and 35 for calculating BW gain (BWG), feed intake (FI), and feed conversion ratio (FCR). At d 35, two birds were randomly selected from each replication (16 broilers/treatment) and slaughtered by cervical dislocation for meat quality. During d 8 to 21, broilers fed with SAL2, SAL3 and DPM diets increased (968.3, 987.5, 994.2 vs. 963.4 g; $P < 0.05$) BWG with those used CON treatment. During d 22 to 35, broilers fed with SAL1, SAL2 and SAL3 diets increased (729.0, 728.2, 729.3 vs. 684.4 g; $P < 0.05$) BWG compared with those used CON treatment. Overall, birds in CON treatment had the lowest BWG and highest feed conversion ratio at d 35, compared with SAL1, SAL2, SAL3 and DPM treatments (1820.4 vs. 1887.3, 1885.1, 1892.1, 1873.8 g; 1.468 vs. 1.388, 1.394, 1.383, 1.406; $P < 0.05$). The application of *S. Herbacea* and *D. Morbifera* had no significant effect on the

organ weights of chicken liver, breast muscle, gizzard, kidneys, or spleen, and was similar among all treatments. The relative weight of abdominal fat, however, was reduced (22.09, 21.30 vs. 29.55%; $P < 0.05$) in the treatments which were supplemented with *S. Herbacea* (SAL2 and SAL3) compared with that of the control. The result of excreta microbial analysis and fecal noxious gas emission did not show any significant effects. In conclusion, the result of this study showed that addition of *S. herbacea, D. morbifera* have a positive influence on growth performance and they can be considered as a growth promoter substitution for broiler chicks.

Key Words: broilers, *Salicornia herbacea, Dendropanax morbifera,* growth performance, meat quality

---

1334 (T197) The effect of salmonella inhibitors supplementation on egg production, egg quality, blood profiles, and excreta salmonella in laying hens.

J. H. Cho*, H. Shin, and I. H. Kim, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

This study was conducted to investigate the effect of salmonella inhibitors supplementation on egg production, egg quality, blood profiles and excreta salmonella in laying hens. A total of 288 ISA-brown laying hens (40-wk-old) were selected for a 5-wk feeding trial. Hens were randomly allocated into 6 treatments with 4 replications per treatment, and 12 hens per replication, according to a completely randomized design. The experimental treatments included: 1) NC (basal diet), 2) PC (basal diet + 0.1% virginiamycin, antibiotics), 3) A (NC + 0.1% *Bacillus subtilis* 1.0×10^{10}cfu/kg), 4) B (NC + 0.1% *Bacillus subtilis* RX71.0 $\times 10^{10}$cfu/kg) and 5) C (NC + 0.1% *Bacillus subtilis* B2A 1.0×10^{10}cfu/kg), 6) D (NC+0.1% *Bacillus subtilis* RX7 1.0×10^{9}cfu/kg). Daily records of egg production and feed consumption were kept throughout the experimental period. Egg production was expressed as an average production of hen per day, which was calculated from the total number of eggs divided by the number of experimental time (week as a unit) and summarized on an average basis. All data were arranged to evaluate by analysis of variance following the GLM procedure in a completely randomized design using the SAS software program (SAS Institute, 1996). Laying hens were blocked with identical age. The difference among treatment was compared using the Duncan's multiple range tests. The treatment effect was observed significant with the probability value below 0.05. Egg production was higher (96 vs. 90, 91%; $P < 0.05$) in treatment B than in NC and PC treatments at 3 wk. Eggshell thickness was higher (40.87 vs. 40.24, 40.32 mm^{-2}; $P < 0.05$) in treatment D than in NC and PC treatments at 1 wk. B and D treatments had higher (41.17, 41.17 vs. 40.48, 40.51, 40.64, 40.53 mm^{-2}; $P < 0.0.5$) eggshell thickness than those in other treatments at 3 wk. But no differences ($P > 0.05$) on eggshell color, egg weight, yolk height, yolk color, haugh unit and eggshell strength were observed during the whole experiment.There was no difference ($P > 0.05$) in WBC, RBC, lymphocyte and haptoglobin among dietary treatments. Excreta salmonella was higher (2.59 vs. 2.23, 2.28, 2.28, 2.28, 2.29 $\log_{10}$cfu/g; $P < 0.05$) in NC treatment compared with those other treatments. In conclusion, dietary salmonella inhibitors have no effects on eggshell color, egg weight, yolk height, yolk color, haugh unit and eggshell strength and blood profiles in laying hens. However, *Bacillus subtilis* supplementation improved egg production, eggshell thickness and excreta salmonella in laying hens.

Key Words: egg production, eggshell thickness, excreta salmonella, laying hens, salmonella inhibitors

---

1335 (T198) Feed additives affects RNA expression in the brush border membrane in broilers.

M. F. Fernandez Alarcon*[1], J. P. Steibel[2,3], L. S. Antonio[4], R. Lunedo[1], G. Baldissera[1], R. L. Furlan[1], and L. R. Furlan[5], *[1]Dep. of Animal Morphology and Physiology, Sao Paulo State University, Jaboticabal, SP, Brazil, [2]Michigan State University, East Lansing, [3]Dep. of Fisheries and Wildlife, Michigan State University, East Lansing, [4]Dep. of Biological Sciences–Biochemistry, University of São Paulo, Bauru, Brazil, [5]Aquaculture Center, Sao Paulo State University, Jaboticabal, Brazil.*

Probiotics and essential oils have been investigated as replacements for antibiotic growth promoters (AGP) by improving the performance and gut health of chickens. However, studies reported contrasting responses from these additives in intestinal digestion and absorption. We investigated the effects of addition of *Bacillus subtilis* (probiotic), an essential oil blend (carvacrol, cinnamaldehyde, cineol and pepper extract) and their combination in the performance and expression of genes related to digestion and absorption in Coob broilers, by RT-qPCR. Basal diet was used as negative control and the avilamycin AGP as positive control. One thousand, three hundred twenty male broiler chicks from Coob strain were divided among five treatments, in six pens of 44 chicks each. Birds were raised following breeder's recommendations. Performance was assessed in terms of feed intake (FI), weight gain (WG) and feed conversion ratio (FCR) recorded at 7, 21, and 42 d of age. At these same ages, one bird per pen ($N = 6$), was slaughtered to collect the mucosa of the ileum for RT-qPCR analysis. The investigated genes were: aminopeptidase N (APN), sucrase isomaltase (SI), maltase-glucoamylase (MGA), intestinal transporter peptide-1 (*P*EPT1), transporter of glucose and galactose Na^+ dependent-1 (SGLT-1), glucose transporter, galactose and fructose independent Na^+-2 (GLUT -2) and ATP ase Na^+/K^+ (ATP1A-1). Except for an increased feed intake presented in birds fed probiotics in relation to fed AGP at 21 d, no differences were found in broiler performance during the experiment. Regarding gene expression, at 7 d, birds treated with AGP presented lower ($P < 0.05$) expres-

sion of ATP1A-1 mRNA than the negative control. At 21 d, birds fed with the combination of probiotics and essential oil showed lower mRNA concentration of MGAM than those fed with AGP. In addition, no difference was observed in gut gene expression at 42 d. The lack of difference in growth performance between treatments could be due to the environment in which the birds were raised, more hygienic than that normally found in poultry farms. Moreover the changes in ATP1A-1 and MGAM RNA expression observed herein highlight the role of feed additives in host gut enzymes and transporter gene expression. These results encourage analysis of brush border enzymes activity, jejunum morphometry and indirect absorption trials of glucose in the jejunum, which are underway.

Key Words: broiler, feed additives, gene expression, intestine, RT-qPCR

1336 (T199) Apparent digestibility of wheat bran nutrients with or without exogen enzymes addition in weaned piglets. J. C. Dadalt*, P. D. A. P. Ribeiro, G. D. V. Polycarpo, C. Gallardo, G. D. Ricci and M. A. D. T. Neto, *University of São Paulo, Pirassununga, Brazil.*

Non-ruminant animals have a limited capacity for food digestion with low digestibility as those with high fiber or phytic acid contents. Some researches indicated that enzyme additions may decrease the effects of antinutritional factors present in vegetable feedstuffs, improving its digestion and nutrient utilization. Using weaned piglets, this study evaluated the apparent digestibility of dry matter (DM), crude protein (CP), mineral matter, energy (DE) and, metabolizable energy (ME) and N retention of the wheat bran (WB) supplied or not with exogen enzymes. Twenty-five crossbred barrows with initial weight 9.35 kg ± 1.61 kg, were allotted in a completely randomized design under five treatments and five replicates. The experimental unit was represented by one pig within its respective metabolic cage. The experimental period was 10 d, in which 5 d for cage adaptation and 5 d for feces and urine collection. The treatments were: Control diet (CD); CD + 30% wheat bran (WB); CD + 30% WB + 200 mg/kg of carbohydrase (WB+Carb); CD + 30% WB + 50 mg/kg of phytase (WB+Phy); CD + 30% WB+ Carb + Phy (WB+Carb+Phy). The control diet was based on corn (61.33%), skim milk powder (10%) and dried whey (15%). The enzymes were commercial phytase (10,000 FTU/g), carbohydrase providing 10% of Galactomananase, 10% of Xilanase, 10% of β-glucanase, 60% of malted barley and 10% of α-galactosidase. Data were analyzed by ANOVA and LS Means using the GLM procedure (SAS Inst. Inc., Cary, NC). Significance was defined as $P < 0.05$. Carbohydrase and phytase combination improved the digestibility coefficients ($P < 0.05$) in most of the variables, excepting nitrogen retention which did not show statistical difference among treatments. Wheat bran without enzyme addition had lower values for DE and ME (2862 and 2804 kcal/kg), respectively. The higher values observed for DE and ME were: WB+Carb+Phy (3164 and 3082 kcal/kg) without statistical difference with WB+Carb (3098 and 3056 kcal/kg) ($P = 0.4785$ and $P = 0.9766$) and WB+Phy (3051 and 2996 kcal/kg) ($P = 0.0970$ and $P = 0.5421$) (values expressed on dry matter). Lower digestibility of CP was observed for WB and WB+Phy (72.52 and 73.98%) respectively, which statistical results were similar to WB+Carb diet (75.69%) ($P = 0.9324$). The enzymes showed an effective improvement on digestibility of wheat bran for young pigs after weaning.

Key Words: carbohydrase, metabolism, phytase

1337 (T200) Evaluating the effects of *Salicornia* extract on performance, egg quality and blood profile of laying hens. I. H. Kim*, H. L. Li, and M. M. Hossain, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

An experiment was conducted to evaluate the effects of adding *Salicornia* extract to the drinking water of laying hens on their performance, egg quality, and blood profile. A total of 216 Hy-line Brown at the age of 40 wk were used in a 10-wk experiment. The birds were allotted into 3 experimental treatments and there were 24 replications per treatment with three birds per pen. Treatments consisted of CON (basal diet), T1 (1 cc *Salicornia* extract water per liter drinking water), and T2 (5 cc *Salicornia* extract water per liter drinking water). Daily records of egg production and feed consumption were kept throughout the experimental period. Egg production was expressed as an average production of hen per d, which was calculated from the total number of eggs divided by the number of experimental time (wk as a unit) and summarized on an average basis. A total of 42 salable eggs (no shell defects or cracks) were randomly collected biweekly from each treatment at 1700 h (three eggs per replication). The egg quality of the collected eggs was then determined at 2000 h on the day of collection. Laying hens were blocked with identical age. The difference among treatment was compared using the Duncan's multiple range test. The treatment effect was observed significant with the P value < 0.05. Addition of *Salicornia* extract to the drinking water of laying hens didn't show any negative effects on performance, egg quality, and blood profile. Treatments T1 and T2 increased egg production remarkably (86.3 vs. 89.0, 91.0%; $P < 0.05$) at the first wk compared with CON. Moreover, at last week, the egg production in T1 was significantly higher (91.3 vs. 86.0%; $P < 0.05$) than CON treatment. Birds in T2 treatment showed improved (111.2 vs. 110.6 g; $P < 0.05$) feed intake compared with CON at first week. The ratio of broken shell was decreased (7.6 vs. 11.3%; 8.3 vs. 12.1%; 7.8 vs. 10.6%; 9.2 vs. 11.1%; 8.6 vs. 13.6%; $P < 0.05$) in T2 treatment than that in CON treatment in 1, 4, 6, 8, and 10 wk. The results of this study showed that addition of *Salicornia* extract can improve the egg shell quality, thereby

decreasing the rate of breaking eggs and increasing the benefit of production in commercial farms.

Key Words: blood profile, breaking eggs rate, egg production, laying hens, *Salicornia*

1338 (T201) Effect of material bioconversion natural complex on the growth performance, nutrient digestibility, fecal microbiota, fecal score, fecal moisture and pH in weanling pigs. M. Jung, Y. Lei, and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

A total of 150 pigs [(Yorkshire × Landrace) × Duroc], BW of 6.57 ± 0.49 kg, were used in a 6-wk trial to investigate the effects of material bioconversion natural complex (STR) on growth performance, nutrient digestibility, fecal microflora, fecal score, fecal moisture, and pH in weanling pigs. STR is a propolis feed additive contained more than 60% propolis and 6% of total flavonoid in powder form and produced from fermentation of mulberry leaves and turmeric with bacterial of mulberry yellow mushroom. Pigs were randomly allocated into 1 of 5 dietary treatments on the basis of BW and sex [6 replicate pens per treatment with 5 pigs (2 gilts and 3 barrows) per pen]. Dietary treatments were: 1) NC (basal diet, free of antibioitics), 2) PC (NC + 3 ppm Tiamulin), 3) STR-1 (NC + 0.1% STR1), 4) STR-2 (NC + 0.1% STR2), 5) STR-3 (NC + 0.1% STR3). STR1, STR2, and STR3 contain 1.5, 3, and 6% of active complex powder, respectively. Apparent nutrient digestibility was measured following the procedures by the AOAC (2000). Throughout the experimental period, pigs fed with STR-2 and STR-3 diets had higher (487, 492 vs. 474 g; $P < 0.05$) ADG compared with pigs fed with NC diet and the G/F ratio of STR-3 treatment was higher (0.720 vs. 0.692; $P < 0.05$) than that of NC treatment. The apparent total tract digestibility (ATTD) of dry matter was higher (1 wk: 83.96 vs. 82.22%; 3 wk: 85.92 vs. 82.47%; 6 wk: 81.05 vs. 77.23%; $P < 0.05$) in STR-3 treatment than in NC treatment. The ATTD of nitrogen was higher (79.98, 78.69, 78.87 vs. 76.54%; $P < 0.05$) in STR-1, STR-2, and STR-3 treatments than in NC treatment at wk 3. The ATTD of energy was higher (83.75 vs. 82.23% and 82.70 vs. 79.23%; $P < 0.05$) in STR-3 treatment than in NC treatment at wk 1 and 6, respectively. The fecal score of pigs fed with STR-3 diet was lower (3.00 vs. 3.18; $P < 0.05$) compared with pigs fed with STR-2 diet during wk 4. Moreover, fecal *Escherichia coli* concentration of pigs fed with STR was lower (5.75, 5.75, 5.76 vs. 5.90 $\log_{10}$cfu/g; $P < 0.05$) compared with pigs fed with NC diet. In conclusion, inclusion of STR3 (an antibiotic free diet) at a level of 0.1% could increase growth performance, nutrient digestibility, and decrease fecal score and fecal microbiota in weanling pigs.

Key Words: growth performance, fecal score, nutrient digestibility, STR, weanling pig

1339 (T202) Effects of microencapsulated *Enterococcus faecalis* and enzyme supplementation on piglet response to an *Escherichia coli* (K88) challenge. H. S Chen[1,2], D. E Velayudhan*[1], A. K Li[3], Y. Z Feng[2], D. Liu[2], Y. L Yin[4], and C. M. Nyachoti[1], *[1]University of Manitoba, Winnipeg, Canada, [2]Institute of Animal Husbandry, Harbin, China, [3]Academy of State Administration of Grain, Beijing, China, [4]Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, China.*

The objective of this study was to determine the effect of dietary probiotic microencapsulated *Enterococcus faecalis* and multi-enzyme complex (MC) in enterotoxigenic *Escherichia coli* K88 (ETEC)-challenged piglets fed wheat-barley soybean based diets. Thirty-six, 21-d-old weanling pigs with an initial BW of 6.7 ± 0.6 kg were allotted in a completely randomized design to 4 dietary treatments; a wheat-barley soybean based negative control (NC) with no antimicrobial growth promoters (Diet A), NC + MC (Diet B), NC + probiotic (Diet C) and NC + MC + probiotic (Diet D). Piglets were housed individually in cages. Diets were formulated to meet or exceed NRC 2012 specifications for weaned pigs. MC supplied 500, 50, 400, 1200, 450, and 45 units of pectinase, cellulase, mannanase, xylanase, glucanase, and galactanase, respectively, per kg of diet. The probiotic was added at the rate of 10 mg (1.0×10^{11} cfu/g) per kilogram of diet. Pigs were acclimated to treatments for a 7-d period. On d 8, pigs were weighed, blood sampled for determining baseline immunological parameters (IL6 and TNF α) and then orally challenged with 6 mL (5×10^{10} cfu/mL) of the freshly grown ETEC K88 inoculum. At 6, 12, 24, 48, and 150 h post-challenge, blood samples were taken, performance measures and fecal consistency scores were recorded, and on d 14 all pigs were killed to obtain intestinal tissue and digesta samples to evaluate GIT morphology, microbial ecology, and immunological parameters. Data were analyzed using the PROC MIXED of SAS. No significant enzyme x probiotic interaction was observed for any of the parameters evaluated. During pre-challenge, pigs receiving enzyme, probiotic and combination of both improved the ADG ($P = 0.03$) by 49, 62, and 51% and G:F ($P = 0.04$) by 25, 32, and 32%, respectively. However, during the post-challenge period only a numerical improvement in G:F was observed for Diet C when compared with Diet A (0.70 vs. 0.59). Also, pigs fed Diet C had greater ($P = 0.05$) ileal villus height than those receiving the NC. Moreover, Diet C significantly reduced the severity of diarrhea ($P = 0.04$) by 12% during the challenge phase compared to pigs fed NC. In summary, the results indicate that dietary supplementation of microencapsulated *Enterococcus faecalis* in weaned pigs challenged with ETEC was effective in maintaining gut health and thereby controlling post-weaning diarrhea.

Key Words: *Escherichia coli,* probiotic, piglets

1340 (T203) Sodium alginate addition improves water stability and utilization of extrudated feed for farmed saltwater crocodiles (*C. porosus*).

M. Francis[1], T. J. Wester[*1], P. C. H. Morel[1], and B. H. P. Wilkinson[2], [1]*Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand,* [2]*Institute of Food, Nutrition and Human Health, Massey University, Palmerston North, New Zealand.*

Saltwater crocodile (*C. porosus*) farming in Papua New Guinea is an emerging industry that supplies high quality raw skins for fashion industries worldwide. Extrudated animal by-product feed (non-heat treated feed forced through a die at low pressure) is used to get a consistent high quality feed; however, this feed disintegrates quickly in water which leads to loss of nutrients, inefficient feed conversion ratio, and water contamination. We evaluated Na alginate as a binding agent to improve feed stability in water and determined its effect on nutrient availability in a digestibility trial. A 24-h in vitro water solubility test of exudated chicken by-product-based diets (35% minced chicken carcasses, 15% chicken blood, 5% poultry offal meal, 5% pulped eggs, 15% wheat millrun, and 25% supplement, as-fed basis) with and without 1.5% Na alginate and 1.9% $CaCO_3$ added showed the inclusion of Na alginate improved the dry matter retention in feed by 12.6-times ($P < 0.05$). These diets were then compared in vivo in a digestibility trial. Ten juvenile crocodiles (2.2 to 2.4 yr of age, 1.2 to 1.9 kg BW) were chosen from farm raised stocks and fed exudated chicken by-product-based diets with and without 1.5% sodium alginate and 1.9% $CaCO_3$ added. Animals were fed 2% BW for 12 d, with feces collected the last 5 d. Animals were then slaughtered and digesta sampled from the ileum. Acid insoluble ash was used as an internal marker. There were no differences in any amino acid, N (65.0 vs. 55.8%, SE = 12.2%), and organic matter (46.8 vs. 39.6%, SE = 12.8%) digestibility at the ileum between diets with and without alginate, respectively. However, fecal digestibility of organic matter (69.8 vs. 39.2% SE = 9.1%) and energy (72.2 vs. 44.4%, SE = 8.3%) were greater in alginate containing diets ($P < 0.05$). This shows that alginate addition does not have deleterious effects on digestion in crocodiles, and because it improves feed stability in water, should greatly enhance nutrient uptake and feed efficiency. Results will be used to formulate diets with increased feed utilisation and decreased feed wastage, with the ultimate goal of increasing economic return to Papua New Guinea while decreasing effluent discharge and pollution of the ecosystem.

Key Words: saltwater crocodile, ileal digestibility, sodium alginate

1341 (T204) Impact of allicin on enzyme activity, cytokine secretion, and gene expression dynamics in oxidative- and endotoxin-stressed porcine intestinal epithelial cells.

N. L. Horn[*1], G. Miller[2], K. M. Ajuwon[1], and O. Adeola[1], [1]*Dep. of Animal Sciences, Purdue University, West Lafayette, IN,* [2]*Biomatrix, Princeton, MN.*

Environmental stress and endotoxins can negatively affect gastrointestinal function by influencing cellular antioxidant systems, tight junctions, and inflammatory mediators. Allicin is a botanical derived from garlic that has anti-inflammatory and antioxidant properties. The objective of the current study was to determine if allicin could mitigate oxidative and endotoxin stress using an IPEC cell model. The experiment was arranged as a 2 × 2 x 2 factorial of allicin (0 or 40 μM), oxidative stressor, hydrogen peroxide (0 or 100 μM), and endotoxin stressor, lipopolysaccharide (0 or 10 μg/ml). Cells were incubated with allicin or lipopolysaccharide (LPS) for 18 h or with hydrogen peroxide for 3 h approximately 1 wk following confluency. Trans-epithelial resistance (TER), reactive oxygen species (ROS), antioxidant enzymes, interleukin 8 and 1 β (IL-8 and IL-1β), and tumor necrosis factor α (TNF-α) secretion were measured. Gene expression was measured by RT-PCR for cytokines IL-8, IL-1β, and TNF-α and tight junction proteins claudin 1 (CL-1), occludin (OC), and zonula occludens 1 (ZO-1). Treatment did not affect TER although addition of allicin to hydrogen peroxide- and LPS-treated cells reduced ($P < 0.05$) ROS. Allicin decreased superoxide dismutase (SOD) activity ($P < 0.001$), whereas hydrogen peroxide increased SOD activity ($P = 0.02$). Furthermore, addition of allicin to hydrogen peroxide-treated cells restored SOD activity similar to untreated cells ($P < 0.05$). Addition of allicin to hydrogen peroxide- and LPS-treated cells decreased catalase activity ($P < 0.05$). There was an increase in TNF-α and IL-8 gene expression due to LPS ($P < 0.001$) although there was no effect of hydrogen peroxide or allicin ($P > 0.05$). Experimental treatment had no effect on tight junction gene expression ($P > 0.05$). There was an increase ($P < 0.001$) in IL-8 secretion due to LPS which was further increased ($P < 0.05$) by addition of allicin to LPS-treated cells and hydrogen peroxide incubation increased ($P = 0.01$) TNF-α secretion. Based on the results from the current study, allicin can ameliorate oxidant effects of hydrogen peroxide and LPS as well as alter cytokine secretion in IPEC cells.

Key Words: allicin, hydrogen peroxide, lipopolysaccharide

1342 (T205) Evaluation of a new probiotic strain of *Bifidobacterium longum* subsp. *infantis* CECT 7210 to improve health status of weaning piglets orally inoculated with *Salmonella* typhimurium.
E. Barba-Vidal[*1], L. Castillejos[2], V. F. Buttow Roll[3], M. Rivero[4], J. A. Moreno Muñoz[4], and S. Martín-Orúe[1], *[1]Animal Nutrition and Welfare Service Dep. of Animal and Food Sciences Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [3]Dep. of Animal Science, Faculty of Agronomy Eliseu Maciel, Federal University of Pelotas, Pelotas, Brazil, [4]Laboratorios Ordesa S. L., Parc Científic de Barcelona, Spain.*

A new probiotic strain of *Bifidobacterium longum* subsp *infantis* CECT 7210 (Laboratorios Ordesa, S.L.) was evaluated on an oral challenge against *Salmonella* typhimurium. Seventy-two animals (28 d old, 7.7 ± 1.27kg) were distributed during an experimental period of 16 d in 24 pens and 4 experimental groups in a 2 × 2 factorial design: with or without probiotic (10^9 CFU/day in 2-mL water suspension) and inoculated with *Salmonella* (5×10^8 CFU) or placebo. Animals were fed ad libitum a multicereal diet with selected protein sources (soybean meal 44, fishmeal and bovine sweet whey), without antibiotics and that met NRC 2012 requirements. The probiotic was administered orally and individually on a daily basis. Feed consumption and body weights were monitored during the whole experimental period. After an adaptation week the animals were challenged. From this moment onward fecal shedding of *Salmonella* [d 0, 1, 3, and 7 post-inoculation (PI)], fecal consistency (d 1, 2, 3, 5, and 7 PI) and rectal temperature (24 and 48 h PI) were assessed. On d 4 and 8 PI, one animal from each pen was euthanized and blood, intestinal content and tissue samples were collected. Blood was obtained to assess the inflammatory response (TNF-α and plasma Pig-Map); intestinal content to assess the presence of *Salmonella* in colon as well as fermentation products (lactic acid and volatile fatty acids) and tissue samples to evaluate microscopic ileal morphology. All parameters responded significantly to infection ($P < 0.05$). The administration of the probiotic tended to increase average daily gain (ADG) of the animals during the postinoculation period (d 0 to 7 PI; 145 vs. 226 g/d, $P = 0.067$) and increased the overall ADG (d 0–16; 90 vs.150 g/d, $P = 0.042$). Moreover, it significantly reduced febrile response of infected animals at 48h PI (39.48 vs. 39.06°C, Probiotic*Day, $P = 0.003$) and improved fecal consistency (1.62 vs. 1.95, $P = 0.014$). A reduction of *Salmonella* counts at 48 h ($P = 0.028$) and d 4 PI ($P = 0.056$) were also observed. In addition, the probiotic promoted an increase of ileal intraepithelial lymphocytes on d 8 PI (0.86 vs. 1.32, $P = 0.015$) and also a numerical reduction in TNF-α (87.70 vs. 72.11 pg/dL, $P = 0.12$). No significant changes in fermentation products were registered related to the probiotic ($P > 0.05$). Results demonstrate that oral administration of the probiotic *Bifidobacterium longum* subsp. *infantis* CECT 7210 improves growth, reduce clinical response and improve some immunitary parameters of pigs orally challenged with *Salmonella* typhimurium.

Key Words: probiotic, *Salmonella,* weaning, *Bifidobacterium*

1343 (T206) A standardized blend of capsicum oleoresin, cinnamaldehyde and carvacrol improves performance of lactating sows.
C. Oguey[1] and C. Bruneau[*2], *[1]Pancosma, Geneva, Switzerland, [2]Pancosma, St.-Hyacinthe, QC, Canada.*

The main concern in sow farming is to optimize progeny performance during suckling and minimize fertility concerns. In monogastric animals, a standardized blend of capsicum oleoresin, cinnamaldehyde and carvacrol (XT, XTRACT 6930, Pancosma) was shown to positively affect fat digestibility and immune modulation. Therefore, given these modes of action, XT should be beneficial to the performance of lactating sows. As scarce information is available on this matter, a study was designed to evaluate the effect of XT supplementation on performance of sows raised under commercial conditions. A total of 428 sows were randomly allocated from 15 d before farrowing until piglets' weaning to one of the two treatments: CT: basal diet and XT: basal diet supplemented with 100 g/t XT. Animals had ad libitum access to feed and water. Sows' ADFI during gestation and lactation, backfat loss during lactation and weaning to estrus interval were individually recorded. Piglet birth weight, number of piglets born alive, mummies and weaned, and piglets weights at birth and weaning were evaluated per sow. Results were statistically analyzed by ANOVA, using the treatment, the parity and their interaction as fixed effects. Results showed that XT did not affect sow ADFI during gestation and lactation, backfat loss, the numbers of piglets born alive and mummies, and piglets' weight gain during suckling ($P > 0.28$). However, the interaction treatment*parity had a significant impact on lactation ADFI ($P < 0.05$). More specifically, XT increased ADFI during lactation of primiparous sows compared to CT (+4.1%, $P < 0.05$). XT supplementation tended to increase the number of piglets weaned per sow (+0.2 piglets/sow, $P = 0.09$) and to reduce pre-weaning mortality (-15.8%, $P = 0.09$). Finally, XT significantly decreased the weaning to estrus interval by 2.2 d ($P = 0.04$). There results suggest that XT has the potential to improve sow performance during lactation under commercial conditions, through more piglets weaned per litter and improved fertility.

Key Words: phytonutrients, sow performance

1344 (T207) Zilpaterol hydrochloride improves growth performance of meat producer Japanese quails. H. Dávila-Ramos and J. C. Robles-Estrada*, *Universidad Autonoma de Sinaloa, Culiacan, México.*

Zilpaterol hydrochloride (ZH) is a β-adrenergic agonist that was approved in México (2002) and the United States (2006) to promote growth and carcass dressing in beef cattle. However has been tested in other species such as lambs and poultry. The objective of this experiment was determinate the effect of zilpaterol hydrochloride supplementation during 21 d on growth performance of meat producer Japanese quail (*Coturnix coturnix japonica*). Two hundred twenty Japanese quails (both sexes; 90.3 ± 1.19 g) were distributed in 20 birdcages with four treatments (five birdcages per treatment). Treatments consisted in different doses (0, 0.20, 0.25, and 0.30 mg/kg of live weight/d) of zilpaterol hydrochloride supplementation, the basal diet contained 55% ground corn grain and 35% soybean meal (24%CP and 2.9 Mcal/kg of ME). Quails were weighted weekly and adjusted zilpaterol dose. The results were analyzed with completely randomized design and comparing means of treatments with orthogonal contrasts and orthogonal polynomials. Zilpaterol supplementation increased final live weight (5.6%; $P \leq 0.01$), total weight gain (9.7%; $P \leq 0.01$), feed conversion (6.1%; $P \leq 0.01$) and feed intake (2.8%; $P = 0.02$). Similarly, supplementation with 0.30 mg/kg of live weight increases the final live weight, total weight gain and feed conversion ($P \leq 0.01$) when compared with control treatment, however this dose showed no changes in feed intake ($P = 0.24$). No significance difference ($P \geq 0.21$) were showed in all variables when compare minimum and maxim dose (0.20 vs. 0.30 mg/kg of live weight), neither differences were detected for linear ($P \geq 0.25$) and quadratic ($P \geq 0.14$) analysis. These results indicated that zilpaterol supplementation in meat producer Japanese quail improve the growth performance without changes between doses. Levels below 0.20 mg/kg live weight need to be tested to determine the max inclusion rate needed.

Key Words: zilpaterol hydrochloride, *Coturnix coturnix japonica*, growth performance

1345 (T208) Effects of increasing levels of curcumin on growth performance and immune response of nursery pigs. M. R. Bible*, S. D. Carter, H. Kim, and K. F. Coble, *Oklahoma State University, Stillwater.*

Curcumin (CUR), a curcuminoid in turmeric, has antimicrobial and anti-inflammatory properties that may be beneficial to pigs. Two experiments (Exp.) were conducted to determine the effect of increasing levels of CUR on growth performance and immune response. Pigs were weaned at 21 d, blocked by BW, and allotted randomly to dietary treatments (trts) in a randomized complete block design (RCBD). Each experiment utilized corn-soybean meal based diets with a 4-phase feeding program. Growth performance was calculated for d 0 to 21 and 0 to 42. Exp. 1 (6 reps/trt) used 168 pigs (6.2 kg) with the following trts: carbadox (55 mg/kg; AB), 12, 23, and 46 mg/kg of CUR. Exp. 2 (7 reps/trt) used 112 pigs (6.0 kg) with the following trts: carbadox (55 mg/kg; AB), 46, 93, and 186 mg/kg of CUR. On d 20, selected pigs were challenged with an *E. coli* lipopolysaccharide (LPS). Rectal temperatures (RT) were measured and blood collected for analysis of tumor necrosis factor-α (TNF-α) and C-reactive protein (CRP) at h 0 and 3, 6, 12, and 24 h post-injection (PI). Data were analyzed as a RCBD using a GLM/PROC MIXED. In Exp. 1, there were no differences ($P > 0.10$) in growth performance for d 0–21. Curcumin did not affect ($P > 0.10$) ADG, but decreased ADFI and improved G:F ($P < 0.08$) for d 0–42 compared to the AB. As CUR increased, ADFI decreased and G:F increased ($P < 0.08$; quad). In Exp. 2, ADG ($P = 0.09$; quad) and ADFI decreased ($P = 0.009$; linear) as CUR increased for d 0 to 21. Compared to the AB, CUR decreased ($P = 0.03$) ADFI. For d 0 to 42, CUR decreased ($P < 0.06$; linear) ADG and G:F; and decreased ($P < 0.04$) ADG and G:F compared to AB. For the LPS challenge in Exp. 1, there was a numerical decrease in TNF- α at h 3 PI followed by a decrease ($P = 0.05$; quad) in CRP at h 6 PI as CUR increased. For Exp. 2, increasing CUR decreased ($P < 0.07$; linear) RT at h 0 and 3 PI. As CUR increased, TNF-α tended ($P = 0.09$; linear) to increase at h 6 PI. However, CUR decreased ($P < 0.10$; linear) CRP at h 0, 3, 6, and 24 PI. Compared to the AB, CUR decreased ($P < 0.03$) CRP at h 0, 3, and 6 PI. When data were combined for both experiments, the optimum response in growth performance and immune response was between 46 and 93 mg/kg of CUR.

Key Words: curcumin, growth performance, immune response

1346 (T209) Mannan oligosaccharides and β-glucan in diets for weaned piglets. U. V. Luna*, J. G. Caramori Junior, G. S. S. Corrêa, S. D. Assis, E. Brusamarelo, J. C. R. Ribas, M. A. Souza, A. B. Corrêa, B. S. Vieira, E. Rovaris, and S. A. P. V. Barbosa, *Federal University of Mato Grosso, Cuiabá, Brazil.*

The objective of this study was to evaluate the effect of supplementation with mannan oligosaccharides, β-glucan and antibiotic in diets for castrated male piglets during the nursery phase (21 to 54 d of age) on performance, morpho-histological characteristics of the intestinal mucosa and occurrence of diarrhea. A total of 368 piglets of the same strain, weaned to 21 d of age, with average weight of 6.9 kg were distributed in a completely randomized design with four treatments: 1) control [basal diet without supplementation: 36.05% corn, 18.4% Soybean meal (45%), 2.9% Soybean oil, 2.5% Crystal sugar, 40% de Pig Mix e 0.15% kaolinite); 2) basal diet + 1500 g mannan oligosaccharides/t of diet; 3) basal diet + 500 g β-glucan/t of diet; and 4) basal diet + 250 g colistin/t of diet. These were used with four replications with 23 animals per experimental unit. The man-

nan oligosaccharides and β-glucan were extracted cell wall of yeas *Saccharomyces cerevisiae*. The piglets were weaned to 21 d of age, heavy and distributed in experimental unit. Performance was assessed through weight gain, feed intake and feed conversion. The morpho-histological characteristics of the intestinal mucosa studied were villus height, intestinal crypt depth, villus circumference and villus height:crypt depth of duodenum, jejunum and ileum ratio. The occurrence of diarrhea was observed daily by the evaluation of fecal score. Not there was a difference for weight gain (P = 0.0750; averages: 14.000, 13.635, 14.018, 12.605 kg), feed intake (P = 0.1574; averages: 28.053, 28.577, 29.202, 26.920 kg) and feed conversion (P = 0.2239; averages: 2.005, 2.098, 2.084, 2.134 kg) the piglets the diets receiving control, mannan oligosaccharides, β-glucan and antibiotic, respectively. Thus, it is concluded, that the use of mannan oligosaccharides, β-glucan and antibiotic in the diet of castrated male piglets in the nursery phase did not affect performance and occurrence of diarrhea. The use β-glucan increases villus height and crypt depth in the duodenum and ileum and the villus circumference the jejunum.

Key Words: additives, diarrhea, intestinal morphology

NONRUMINANT NUTRITION: EVALUATION OF FEED INGREDIENTS FOR MONOGASTRIC DIETS

1347 (W165) Nutritional value of macauba pulp presscake (*Acrocomia aculeata*) for growing pigs. *J*. H. B. Pereira[1], S. L. S. Cabral Filho[1], C. G. D. Q. Roriz[1], C. B. Bernardes[1], T. M. Barbosa[1], L. R. Roos[1], A. P. Santana[1], J. B. Lopes[2], and L. S. Murata[*1], *[1]University of Brasilia, Brazil, [2]Federal University of Teresina, Brazil.*

The aim of this study was to determine the apparent digestibility coefficients of the dry matter (DCDM), crude protein (DCCP) and fiber (DCFB). Also, we aimed at determining the apparent digestible (DE) and metabolizable energy (ME) in macauba pulp presscake (*Acrocomia aculeata*) for pig feeding. The apparent digestibility of dry matter (DM), crude protein (CP), fiber (NDF), DE and ME of treatments was also assessed for growing pigs. The study was conducted using a randomized block design with three treatments distributed in two blocks of four replications/block. Twenty-four commercial barrows with an initial weight of 28+0.13 kg were used with an adaptation period of 10 d followed by a 5-d total collection of feces and urine. The diets were formulated by replacing the reference diet (corn and soybean meal) with 0, 10 or 20% macauba pulp presscake. The treatments were: T1 = Reference diet (RD), T2 = 90% RD+10% macauba pulp presscake, and T3 = 80% RD+20% macauba pulp presscake. The DCDM, DCCP, and DCFB for a 20% dietary inclusion level of macauba presscake were 16.5%, -2.25%, and 30.80%, respectively, which were not significantly different from the values observed with a 10% dietary inclusion level. The DE value for macauba pulp presscake in T2 (10%) was 2888.3 and T3 (20%) was 2900.6 kcal/kg. The ME for the same treatments was 2690.0 and 2680.5 kcal/kg, respectively. Diet DM digestibility values were 79.1% in T2 and 72.0% T3, while CP digestibility in T2 and T3 were 77.9% and 71.2%, respectively. Diet NDF digestibility for T2 was 64.3% and T3 was 55.7%. Significant difference ($P < 0.05$) for diet nitrogen balance (NB) was found only in fecal nitrogen (FN), showing that diet fiber increased the excretion of endogenous nitrogen. The inclusion level of macauba pulp presscake in the diet had an effect on the digestibility of DM, CP, and NDF, where the apparent digestibility coefficient decreased with the increase of macauba pulp inclusion, without influencing the DE, ME and NB values. This diet is considered to have a low nutritional value and its use is not recommended for growing pigs with 28 to 40 kg of body weight. The possible usage as alternative foods to feed pigs will depend on the understanding of their possibilities and limitations as well as reduction of production costs. Inclusion rates of this ingredient in pork diet must be considered, especially the fiber content values.

Key Words: alternative feed, biodiesel, by-products

1348 (W166) Different corn hybrids fed to growing pigs. I. Chemical composition, energy concentration, and digestibility of nutrients. Y. Liu[*1], R. C. Sulabo[1], T. E. Sauber[2], and H. H. Stein[1], *[1]University of Illinois at Urbana-Champaign, Urbana, [2]Pioneer Hi-Bred International Inc., Johnston, IA.*

Fifty-two barrows (26.8 ± 3.42 kg) were used in five experiments to determine the variability in the chemical composition, energy concentration, and digestibility of nutrients in 48 different corn hybrids sourced from DuPont Pioneer (Johnston, IA) and fed to growing pigs. In Exp. 1, 12 ileal cannulated barrows were allotted to a 12 × 12 Latin square design with 12 diets and 12 7-d periods. In Exp. 2 to 5, 10 ileal cannulated barrows were allotted to a 10 × 10 Latin square design with 10 diets and 10 7-d periods. In all experiments, corn was 97.0% (as-fed basis) of the diet and the only ingredient contributing energy, starch, ADF, NDF, lipids, and AA to the diets. The only difference in diet composition among diets was that different corn hybrids were used. Descriptive statistics for chemical component, energy concentration, and digestibility of nutrients in corn hybrids were determined using PROC MEANS. Correlation coefficients among chemical components, energy concentration, and digestibility of nutrients in all corn hybrids were determined using PROC CORR. On an as-fed basis, the GE concentration of the corn hybrids ranged from 3736 to 3989 kcal/kg, with an average of 3884 ± 63.6 kcal/kg. The average concentration of acid-hydrolyzed ether extract (AEE), starch, NDF, ADF, and ash was 3.86 ± 0.59%, 62.91 ± 1.79%, 8.13 ± 1.40%, 2.43 ± 0.53%, and 1.02 ± 0.28%, respectively. The average apparent ileal digestibility of GE, CP, AEE, NDF, ADF, and starch of the corn hybrids was 75.44 ± 4.38%, 62.63 ± 7.62%, 57.64 ± 7.62%, 19.02 ± 21.52%, −7.56 ± 19.53%, and 95.35 ± 2.48%, respectively, whereas the average apparent total tract digestibility of GE, CP, AEE, NDF, ADF, and starch was 87.78 ± 1.70%, 77.62 ± 4.36%, 53.53 ± 7.85%, 54.20 ± 13.03%, 38.46 ± 16.36%, and 99.90 ± 0.09%. On a DM basis, DE of the corn hybrids ranged from 3803 and 4217 kcal/kg DM with an average of 4058 ± 93 kcal/kg. The DE of corn hybrids may be predicted using the model: DE, kcal/kg DM = 1.719 × CP– 11.600 × AEE + 2.188 × NDF + 5.198 × ADF + 0.378 × Starch + 2.480 × GE– 7320.52 ($R^2 = 0.77$, RMSE = 54.3; $P < 0.001$). In summary, the chemical composition, energy concentration, and digestibility of nutrients varied among corn hybrids.

Key Words: chemical compositions, corn, pigs

1349 (W167) Different corn hybrids fed to growing pigs. II. Concentrations and digestibility of amino acids.

Y. Liu*[1], R. C. Sulabo[1], T. E. Sauber[2], and H. H. Stein[1], [1]*University of Illinois at Urbana-Champaign, Urbana,* [2]*Pioneer Hi-Bred International Inc., Johnston, IA.*

A total of 42 barrows (initial BW: 28.2 ± 2.91 kg) were used in four experiments to determine the variability in concentration and digestibility of AA in corn hybrids sourced from DuPont Pioneer (Johnston, IA) and to develop prediction equations to estimate the concentration of digestible AA in corn hybrids fed to growing pigs. In Exp. 1, 12 ileal cannulated barrows were allotted to a 12 × 12 Latin square design with 12 diets and 12 7-d periods. In Exp. 2, 3, and 4, 10 ileal cannulated barrows were allotted to a 10 × 10 Latin square design with 10 diets and 10 7-d periods. All diets had the same composition with the only difference being that different corn hybrids were used in each diet. Corn was included as 97.0% (as-fed basis) of the diet and was the only AA-contributing ingredient. Descriptive statistics for each chemical component of corn hybrids were determined using PROC MEANS. Simple linear regression analyses were performed using PROC REG of SAS. On an as-fed basis, the average concentration of CP, Arg, His, Ile, Leu, Lys, Met, Phe, Thr, Trp, and Val in the corn hybrids was 7.95 ± 0.79%, 0.36 ± 0.03%, 0.22 ± 0.02%, 0.30 ± 0.03%, 1.00 ± 0.14%, 0.21 ± 0.04%, 0.16 ± 0.02%, 0.41 ± 0.04%, 0.28 ± 0.03%, 0.05 ± 0.01%, and 0.40 ± 0.03%, respectively. The average standardized ileal digestibility (SID, %) of CP in the corn hybrids was 84.59 ± 4.92%. The average SID of indispensable AA was 92.63 ± 3.34% for Arg, 87.75 ± 3.99% for His, 86.96 ± 3.30% for Ile, 89.87 ± 2.58% for Leu, 85.25 ± 14.34% for Lys, 91.93 ± 2.49% for Met, 89.29 ± 2.74% for Phe, 80.75 ± 4.81% for Thr, 79.46 ± 6.74% for Trp, and 86.02 ± 3.89% for Val, respectively. The concentrations of standardized ileal digestible AA is not accurately estimated from the concentration of CP ($0.11 \leq R^2 \leq 0.78$). However, the concentration of each AA can be used to predict the concentration of digestible AA in corn ($R^2 \geq 0.80$). In summary, the variability in AA composition and digestibility of corn hybrids differed between individual AA. The concentration of digestible AA cannot be predicted from CP, but the concentration of each AA can be used to predict the concentration of digestible AA in corn.

Key Words: amino acid digestibility, corn, pigs

1350 (W168) A high dietary electrolyte balance reduces growth performance and CP and Zn total tract apparent digestibility in weanling piglets.

S. A. Guzmán-Pino[1], D. Solà-Oriol[1], R. Davin*[1], E. G. Manzanilla[1], C. Torrente[2], and J. F. Pérez[1], [1]*Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain,* [2]*Servei d'Emergències i Cures Intensives de la Fundació Hospital Clínic Veterinari-UAB, Departament de Medicina i Cirurgia Animals, Universitat Autònoma de Barcelona, Bellaterra, Spain.*

It is generally accepted that dietary electrolyte balance (dEB, Na + K– Cl, in mEq/kg diet) influences feed intake and growth performance of pigs. However, there is a not clear optimal recommendation for piglets. The objective of this study was to assess the effect of diets differing in the mineral source and dEB on feed intake, total tract apparent digestibility and growth of weanling pigs. A total of 240 piglets (21 d after weaning, initial BW 13.4 ± 1.17 kg) were blocked by BW into three blocks (heavy, middle and light), and then distributed into eight pens per block (10 pigs/pen) and randomly assigned to one of four experimental diets differing in the dEB level: 16 and 133 mEq/kg diets (VL, L), based on the incorporation of CaCl (3.6 g/kg); and 152 and 269 mEq/kg diets (H, VH), based on the addition of calcium carbonate (10.6 g/kg), without or with sodium bicarbonate (10 g/kg), respectively. Titanium dioxide (3 g/kg) was used as indigestible marker. The diets were offered for 16 d when performance was evaluated. One fecal sample was collected per pen on d 7 to measure whole-tract digestibility, and five venous blood samples per treatment were collected on d 12 to measure acid-base status of animals. Piglets fed VL and L diets reached higher BW on d 16 (19.01 kg and 19.46 kg, respectively) than did piglets fed VH diet (17.05 kg, $P < 0.05$). Diet L also promoted a lower ($P < 0.05$) feed:gain ratio (2.10) and a higher ($P < 0.05$) digestibility of the CP (74.6%) and Zn (13.0%) than did diet VH (3.23, 68.2 and 1.1%, respectively). The VL diet reduced blood TCO2, bicarbonate and base excess values, as compared with L, H and VH diets ($P < 0.01$), reflecting the acidogenic nature of that diet. In conclusion, the results show that a high dEB diet (269 mEq/kg) may reduce piglets' performance and the total tract digestibility of nutrients, possibly associated to its higher acid-binding capacity (427 mEq/kg).

Key Words: dietary electrolyte balance, digestibility, growth performance

1351 (W169) Acceptance and palatability of different inclusion levels of protein solutions by feed restricted and non-restricted nursery pigs.

J. E. Figueroa[1,2], D. Solà-Oriol[3], R. Davin[*4], J. F. Pérez[4], and D. Dwyer[5,6], *[1]SNiBA, Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Universidad de Chile, Santiago, [3]Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [4]Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [5]Cardiff University, Wales, [6]School of Psychology, University of New South Wales, Australia.*

The aim of the present work was to study the productive performance of nursery pigs when sweet milk whey (SMW) is replaced by porcine digestive peptides (PDP; 620 g/kg of CP, Bioibérica SA, Palafolls, Barcelona, Spain). A total of 240 pigs were randomly distributed after weaning into two groups (12 pens/group) depending on the presence of SMW or PDP on their diets. The SMW group was fed a pre-starter (0 to 14 d) and starter (15 to 33 d) diet with 142 g/kg and 49 g/kg SMW respectively; the PDP group was offered an iso-caloric and iso-proteic diet with 20 g/kg of PDP and 300 g/kg of wheat replacing dairy products. Feed intake and body weight were measured weekly to calculate average daily feed intake (ADFI), average daily gain (ADG) and gain: feed ratio (GFR). A choice test and one-feeder test of 30 min each were performed in another group of animals 3 wk wk weaning (36 pen pairs) to evaluate the preference and acceptance for both diets, respectively. Feed intake was recorded by measuring the initial and final weight of the feeders. SMW and PDP diet positions were balance across pig's pairs. Data were analyzed with ANOVA using the GLM procedure (performance values) or the PROC MIXED (preference and acceptance values) of the statistical package SAS. Despite clear differences on feed preference (211 vs. 77 g; $P = 0.039$) and acceptance (287 vs. 192 g; $P = 0.001$) between diets with or without whey respectively, no effects were observed on performance at the end of the nursery period (20.92 vs. 21.13 kg for BW, 0.62 vs. 0.63 kg/d for ADFI and 0.52 vs. 0.53 kg/d for ADG). Despite the reduced preferences and acceptance observed, the use of dairy products appears to be unnecessary if a high valuable protein source is offered during nursery.

Key Words: familiarity, feed preferences, lactose

1352 (W170) Nutritional value of whey permeate and egg products fed to growing pigs.

T. A. Woyengo[*1], E. Sánchez[1,2], J. Yanez[3], M. Cervantes[4], and R. T. Zijlstra[1], *[1]University of Alberta, Edmonton, Canada, [2]Universidad Autónoma de Baja California, Mexicali, México, [3]Universidad Autnonoma de Tlaxcala, México, [4]ICA, Universidad Autónoma de Baja California, Mexicali, México.*

Inedible eggs from egg-breaking plants have high AA and fat content. Instead whey permeate (WP), co-product from dairy industry, has high lactose content. Thus, blends of eggs and WP can be good sources of protein and energy in swine diets; however, their nutritional value is unknown. A study was conducted to determine standardized ileal digestibility (SID) of AA and calculated NE value for dried whole egg (egg), and two blends of WP and egg (70% WP and 30% egg, 7030PE; and 60% WP and 40% egg, 6040PE). Eight ileal-cannulated barrows (35.1 kg BW) were fed four diets in a replicated 4 × 4 Latin square design. The diets were a pre-grower-corn-starch-based basal diet, and this basal diet with energy- and AA-yielding ingredients replaced with 30% of egg, or 40% of 7030PE or 6040PE. Energy and nutrient digestibility in the test products was determined by difference method. The SID of AA were calculated using published values for basal ileal endogenous AA losses. On DM basis, egg, 7030PE, and 6040PE contained 48.9, 18.6, and 21.4% CP; 3.60, 0.98, and 1.17% Lys; and 39.3, 8.89, and 12.4% ether extract, respectively. The SID of Lys was greater ($P < 0.05$) for egg (86.9%) than for 7030PE (73.6%) or 6040PE (70.8%). However, egg had lower ($P < 0.05$) SID of Arg, Ile, and Phe than 7030PE or 6040PE. The 7030PE and 6040PE were similar in apparent total tract GE digestibility and SID of all AA except His. The NE (on DM basis) for egg (4.67 Mcal/kg) was greater ($P < 0.05$) than that for 7030PE (3.34 Mcal/kg), which was lower ($P < 0.05$) than that of 6040PE (3.61 Mcal/kg). In conclusion, the proportion of egg (30 vs. 40%) in the egg-WP blend did not affect the digestibility of GE and of most AA; however, the NE value was greater for the blend with 40% egg due to the high fat content in egg. Egg-WP blends had lower Lys digestibility than egg, implying that Lys was partly damaged by the blending and drying process. Nonetheless, the egg-WP blends had high AA digestibility and NE values, and hence they can be good sources of AA and energy in swine diets.

Key Words: egg, whey permeate, pig

1353 (W171) Inclusion of recycled wastes from the food industry in phase I diets for piglets: Effects on nutrient digestibility and growth performance.
B. Saldaña[1], P. Guzmán[1], G. Fondevila[1], J. F. Diaz Berrocoso[1], L. Cámara[1], X. Roca[2], and G. G. Mateos*[1], *[1]Universidad Politecnica de Madrid, Spain, [2]Promic, S. A., Barcelona, Spain.*

We studied the effects of inclusion of food by-products in the phase I diet on growth performance and total tract apparent digestibility (TTAD) of nutrients in 288 weaned pigs (7.9 ± 0.15 kg BW). On DM bases, the ingredients tested were a) lactal, a combination of yogurt (52%), milk (26%), and 22% of a wheat flour + broken rice meal mixture, b) lactal-cheese, a combination of yogurt (39%), milk (20%), cheese (19%), and 22% of the cereal mixture, and c) Infant, a mixture of out of date infant formulas based on cereals. In phase I (d 0 to 21 of experiment) there were eight dietary treatments arranged as a 2 × 4 factorial with two levels of lactose (7% and 10%) and four feed formulation: 1) a control commercial diet, 2) a diet with 15% lactal (LACTAL), 3) a diet with 15% lactal-cheese (LACTAL-cheese), and 4) a diet with 15% lactal-cheese and 20% Infant formula (INFANT). All diets were formulated to be isonutritives. On d 13 to 15 of the experiment, 300 g of feces per pen were collected by rectal massage for the TTAD analysis. From d 21 to 35 (phase II) all pigs received a common diet. Each treatment was replicated six times and the experimental unit was the individual pen with six pigs. Data were analyzed as a completely randomized design, with level of lactose and feed formulation as main effects. In phase I, an increase in dietary lactose increased ($P < 0.05$) ADFI and ADG but did not affect G:F. Pigs fed the INFANT diets (with 7 or 10% lactose) had higher ADFI ($P < 0.05$) than pigs fed the LACTAL diets, with pigs fed the other diets being intermediate. In phase II, pig growth was not affected by previous dietary treatment. Cumulatively, ADFI was higher ($P < 0.05$) for pigs fed the INFANT diet than for pigs fed the LACTAL diets. TTAD of DM, OM, GE, and CP was higher ($P < 0.05$) for pigs fed the high lactose level diets. Similar results were obtained for pigs fed the INFANT diets ($P < 0.05$). It is concluded that an increase in lactose content of the diet improved piglet performance and that the food by-products tested can substitute successfully high quality ingredients, such as dried whey and heat processed cereals, in phase I diets for weanling pigs.

Key Words: cheese, food by-products, infant formulas, lactose, yogurt

1354 (W172) Effect of wheat and wheat with corn distillers grain on growth performance in nursery pigs.
D. J. Bloxham*, R. Dove, and M. J. Azain, *University of Georgia, Athens.*

An experiment was conducted to evaluate the effect of substituting wheat or wheat and corn distiller's grains with solubles (DDGS) for corn in the phase 2 and 3 starter diets. The objective of this study was to determine if wheat is a viable alternative to corn in starter diets. A total of 126 pigs (4 to 6 pigs per pen and 8 pens per treatment) were blocked by weight and randomly assigned treatments within block. Pigs were weaned at 20 ± 2 d and fed a common diet (ME 3.4 kcal/kg; 1.5% SID lysine) 0 to 7 d post weaning, initial weight of 6.3 kg, NS. The three experimental diets [1, control, corn diet (C); 2, 30% wheat (W); and 3, 30% wheat and 30% DDGS (WCD)] were fed in two phases: phase 2 (ME:3.3 kcal/g, 1.4% SID lysine) from d 7 to 21 post-weaning, and phase 3 diets (ME: 3.3 kcal/g, 1.2% SID lysine) from d 21 to 35. All diets were formulated to meet the dietary requirements according to the 2012 Swine NRC. Body weight gain and feed disappearance were determined weekly. Data were analyzed using PROC GLM of SAS. Overall, pigs fed 30% W (21.6 kg) had body weights that were similar to those fed the C diet (21.0 kg, $P = 0.17$). Pigs fed the WCD diet were significantly heavier (22.6 kg, $P < 0.01$) than those fed C (21.0 kg). The ADFI was similar among treatments in phase 2 (569 g/d, NS), but was greater in those fed WCD in phase 3 (C, 888; W, 870; WCD 1006 g/d; $P < 0.02$) and overall (C, 728; W, 718; WCD 791 g/d; $P < 0.02$). The G: F was improved in pigs fed WCD in phase 2 (C, 0.62; W, 0.62; WCD 0.67; $P < 0.02$), but not in phase 3 or overall. In conclusion, these results indicate that wheat can be substituted for corn in nursery diets and that wheat in combination with DDGS may be superior to corn based diets.

Key Words: wheat, DDGS, nursery pig performance

1355 (W173) Effects of dietary protein and rapidly fermentable carbohydrate contents on microbial fermentation profile in the hindgut of weanling pigs.
V. V. Almeida[1], M. C. Thomaz[1], A. J. C. Nuñez[2], P. V. A. Alvarenga[1], F. R. Castelini[1], D. Perondi[1], R. G. Isola[1], A. Remus[1], Y. V. Silva-Guillen[1], E. Daniel[1], and S. L. Silva*[2], *[1]Dep. of Animal Science, FCAV/UNESP, Jaboticabal/SP, Brazil, [2]Dep. of Animal Science, FZEA/USP, Pirassununga/SP, Brazil.*

Protein fermentation in the hindgut of piglets leads to the production of potentially toxic metabolites such as ammonia, which may increase the risk of postweaning diarrhea. In this way, the objectives in this study were to determine the effects of dietary CP and dried citrus pulp (DCP, rapidly fermentable carbohydrate source) contents on short-chain fatty acids (SCFA), branched-chain fatty acids (BCFA), and ammonia concentrations in the colon digesta of weanling pigs. One hundred eight barrows weaned at 21 d of age were blocked by initial BW (5.82 ± 0.16 kg) and randomly assigned to one of four treatments with nine replicate pens per treatment and three pigs per pen. Treatments were arranged in a 2 × 2 factorial, with 2 CP contents (HCP and LCP, high- and low-CP diets, respectively) and 2 DCP contents (0 and 7.5%, as-fed basis). The HCP treatments consisted of feeding a 20 and 21%

CP diet (as-fed basis) during the pre-starter I (1 to 14 d) and pre-starter II (15 to 28 d) phases, respectively. For the LCP treatments, diets were reduced by 4% units compared with the HCP diets in both phases. The AA contents in the diets were balanced by supplementation with crystalline AA, such as L-Lys, DL-Met, L-Thr, L-Trp, L-Val, and L-Ile to maintain constant ratios in relation to standardized ileal digestible Lys. Colon digesta samples were collected from one randomly selected pig per pen on d 7 and 28 postweaning for determinations of SCFA and BCFA by gas chromatography, and ammonia concentrations by colorimetry. Statistical analyses were conducted using the PROC MIXED of SAS. Feeding pigs diets containing 7.5% DCP increased ($P < 0.01$) acetic acid concentrations, and decreased propionic ($P < 0.05$) and valeric ($P < 0.01$) acids concentrations, whereas butyric acid production was not affected ($P > 0.05$) by treatments. Dietary DCP inclusion increased ($P < 0.05$) isobutyric acid concentrations in the colon only at 28 d postweaning. Adding 7.5% DCP to the diet resulted in lower isovaleric acid ($P < 0.01$) and ammonia ($P < 0.01$) concentrations in the colon only for pigs fed the LCP diet. In conclusion, low-protein AA-supplemented diets with 7.5% DCP inclusion depresses harmful protein fermentation in the hindgut, and therefore may be contributing to enhance intestinal health of weanling pigs.

Key Words: intestinal health, piglets, protein fermentation

1356 (W174) Effects of dietary supplementation rice bran extracton production performance, feed intake, egg quality and excreta microbiota in laying hens.

H. L. Li, Y. Lei, and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

This experiment was conducted to evaluate the effects of dietary supplementation of rice bran extract on production performance, feed intake, egg quality and excreta microbiota in laying hens. A total of 288 Hy-line Brown (46-wk old) laying hens were randomly assigned to 1 of 3 treatments. The trial lasted for 20 wk. The dietary treatments were as follows: 1) CON, free antibiotics diet; 2) RB01, CON +0.01% rice bran extract; 3) RB02, CON + 0.02% rice bran extract. There were 8 replicates per treatment with 12 birds per replicate. Daily records of egg production and feed consumption were kept throughout the experimental period. Egg production was expressed as an average production of hen per day, which was calculated from the total number of eggs divided by the number of experimental time (week as a unit) and summarized on an average basis. A total of 42 salable eggs (no shell defects or cracks) were randomly collected biweekly from each treatment at 1700 h (3 eggs per replication). The egg quality of the collected eggs was then determined at 2000 h on the day of collection. All data were arranged to evaluate by analysis of variance following the GLM procedure in a completely randomized design using the SAS software program (SAS Institute, 1996). Laying hens were blocked with identical age. The difference among treatment was compared using the Duncan's multiple range test. The treatment effect was observed significant with the probability value below 0.05. The egg production of RB02 was higher (92.3 vs. 88.1%; 93.3 vs. 90.3%; $P < 0.05$) than CON at wk 5 and 6. Moreover, the *E. coli* content of excreta microflora of CON was higher (6.62 vs. 6.37 $\log_{10}$cfu/g; $P < 0.05$) than RB02. The Lactobacillus content of CON was lower (7.44 vs. 7.72 $\log_{10}$cfu/g; $P < 0.05$) compared with RB02. In conclusion, dietary supplementation of 0.02% rice bran extract can increase egg production performance and *Lactobacillus content*, and decrease *E. coli* content in laying hens.

Key Words: egg quality, excreta microbiata, feed intake, laying hens, production performance, rice bran extract

---

1357 (W175) Injection of glycosaminoglycans and vitamin C in incubation on the weight loss and shell conductance of the eggs.

E. T. T. Santos*[1], D. M. C. C. Castiblanco[1], L. L. Borges[1], C. H. D. F. Domingues[2], T. C. O. D. Quadros[1], S. Sgavioli[1], G. M. D. A. R. Garcia[1], R. D. G. Isola[2], and S. M. B. Artoni[1], *[1]Dep. of Morphology and Animal Physiology, São Paulo State University, Jaboticabal, Brazil, [2]Dep. of Animal Science, São Paulo State University, Jaboticabal, Brazil.*

Injection of nutrients into eggs can improve the incubation process. This study injected different percentages of a supplement consisting of glycosaminoglycans and vitamin C into eggs and evaluated the effect during incubation on weight loss and shell conductance of the eggs. Two hundred forty fertile broiler (Cobb) eggs from breeder hens at 43 wk of age were used. The eggs were 64 ± 4 g each. The experimental design was completely randomized with five treatments (non-injected eggs, eggs injected with milli-Q water, eggs injected with glycosaminoglycans and vitamin C at 2, 4, and 6% diluted with 100 µL of milli-Q water), distributed in three horizontal Ecological Premium, model IP 120, incubators, with three repetitions and 16 eggs per treatment. Each 100 g of the supplement were composed of: 30,000 mg of chondroitin sulfate, 30,000 mg of glucosamine and 5000 mg of vitamin C and vehicle q.s 100 g. The supplement was injected into the albumen, approximately 6 mm below the eggshell on d 4 of incubation. The injection site was then covered with a label identifying the treatment and repetition. Statistical analsyses were performed using the Statistical Analysis System SAS (2002) program with the averages compared by Tukey test at 5% probability. The weight loss was calculated as a percent from the difference between the weight of the egg at the start of the incubation and at d 18 of incubation. Shell conductance was calculated by weight loss in grams until the transfer/saturation vapor pressure (23.86 mm/Hg at 25°C). Shell conductance is the ability to exchange gases between the egg and the environment, and

is related to the weight loss. The higher the conductance and loss of mass, the greater the evaporative heat loss from the egg will be. In this study, the weight loss was approximately 7.6% and conductance was 0.320 and both were not significantly affected ($P > 0.05$) by the treatments. Therefore, the intra-egg injection of the glycosaminoglycans and vitamin C supplement did not alter the heat loss from evaporation.

Key Words: ascorbic acid, chondroitin, nutrition in ovo

1358 (W176) Effect of material bioconversion natural complex on growth performance, nutrient digestibility, blood characteristics, and fecal microbiota in weanling pigs. J. H. Cho*, M. Begum, and I. H. Kim, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

A total of 150 weanling pigs [(Yorkshire × Landrace) × Duroc] with an average initial body weight (BW) of 5.76 ± 1.36 kg were used in a 6-wk trial to investigate the effect of material bioconversion natural complex on growth performance, nutrient digestibility, blood characteristics, fecal characteristics in weanling pigs. All these weanling pigs were randomly allotted into one of the five experimental diets according to their initial BW and sex (6 replicate pens/treatment, 5 pigs/pen, 2 barrows and 3 gilts/pen). Dietary treatments consisted of 1) NC, free antibiotics diet; 2) PC, NC + 0.1% tiamulin; 3) STR1, NC + 0.1% fermented material 1; 4) STR2, NC + 0.1% fermented material 2; and 5) STR3, NC + 0.1% fermented material 3. STR is material bioconversion natural complex powder produced from fermentation of mulberry leaves and turmeric with bacterial of mulberry yellow mushroom. STR1, STR2, STR3 contains 1.5, 3, and 6% of active complex powder, respectively. All diets, in mash form, were formulated to meet or exceed the nutrient requirements (NRC, 2012) for weanling pigs. During wk 3 to 6, pigs fed with PC, STR2 and STR3diets had higher (457, 463, 453 vs. 393 g; $P < 0.05$) ADG than NC treatments. During the overall period, pigs fed NC diet had lower (342 vs. 385, 388 g; $P < 0.05$) ADG than PC and STR2 treatments and the G:F in PC, STR2 and STR3 treatments was significantly higher (0.745, 0.740, 0.715 vs. 0.638; $P < 0.05$) compared with NC treatment. The ATTD of dry matterin STR2 treatment was higher (83.35 vs. 81.36%; 81.27 vs. 79.06%; $P < 0.05$) than NC treatment atthe end of wk 3 and 6. Moreover, the ATTD of nitrogen in PC and STR2 treatments was higher (81.81, 81.35 vs. 78.54%; $P < 0.05$) than NC treatment at the end of 3 wk. Pigs fed with PC diet had higher (8.21 vs. 7.43 $\log_{10}$cfu/g; $P < 0.05$) *Lactobacillus* population than those fed with NC diet. But there was no difference ($P > 0.05$) detected on *E. coli*, and *Salmonella* content at 6 wk. Through the experimental period, there was no difference ($P > 0.05$) observed on fecal score among dietary treatments. During the whole experimental period, no significant difference ($P > 0.05$) was observed on fecal moisture or fecal pH among dietary treatments. In conclusion, supplementation of material bioconversion natural complex may be helpful to improve the growth performance and nutrient digestibility, increase *Lactobacillus* concentrations of weanling pigs.

Key Words: nutrient digestibility, growth performance, *Lactobacillus* population, material bioconversion natural complex, weanling pigs

---

1359 (W177) The effects of fermented cotton seed meal on growth performance and egg quality in laying hens. Y. Wang*[1], A. Li[1], Y. Hou[1], Y. Li[2], X. Zhang[1], and H. Wei[1], *[1]Academy of State Administration of Grain, Beijing, China, [2]Animal Diseases Control and Prevention Centre of Miyun City, Beijing, China.*

Cottonseed meal (CSM) is very rich in China, but its nutrient bioavailability is low. Microbial solid-state fermentation is an effective way to improve the nutrient bioavailability of CSM. Therefore, deeply evaluating the nutritional value of fermented cottonseed meal (FCSM) in poultry, pig and ruminants can provide important data support for its reasonable application in animal feed and alleviate the shortage of high quality protein feedstuff. The objective of this study was to evaluate the effects of FCSM on growth performance and egg quality in laying-hens. A total of 660 47-wk-old laying hens were randomly divided into two groups with 110 birds/replicate. A corn-soybean meal (SBM) based control diet was formulated and the experimental diets included FCSM to replace 15% SBM on a kg basis. The trial period was 2 mo. Laying rate, feed to egg ratio, and egg quality were measured. The statistical analysis was performed with SPSS 18.0 software for Windows. Independent sample *t* test was used and a probability level of $P \leq 0.05$ was considered statistically significant. The results indicated that, compared to non-fermented CSM, free gossypol (FG) content of FCSM declined from 706 mg/kg to 257mg/kg, apparent metabolism energy (AME) increased from 8.93 MJ/kg to 9.37 MJ/kg. The number of *Saccharomyces cerevisiae* and *Bacillus subtilis* in FCSM was 1.86×10^8 and 3.1×10^8, besides, the content of small peptides (molecular weight < 600 Da) in FCSM was higher than CSM. No difference was found between treatments regarding the laying rate ($P = 0.383$), feed to egg ratio ($P = 0.318$). Compared to control diet, the FCSM had no adverse effects on yolk relative weight ($P = 0.201$), Haugh unit ($P = 0.499$), yolk color ($P = 0.817$), egg shell strength ($P = 0.923$). In conclusion, FCSM can be used in laying hen diets at up to 15% of the total diet as a promising alternative protein source.

Key Words: laying hen, fermented cotton seed meal, growth performance

1360 (W178) Soybean meals and soy protein concentrates as main source of protein in phase 1 diets for piglets: Growth performance data.

P. Guzmán, B. Saldaña, L. Cámara, and G. G. Mateos*, *Universidad Politecnica de Madrid, Spain.*

In total, 192 weanling pigs were used to study the growth performance and incidence of post-weaning diarrhea (PWD) in piglets fed diets based on soybean meals (SBM) of different origins or soy protein concentrates (SPC) from 21 to 58 d of age. In phase 1 (21 to 49 d of age) piglets received one of eight diets that differed in the source of soy protein used. Six of the diets were based ($n = 2$) on SBM from three different origins [USA, Argentina (ARG), and Brazil (BRA)] and the other two diets were based on 2 SPC with 60 or 65% CP, respectively. All diets were isonutritive and contained the same amount of dietary CP from soy origin. In phase 2 (49 to 58 d of age) all pigs received a common commercial diet. In phase 1, growth performance was not affected by diet but PWD was higher in pigs fed the ARG SBM than in pigs fed the other diets ($P < 0.05$). From 28 to 35 d of age, piglets fed the SPC tended to grow faster ($P = 0.056$) than piglets fed the SBM. From 35 to 42 d of age piglets fed USA SBM showed higher ADG ($P < 0.05$) and better G:F ratio ($P < 0.05$) than the average of piglets fed the other diets. However, no differences among diets were observed in phase 2. Cumulatively (21 to 58 d of age), the only difference observed among treatments was for G:F ratio that tended to be better for pigs fed the USA SBM as compared with the average of pigs from all the other treatments ($P = 0.064$). Also, PWD was higher in piglets fed ARG SBM than in piglets fed the other diets ($P < 0.01$). In conclusion, soy source had little effect on performance of pigs but G:F ratio tended to be better in pigs fed SBM of USA origin and PWD was higher in pigs fed the ARG SBM. Therefore, the choice of soy source (SPC and SBM) and SBM origin (USA, ARG, and BRA) might depend at high extent on the objectives and the relative cost of available sources.

Key Words: piglet growth, soybean meal origin, soy protein concentrate

1361 (W179) Standardized total tract digestibility of phosphorus in camelina (*Camelina sativa*) meal fed to growing pigs without or with phytase supplementation.

P. A Adhikari, and C. M. Nyachoti*, *University of Manitoba, Winnipeg, Canada.*

A study was conducted to determine the apparent (ATTD) and standardized (STTD) total tract digestibility of phosphorus (P) in camelina meal fed to growing pigs and the effect of phytase supplementation on STTD of P in camelina meal. Eighteen growing pigs (average initial BW of 18.1 ± 0.70 kg) were placed individually in metabolism crates which allowed for the total but separate collection of feces and urine. Pigs were allotted to one of three experimental diets, containing either 1) 20% camelina meal without phytase, 2) 20% camelina meal with 500 FTU/kg phytase or 3) a constarch-gelatin based P-free diet, in a completely randomised design to give six replicates per diet. The P-free diet formulated to contain 18.0% CP was used to determine endogenous P losses (EPL) to estimate STTD of P in camelina meal. Pigs were fed their respective diets in two equal portions at 0830 and 1630 h. Daily feed allowance was based on the body weight at the beginning of experiment and was calculated to supply 2.6 times the estimated maintenance energy requirements. The experiment lasted for 14 d, and pigs were adapted to their respective diets for the initial 9 d followed by a 5-d period of total collection of feces and urine. The ATTD of P and EPL were 55.4% and 108 ± 48.9 mg/kg DMI, respectively, whereas the STTD of P was 57.4%. Phytase supplementation increased ($P < 0.05$) the ATTD and STTD of P in camelina meal to 68.3 and 70.0%, respectively. Phytase supplementation increased ($P < 0.05$) P retention (66.8 vs. 54.6%) and reduced ($P < 0.05$) P output in the feces (0.50 vs. 0.71 g/d). The standardized total tract digestible P content in camelina meal was estimated at 5.45 g/kg.

Key Words: camelina meal, endogenous losses, phosphorus, pig

1362 (W180) Effects of adding a dried food waste product to the diets of finishing pigs on growth, feed intake, and nutrient digestibility.

H. L. Acuff* and L. A. Pettey, *California State Polytechnic University, Pomona.*

A study was conducted to measure the effects of adding a dried food waste product (DFWP) to the diets of late finishing pigs. The product was derived from bakery and vegetable food waste being aerobically digested (BioGreen 360) and heated to over 150°C during drying. Before mixing the diets, the DFWP used in the study was analyzed for nutrient content and found to have 84.0% DM, 10.95% CP, 15.42% EE, 0.42% Lys, 0.17% Ca, and 0.22% P. Nine finishing pigs (132 kg BW) were allotted randomly to one of three dietary treatments: 1) corn-SBM-based control diet; 2) control with 5% DFWP added; and 3) control with 10% DFWP added. All diets were balanced for lysine, Ca, and P (NRC, 2012). The study was conducted in three 1-wk periods, with each pig being fed a different diet each week with a 5-d adjustment period followed by a 2-d collection of feces. Pigs were weighed weekly and feed disappearance was measured daily. Fecal grab samples were dried and analyzed for DM, CP, EE, and ADF. Acid-insoluble ash was used as an indigestible marker for digestibility calculations. During the experiment, average daily gain (ADG) increased linearly ($P < 0.05$) with increasing DFWP addition to the diet. Average daily feed intake (ADFI) decreased numerically in pigs fed diets with 10% DFWP, as expected due to the high fat content of DFWP. Digestibility

estimates for DM, CP, fat, and ADF were not influenced by collection period and were pooled across period to estimate the effect of dietary DFWP addition. DM digestibility averaged 94.6% for all diets and was not influenced ($P > 0.10$) by DFWP addition. CP digestibility was also not affected ($P > 0.10$) by DFWP addition to the diet and were 81.1%, 81.2%, and 80.9% for Diets 1, 2, and 3, respectively. Fat digestibility (51.9%, 55.3%, and 62.8% for Diets 1, 2, and 3, respectively) increased linearly ($P < 0.01$) with increasing DFWP addition to the diet and was higher ($P < 0.10$) than the control diet when 5 or 10% DFWP was added. ADF digestibility was not affected ($P > 0.10$) by DFWP addition to the diet. Based on this experiment, the DFWP produced by the Biogreen 360 food waste digester is palatable for growing pigs, increases the fat digestibility of a corn-SBM based diet, and does not negatively influence protein or ADF digestibility when added up to 10% of the diet.

Key Words: pigs, food waste, digestibility

1363 (W181) Determination of the effect of the level of corn starch in the diet on the energy value of crude glycerin in swine. C. Ordoñez-Gomez*[1,2], C. Ariza-Nieto[3], and G. Afanador-Tellez[2], *[1]Universidad Francisco de Paula Santander-Ocaña, Colombia, [2]Universidad Nacional de Colombia, Bogotá, [3]CORPOICA, Mosquera, Colombia.*

Crude glycerin (CG), a byproduct of biodiesel, generates interest in animal feed because of its energy value. To determine the effect of the level of starch in the diet on the digestible energy (DE) of crude glycerin in swine this study was developed. The DE was determined for crude glycerin with 10 barrows placed in metabolic cages using 0.5% chromium oxide as an indigestible dietary indicator. The treatments consisted in two starch levels (SL) 10 and 12%, and five levels of CG substitution 0, 2.5, 5, 7.5 and 10%. Each period consisted of 5-d adjustment period, a 2-d collection period. During the collection period, feces and urine were collected separately and stored at 0°C until analysis to calculate metabolized energy (ME). The data were subjected to multiple linear regression analysis determining the value of the DE and ME of CG, as the slope of the line and N metabolism data as a Latin square design using the GLM and REG modules of SAS ver. 9.2. DE value of diet corrected by dietary starch content was described as, DE of diet corrected by starch (Kcal/kg) = 2952.1 +30.9(period) +4427.3(CG) + 31.5(SL)- 691.5(CG: SL). According to the slope, DE value of CG depended of SL ($P < 0.001$) estimated in 4427 and 3769 Kcal/kg DM for 10 and 12% of SL, respectively. ME of CG was determined as 3436 Kcal/kg DM, no effect ($P > 0.05$) of SL on the value of the ME of the CG was observed, although no quadratic effect of level of CG was observed ($P > 0.05$). An increase ($P < 0.001$) in urinary energy (UE) was observed as CG increased in the diet; UE (Kcal/kg DMI) = 159.6 +7.99(CG). There was an interaction between CG and SL ($P < 0.001$) which caused an increased in the amount of nitrogen digestible (AND) when CG increased by the 10% SL. However, the AND decreased when CG was increased by the 12% SL. According to these results, it was established that SL affects DE value of CG and the nitrogen metabolism in pigs.

Key Words: energy, crude glycerin, starch

1364 (W182) Effect of the substitution of soybean meal and sorghum for cull chickpeas on the apparent digestibility of nutrients in diets for growing pigs. J. M. Uriarte*, R. Barajas Cruz, J. A. Romo Rubio, H. R. Guemez Gaxiola, J. M. Romo Valdez, J. F. Nuñez, and N. A. López, *Universidad Autónoma de Sinaloa, Culiacán, México.*

The objective of this experiment was to determine the effect of the substitution of soybean meal and sorghum for cull chickpeas (CP average value of 24%, and 3.0 Mcal ME/kg, crude fat 5%) on apparent digestibility of nutrients in diets for growing pigs. Six pigs (BW = 36.15 ± 1.5 kg; Large White × Landrace × Large White × Pietrain) were used in a replicated Latin square design. Pigs were assigned to consume one of three diets: 1) Diet with 18.2% CP and 3.2 Mcal ME/kg, containing sorghum 68.6%, soybean meal 27.4%, and premix 4.0% (CONT); 2) Diet with 17% CP and 3.2 Mcal ME/kg with sorghum 48.5%, cull chickpeas 35%, soybean meal 10.0%, vegetable oil 2.5%, and premix 4.0% (CHP35), and 3) Diet with 20.5% CP and 3.1 Mcal ME/kg with sorghum 17.0%, cull chickpeas 70%, soybean meal 5.0%, vegetable oil 4.0%, and premix 4.0% (CHP70). Pigs were individually placed in metabolic crates (0.6 × 1.2 m). The adaptation period was 6 d and sample collection period was 4 d. From each diet and period, one kg of diet was taken as a sample and the total fecal production was collected. Feed Intake (1.88, 1.86 and 1.68 kg/day) was not affected by treatments ($P = 0.10$) for CONT, CHP35 and CHP70, respectively. Apparent digestibility of DM (82.9, 83.7 and 82.9%) was equal ($P = 0.81$) across treatments. Apparent digestibility of crude protein was not altered ($P = 0.35$) by CHP inclusion (78.4, 77.5 and 76.0%). These results suggest that cull chickpeas can be used up to 70% in growing pig diets without affecting nutrient digestibility.

Key Words: chickpeas, digestibility, pigs

NONRUMINANT NUTRITION: FACTORS IMPACTING FEED INTAKE

1365 (W183) Antioxidant activity of intestinal mucosa in piglets fed deoxynivalenol naturally contaminated diet. F. Guay[1], M. Lessard[2], Y. Chorfi[3], and B. V. Le Thanh[*4], *[1]Universite Laval, Quebec City, Canada, [2]Agriculture and Agri-Food Canada, Sherbrooke, QC, [3]Université de Montréal, Faculté de Médecine Vétérinaire, St-Hyacinthe, QC, Canada, [4]Universite Laval, Quebec City, Canada.*

Deoxynivalenol (DON) is a mycotoxin commonly detected in cereals and grains, and is the most prevalent contaminating trichothecene in North American crops. In young piglets, the main effects of DON are reduced feed intake and weight gain, impaired immune response and enhanced oxidative stress. The influence of DON-contaminated feed on the antioxidant status of the intestinal mucosa in weaned piglets is not well known. Therefore, the aim of this study was to evaluate the activity of antioxidant enzymes and markers associated with oxidative stress in jejunal and ileal mucosa of piglets fed DON naturally contaminated diet. A total of 24 castrated weanling piglets with an initial weight of 6.0 ± 0.5 kg were used for a 14-d experimental period. After 1 wk post-weaning on a commercial diet, piglets were randomly assigned to either control diet or 4 ppm DON diet and housed individually. Samples of jejunum and ileum mucosa were collected at the end of the experiment to determine the total activity of glutathione peroxidase (GPx), catalase (CAT), superoxide dismutase (SOD) and xanthine oxidase (XO) as well as malondialdehyde (MDA) concentration and total antioxidant capacity (TAC). Data were analyzed using the SAS PROC MIXED in a randomized complete block design (initial body weight) with DON contamination as main independent factor. DON-contaminated diet decreased catalase activity (3.69 vs. 3.03 μmol/min/g, $P = 0.045$) and tended to increase MDA concentration in jejunal mucosa (7.09 vs. 9.86 nmol/g, $P = 0.087$). Also it decreased total SOD activity (48.1 vs. 35.9 μU/g, $P = 0.021$), but increased the total GPx activity (2.49 vs. 2.95 μmol/min/g, $P = 0.035$) in ileal mucosa. Activity of XO and TAC were not affected by DON-contaminated diet neither in jejunal nor in ileal mucosa. These results showed that DON affect intestinal enzyme activities involved in the oxidative stress reaction, which can affect the function and the integrity of the intestinal mucosa.

Key Words: piglet, deoxynivalenol, antioxidants

1366 (W184) Effects of different feed processing procedures with expander on broiler performance. M. Gierus[*1], C. Elwert[2], and S. Sternowsky[3], *[1]University of Natural Resources and Life Sciences–Institute of Animal Nutrition, Products, and Nutrition Physiology, Vienna, Austria, [2]Feedtest, Wettin-Löbejün, Germany, [3]Amandus Kahl GmbH & Co KG, Reinbek, Germany.*

For particle agglomeration after grinding, pelleting is successfully used, but it does not increase considerably starch gelatinization, which would be maximized after hydrothermic treatment (HT). Among feed processing methods with HT, expanding may achieve the most efficient feed conversion rate (FCR). The objective was to compare different feed processing methods of broiler ration on animal performance. Ration was mixed with the same ingredients, differing in composition between phase I and II only. Rations were processed to obtain mash (negative control), pelleted only (positive control), or four expander processes [crumble I (2.7 kWh/t) and II (12 kWh/t), shaped crumble (30 kWh/t), and pelleting after expander processing (exp. + pel., 15 kWh/t)]. Broilers were kept in boxes of 10 animals each and were fed in two phases [age 1 to 21 d (phase I), and 22 to 36 d (phase II)]. Body weight gain and feed intake were measured. Treatments were arranged in a completely randomized design ($r = 8$); means separated by Tukey ($P < 0.05$). Among feed processing methods, feed intake was highest for pellets, crumbles I and II. Expanding could preserve coarse structure inside the expandat, in contrast to the pelleted ration. The most efficient FCR among expander treatments was achieved with the shaped crumble, next to pelleted feeds. Whereas crumble I (low energy input as kWh/t) contributed to particle agglomeration, this expander treatment was not able to increase substantially starch gelatinization or avoid selective feed intake. The shaped crumble had higher energy input (as kWh/t) than crumble II, which may explain the comparable FCR to pelleted rations. The reduced bulk density however may explain the lower feed intake for the shaped crumble treatment. The FCR of broilers fed on shaped crumbles compared to the pelleted treatments is attributed to the coarse particles inside the expandate after processing and the HT on improved starch gelatinization.

Key Words: broiler, feed processing, feed conversion

1367 (W185) Influence of pre-pelleting inclusion of whole corn on performance, nutrient utilization and digestive tract measurements of young broilers. Y. Singh[1], V. Ravindran[*1], and T. J. Wester[2], *[1]Massey University, Palmerston North, New Zealand, [2]Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand.*

The objective of the present study was to examine the effects of pre-pelleting inclusion of whole corn on performance, digestive tract measurements and nutrient utilization in broiler starters. Five diets, containing 60% ground corn or 15, 30, 45, and 60% whole corn replacing (w/w) ground corn, were formulated and cold-pelleted at 65°C. Each diet was offered ad libitum to six replicates (eight birds per replicate cage) from d 1 to 21 post-hatch. Weight gain (1005, 990, 919, 933, and 857 g/bird, respectively) and feed intake (1303, 1312, 1214, 1226, and 1136 g/bird, respectively) decreased linearly ($P < 0.001$) with increasing pre-pelleting inclusion of whole corn. Feed per gain (quadratic effect, $P < 0.05$) increased as the inclusion level of whole corn increased to 30% and then plateaued with further inclusions. Relative gizzard weight (12, 14, 15, 16, and 16 g/kg body weight, respectively; quadratic effect, $P < 0.05$) and apparent metabolizable energy (3400, 3450, 3466, 3424, and 3435 kcal/kg, respectively; quadratic effect, $P < 0.05$) increased with increasing inclusion of whole corn up to 30% and then leveled off. Ileal digestibility of starch (linear effect, $P < 0.001$) and nitrogen (linear effect, $P = 0.07$) increased with increasing inclusion levels of whole corn. Pellet quality, measured as pellet durability index (64, 78, 78, 82, and 84, respectively; quadratic effect, $P < 0.001$), increased sharply with the inclusion of whole corn to 15%, then plateaued and a further increase was observed at the inclusion level of 45%. The present data showed that, despite improvements in gizzard development, nutrient utilization and pellet quality, weight gain of broilers were poorer with pre-pelleting inclusion of whole corn due largely to the reduced feed intake.

Key Words: broilers, pre-pelleting, whole corn

Table 1367.

	Feed intake, g/day		Body weight gain, g/day		FCR
Treatment	Phase I	Phase II	Phase I	Phase II	0–36 d
mash	55.8 [a]	169.6 [c]	40.2 [bc]	94.5 [b]	1.62 [b]
pelleted	57.8 [a]	181.2 [ab]	47.1 [a]	94.6 [b]	1.55 [a]
crumble I	60.7 [a]	185.0 [a]	47.2 [a]	99.2 [a]	1.65 [c]
crumble II	60.6 [a]	180.4 [ab]	42.7 [b]	103.0 [a]	1.60 [b]
shaped	55.1 [a]	166.6 [c]	39.0 [c]	93.9 [b]	1.53 [a]
exp.+pel.	54.7 [a]	175.6 [bc]	41.7 [bc]	97.9 [ab]	1.52 [a]
SE	0.38	0.55	0.30	0.41	0.01

1368 (W186) Divergent selection for residual feed intake may be impacted by differences in feeding behavior. S. Vigors[*1], T. Sweeney[2], A. G. Fahey[1], C. J. O'Shea[1], and J. V. O'Doherty[1], *[1]School of Agriculture and Food Science, University of College Dublin, Ireland, [2]College of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Ireland.*

Reduced activity related to feeding behaviour traits may explain the reduced feed intake and improved feed efficiency in low residual feed intake (LRFI) pigs, as less active animals will have a lower maintenance requirement. The objective of this study was to examine the effect of divergent selection for RFI on selected feeding behavior traits. Male pigs [$n = 75$; initial BW 22.42 kg (SD = 2.03)] were fed a standard finishing diet (12.5 g/kg lysine and 14.5 MJ/kg Digestible Energy) for 43 d to evaluate feed intake and growth for the purpose of calculating RFI. Feeding behavior was measured using electronic feeders that recorded consumption per visit and feeding time. Phenotypic RFI was calculated as the residuals from a regression model regressing DMI on ADG and midtest $BW^{0.75}$ (MWT). Fifteen high RFI (HRFI) and 15 LRFI pigs were chosen for the purpose of examining feeding behavior parameters. RFI was strongly correlated with both ADFI ($r = 0.67$) and FCR ($r = 0.73$). LRFI pigs had lower ADFI (2.44kg vs. 1.87kg) and improved feed conversion ratio (1.96 vs. 2.48) relative to HRFI pigs ($P < 0.001$) with no difference in ADG or MWT. Behavioral analysis indicated that LRFI pigs ate less ($P < 0.0001$), spent less time eating per d ($P < 0.05$), had smaller meals ($P = 0.05$) and spent less time eating each meal than HRFI pigs ($P = 0.09$). LRFI pigs had less variation in there time spent eating ($P = 0.09$) than HRFI pigs, indicating that LRFI pigs had a more consistent feeding pattern. There was interactions between residual feed intake and the number of visits per d ($P < 0.05$) with LRFI pigs having fewer visits to the feeder than HRFI pigs across the experimental period. The results from this study suggest that LRFI pigs have lower activity related to feeding actions. This may partly explain the reduced feed intake in LRFI pigs.

Key Words: residual feed intake, feeding behavior, pigs

1369 (W187) Effect of dietary aflatoxin from contaminated corn on performance of turkey poults. A. S. Oyegunwa, E. O. Ewuola, A. F. Agboola, and E. A. Iyayi*, *University of Ibadan, Nigeria.*

Eighty 21-d-old Nicholas turkey poults were fed diets containing different levels of aflatoxin from naturally contaminated corn using *Aspergillus flavus*. The aim of the study was to investigate growth and feed intake responses in the birds to the dietary aflatoxin levels to determine the safe level of the toxin in the diets of turkey poults. The birds were weighed and assigned to 4 treatments of 4 replicates each and 5 poults per replicate in a randomized complete block design with an aver-

age initial body weight of 341 g. The diets were T1 = control; T2 = 400ppb aflatoxin; T3 = 800ppb aflatoxin; T4 = 1200ppb aflatoxin/diet. The poults were fed the experimental diets for 2 wk, at the end of which feed intake and body weight records were taken and statistically analyzed using linear regression. At d 14 there was a significant ($P < 0.05$) reduction in feed intake (1316, 710, 519, and 306 g) and body weight (1055, 554, 383, and 306 g) for diets T1, T2, T3 and T4, respectively. Mortality was significantly higher ($P < 0.05$) in the 400, 800, and 1200 ppb aflatoxin diets compared to the control diet. Results of the study showed that dietary aflatoxin concentration of 400 ppb and above from contaminated corn is deleterious to turkey poults reared from d 21 to 35.

Key Words: dietary aflatoxin, turkey poults, performance

1370 (W188) Worldwide occurrence of mycotoxins in feeds and feed components in the year 2013.

S. Schaumberger*, K. Nährer and U. Hofstetter,
Biomin Holding GmbH, Herzogenburg, Austria.

In 2013, a follow-up on the worldwide Biomin mycotoxin survey (started in 2004) covering the most important mycotoxins in feedstuffs was conducted. Information was collected concerning the presence of mycotoxins in commodities most commonly used for feed production. A total of 4218 samples (mainly corn/corn silage, soybean meal, wheat, finished feed and other grains) sourced in America, Europe and Asia were analyzed for the presence of mycotoxins including aflatoxins (Afla), zearalenone (ZEN), deoxynivalenol (DON), fumonisins (FUM) and ochratoxin A (OTA). Samples were analyzed by high performance liquid chromatography (HPLC) and Enzyme-Linked Immunosorbent Assay (ELISA). Only single commodities were analyzed by ELISA. More complex matrices which could interfere with the ELISA method such as DDGS and finished feed were tested by HPLC. For the purpose of data analysis, the quantification limits (LOQ) of the test method for each toxin were implemented. In the more than 4000 samples analyzed worldwide, Afla were present in 30%, ZEN in 37%, DON in 59%, FUM in 55% and OTA in 23%. Average contamination levels of all positive samples were 10 ppb for Afla, 49 ppb for ZEN, 458 ppb for DON, 778 ppb for FUM and 2 ppb for OTA. In total, only 19% of the samples were tested negative for the presence of the five investigated mycotoxins. Thirty-six percent of all samples contained one mycotoxin and 45% of the samples showed a co-contamination with two or more mycotoxins. Results of this survey highlight the necessity of mycotoxin testing before the feeding of animals. More than 80% of the samples were positive for at least one mycotoxin. The presence of more than one mycotoxin in almost half of the samples draws attention to the multi-mycotoxin contamination. The results underline the necessity of constant monitoring of mycotoxins in feedstuffs and a proper mycotoxin risk management.

Key Words: mycotoxins, worldwide survey

PHYSIOLOGY AND ENDOCRINOLOGY I

1371 (M188) Comparison of endocrine changes, timing of ovulations, ovarian follicular growth, and efficacy associated with Estradoublesynch and Heatsynch protocols in Murrah buffaloes (*Bubalus bubalis*). R. Mirmahmoudi[*1] and B. S. Prakash[2], *[1]Dep. of Animal Science, Faculty of Agriculture, University of Jiroft, Iran, [2]National Dairy Research Institute, Karnal, India.*

Experiments were conducted on 135 cycling and 31 anestrus buffalos to compare a) the endocrine changes, timing of ovulations, ovarian follicular growth and efficacy of Estradoublesynch (*P*$GF_{2\alpha}$ 0, GnRH 2, $PGF_{2\alpha}$ 9, Estradiol Benzoate; EB 10) and Heatsynch (GnRH 0, $PGF_{2\alpha}$ 7, EB 8) protocols in cycling buffaloes, and b) the efficacy of Estradoublesynch and Heatsynch protocols for fertility improvement in cycling and anestrus buffaloes. Ovulation was confirmed following all GnRH and EB treatments by ultrasonographic examination at 2-h intervals. Plasma progesterone and total estrogen concentrations were determined in blood samples collected at daily intervals, beginning 2 d before onset of protocols until the day of second ovulation detection. Ovulatory follicle size was measured at the time of a) first $PGF_{2\alpha}$ administration/2 d before onset of protocol, b) GnRH administration, c) 2 h before ovulation detection post GnRH administration, d) second $PGF_{2\alpha}$/$PGF_{2\alpha}$ injection, e) EB injection and, f) 2 h before ovulation detection post EB injection. Plasma LH, total estrogen and progesterone concentrations were determined in blood samples collected at 30-min intervals for 8 h, beginning GnRH and EB injections, and thereafter at 2-h intervals until 2 h after detection of ovulation. The first ovulatory rate was significantly ($P < 0.05$) higher in Estradoublesynch (84.6%) protocol than that in Heatsynch protocol (36.4%). The first LH Peak concentration in Estradoublesynch (74.6 ± 10.4 ng/ml) protocol was significantly ($P < 0.05$) higher than that of Heatsynch (55.3 ± 7.4 ng/ml) protocol. In Estradoublesynch protocol, the total estrogen concentration gradually increased from the day of GnRH administration coinciding with LH peak, and then gradually declined to the basal level until the time of ovulation detection. However, in Heatsynch protocol, the gradual increase in total estrogen concentration after GnRH was observed only in those buffaloes which responded to treatment with ovulation. In both Estradoublesynch and Heatsynch protocols, ovulatory follicles size increased from GnRH/EB injections until ovulation. The pregnancy rate after Estradoublesynch (60.0%) protocol was significantly ($P < 0.05$) higher than that achieved after Heatsynch protocol (32.5%). Satisfactory success rate using Estradoublesynch protocols was attributed to the higher release of LH following GnRH injection, leading to most of the animals ovulating post GnRH injection and hence creating the optimum follicular size at EB injection for ovulation and pregnancy to occur.

Key Words: estradoublesynch, heatsynch, endocrine changes

1372 (M189) Development of a novel strategy for synchronization of ovulation and fertility augmentation in cycling buffalo cows. R. Mirmahmoudi[*1] and B. S. Prakash[2], *[1]Dep. of Animal Science, Faculty of Agriculture, University of Jiroft, Iran, [2]National Dairy Research Institute, Karnal, India.*

The aim of present study was to investigate the endocrine changes (progesterone, total estrogens, and LH), ovarian follicular growth, timing of ovulation and efficacy in terms of pregnancy rate in cycling Murrah buffaloes subjected to a novel protocol named Estradoublesynch ($PGF_{2\alpha}$ 0, GnRH 2, $PGF_{2\alpha}$ 9, Estradiol Benzoate; EB 10, timed artificial insemination (TAI) 48 and 60 h later). Twelve cycling buffaloes were subjected to the Estradoublesynch protocol. Ovarian follicle size and the rate of induction of ovulation were examined using transrectal ultrasonography at two hourly intervals post EB injection. Plasma progesterone and total estrogens concentrations were measured in blood samples collected at daily intervals. In addition, plasma LH and total estrogens concentrations were determined in intensive blood samples collected post EB administration. Ovulation occurred in all buffaloes 48.5 ± 1.6 h post EB treatment. Follicle size was gradually increased from second $PGF_{2\alpha}$ injection (9.7 ± 0.3 mm) until ovulation (12.9 ± 0.4 mm). Peak LH concentration of 34.2 ± 7.7 ng/ml occurred 18.3 ± 0.8 h after EB treatment. Peak total estrogen of 50.8 ± 6.9 pg/ml occurred 5.7 ± 1.0 h after EB treatment. Fourteen cycling buffaloes were subjected to the Estradoublesynch protocol, with TAI 48 and 60 h following EB injection, and 58 cycling buffaloes were inseminated after spontaneous estrus (control group). Pregnancy rates were 62% for TAI of cycling buffaloes and 34.5% for control group. These results demonstrated that the Estradoublesynch protocols can be potentially used to obtained satisfactory fertility after TAI in cycling buffaloes. This is a practical application of endocrine study toward fertility augmentation at farm level.

Key Words: Estradoublesynch, ovulation, ovarian follicle

1373 (M190) Maternal dietary effects on embryonic ovarian development in cattle. S. E. Echternkamp[*], D. R. Eborn, and R. A. Cushman, *USDA, Agricultural Research Service, Clay Center, NE.*

Ovarian gametogenesis and folliculogenesis begins early in fetal development with peak numbers of follicles present in bovine fetal ovaries in the second trimester of gestation and may be altered by maternal nutrition. The objective was to

determine whether maternal dietary energy intake by replacement beef heifers before breeding affects ovarian development in female progeny. Over three breeding seasons, puberal heifers were fed either a high (HE) or low (LE) energy diet for 6 mo before breeding plus the first 22 d of a 47-d breeding period to achieve 55 vs. 65% of mature BW; heifers were subsequently managed together on pasture. Female progeny (n = 68 LE and 67 HE) were developed on a standard management protocol for replacement beef heifers. Numbers of antral follicles (AFC), corpora lutea (CL), and ovarian length and height were measured in progeny ovaries by transrectal ultrasonography at 14 mo of age before a 29-d breeding period with fertile bulls; pregnancy was diagnosed at about 75 d of gestation. Data were analyzed by ANOVA with diet, year and diet x year as fixed effects. Progeny of LE vs. HE dams did not differ in birth (33.8 vs. 34.4 ± 0.6 kg, respectively) or prebreeding BW (381.2 vs. 385.0 ± 3.6 kg, respectively). Ovaries of LE progeny contained fewer small (2 to 5 mm) (18.0 vs. 21.9 ± 1.0, LE vs. HE; P = 0.02) and total antral follicles (AFC, 19.9 vs. 24.0 ± 1.0, LE vs. HE; P = 0.01). Overall, 96.5% of progeny had a CL at examination. Although AFC was correlated positively (r = 0.36; P < 0.01) with ovarian size (length x height), size did not differ between diets (357.4 vs. 348.4 mm^2 ± 12.6, LE vs. HE, P > 0.10). The AFC was similar between left and right ovary (r = 0.77; P < 0.01), but not between progeny and dam AFC (r = 0.05). Proportion of daughters pregnant to the 29-d breeding period did not differ between maternal diets (72.4 vs. 70.7 ± 0.5%, LE vs. HE) and was not influenced by prebreeding AFC. Results indicate that nutrient intake by first-parity heifers during early embryonic development may affect fetal ovarian development. USDA is an equal opportunity provider and employer.

Key Words: beef heifers, diets, developmental programming

1374 (M191) Effects of excessive energy intake and supplementation with chromium propionate on insulin resistance parameters in lactating dairy cows: I. Performance and weekly physiological measurements. T. Leiva[1], R. F. Cooke[2], F. G. Dantas[1], F. P. Santos[1], A. P. Brandao[1], J. Ranches[1], A. C. Aboin[1], and J. L. M. Vasconcelos[*1], *[1]UNESP–FMVZ, Botucatu, Brazil, [2]Oregon State University–EOARC Burns, Burns.*

The objective of this experiment was to compare performance and insulin resistance parameters in lactating dairy cows with adequate or excessive energy intake, as well as in lactating dairy cows with excessive energy intake receiving Cr-propionate supplementation. Seventeen primiparous and multiparous, lactating Holstein cows were ranked by parity, BW, and BCS, and assigned to 1 of 3 dietary treatments on d 0: 1) diet to meet their NE_l requirements without Cr supplementation (MAN; n = 5), 2) diet to exceed their NE_l requirements without Cr supplementation (HIGH; n = 6), and 3) HIGH with 2.5 g/d of Cr-propionate (HIGHCR; n = 8, with 10 mg of Cr/cow daily). Cows were maintained in a single group and offered corn silage for ad libitum consumption, but received a corn-based concentrate twice daily via individual self-locking head gates from d 0 to 210. Concentrate intake was formulated to provide 100% of daily NE_l requirements of MAN and 160% of daily NE_l requirements of HIGH and HIGHCR cows. Cow BW, BCS, and milk production were recorded weekly. Blood samples were also collected weekly, before and at 2 and 4 h after the morning concentrate feeding, and analyzed for serum glucose, insulin, and NEFA. Pre-prandial revised quantitative insulin sensitivity check index (RQUICKI) was determined using serum glucose, insulin, and NEFA concentrations obtained before concentrate feeding. No treatment effect was detected for BW change (P = 0.74), although BCS change from d 0 to 210 was greater (P = 0.02) in HIGH and HIGHCR compared with MAN. Milk production was similar between treatments (P = 0.92). Serum glucose concentrations and RQUICKI were also similar ($P \geq 0.68$) across treatments, whereas mean serum NEFA concentrations (pre-prandial samples only) were greater (P = 0.04) for MAN compared with HIGH and HIGHCR. Treatment × parity × day interactions were detected (P < 0.01) for serum insulin and insulin:glucose ratio. These parameters were generally greater ($P \leq 0.05$) for HIGH, intermediate for HIGHCR cows, and lesser for MAN beginning on d 70 of the experiment for multiparous cow, and beginning on d 168 for primiparous cows. In conclusion, lactating dairy cows consuming excessive energy experienced reduced insulin sensitivity compared to cows consuming adequate amounts of energy, characterizing a state of insulin resistance, whereas Cr-propionate supplementation alleviated this outcome. However, milk production was not impacted by excessive energy intake or Cr-propionate supplementation.

Key Words: chromium, dairy cows, energy intake, insulin resistance

---

1375 (M192) Association of monocyte chemoattractant protein-1 and vascular endothelial growth factor in subcutaneous and visceral adipose tissue of early lactating dairy cows. S. Häussler[*1], C. Sacré[1], P. Friedrichs[2], S. Dänicke[3], and H. Sauerwein[1], *[1]University of Bonn, Institute of Animal Science, Germany, [2]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Germany, [3]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany.*

Adipose tissue (AT) is an endocrine organ, producing and secreting a wide range of adipokines, which are known to regulate metabolism and immune function. Metabolic adaptations during early lactation in dairy cows may be accompanied by changes in vascularization within AT to ensure nutrient supply for the adipocytes and/or to support the release of NEFA and

glycerol through increased blood flow. Small concentrations of monocyte chemoattractant protein-1 (MCP-1) can stimulate AT vascularization through the vascular endothelial growth factor (VEGF). Based on the virtual absence of macrophages in bovine AT, we hypothesized that MCP-1 in bovine AT is rather related to vascularization than to recruiting monocytes. Therefore, we aimed to investigate MCP-1 together with VEGF in different bovine AT. Primiparous German Holstein cows (n = 25) from a feeding trial were allocated to 3 groups that were slaughtered on Day 1 (n = 5), 42 and 105 (each n = 10) postpartum (P.p.). Subcutaneous (sc) AT (tailhead, withers, sternum) and visceral (vc) AT (omental, mesenteric, retroperitoneal) were sampled. Quantification of MCP-1 and VEGF was done by qPCR; mRNA abundance was summarized for sc and vc AT (means ± SEM). Differences throughout lactation were analyzed using the Kruskal–Wallis test, comparison between the sc and vc AT was done by Mann–Whitney-U test, and Spearman correlation was used to investigate the relation between the two variables (SPSS 21, $P \leq 0.05$). From d 1 to d 105 p.p. the mRNA abundance of MCP-1 and VEGF decreased 1.6-fold (P = 0.008) and twofold (P = 0.002), respectively, irrespective of AT depot. Comparing different AT across all days, MCP-1 mRNA abundance was 2.5-times ($P < 0.001$) and VEGFA mRNA abundance was 1.4-times ($P < 0.001$) higher in vc than in sc AT. Together with the previous finding that hardly no macrophages were observed in bovine AT, the positive correlation between MCP-1 and VEGF (r = 0.297; $P < 0.001$) indicates that MCP-1 may play a role in vascularization of bovine AT. High levels of MCP-1 and VEGF at the onset of lactation might increase vascularization to improve the essential blood flow in bovine AT right after calving. The higher expression of both MCP-1 and VEGF in vc than in sc AT might be due to the higher metabolic activity of vc AT.

Key Words: VEGF, MCP-1, adipose tissue

1376 (M193) Reactive oxygen metabolites (ROM) and advanced oxidation protein products (AOPP) as influenced by energy intake and niacin supplementation in the periparturient dairy cow.

H. Sadri*[1], D. Nakov[2], S. Dänicke[3], U. Meyer[3], R. Tienken[3], and H. Sauerwein[4], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Germany, [2]Institute for Animal Biotechnology, University St. Cyril and Methodius, Skopje, Macedonia, [3]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany, [4]University of Bonn, Institute of Animal Science, Germany.*

Increasing metabolic requirements related to late pregnancy, calving, and initiation of lactation may result in augmented production of ROM and, if not compensated by endogenous antioxidants, in oxidative stress. Niacin, as a precursor for NAD+ synthesis, upregulates the expression of glucose-6-phosphate dehydrogenase, the rate-limiting enzyme in the pentose phosphate pathway and the principal source of cellular NADPH. Increased levels of NADPH decrease cellular ROM through regulating ROM-generating oxidases or by maintaining anti-oxidant enzymes in active form. We hypothesized that niacin by increasing NAD(p)H levels ameliorates oxidative stress in dairy cows and that this effect will differ depending on the portion of concentrate in the diet fed during late pregnancy and the first 100 d of lactation. Fifty-six Holstein cows were studied from d 42 ante partum (a.p.) through d 100 post partum (p.p.), and were assigned to 1 of 4 treatment groups (n = 14 each) in a 2 × 2 factorial arrangement of the level of concentrate feeding (high or low concentrate portion in the diet), with or without 24 g/d of niacin from d −42 to d 24. Blood was collected in weekly intervals (3-d intervals around calving). Derivatives of ROM (dROM; indirect photometric assessment of free radicals) were measured in all serum samples, and AOPP (marker of oxidative protein damage) in sera from d −42, -21, 14, 21, 28, and 35. Data were analyzed by the PROC MIXED of SAS using repeated measure analysis ($P < 0.05$). The model included the effects of diet, niacin, time, and two- and three-way interactions of main effects with time. Serum concentrations of dROM were not affected by concentrate level or niacin supplementation, and no interactions between concentrate and niacin, as well as no three-way interactions between treatments and time on dROM concentrations were observed. Serum concentrations of dROM were affected by time reaching a nadir around calving, and increasing immediately thereafter to relatively constant concentrations slightly higher than a.p. Serum AOPP was not different between treatment groups, but changed over time. Decreasing dROM values around calving might result from increased antioxidant protection. The two serum markers of oxidative stress selected herein yielded no effects of diet or niacin, however, markers of antioxidant status should additionally be considered.

Key Words: niacin, energy intake, oxidative status, dairy cow

---

1377 (M194) The effect of aspirin on prostaglandin $F_{2\alpha}$ secretion in lactating dairy cows during the luteal phase of the estrous cycle.

J. A. Spencer*, K. Steinkamp, B. Shafii, and A. Ahmadzadeh, *University of Idaho, Moscow.*

Approximately, 70 to 80% of total embryonic loss in dairy cattle occurs between Days 8 and 16 after artificial insemination (AI). Early embryonic loss may be due to the premature secretion of prostaglandin $F_{2\alpha}$ ($PGF_{2\alpha}$) during Days 14–16 after fertilization. The objective of this study was to examine the effect of Aspirin, a non-steroid anti-inflammatory drug (NSAID), on $PGF_{2\alpha}$ secretion in lactating dairy cows by characterizing blood plasma prostaglandin metabolites (PGFM) and progesterone (P_4) during the luteal phase of the estrous cycle. Twenty-four lactating Holstein cows were synchronized

to ovulation. The ovulation was confirmed by ultrasonography (d 1). On d 14 and after detection of corpora lutea, cows were assigned randomly to receive Aspirin (total of 140 g) or no Aspirin (control) and the blood sample was obtained from each cow. Aapirin was given orally on d 14 (2×) and d 15 (1×), 12 h apart. On d 15, 6 h after the last dose of aspirin, hourly blood samples were taken for 6 h for PGFM concentrations. Daily blood samples were also collected (d 15 to 23) to examine P_4concentrations. One cow was eliminated from the study for having < 1 ng/mL P_4 on d 15. Analyses of repeated measures, using the mixed model procedure of SAS were utilized. The model included treatment, the repeated factor time, and treatment × time interaction. Cow was the random effect. On d 14, mean P_4 was > 1 ng/mL for all cows and it was similar between groups. Before treatment, there was no difference in mean PGFM concentrations between the groups, (203 vs. 224 ng/mL; SE ± 39 for aspirin and control, respectively). There was an effect of treatment and treatment × time on mean PGFM ($P < 0.05$). Mean PGFM concentrations were decreased ($P < 0.05$) 30 h after initiation of treatment and remained low for 5 h after last treatment, whereas they remained unchanged in the control. Overall, mean PGFM concentrations were 106 and 190 ng/mL (SE ± 33) for aspirin and control, respectively. Blood P_4 concentrations post-treatment were similar between the two groups (3.6 vs. 3.2 ng/mL; SE ± 0.6), but declined from d 15 to d 23 ($P < 0.01$). The study indicated that oral administration of aspirin treatment may suppress $PGF_{2\alpha}$ during d 14 to 15 after estrus and prevent early luteal tissue regression; however, no effect on P_4 was observed.

Key Words: dairy cows, NSAID, prostaglandin $F_{2\alpha}$

1378 (M195) Association between oxidative stress through excessive fat accumulation and the number of mitochondrial DNA copies in adipose tissue of dairy cows.

L. Laubenthal[*1], L. Locher[2], J. Winkler[3], U. Meyer[3], J. Rehage[2], S. Dänicke[3], H. Sauerwein[1], and S. Häussler[1], *[1]University of Bonn, Institute of Animal Science, Germany, [2]University for Veterinary Medicine Foundation, Hannover, Germany, [3]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany.*

In the transition period, overconditioned cows usually have more problems to adapt to the needs of lactation than leaner cows and are thus more prone to health problems. The mitochondrial DNA (mtDNA) copy number reflects the abundance of mitochondria in a cell and may change under different energy requirements and physiological conditions. Increased metabolic demands as well as increased mtDNA copies per cell are associated with elevated oxidative stress. However, the association between oxidative stress through excessive fat accumulation and mtDNA copy numbers in bovine adipose tissue (AT), being considered as a major contributor to systemic oxidative stress, has not been investigated so far. We hypothesized that the mtDNA copy number in AT will increase concomitant with oxidative stress [assessed by quantifying the derivates of reactive oxygen species (dROM)] during fat accretion in cows. Eight non-lactating, non-pregnant pluriparous German Holstein cows (age: 4 to 6 yr) were fed diets with increasing portions of concentrate feed during the first 6 wk of the experiment until 60% were reached, which was maintained for 9 wk. Within this period cows had an average body weight (BW) gain of 243 ± 33.3 kg. Blood samples were collected monthly and dROM were photometrically quantified in serum using N,N,diethyl-1,4-phenylendiamine as chromogen. Biopsies from the subcutaneous tailhead AT were taken every 8 wk and immediately snap frozen for genomic DNA isolation. The number of mtDNA copies/cell was measured by a multiplex quantitative PCR using β-globin as reference gene. Data (mean ± SEM) for mtDNA copies and dROM as well as for BW were analyzed using non-parametric tests or repeated measurement ANOVA, respectively. Correlations were calculated using the Spearman (r) correlation coefficient. Throughout the fat accumulation period mtDNA copies/cell and dROM increased fourfold (329 ± 57.5 to 1385 ± 160; $P = 0.002$) and 2.5-fold (49.9 ± 9.24 to 125 ± 16.0 µg H_2O_2equivalents/mL; $P = 0.003$), respectively. We observed a positive correlation between mtDNA copy numbers and BW ($r = 0.596$, $P = 0.003$) and dROM ($r = 0.550$, $P = 0.005$). Increased mtDNA copies in AT might be an adaptation in response to oxidative stress that evolves from excessive fat accumulation in overconditioned cows. It is known, that mtDNA copy numbers increase as a compensatory response mechanism to mtDNA damage. Therefore, increased numbers of mitochondria and thus increased numbers of mtDNA copies per cell might then amplify the production of ROM leading to further mtDNA damage.

Key Words: mtDNA, oxidative stress, fat accumulation

1379 (M196) Telomere length shortening in response to an excessive fat accumulation in subcutaneous adipose tissue of dairy cows.

L. Laubenthal[*1], L. Locher[2], J. Winkler[3], U. Meyer[3], J. Rehage[2], S. Dänicke[3], H. Sauerwein[1], and S. Häussler[1], *[1]University of Bonn, Institute of Animal Science, Germany, [2]University for Veterinary Medicine Foundation, Hannover, Germany, [3]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany.*

With the onset of lactation, overconditioned cows mobilize more body tissue than thin cows and are prone to develop metabolic disorders. The metabolic stress in cows with higher body condition score (BCS) before calving and greater loss of BCS after calving comprises oxidative stress. Increased production of reactive oxygen metabolites may damage cells and accelerate telomere shortening which serves as biological marker for age and stress-related conditions. Herein we aimed to investigate the telomere length (TL) in subcutaneous

adipose tissue (AT) during exemplarily induced excessive fat accumulation in cows. We hypothesized that TL is associated with the production of derivates of reactive oxygen metabolites (dROM), as indicator for oxidative stress, in overconditioned cows. Eight non-lactating, non-pregnant German Holstein cows (4 to 6 yr) received diets with increasing concentrate feed proportions (0 to 60% of the total daily dry matter intake) during the first 6 wk of the experiment which was maintained for 9 wk. The BCS (5-point scale) increased from 2.3 ± 0.12 to 4.57 ± 0.14 and the average body weight (BW) gain was 243 ± 33.3 kg. Blood samples were taken monthly for photometric quantification of dROM in serum using N,N,diethyl-1,4-phenylendiamine as chromogen. Subcutaneous AT from tailhead was collected at the beginning and of the experiment and after 15 wk. Samples were snap frozen for isolation of genomic DNA. A multiplex quantitative PCR was used to analyze the relative quantity of telomere (qT) products compared with β-globin products which served as reference gene to estimate TL in AT. Data (mean ± SEM) for TL, BCS and BW as well as for dROM were evaluated using repeated measurement ANOVA or non-parametric tests, respectively. Correlations were calculated using the Spearman (*r*) and Pearson (*r*) correlation coefficient. Relative qT decreased throughout the experiment (51.8 ± 3.26 to 43.6 ± 1.76; $P = 0.01$) whereas dROM increased more than two-fold ($P = 0.003$). Shorter TL were correlated with BCS ($r = -0.586$, $P = 0.017$), BW ($r = -0.653$, $P = 0.008$) and dROM ($r = -0.596$, $P = 0.015$). Increasing dROM indicating oxidative stress were observed in overconditioned cows. Fat accumulation was accompanied by reduced TL in bovine AT. Shortening of telomeres might indicate fibrosis and would thus result in AT dysfunction which might compromise the adaptive capability of AT to the needs of lactation in overconditioned cows.

Key Words: telomere length, adipose tissue, oxidative stress

1380 (M197) Pregnancy per AI of high producing Holstein cows treated with norgestomet ear implant or progesterone intravaginal device.

H. Ayres[*1,2], C. M. Azevedo[3], J. B. Solak[4], O. Corso[4], S. Soriano[5], M. C. Wiltbank[6], and R. M. Ferreira[2], *[1]MSD Animal Healtg, São Paulo, Brazil, [2]Departamento de Reprodução Animal, USP, São Paulo, Brazil, [3]Qualy Calf Consultoria Ltda, Venceslau Braz, Brazil, [4]Castrovet Consultoria Veterinária, Castro, Brazil, [5]Fazenda Colorado, Araras, Brazil, [6]University of Wisconsin, Madison.*

The aim of present study was to compare pregnancy per AI (p/AI) of high producing Holstein cows subjected to timed artificial insemination (TAI) using a new or previously used progesterone intravaginal device or a Norgestomet ear implant. In Experiment 1, 359 cows (173 primiparous and 186 multiparous) received 2 mg estradiol benzoate i.m. (Gonadiol, MSD Animal Health, Brazil) at random days of the estrous cycle (d 0) and were homogenously distributed in two groups. Cows on group NEW-PROGESTERONE received a new progesterone releasing intravaginal device (CIDR, Zoetis, Brazil), while cows on group NEW-NORGESTOMET received a new Norgestomet ear implant (Crestar, MSD Animal Health, Brazil). On d 8, 500 mg Cloprotenol (Ciosin, MSD Animal Health, Brazil) and 1 mg estradiol cypionate (E.C.P., Zoetis, Brazil) were administered and the ear implants or intravaginal devices were removed. On d 10, 100 μg gonadorelin (Fertagyl, MSD Animal Health, Brazil) was administered and TAI was performed 10 h later. In Experiment 2, 293cows (146 primiparous and 147 multiparous) were subjected to the same experimental design described above except for using implants and devices previously used for 8 d (USED-PROGESTERONE = 146 cows vs. USED-NORGESTOMET = 147 cows). The experimental period began in May and ended in September 2012. Statistical analyses were performed using logistic regression (*P*ROC GLIMMIX of SAS). There were no interactions for treatment and parity, farm, and times in bred. The P/AI 30 d after TAI was similar ($P > 0.10$) between groups NEW-PROGESTERONE [31.6% (50/158)] and NEW-NORGESTOMET [35.3% (71/201)], and between groups USED-PROGESTERONE [35.6% (52/146)] and USED-NORGESTOMET [36.7% (54/147)]. These results indicate that both CIDR and Crestar, either new or previously used for 8 d, can be used for TAI treatments producing similar P/AI.

Key Words: norgestomet, pregnancy per AI, Holstein

1381 (M198) Telomere length in different visceral and subcutaneous adipose tissue depots of overconditioned cows.

L. Laubenthal[*1], L. Locher[2], J. Winkler[3], U. Meyer[3], J. Rehage[2], S. Dänicke[3], H. Sauerwein[1], and S. Häussler[1], *[1]University of Bonn, Institute of Animal Science, Germany, [2]University for Veterinary Medicine Foundation, Hannover, Germany, [3]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany.*

Telomeres are short and repetitive sequences of the chromosomes which shorten with every cell-division. Therefore telomere length (TL) is considered as a biological marker for aging and cell proliferation depending on the tissue type. Increasing oxidative stress in response to nutrient surplus, e.g., in overconditioned dairy cows at the onset of lactation, accelerates telomere attrition. Adipose tissue (AT) is mobilized in early lactating cows to cope with the nutrient demands for milk synthesis. The different AT depots are divided into visceral (vc) and subcutaneous (sc) depots which exhibit different metabolic functions and cellular composition. We hypothesized that TL shortening within AT is depot specific in overconditioned cows due to different metabolic activities of sc and vcAT. Herein, we aimed to characterize the TL in seven different fat depots after rapid, diet-induced fat accumulation in cows. Eight German Holstein

cows (non-lactating, non-pregnant, age: 4 to 6 yr) were gradually adapted to a high-energy ration by increasing the portion of concentrate in the ration from 0 to 60% of daily dry matter intake within 6 wk. Animals were fed the 60% diets for further 10 wk and were then slaughtered; tissue samples from scAT (sternum, withers and tailhead) and vcAT (*P*ericardial, mesenteric, omental and retroperitoneal) were collected and snap frozen for further analyses. After isolation of genomic DNA, a multiplex quantitative PCR was used to analyze the relative quantity of telomere (qT) products compared with β-globin products which served as reference gene to estimate TL in AT. Differences between qT in the single AT depots were analyzed using the Student's *t* test (SPSS; mean ± SEM). Mesenteric AT exhibited 1.3-fold lower qT compared to omental (59.1 ± 7.4; $P = 0.01$) and pericardial (57.7 ± 7.9; $P = 0.004$) depots and 1.2-fold lower qT than retroperitoneal (53.5 ± 4.9; $P = 0.01$) AT. In scAT depots, fat from withers displayed 1.3-fold higher qT values than sternum (47.3 ± 3.5; $P = 0.005$) AT and 1.1-fold higher qT compared to tailhead (54.1 ± 8.2; $P = 0.05$) fat. Although vcAT is known to have a higher metabolic activity than scAT in dairy cows, we did not observe any differences in TL when comparing all sc versus all vcAT. Depot specific differences of TL might nevertheless be a hint to depot specific roles

Key Words: telomere length, adipose tissue, dairy cow

1382 (M199) Liveability of buck spermatozoa after cold storage using egg yolk citrate extender.

A. O. Ladokun*, J. A. Abiona, J. O. Daramola, E. O. Oke, and A. M. Onifade, *Federal University of Agriculture, Abeokuta, Nigeria.*

Preservation and extension of West African Dwarf (WAD) buck semen has been a challenge, because AI centres are far from farms where they are needed. This study was performed to investigate the liveability of buck spermatozoa extended with egg yolk citrate of West African dwarf goat buck spermatozoa. Twenty matured bucks were used for this experiment. Semen from these bucks was collected by means of artificial vagina after which evaluation was done. Buffer and extender were prepared using egg Yolk Citrate to preserve the semen and it was stored at 5°C in a refrigerator. Data were collected for 5 d at 0, 24, 48, 72, and 96 h on sperm concentration, percentage liveability, percentage dead, intact, damage, missing acrosome and sperm morphology. Data were analyzed using Statistical Package for Social Sciences (SPSS). Results show that the percentage sperm liveability at 0, 24, 48, 72, and 96 h were 57.50, 56.30, 54.03, 51.27, 47.00 respectively indicating a decrease with time. However, the percentage sperm dead increased with time: 42.50, 43.68, 45.97, 48.73, and 50.92% for 0, 24, 48, 72, and 96 h, respectively. The sperm motility (percentage) also reduced as the length of storage increased. The morphological characteristics of the spermatozoa also decreased with increase in the length of storage. It was concluded that liveability of sperm reduced as the storage time increased in West African Dwarf buck even with egg yolk citrate extender.

Key Words: egg yolk citrate, liveability, goat buck

1383 (M200) Bedding surface does not alter circulating patterns of cortisol, corticosteroid-binding globulin, or free cortisol index in preweaned Jersey calves.

H. G. Kattesh*, C. A. Kurman, B. E. Gillespie, P. D. Krawczel, and A. M. Saxton*, University of Tennessee, Knoxville.*

Previous research found no significant treatment differences in behavior or performance of Jersey calves residing at one farm when housed individually in hutches bedded with gravel ($n = 11$), sand ($n = 12$), or rubber mat ($n = 11$) from birth to 10 wk of age. The aim of the present study was to further examine the effects of these bedding surfaces on plasma total cortisol (CORT) and corticosteroid binding globulin (CBG) concentrations, and free cortisol index (FCI) analyzed from blood samples (10 mL) collected weekly from each of the calves during this earlier study beginning within 24 h of birth. Calves were provided 4 L of waste milk 1x/d from birth to 6 wk of age, and 2 L of waste milk 1x/d with calf starter and water ad libitum during the remaining 4 wk. Serum CORT was analyzed using a commercial RIA kit procedure and bovine CBG by an indirect ELISA developed and validated in our laboratory. The FCI was calculated using the ratio of serum CORT (nmol/L) to CBG (mg/L) concentrations. Data were analyzed by PROC MIXEDs in SAS 9.3 for repeated measures. No differences were found ($P > 0.10$) in CORT, CBG or FCI among treatment groups at any time point measured. Age-related changes ($P < 0.01$) among the three variables were found such that CORT was greatest (132.7 ± 32.0 nmol/L) at birth, reached a nadir (2.1 ± 0.5 nmol/L) at 6 wk of age, and increased ($P < 0.05$) to 8.0 ± 2.0 nmol/L by 9 wk of age. Serum CBG increased ($P < 0.01$) between birth and 1 wk of age (1.1 vs. 1.4 mg/L; SE = 0.1) and remained unchanged until the calves reached 6 wk of age at which time CBG was at its lowest (0.8 ± 0.1 mg/L; $P < 0.05$). Subsequently, CBG increased (1.4 ± 0.1 mg/L; $P < 0.05$) at 7 wk of age where it persisted thereafter. The FCI reflected the changes observed in CORT. The data are consistent with our previous results indicating that any of these bedding types may be used without compromising the welfare of preweaned Jersey calves. Whether the changes in CORT, CBG and calculated FCI noted here are age and/or diet related await further study.

Key Words: dairy calf, free cortisol index, bedding

1384 (M201) Niacin increases chemerin mRNA abundance in differentiated bovine preadipocytes in vitro. C. Kopp[1], H. Khalilvandi-Behroozyar[1,2], H. Sauerwein[*3], and M. Mielenz[1,4], *[1]Institute of Animal Science, Physiology & Hygiene Unit, University of Bonn, Germany, [2]Dep. of Animal Science, Urmia University, Iran, [3]University of Bonn, Institute of Animal Science, Germany, [4]Leibniz Institute for Farm Animal Biology (FBN), Institute of Nutritional Physiology, Dummerstorf, Germany.*

Chemerin is thought to be involved in controlling immune responses as a chemoattractant for antigen-presenting cells and has anti-inflammatory as well as pro-inflammatory functions; the latter are linked with obesity and insulin resistance. It is highly expressed as prochemerin in liver and adipose tissue and was recently identified as adipokine that regulates adipogenesis and adipocyte metabolism. The role of chemerin on glucose metabolism is controversially discussed. However, chemerin enhances insulin-stimulated glucose uptake, insulin signaling and increases insulin sensitivity in murine adipocytes. Niacin (NA) is an antilipolytic and lipid-lowering compound which is used since decades to treat dyslipidemia in humans. Furthermore, NA affects the secretion of several adipokines (e.g., adiponectin) and improves insulin sensitivity in humans. These effects are mediated through binding the G protein coupled receptor 109A (GPR109A). Our objective was thus to examine both, the effect of NA on chemerin mRNA expression in bovine adipocytes and the involvement of GPR109A in NA sensing. A primary cell culture system using differentiated bovine preadipocytes was established. Subcutaneous adipose tissue was collected from five Holstein-Friesian cows. Stromal-vascular cells were isolated, pooled and seeded at 2500 cells/cm^2. Preadipocytes after 12 d of differentiation were used. After serum starvation (4 h), cells were incubated either with 100 ng/mL pertussis toxin (*P*TX), a non-selective G protein uncoupling agent, or PBS for 16 h to characterize the NA mediating pathway. Cells were then treated with NA (10 or 15 μM) for 12 or 24 h or with PBS as controls, respectively. Chemerin mRNA abundance was quantified by qPCR. Data normalization was based on five stable reference genes. Statistical analyses were performed using ANOVA with Bonferroni post hoc tests ($P < 0.05$). The mRNA abundance of chemerin was increased 3.3-fold compared to controls after treatment with 10 μM NA for 24 h ($P = 0.006$). Treatment for 12 h or with 15 μM NA showed no difference in the mRNA abundance of chemerin. Pre-incubation with PTX abolished the observed NA-induced increase of chemerin mRNA abundance. Our results showed a NA-stimulated increase of chemerin mRNA expression in differentiated bovine adipocytes, which may point to improved insulin sensitivity by NA. Due to the annihilated increase after PTX treatment, we suggest that GPR109A mediates the effect of NA.

Key Words: chemerin, niacin, bovine adipocytes

1385 (M202) Macrophage infiltration into subcutaneous adipose tissue in overconditioned cows after excessive fat accumulation. S. Häussler[*1], L. Laubenthal[1], L. Locher[2], J. Winkler[3], U. Meyer[3], J. Rehage[2], S. Dänicke[3], and H. Sauerwein[1], *[1]University of Bonn, Institute of Animal Science, Germany, [2]University for Veterinary Medicine Foundation, Hannover, Germany, [3]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany.*

Adipose tissue (AT) secretes adipokines regulating both metabolism and immune function. In monogastrics, diet-induced obesity is associated with changing adipokine profiles and increased macrophage (Ms) infiltration. However, in early lactating dairy cows we found virtually no Ms infiltration in different AT depots; non-lactating overconditioned heifers had increased accumulation of Ms in AT related with larger adipocytes, albeit in low total numbers. We hypothesized that the portion of Ms in bovine AT will remain small, even if fat is excessively accumulated in short time. Therefore we aimed to investigate the Ms infiltration in subcutaneous (sc)AT after rapid, diet-induced fat accumulation in cows. Eight non-pregnant, non-lactating pluriparous German Holstein cows, were adapted to diets with increasing concentrate feed proportions (from 0 to 60% of total dry matter intake) during the first 6 wk of the experiment which was maintained for 9 wk at 60% concentrate feeding. The body condition score (5-point scale) increased from 2.31 ± 0.12 to 4.53 ± 0.14, and the body weight increased from 540 ± 20 kg to 792 ± 29 kg. Three biopsies were taken every 8 wk of the entire experimental period from scAT of the tailhead region. Immunohistochemistry was performed on cryosections (12 μm) using the Ms-specific marker CD68. Bovine lymph nodes were used for positive and negative controls. The number of Ms and adipocytes per mm^2 were counted (100-fold magnification; 10 fields per sample). The portion of Ms was calculated from the mean number of positive stained cells/mean number of total adipocytes × 100. In total, 12 out of 23 samples yielded CD68-positive stainings. Considering the different time points, 5 out of 7, 5 out of 8 and 2 out of 8 samples were Ms-positive at the beginning, the middle and the end of the experiment, respectively. However, the average portion of Ms was only marginal: 3.7 ± 3.0% (n = 7) at the beginning, 0.9 ± 0.3% (n = 8) at the middle and 0.5 ± 0.3% (n = 8) at the end of the experiment. Thus even a rapid and pronounced increase of fat mass was not accompanied by Ms infiltration into subcutaneous AT. In consideration of the virtual absence of Ms in AT in earlier studies about cows during the first weeks of lactation, and the low portion of Ms in overconditioned heifers and in the present study, we assume that Ms infiltration is of no importance for bovine AT.

Key Words: macrophages, adipose tissue, cow

1386 (M203) Rumen-protected methionine, histidine, and slow-release urea: Effects on plasma 3-methylhistidine and ubiquitin proteasome-related gene expression in skeletal muscle of dairy cows receiving a diet deficient in metabolizable protein. H. Sadri*[1], F. Giallongo[2], A. N. Hristov[2], C. Lang[3], J. Werner[2], C. Parys[4], B. Saremi[5], and H. Sauerwein[1], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Germany, [2]Dep. of Animal Science, Pennsylvania State University, University Park, State College, [3]Dep. of Cellular and Molecular Physiology, Hershey Medical Center, Penn State College of Medicine, [4]Evonik Industries AG, Hanau, Germany, [5]Evonik Industries AG, Hanau, Germany.*

Skeletal muscle, the largest organ in vertebrates, plays a major role in homeostasis. The ubiquitin-proteasome system (UPS) is regarded as the main proteolytic pathway in muscle. It requires the coordinated reactions of three enzymes including ubiquitin-activating enzyme (E1), ubiquitin-conjugating enzyme (E2), and ubiquitin_ligases (E3). We hypothesized that supplementation of diets deficient in metabolizable protein (MP) with slow-release urea or rumen-protected (RP) Met and His will affect the gene expression of UPS-related factors in skeletal muscle of dairy cows in support of decreased proteolysis. Sixty Holstein cows were blocked based on DIM and milk yield and randomly assigned to one of five diets: MP-adequate diet (AMP); MP-deficient diet [DMP; 5% below the requirements (NRC, 2001)]; DMP supplemented with slow-release urea as Optigen (Alltech Inc., Nicholasville, KY; DMPO); DMPO supplemented with RPMet (Mepron; Evonik Industries AG, Hanau, Germany; DMPOM); and DMPOM supplemented with RPHis (Balchem Corp., New Hampton, NY; DMPOMH). The experimental period was 10 wk, with first 2 wk as covariate period. Muscle biopsies were collected from *M. longissimus dorsi* during the last week of the experiment. The mRNA abundance of the following UPS-related target genes was quantified by qPCR: F-box protein 32 (FBXO32), muscle ring-finger protein 1 (MuRF-1), both being muscle-specific E3 ubiquitin ligases, ubiquitin-like modifier activating enzyme 1 (UBA1), and ubiquitin-conjugating enzymes (UBE2G1 and UBE2G2). Data were normalized based on the geometric mean of the 4 most stable reference genes: lipoprotein receptor-related protein 10, marvel domain containing 1, RNA polymerase II, and emerin. The concentration of 3-methylhistidine (3-MH) as marker of muscle catabolism was measured in plasma samples collected at the end of the experiment. Data were analyzed by the PROC MIXED of SAS. With the exception of MuRF-1, the mRNA abundance of the target genes was not affected by treatment. In DMP cows, about twofold more (P = 0.05) MuRF-1 mRNA than in DMPO was observed. Plasma 3-MH did not differ among treatments. In conclusion, the UPS seemed to be upregulated at the level of the mRNA during protein deficiency but this effect was apparently not sustained to increased 3-MH plasma concentrations.

Key Words: rumen-protected amino acid, ubiquitin-proteasome system, dairy cow

1387 (M204) Antioxidant supplementation during in vitro maturation increased oocyte mitochondrial membrane potential and bovine embryo development. B. C. D. S. Leão*, N. A. D. S. Rocha Frigoni, P. C. Dall'Acqua, and G. Z. Mingoti, *University of Sao Paulo State (UNESP), Araçatuba, Brazil.*

This study evaluated the effects of bovine oocytes IVM medium supplementation with intracellular (cysteine and cysteamine) and extracellular (catalase) antioxidant on the oocyte competence, based on evaluation of nuclear maturation rates, occurrence of apoptosis, mitochondrial membrane potential and the subsequent embryonic development. Oocytes were matured during 22h in TCM-199 medium with bicarbonate, hormones and 10% FCS, without supplementation (Control group) or supplemented with: 0.6 mM cysteine associated with 100 µM cysteamine (C+C group); 100 UI catalase (CAT group); or 0.6 mM cysteine associated with 100 µM cysteamine and 100 UI catalase (C+C+CAT group), at 38.5°C and 5% CO_2 in air. A sample of matured and immatured oocytes were stained with 500 nM of the fluorescent probe MitoTracker Red (CMXROs, Molecular Probes, Invitrogen, Oregon, USA) or TUNEL (In Situ Cell Death Detection Kit, Fluorescein, Roche Applied Science, IN, USA), to evaluate mitochondrial membrane potential (n = 344) and apoptotic index (n = 565), respectively. Stained oocytes were evaluated under an epifluorescence inverted microscope (excitation 579/510–550nm and emission 599/590nm, respectively for MitoTracker and TUNEL) and the mitochondrial membrane potential (quantified in arbitrary fluorescence units- AFU) were measured by Q-Capture Pro image software. The intensity values of the fluorescence signal obtained from oocytes were subtracted from mean values of "background" in the images. The rest of oocytes were submited to IVF and presumptive zygotes were IVC in SOFaa, at 38.5°C and 5% CO_2 in air, for 7 d. Cleavage and blastocyst rates were evaluated at 72 and 168 hpi, respectively. Were made 10 replicates with 50 oocytes per dish, and it was considered the experimental unit. The mitochondrial membrane potential was analyzed by ANOVA followed by Tukey's test and percentage of apoptosis, cleavage and blastocyst rates by Chi-square test ($P < 0.05$). Data are presented as mean ± SEM. The AFU for membrane mitochondrial potential were 1.00 ± 0.05^{a} (immature oocytes), 1.60 ± 0.05^{b} (Control), 0.94 ± 0.03^{a} (C+C), 1.41 ± 0.05^{c} (CAT) and 1.81 ± 0.07^{d} (C+C+CAT). The oocyte maturation rates were 0.0% (immature) 76.7% ± 1.7 (Control), 80.3% ± 4.1 (C+C), 80.5% ± 5.2 (CAT) and 78.2% ± 1.1 (C+C+CAT), and the percentage of apoptotic oocytes were $1.55\%^{a}$ (immature), $5.83\%^{ab}$ (Control), $5.45\%^{ab}$ (C+C),

1.92%[a] (CAT) and 10.78%[b] (C+C+CAT). Cleavage and embryo development were 72.5%[a] and 28.2%[a] (Control), 75.7%[a] and 31.1%[a] (C+C), 75.4%[a] and 33.3%[a] (CAT) and 73.1%[a] and 46.2%[b](C+C+CAT). In conclusion, supplementation with association of cysteine, cysteamine and catalase improved blastocyst development that can be associated with the increase mitochondrial membrane potential and oocyte competence.

Key Words: mitochondrial membrane potential, antioxidant, in vitro maturation, blastocyst development

---

1388 (M205) Hepatic and adipose mRNA expression of genes related to FGF21 in response to conjugated linoleic acid (CLA) supplementation in dairy cows during early lactation. H. Sadri[*1], S. Dänicke[2], J. Rehage[3], and H. Sauerwein[1], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Germany, [2]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany, [3]University for Veterinary Medicine Foundation, Hannover, Germany.*

The hepatokine fibroblast growth factor 21 (FGF21), a member of the FGF super-family, is emerging as an important regulator of metabolism. It is induced by fasting, ketogenic diets, and by peroxisome proliferator-activated receptor (PPAR) agonists. The glycemic and insulin sensitizing effects of FGF21 are mediated through the adipokine adiponectin that is induced by FGF21. We recently reported that the postpartal increase of adiponectin is attenuated in dairy cows receiving the PPAR-agonistic CLA and thus hypothesized that supplementation of cows with CLA in early lactation will affect the expression of FGF21, of the FGF receptor (FGFR) isotopes FGFR1c and FGFR2c, and of the essential co-receptor b-Klotho in liver and adipose tissue. German Holstein cows receiving 100 g/d CLA (n = 11; Lutrell pure, BASF, Germany; each 12% of *trans*-10, *cis*-12 and *cis*-9, *trans*-11 CLA) or a control fat supplement (Silafat, BASF; CTR; n = 10) from DIM 1 to 182 were biopsied (liver and subcutaneous fat) on d -21, 1, 21, 70, and 105 relative to calving. The target mRNAs were quantified by real-time RT-PCR. Data were analyzed by the PROC MIXED of SAS 9.2. Hepatic FGF21 and FGFFR2c mRNA abundance were affected by time ($P < 0.05$) and by treatment (FGF21: $P = 0.08$; FGFR2c: $P < 0.01$). In CTR cows, a 4.5-fold increase in FGF21 mRNA was observed from d -21 to d 21, followed by a decline to nearly prepartum values by d 105. The CLA cows had less FGF21 mRNA than the CTR cows. The mRNA abundance of FGFR2c increased during lactation in CTR but not in CLA; the greatest difference (1.5-fold) between the CLA and the CTR group was observed on d 70. The mRNA abundance of b-Klotho in the liver and adipose tissue changed over time ($P < 0.05$), while CLA had no effect. Expression of FGFR1c mRNAin adipose tissue was neither affected by time nor by treatment. The observed upregulation of hepatic FGF21 expression during the first 3 wk in liver supports a role of FGF21 in metabolic regulation and nutrient partitioning during early lactation. The inhibiting effects of CLA supplementation on hepatic mRNA expression of FGF21 and its receptor might promote glucose availability for the mammary gland by reducing peripheral insulin sensitivity.

Key Words: FGF21, CLA, liver and fat tissues, dairy cow

1389 (M206) Effect of melatonin (MEL) or maternal nutrient restriction on vascularity of the ovine placenta. K. A. Vonnahme[*1], M. E. Wilson[2], S. Romero[1], S. T. Dorsam[1], J. Haring[1], P. P. Borowicz[1], D. A. Redmer[1], and C. O. Lemley[3], *[1]North Dakota State University, Fargo, ND, [2]West Virginia University, Morgantown, WV, [3]Mississippi State University, Starkville.*

Objectives were to determine placental vascularity following dietary MEL treatment in a maternal nutrient restriction model. A second experiment was performed to assess MEL receptor dependent modulation in placental vascularity. For Exp. 1, 31 ewes were supplemented with 0 (CON) or 5 mg of MEL per d and allocated to receive 100% (adequate fed; ADQ) of daily nutrient requirements or a 40% restriction in total feed intake (RES) from d 50 to 130 of gestation. Placentomes were collected on d 130 of gestation. For Exp. 2, 14 ewes were fitted with Alzet mini osmotic pumps and infused with vehicle, MEL, or MEL receptor 1 and 2 antagonist (luzindole, LUZ) from d 62 to 90 of gestation. Placentomes were collected on d 90. Placentomes from both Exp. 1 and 2 were fixed, paraffin embedded, and examined for capillary area density (CAD, total capillary area as a proportion of tissue area), capillary number density (CND, total number of capillaries per unit of tissue area), capillary surface density (CSD, total capillary circumference per unit of tissue area), and average cross-sectional area per capillary (APC) for both maternal (caruncular) and fetal (cotyledonary) compartments. For Exp. 1, a MEL x nutritional plane interaction ($P = 0.02$) was observed for caruncle CAD, which was decreased in MEL-RES vs. CON-RES (0.145 vs. 0.269 ± 0.031). A MEL x nutritional plane interaction ($P = 0.01$) was observed for caruncle APC, which was decreased in MEL-RES vs. all other groups (95.8 vs. 171.7, 195.2, 165.6 ± 18.2 μm^2). Cotyledon CND tended to be higher in MEL versus CON, while a tendency ($P = 0.06$) for a MEL x nutritional plane interaction was observed for cotyledon APC, which was decreased in MEL-RES vs. all other groups (85.9 vs. 122.3, 122.2, 124.9 ± 10.2 μm^2). For Exp. 2, LUZ infusion tended ($P = 0.08$) to increase caruncle CAD (0.171 vs. 0.083 ± 0.026) and APC (129.2 vs. 48.1 ± 23.4 μm^2) compared to vehicle infusion. Measurements of cotyledon vascularity were not different ($P > 0.10$) across infusion treatments. *Supported in part by USDA-NIFA-AFRI grant 2011–67012–30683.*

Key Words: placenta, sheep, vascularity

1390 (M207) Follicle-stimulating hormone stimulates β-catenin via protein kinase B in granulosa cells.
B. I. Gomez*[1], C. A. Gifford[1], D. M. Hallford[2], and J. Hernandez Gifford[1], *[1]Oklahoma State University, Stillwater, [2]New Mexico State University, Las Cruces.*

Follicle-stimulating hormone regulation of ovarian estradiol production requires involvement of β-catenin (CTNNB1), a transcriptional co-factor. In cultured bovine granulosa cells, FSH treatment increases protein abundance of CTNNB1 as well as protein kinase B (AKT), a molecule known to regulate components of the CTNNB1 degradation complex. However, whether FSH induction of CTNNB1 is through direct modulation of AKT remains to be determined. To elucidate the effects of AKT signaling on CTNNB1 induction and subsequent estradiol production, bovine granulosa cells were cultured in the presence or absence of known AKT activators and inhibitors. Total protein was collected for analysis by Western blot and culture medium for estradiol quantification by RIA. Values were analyzed using one-way ANOVA procedure of SAS. To investigate specific contributions of AKT to CTNNB1 accumulation, granulosa cells were treated with IGF-1, a well-established AKT activator, in the presence or absence of FSH. Granulosa cells treated with FSH, IGF-1, and FSH+IGF-1 increased (0.68-fold) CTNNB1 accumulation compared to controls ($P = 0.09$; $n = 6$). Estradiol medium concentrations increased ($P = 0.001$; $n = 4$) in cells treated with FSH, IGF-1, and FSH+IGF-1 (166, 379, and 397%, respectively) compared to non-treated controls. A subsequent study utilizing lithium chloride (LiCl), another activator of the AKT pathway, demonstrated similar results. Granulosa cells were cultured in the presence or absence of LiCl with and without FSH. Consistent with data from IGF-1 treated cells, LiCl, FSH, and FSH+LiCl increased CTNNB1 accumulation (0.79-fold) compared to non-treated controls ($P = 0.03$; $n = 3$). In contrast, inhibition of AKT signaling with LY294002 suppressed ($P = 0.02$; $n = 3$) CTNNB1 by 1.93-fold compared to controls. Co-treatment of FSH and LY294002 reduced the ability of FSH to increase CTNNB1 ($P = 0.03$). LY294002 treatment reduced estradiol medium concentrations 1.14-fold when compared to control levels, while co-incubation of FSH+LY294002 and FSH treatment induced estradiol to similar levels above controls ($P = 0.0001$; $n = 4$). Results demonstrate activation of AKT is required for CTNNB1 accumulation and estradiol production in bovine granulosa cells. These data suggest that induced CTNNB1 accumulation by FSH and IGF1 activation of AKT may be the lynch pin molecule responsible for FSH and IGF1 synergistic steroidogenic activity.

Key Words: protein kinase B, β-catenin, granulosa cells

1391 (M208) Ileal tight junction gene expression in glucagon-like peptide 2-treated dairy bull calves with and without coccidiosis.
M. P. Walker*[1], E. E. Connor[2], R. L. Baldwin[3], and S. Kahl[1], *[1]USDA-ARS, BFGL, Beltsville, MD, [2]USDA-ARS, Bovine Functional Genomics Laboratory, Beltsville, MD, [3]USDA-ARS, Beltsville, MD.*

Intestinal gut permeability is partially regulated by the intestinotrophic hormone glucagon-like peptide 2 (GLP-2). Specifically, disease models in mice and human cell lines have implicated GLP-2 in the regulation of the tight junction milieu within the intestinal tract. Therapeutic administration of GLP-2 ameliorates gastrointestinal lesions and mechanical damage in rodent models of ileitis, porcine models of bowel resection, and humans with small bowel disease. These damages can reduce nutritional absorption and increase bacteria in the blood stream, both of which are in part attributed to tight junction protein disregulation. The purpose of the present study was to determine whether GLP2 therapy alters tight junction gene expression in ileum of neonatal dairy calves with scours induced by *Eimeria bovis* infection. Neonatal Holstein bull calves ($n = 18$) were separated into 4 treatment groups; uninfected-buffer ($n = 5$), uninfected-GLP-2 ($n = 4$), *E. bovis*-buffer ($n = 5$), and *E. bovis*-GLP-2 ($n = 4$). On d 0, calves in the *E. bovis*-buffer and *E. bovis*-GLP-2 groups were orally dosed with 200,000 sporulated oocysts of *E. bovis*. For 10 d (d 18 to d 27 of the study), uninfected-GLP-2 and *E. bovis*-GLP-2 calves were injected every 12 h with 50 µg of GLP-2/kg BW and at d 28 calves were sacrificed for collection of intestinal tissues for RNA extraction. Tight junction genes including CAR, CLDN1, CLDN2, CLDN4, F11R/JAMA, JAM2/JAMB, and TJP1/ZO-1 were evaluated in ileal epithelium by realtime quantitative PCR. Relative mRNA expression normalized to ATP5B and HMBS revealed greater expression of TJP1/ZO-1 in *E. bovis*-infected calves compared to uninfected calves ($P \leq 0.03$) and an *E. bovis* infection vs. GLP2 treatment interaction ($P \leq 0.004$). Expression of all other genes did not differ ($P > 0.05$) with GLP-2 treatment or *E. bovis*infection status. The lack of significant findings among the majority of genes investigated may be explained by large variation among individuals or the timing of sample collection relative to infection status and GLP-2 treatment. Alternatively, tight junctions may not be regulated at the RNA level, whereby analysis at the protein level may be more appropriate. Finally, the cellular localization of tight junction proteins may become altered during infection and with GLP2 treatment due to post-translational modifications or other regulating molecules. A more in-depth histological study could reveal significant findings that analysis of RNA levels alone cannot detect.

Key Words: dairy cattle, ileum, tight junction

1392 (M209) Effects of heat stress on the metabolic transcriptional profile of peripheral tissues in growing pigs. M. Sanz Fernandez[*1], J. S. Johnson[1], J. T. Seibert[1], R. L. Boddicker[1], S. C. Isom[2], L. Cox[2], J. W. Ross[1], R. P. Rhoads[3], and L. H. Baumgard[1], *[1]Iowa State University, Ames, [2]Utah State University, Logan, [3]Virginia Tech, Blacksburg.*

Heat stress (HS) alters postabsorptive metabolism and nutrient partitioning, independently of reduced nutrient intake. Surprisingly, despite marked hypophagia, heat-stressed animals have reduced plasma non-esterified fatty acids (NEFA), and decreased sensitivity to lipolytic signals. In addition, HS increases plasma insulin parameters in a variety of animal models. Further, HS seems to alter systemic fuel utilization, favoring aerobic glycolysis rather than oxidative phosphorylation. Study objective was to determine if these metabolic changes have their origin at the transcriptional level. Seventeen crossbred gilts (57 ± 5 kg BW) were subjected to one of two environmental treatments: 1) constant HS conditions (32°C, 23% RH) and ad libitum feeding (n = 7), or 2) pair-feeding in thermoneutral conditions (20°C, 36% RH; PFTN; n = 10) to eliminate the confounding effects of dissimilar intake. Feed intake decreased 38% on average and was not different between treatments (P = 0.75). After 8d of environmental exposure, pigs were sacrificed and liver, subcutaneous adipose tissue (AT) and muscle (longissimus dorsi, LD) immediately collected. Gene expression was determined using qPCR (BioMark System, Fluidigm Corporation) on an average of 42 genes per tissue. Genes were selected based on the RNA-Seq output of a similar experiment. Gene expression was normalized to housekeeper genes and statistical analysis was performed in delta delta Ct values (*P*ROC GLM, SAS 9.2). Data is reported as fold change. As expected, heat shock protein-related genes (e.g., HSF2, HSPA4, HSPB8, HSPCB, HSPE1, HSP90AA1) were up-regulated (41–156%, $P \leq 0.10$) across all tissues in HS compared to PFTN conditions. Supporting the phenotypic observation, adipose triglyceride lipase was downregulated (36%, P = 0.07), hepatic fatty acid synthase was up-regulated (1.5-fold, $P < 0.01$), and TCA cycle and electron transport chain proteins (i.e., IDH2, NDUFB7, NDUFS7) were downregulated (43%, P = 0.06; 22%, P = 0.05; 23%, P = 0.10; respectively) in liver and LD of HS pigs. Unexpectedly, AT insulin receptor and LD pyruvate dehydrogenase kinase 4 were downregulated (32%, P = 0.07; 61%, P = 0.05; respectively) in HS compared to PFTN pigs. Abundance of most of the genes involved in bioenergetic pathways did not differ between treatments. These data suggest that changes in metabolism and fuel selection after chronic HS (8d) may partially arise from differences in post-transcriptional regulation. Whether gene expression control at the transcriptional level has a role on metabolic adaptation to acute HS remains unknown.

Key Words: heat stress, pig, postabsorptive metabolism

1393 (M210) Effect of feeding high or low portions of concentrate during the transition period on serum adiponectin concentrations and mRNA expression of adiponectin and its receptors in subcutaneous and retroperitoneal fat of dairy cows. P. Friedrichs[1], M. Weber[1], L. Locher[2], S. Dänicke[3], U. Meyer[3], R. Tienken[3], H. Sauerwein[*1], and M. Mielenz[4], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Germany, [2]University for Veterinary Medicine Foundation, Hannover, Germany, [3]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany, [4]Leibniz Institute for Farm Animal Biology (FBN), Institute of Nutritional Physiology, Dummerstorf, Germany.*

The mRNA expression of adiponectin (ADIPOQ) and its receptors ADIPOR1/2 in adipose tissue (AT) decreases with the onset of lactation in dairy cows; the serum concentrations of ADIPOQ have also been demonstrated to drop during the lactation-induced negative energy balance (NEB) but not during feed-restriction induced NEB at later stages of lactation (Singh et al. (2014), doi:10.3168/jds.2013–7598). As to whether the extent of NEB during the lactation-induced NEB may affect ADIPOQ system was not known and we thus hypothesized that the ADIPOQ system will be affected by feeding different portions of concentrate in the diet throughout the transition period, and that visceral (VC) and subcutaneous (SCAT) respond concordantly. Twenty pluriparous German Holstein cows were fed with rations containing either 60% (HC) or 30% (LC) concentrate (DM basis, n = 10 per group) from d 1 to 21 postpartum. The SCAT (tail head) and RPAT were biopsied at d -21, 1, and 21 relative to parturition. Blood samples were collected weekly. ADIPOQ and AdipoR1/2 mRNA abundances were quantified by qPCR, and serum ADIPOQ by ELISA. The statistical analyses were performed using SPSS 21.0 ($P < 0.05$). The NEB was more negative in LC than in HC animals (Δ = 18.5 MJ/d, third week of lactation). Effects of diet were limited to ADIPOQ in SCAT, with 4.1-fold lower mRNA abundance in LC than in HC at d 21 ($P < 0.02$). With the exception of AdipoR2 mRNA in RPAT, we detected time-related changes in SC and RPAT with higher abundances ante partum ($P < 0.05$) for all target mRNAs, and for ADIPOQ in serum. AdipoR2 mRNA abundance in RPAT was highest at d 1. Irrespective of time, ADIPOQ and AdipoR2 expression was higher in RPAT than in SCAT ($P < 0.05$), whereas AdipoR1 mRNA abundance was not different between both tissues. ADIPOQ and AdipoR1 mRNA abundance were positively correlated in SCAT (r = 0.461, $P < 0.01$) and RPAT (r = 0.745, $P < 0.01$). AdipoR1 and AdipoR2 were correlated in SCAT (r = 0.422, $P < 0.01$). The lower ADIPOQ mRNA abundance in SCAT of the LC group points to greater responsiveness towards dietary effects in this depot; however, this was apparently not reflected in serum ADIPOQ indicating that other fat depots might compensate the decrease. The observed time-related changes in SCAT and of

serum ADIPOQ confirm earlier reports, whereas the likewise regulation in RPAT for ADIPOQ and AdipoR1 has not been previously investigated in cows. The correlation between ADIPOQ and AdipoR1 mRNA abundances points to a co-regulation of both genes in AT.

Key Words: adiponectin

1394 (M211) Heat stress affects insulin sensitivity in primary bovine adipocytes.

P. P. Faylon[*1], L. H. Baumgard[1], R. P. Rhoads[2], and D. M. Spurlock[1], *[1]Iowa State University, Ames, [2]Virginia Tech, Blacksburg.*

Animals experiencing heat stress (HS) have diminished lipolytic response. Current research on lipid metabolism in lactating cows shows a clear disconnect between in vivo and in vitro data, wherein bovine cells cultured under HS conditions were found to be more sensitive to lipolytic stimuli. The objective of this study was to determine if HS affects insulin sensitivity in subcutaneous adipose tissue (AT) of dairy cattle. Bovine primary adipocytes, isolated from 7 multiparous Holstein cows in late lactation, were cultured at either 42°C (HS) or 37°C (thermal neutral, TN) and incubated with varying concentrations of insulin (0 to 2.5 mU) in combination with isoproterenol (ISOP, 10^{-6} M). Glycerol release was measured as an indicator of lipolytic response. The effects of temperature and insulin concentration, as well as their interaction on AT lipolysis were evaluated. Likewise, the abundance of several lipolytic proteins in relation to HS was analyzed. A significant insulin concentration by temperature interaction was observed in HS ($P < 0.001$) but not TN ($P = 0.34$) cells. Insulin significantly reduced the amount of glycerol released ($P < 0.001$), indicating a decline in response to lipolytic stimuli. Meanwhile, in the absence of insulin, adipocytes cultured under HS exhibited an elevated response to ISOP ($P < 0.001$) relative to their TN counterparts. Basal lipolytic (-ISOP/-insulin) response was not different between HS and TN cells ($P > 0.05$). Furthermore, a significant decrease in the phosphorylation of hormone sensitive lipase (HSL) at Serine 563 ($P = 0.03$) and perilipin ($P = 0.04$) with respect to increasing insulin concentrations was observed for cells cultured under HS but not TN conditions. These data support the view that HS affects insulin sensitivity of bovine adipocytes, suggesting that HS may indirectly prevent in vivoadipose tissue mobilization as a result of heat-induced increase in circulating insulin concentrations, combined with higher AT sensitivity to insulin.

Key Words: heat stress, adipose tissue, insulin, lipolysis

1395 (M212) mRNA expression of chemerin and its receptor in a subcutaneous and a visceral fat depot of dairy cows fed with high or low portions of concentrate during the transition period.

P. Friedrichs[1], H. Khalilvandi-Behroozyar[2], L. Locher[3], S. Dänicke[4], U. Meyer[4], R. Tienken[4], H. Sauerwein[*1], and M. Mielenz[5], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Germany, [2]Dep. of Animal Science, Urmia University, Iran, [3]University for Veterinary Medicine Foundation, Hannover, Germany, [4]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany, [5]Leibniz Institute for Farm Animal Biology (FBN), Institute of Nutritional Physiology, Dummerstorf, Germany.*

Chemerin (RARRES2) is involved in adipogenesis and in mediating fat mobilization in mature adipocytes, exerting its effects via its receptor ChemR23. In humans, circulating chemerin levels are regulated by the energy intake. We hypothesized that the expression of RARRES2 or ChemR23 in subcutaneous (SC) and retroperitoneal (RP) adipose tissue (AT) of dairy cattle will change throughout the transition period and will be affected by different portions of concentrate in the diet. Twenty pluriparous German Holstein cows were divided into a high-concentrate group (HC, $n = 10$) receiving a diet with 60% and a low-concentrate group (LC, $n = 10$) receiving a diet with 30% concentrate on DM basis from d 1 until d 21 post partum. The SCAT from tail head and RPAT were biopsied at d -21, 1, and 21 relative to calving. RARRES2 and ChemR23 mRNA abundance were quantified by qPCR. The statistical analyses were performed with SPSS 21.0 ($P < 0.05$). The mRNA abundances of both genes were not different between the HC versus the LC group neither in SCAT nor in RPAT, thus, groups were pooled for further analyses. In both tissues RARRES2 and ChemR23 mRNA expression were time-dependent, i.e., less RARRES2 and ChemR23 mRNA was observed ante partum than post partum in both AT ($P < 0.05$). When comparing both AT depots within the individual sampling times, RPAT had 1.33-fold higher RARRES2 mRNA abundance than SCAT on d 1 ($P = 0.004$), whereas no differences between both depots were seen on d -21 and 21. For ChemR23, RPAT and SCAT did not differ at any time point. In conclusion, the different concentrate portion and the difference in energy balance ($\Delta = 18.5$ MJ/d in the third week of lactation) between HC vs. LC group were apparently not relevant for the expression of RARRES2 or ChemR23. Considering time-related differences we observed that RARRES2 and its receptor are regulated in a likewise manner in bovine AT. Due to their functions, the higher mRNA abundances of RARRES2 and its receptor in both AT after parturition may reflect the paracrine/autocrine involvement of RARRES2 in stimulation of lipolysis to provide non-esterified fatty acids as energy source to other peripheral tissues.

Key Words: chemerin, adipose tissue, transition period

1396 (M213) Individual *trans* monounsaturated fatty acids have distinct effects on lipogenesis in 3T3-L1 adipocytes. P. Vahmani*[1], T. D. Turner[1], P. D. Duff[1], D. C. Rolland[1], C. Mapiye[2], W. J. Meadus[1], and M. E. R. Dugan[1], *[1]Agriculture and Agri-Food Canada, Lacombe, AB, Canada, [2]Stellenbosch University, Western Cape, South Africa.*

The objective of this research was to determine the isomer specific effects of *trans* 18:1 isomers on lipogenic gene expression and fatty acid composition in adipocytes. Differentiated 3T3-L1 adipocytes were treated with 200 μM of either *trans*-9 18:1, *trans*-11 18:1, *trans*-13 18:1, or *cis*-9 18:1 (control) for 120 h. Cells were then analyzed for changes in gene expression and fatty acid composition using real-time PCR and gas liquid chromatography, respectively. The experiment was repeated three times and data were analyzed using the PROC MIXED of SAS. The *trans*-9 18:1 treatment increased the expression of acetyl-CoA carboxylase (1.6-fold, $P = 0.08$), fatty acid synthase (1.5-fold, $P = 0.03$) and stearoyl-CoA desaturase-1 (1.7-fold, $P = 0.03$) compared to the control, whereas *trans*-11 18:1 and *trans*-13 18:1 did not affect ($P > 0.10$) the expression of these genes. Consistent with the gene expression results, the content of *cis*-9 16:1 ($P = 0.01$; SEM = 8.63), total monounsaturated fatty acids ($P = 0.002$; SEM = 31.5) and total fatty acids ($P = 0.04$; SEM = 41.7) were higher in *trans*-9 18:1 (191, 986, and 1502 μg/well respectively) compared with *cis*-9 18:1 (144, 783, and 1272 μg/well respectively), *trans*-11 18:1 (141, 716, and 1370 μg/well respectively) or *trans*-13 18:1 (128, 659, and 1349 μg/well respectively). The *trans*-9 18:1 treatment also increased the *cis*-9 16:1/16:0 ratio ($P < 0.01$; SEM = 0.016) compared to the *cis*-9 18:1, *trans*-11 18:1 or *trans*-13 18:1 treatments (0.61, 0.52, 0.41 and 0.42 respectively). The amount of treatment fatty acid deposited in cells was highest ($P = 0.01$; SEM = 31.5) for *trans*-9 18:1 (585 μg/well) followed by *cis*-9 18:1 (493 μg/well), *trans*-11 18:1 (382 μg/well) and *trans*-13 18:1 (339 μg/well). About 32% of *trans*-13 18:1 was desaturated to *cis*-9, *trans*-13 18:2, whereas 19% of *trans*-11 18:1 was desaturated to *cis*-9, *trans*-11 18:2. Our results suggest that *trans*-9 18:1, the most abundant industrial *trans* fatty acid, is more lipogenic than *trans*-11 18:1 or *trans*-13 18:1. We also found that *trans*-13 18:1 is used as a preferred substrate for delta-9 desaturation. Our results demonstrate that *trans*-13 18:1, the second most abundant *trans*-18:1 isomer in beef when feeding forage based diets, is metabolized differently and may have differing bioactivity than major industrially produced *trans* fatty acids. Consequently, potential bioactivities of *trans*-13 18:1 and its delta-9 desaturation product deserve further investigation.

Key Words: adipocytes, mouse, *trans* monounsaturated fatty acids

1397 (M214) Modeling diurnal variation in ruminal temperature of beef cows. B. H. Boehmer*, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station, Stillwater.*

Ruminal temperature (RuT) of beef cows is an effective measure of core body temperature. Monitoring RuT may be useful for the prediction of physiological events in cattle including estrus, parturition, and health status. Daily variation in core body temperature of cattle is well documented and may influence prediction models using temperature. The objective of this experiment was to develop a method to reduce the impact of diurnal variation in RuT of beef cows. Hourly reporting temperature boluses (SmartStock, LLC) were administered to postpartum, lactating, Angus cows. The data set used for modeling contained 12,358 RuT values (58 cows; 14 d), with a daily mean of 19.3 ± 0.3 RuT readings per cow. Models were developed to generate hourly correction factors for RuT, which reduce the impact of diurnal variation. Briefly, the RuT for a cow at an hour was subtracted from the mean RuT of all cows at all hours in the experimental group (Ac), or mean RuT of an individual cow for all hours (Cc), or all RuT during a 72 h running average for an individual cow (Ra). Correction factors for each daily hour (0000 to 2300 h) were calculated as the hourly least squares mean for the hourly deviations from the means (Ac, Cc, Ra). Hourly least square means of the deviations for an hour were calculated for all cows (AM) or for individual cows (CM). Unadjusted RuT and RuT excluding drinking events (W; less than 2 x SD of mean RuT) were used for model evaluation. Ruminal temperature for each model was analyzed using PROC UNIVARIARTE, PROC REG, and PROC MIXED (SAS Inst. Inc.). All six correction models reduced the variation (> 54%) and skewdness (> 30%) of RuT. Hourly variation in RuT occurred for unadjusted RuT, W, and RaAM ($P < 0.05$), but was eliminated in AcAM, AcCM, CcAM, CcCM, and RaCM models. Bayesian information criterion values (goodness of fit), were least when AcCM was used to model RuT. When the AcCM model was used, variation in RuT was greatly diminished. Daily hour did not influence RuT when AcCM, CcCM, and RaCM models ($P = 0.87$, 0.83, 0.91, respectively) were used to adjust RuT. These results indicate models can be developed to greatly reduce diurnal variation in RuT. The usefulness of RuT can be enhanced through the use of models to reduce diurnal variation in body temperature of cows.

Key Words: beef cow, diurnal variation, ruminal temperature

1398 (M215) β-Hydroxybutyrate profile of high-yielding dairy cows of a Brazilian intensive system.

C. Bespalhok Jacometo*[1], J. Oliveira Feijó[1], P. Mattei[1], A. Marangon Oliveira[1], E. Schmitt[2], V. Coitinho Tabeleão[1], C. Cassal Brauner[1], F. B. Del Pino[1], S. Soriano[3], and M. Nunes Corrêa[1], *[1]Federal University of Pelotas, Brazil, [2]Embrapa, Porto Velho–RO, Brazil, [3]Fazenda Colorado, Araras, Brazil.*

This study aimed to investigate the β-hydroxybutyrate (BHB) profile of high-yielding primiparous and multiparous cows according to milk yield level. A total of 174 Holstein cows was evaluated and divided as: 1) primiparous with mean milk yield equal to or higher than 35 kg/d (42.92 ± 0.78 kg/d) (HP group, n = 37); 2) primiparous with mean milk yield lower than 35 kg/d (26.44 ± 0.91 kg/d) (LP group, n = 50); 3) multiparous with mean milk yield equal to or higher than 35 kg/d (44.28 ± 0.87 kg/d) (HM group, n = 37), and 4) multiparous with mean milk yield lower than 35 kg/d (24.87 ± 0.91 kg/d) (LM group, n = 50). The animals belonged to a commercial herd located in São Paulo State, Brazil, and were kept in free stall barns, according to their production level, and were given high-concentrate diet based on NRC recommendations (NE_L: H groups: 1.74 MCal/kg DM and L groups: 1.56 MCal/kg DM). Blood samples were collected from the coccygeal vein to evaluate BHB by an enzymatic method using a commercially available kit (Randox-Ranbut Laboratories, Oceanside, CA). The mean lactation period of all evaluated cows was 216 ± 12. Statistical analysis was performed using SAS software by One-way ANOVA and Pearson Correlation Test. The mean dry matter intake of each free stall barn during the period in which blood samples were collected was similar between groups (HP: 24 kg/d; LP: 22.7 kg/d; HM: 26.9 kg/d and LM: 22.7 kg/d). There were no statistical differences between groups ($P > 0.05$). The BHB concentrations for primiparous groups were: HP 0.45 ± 0.05 mmol/L, and LP 0.48 ± 0.08 mmol/L; for the multiparous ones, HM 0.42 ± 0.04 mmol/L, and LM 0.42 ± 0.09 mmol/L. When the same production level was compared, HP and HM tended to have a negative correlation, and so did LP and LM (Pearson´s correlation coefficients: -0.26 and -0.22, respectively); when the same category was compared, both HP– LP and HM– LM combinations tented to have a positive correlation (0.21 and 0.40, respectively). The results suggest that the cows with the mean lactation period in this study did not show a negative energy balance (NEB), probably due to the fact that milk production requirements were provided by their diet, which did not alter BHB concentration levels, an NEB marker.

Key Words: β-hydroxybutyrate, dairy cows, negative energy balance

1399 (M216) Analysis of transcription regulator gene networks in peripartal bovine liver during summer and spring seasons.

K. Shahzad*[1], H. Akbar[1], L. Basiricò[2], P. Morera[2], U. Bernabucci[2], and J. J. Loor[1], *[1]University of Illinois, Urbana-Champaign, Urbana, [2]Università degli Studi della Tuscia, Viterbo, Italy.*

Gene network analysis was used on hepatic transcriptome data from cows calving during spring (SP) or summer (SU) to uncover transcription regulators (TR) and their target genes. Liver tissue was harvested from multiparous Holstein cows at -30, 3, and 35 d relative to parturition during SP. (March–April, n = 6) and SU (June–July, n = 6). Mean temperature-humidity indeces for SP. (day/night, below 72) and SU (day, 79.5 ± 2.9; night, 70.1 ± 4.7) were recorded. Transcriptomics was conducted using the 45K-Agilent bovine microarray. Statistical analysis with FDR $\leq$ 0.10 resulted in 618, 1030 and 894 differentially expressed genes during SU vs. SP. at -30, 3, and 35 d, respectively. Ingenuity pathway analysis (IPA) was used for gene network reconstructions. Among molecular and cellular functions, the IPA analysis identified cell death and survival and cellular growth and development as the most-enriched functions. Carbohydrate metabolism was the most enriched at -30 and 3 d, while nucleic acid metabolism and cellular development were the most enriched at 3 and 35 d. A total of 50, 78, and 74 TR were identified at -30, 3, and 35 d. The IPA analysis uncovered HNF4A, MYC, and NCOA1 (-30, 3, and 35 d), STAT3, and RELA (-30 and 35 d), BCL6 (3 and 35 d), KAT2B (-30 d), and GATA2 (3 d) as key TR. Comparing SU vs. SP. at -30d uncovered HNF4A and MYC (both triggered by RELA) as key TR. Both are linked with several downstream up-regulated target genes involved in oxidation of xenobiotic compounds (CYP3A4), tryptophan catabolism (ACMSD1), arginine catabolism (ARG1), apoptosis regulation, and ER Calcium homeostasis (CFLAR, TMBIM6). In contrast, among the downregulated targets there were several involved in cellular proliferation, anti-apoptotic activities, immune related disorders (CDKN1, LGALS1, TSPO), and liver disease (SERPINA1, FTH1). At 3 d, both HNF4A and MYC were downregulated. Up-regulation of BCL6 was directly linked with the IL-6-dependent immune-response and cell growth. In contrast, BCL6 was associated with downregulation of IL7R, IL13R1 and CXCL10-dependent immune responses. At 35 d, the up-regulation of RELA was associated with target genes involved in activation of anti-inflammatory responses (CCL3, B2M), extracellular matrix breakdown (MMP1), regulation of cell cycle (MYC, PTEN, CASP8) and gluconeogenesis (*P*CK1). These results suggests that the molecular phenotype of the liver differs when calving during the summer compared with spring.

Key Words: temperature-humidity index, transcription regulator network analysis, transition cows

PHYSIOLOGY AND ENDOCRINOLOGY II

1400 (T210) Fertility of lactating dairy cows treated with gonadotropin-releasing hormone at estrus, 5 d after AI, or both, during summer heat stress. L. G. D. Mendonça*[1], F. M. Mantelo[1], and J. S. Stevenson[2], [1]*Dep. of Animal Sciences and Industry, Kansas State University, Manhattan,* [2]*Kansas State University, Manhattan.*

Objective was to evaluate fertility of lactating dairy cows after treatment with GnRH on the day of estrus, 5 d after AI, or both, under heat stress conditions in two Kansas dairies. Cows (n = 2855) detected in estrus based on tail paint removal were assigned to four treatments in a 2 × 2 factorial arrangement: 1) control (CON = 722); 2) GnRH treatment at AI (G0 = 739); 3) GnRH treatment 5 d post-AI (G5 = 697); or 4) GnRH treatment at AI and 5 d post-AI (G0G5 = 697). Daily temperature and humidity data were collected during study enrollment and temperature humidity index (THI) was calculated. Blood samples were collected from a subgroup of cows at AI (d 0), d 5 and d 12 to determine progesterone concentrations (CON = 58, G0 = 57, G5 = 58, G0G5 = 65). Pregnancy diagnosis was conducted by transrectal ultrasonography on d 36 and 94. Treatment with GnRH at AI did not affect pregnancy per AI (P/AI) on d 36 (P = 0.89) or d 94 (P = 0.53). Treatment with GnRH 5 d after AI did not affect P/AI on d 36 (P = 0.49) or d 94 (P = 0.36). Furthermore, the interaction between GnRH treatments on d 0 and 5 did not affect P/AI on d 36 (P = 0.90) or d 94 (P = 0.75). In contrast, the interaction between lactation number and treatment with GnRH on d 5 affected P/AI on d 36 (P = 0.01) and d 94 (P = 0.03) because GnRH treatment increased P/AI of ≥ 3-lactation cows (27.0 vs. 19.3%, 23.1 vs. 16.1%, respectively). Average THI at AI was 83.8 ± 0.1 and tended (P = 0.08) to be associated with P/AI at d 36, but was not (P = 0.34) associated with P/AI on d 94. Overall, treatment with GnRH on d 0 (P = 0.82), d 5 (P = 0.61), and the interaction between treatments on d 0 and 5 (P = 0.28) did not affect progesterone concentration on d 5 and 12 (1.8 ± 0.1 and 6.7 ± 0.2 ng/mL, respectively). Treating cows under heat stress conditions with GnRH at AI did not increase P/AI, but treatment with GnRH 5 d post-insemination increased fertility of ≥ 3-lactation cows.

Key Words: fertility, summer heat stress, dairy cow

1401 (T211) Luteolysis and pregnancy outcome in 5-d Resynch dairy cows after 1 or 2 injections of prostaglandin $F_{2\alpha}$. J. S. Stevenson*, S. L. Pulley, and S. L. Hill, *Kansas State University, Manhattan.*

Our objective was to determine pregnancy outcome after 50 mg PG administered on d 6 or 25 mg PG delivered on d 5 and 6, respectively, in a 5-d Ovsynch-Resynch (GnRH 5 d before [d 0] and 56 [p.m. on d 7] or 72 h [d 8] after 25-mg doses of PG [d 5 and 6 after GnRH]; timed artificial insemination [AI] on d 8). Lactating Holsteins in herd 1 diagnosed not pregnant between 30 and 36 d since last AI were enrolled randomly to receive either 50 mg PG on d 6 (1 × 50; n = 134) or 25 mg PG on d 5 and 6 (2 × 25; n = 139) after GnRH-1 (d 0), with GnRH-2 at 56 h after PG (d 5) and timed AI 16 h after GnRH-2. In herd 2, even-tagged cows received the 2 × 25 (n = 422) treatment and odd-tagged cows received the 1 × 50 (n = 450) treatment after a not pregnant diagnosis between 34 and 40 d since last AI. Blood collected from all cows in herd 1 at d 0, 5, 6, and 8 was assayed for progesterone. Defined luteolysis occurred when progesterone was ≥ 1 ng/mL on d 5 and 72 h later was < 0.5 ng/mL or < 1 ng/mL on d 8. Progesterone was similar between treatments on pretreatment d 0 and 5, but was greater (P < 0.01) in 1 × 50 than 2 × 25 cows on d 6 (4.7 ± 0.2 vs. 1.1 ± 0.2 ng/mL) and d 8 (0.43 ± 0.04 vs. 0.19 ± 0.04 ng/mL), respectively. Luteolysis was greater (P < 0.01; 93.3 vs. 78.5%) in the 2 × 25 vs. 1 × 50 treatment when the cutpoint was 0.5 ng/mL on d 8, whereas no difference was detected when the cutpoint was < 1 ng/mL (100 vs. 96.3%), respectively. Luteolytic failure was greater in cows classified as early cycle on d 0 or having a new corpus luteum after d 0 than for cows classified as late cycle on d 0 or having low progesterone on d 0 and 5. Luteolytic failure also was greater (P < 0.01) in 1 × 50 than 2 × 25 cows with a cutpoint of 0.5 ng/mL at AI and pregnancy per AI in combined herds was slightly reduced (30.4 vs. 25.1%), respectively.

Key Words: luteolysis, pregnancy per AI, progesterone

1402 (T212) Physiological characteristics of cows with divergent genetic merit for fertility traits during the transition period. S. Moore*[1,2], P. Lonergan[2], T. Fair[2], and S. Butler[3], [1]*Teagasc Moorepark, Fermoy, Ireland,* [2]*University College Dublin, Ireland,* [3]*Animal & Grassland Research and Innovation Centre, Teagasc, Moorepark, Fermoy, County Cork, Ireland.*

Cows with similar genetic merit for milk production, but with extremes of good (Fert+; n = 15) or poor (Fert-; n = 10) genetic merit for fertility traits were monitored. DMI was recorded daily from wk -2 to 5 relative to calving. Blood metabolites and metabolic hormones were measured from wk -2 to 8 relative to calving. Vaginal mucus (VM) was scored weekly on a scale 0 (no pus) to 3 (≥ 50% pus) from parturition to wk 6. Uterine polymorphonuclear neutrophil count was measured at

wk 3 and 6. Continuous data were analyzed using mixed model procedures. PROC NPAR1WAY was used to analyse VM score data. Logistic regression was performed to analyse the proportion of animals classified as having endometritis or to have resumed cyclicity by wk 6 postpartum. Prepartum DMI was similar between genotypes, but during the postpartum period, Fert+ cows had greater DMI than Fert- cows (19.7 vs. 16.8 kg DM/d, $P = 0.02$). Energy balance at wk 1 was greater in Fert+ cows than Fert- cows (2.3 vs. -1.12 UFL/d, $P = 0.02$). Fert+ cows had greater milk solids production (1.89 vs. 1.74 kg/d, $P = 0.05$). Fert+ cows had greater mean circulating insulin-like growth factor-I (102.62 vs. 56.85 ng/mL, $P = 0.001$) and tended to have greater mean circulating insulin (3.25 vs. 2.62 µIU/mL, $P = 0.08$) compared with Fert- cows from wk -2 to 8 relative to parturition. Mean circulating glucose (3.40 vs. 3.01 mmol/L, $P = 0.04$) concentrations were greater in Fert+ cows compared with Fert- cows from wk -2 to 3 relative to parturition. Fert+ cows maintained greater mean BCS throughout lactation compared with Fert- cows (2.98 vs. 2.74 units, $P < 0.0001$). Fert+ cows had better uterine health compared with Fert- cows as evidenced by lower weekly VM scores during wk 2 to 6 postpartum, and based on uterine cytology a smaller proportion were classified as having endometritis at wk 3 (0.42 vs. 0.78, $P = 0.09$) and 6 (0.25 vs. 0.75, $P = 0.04$). A greater proportion of Fert+ cows had resumed cyclicity by wk 6 postpartum (0.86 vs. 0.20, $P = 0.009$) compared with Fert- cows. These results indicate that good genetic merit for fertility traits is associated with a more favourable bioenergetic and uterine health status, earlier resumption of cyclicity and greater BCS, without antagonizing milk production.

Key Words: genetic merit for fertility, transition period, endometritis

---

1403 (T213) Characterization of luteal dynamics in lactating dairy cows for 32 d after synchronization of ovulation and timed artificial insemination.

A. Ricci*[1], P. D. Carvalho[2], M. C. Amundson[1], and P. M. Fricke[1], *[1]Dep. of Dairy Science, University of Wisconsin–Madison, Madison, [2]University of Wisconsin, Madison.*

Approximately 20% of cows diagnosed not pregnant 32 d after TAI do not have a CL, and cows that begin a resynchronization protocol in the absence of a CL have about 10% fewer pregnancies per AI compared to cows with a CL. An understanding of luteal dynamics after synchronization of ovulation and timed AI (TAI) may help to refine strategies for resynchronizing cows failing to conceive. Lactating Holstein cows ($n = 141$) were synchronized for first TAI (80 to 86 DIM) using a Double Ovsynch protocol. Thrice weekly (MWF) from 4 to 32 d after TAI, luteal diameter was measured using ultrasonography and blood samples were collected for evaluation of progesterone (P4) concentrations. Pregnancy status was determined using ultrasound 32 d after TAI. Cows ($n = 13$) were removed if they had twins ($n = 2$), if they did not synchronize ($n = 4$), or if they had pregnancy loss ($n = 7$). For cows diagnosed pregnant ($n = 48$), luteal volume increased from 4 to 13 d after TAI then remained constant until 32 d, whereas P4 increased from 4 to 15 d after TAI then remained constant until 32 d. For cows diagnosed not pregnant 32 d after TAI ($n = 80$), P4 profiles were evaluated using statistical cluster analysis (PROC CLUSTER of SAS) based on the day after TAI that P4 decreased to < 1 ng/mL. Cows diagnosed not pregnant were segregated into 5 clusters: 1) luteal regression 15 d after TAI (1.3%, 1/80); 2) luteal regression 18 to 22 d after TAI (55.0%, 44/80); 3) luteal regression 25 to 27 d after TAI (18.8%, 15/80); 4) luteal regression 29 to 32 d after TAI (3.8%, 3/80); and 5) original CL present 32 d after TAI (21.3%, 17/80). Pregnancy-associated glycoproteins (PAG) were measured in serum samples collected 25 and 32 d after TAI using a commercial assay (IDEXX Laboratories, Inc., Westbrook, ME). Relative serum PAG levels (mean ± SEM S-N values) differed among clusters at both 25 ($P = 0.03$) and 32 ($P < 0.01$) d after TAI and were similar for cows in clusters 2, 3, and 4 but were greater for cows in cluster 5. We conclude that cows maintaining their original CL for 32 d after TAI were initially pregnant but underwent pregnancy loss based on residual serum PAG levels at 24 and 32 d after TAI. *Supported by Hatch project WIS01171.*

Key Words: progesterone, luteal dynamics, pregnancy loss

1404 (T214) Influence of fat supplementation on LH pulses and FSH concentration in Nellore heifers.

R. S. Cipriano*[1], M. C. V. Miguel[2], H. F. Costa[2], J. S. Souza[2], L. M. Pavanello[2], M. A. Maioli[2], D. Giraldo-Arana[2], D. M. Pinheiro[2], F. M. Abreu[3], L. H. Cruppe[3], M. L. Day[3], and G. Nogueira[2], *[1]UniSalesiano, Araçatuba, Brazil, [2]Unesp, Araçatuba, Brazil, [3]Ohio State University, Columbus.*

The aim of this study was to verify whether protected fat supplementation, after weaning increases LH pulses and FSH concentration in Nellore heifers (*Bos taurus indicus*). Contemporary heifers ($n = 30$; 167 ± 13 kg; 9 mo) were sorted into three experimental groups: Control Group (CG, $n = 10$), sugarcane bagasse plus 4.2 kg concentrate and 500 g of ground corn; Fat Group (FG, $n = 10$), sugarcane bagasse, plus 4.2 kg of concentrate and plus 200 g of rumen protected fat (Ca salts of soybean oil); and Excess Group (EG, $n = 10$), sugarcane bagasse plus 4.2 kg of concentrate, 500 g of ground corn plus 200 g of rumen protected fat per animal per day (13.85% of palmitic acid, 17.92% of oleic acid and 49.09% of linoleic acid). After an adaptation period, animals remained under nutritional treatments for 92 d (13 to 16 mo of age). Blood samples were collected every 24 h during 17 d, in 10, 12, 14, and 16 mo of age, and every 20 min per 12 h on 11, 13, 14, and 16 mo of age for FSH and LH quantification. The

results were evaluated by repeated measures ANOVA and the Duncan´s test was the post-test of SAS. During the treatment, the FG presented a higher number LH pulses (3.12 ± 1.64; P = 0.05) in comparison with EG (1.86 ± 0.90) and CG (2.63 ± 0.74), from samples collected every 20 min per 12 h. The CG showed higher FSH concentration area (15.71 ± 3.72 ng/ml/day), P = 0.06) than GG (11.23 ± 2.51 ng/ml/day) and EG (14.17 ± 4.22 ng/ml/day) at the 14 mo of age. There was no difference on FSH concentration area between groups in 10 (P = 0.80), 12 (P = 0.55) and 16 (P = 0.35) mo of age. The CG showed higher FSH amplitude (1.86 ± 0.72 ng/ml, P = 0.08) than GG (1.12 ± 0.51 ng/ml) and EG (1.54 ± 0.22 ng/ml) also at the 14 mo of age. There was no difference on FSH amplitude between groups at the 10 (P = 0.89), 12 (P = 0.78) and 16 (P = 0.36) mo of age. We concluded that fat treatment increased frequency LH pulses, decreased FSH amplitude and FSH concentration area during supplement period.

Key Words: *Bos indicus*, LH, pulses, FSH, fat, supplementation

1405 (T215) Pregnancy outcomes based on pregnancy-associated glycoproteins in milk and serum during the first trimester of gestation in Holstein dairy cows.

A. Ricci[*1,2], P. D. Carvalho[3], M. C. Amundson[1], S. Koller[4], R. H. Fourdraine[5], L. Vincenti[2], and P. M. Fricke[1], *[1]Dep. of Dairy Science, University of Wisconsin-Madison, Madison, [2]University of Turino, Italy, [3]University of Wisconsin, Madison, [4]IDEXX Laboratories, Inc, Westbrook, ME, [5]AgSource Laboratories, Verona, WI.*

Our objective was to compare pregnancy outcomes based on pregnancy-associated glycoproteins (PAGs) in milk and serum samples from cows of known pregnancy status during the first trimester of gestation. Lactating Holstein cows (n = 141) were synchronized using a Double-Ovsynch protocol for first timed AI (TAI). Blood and milk samples were collected from all cows 25 and 32 d after TAI, and pregnancy status was determined 32 d after TAI using ultrasound. Pregnant cows with singletons (n = 48) continued the experiment in which blood and milk samples were collected and pregnancy status was assessed weekly from 39 to 102 d after TAI. Milk samples were assayed for PAGs by AgSource Laboratories (Menomonie, WI) and serum samples were assayed for PAGs by IDEXX Laboratories (Westbrook, ME). Milk and serum assay outcomes included relative PAG levels (S-N values), and cows were classified as pregnant (PG), nonpregnant (NP), or recheck (RC) based on threshold S-N values. Sensitivity, specificity, negative predictive value, positive predictive value, accuracy for milk PAG outcomes were 88, 87, 92, 83, and 88%, respectively 25 d after TAI, and 98, 83, 98, 79, and 88%, respectively 32 d after TAI. These values for serum PAG outcomes were 94, 92, 96, 88, and 93%, respectively, 25 d after TAI, and 100, 88, 100, 83, and 92%, respectively, 32 d after TAI. Overall, 87% (48/57) of cows maintained their pregnancy until 102 d after TAI. For the milk assay, NP and RC outcomes occurred for pregnant cows 25 (11 and 36%), 46 (4 and 17%), 53 (4 and 20%), 60 (5 and 18%), and 67 (7 and 20%) d after TAI when relative PAG levels were low. For the serum assay, NP and RC outcomes occurred for pregnant cows 25 d after TAI (6 and 35%), whereas RC outcomes occurred for pregnant cows 39 (30%), 46 (46%), 53 (59%), 60 (70%), 67 (52%), 74 (28%), 81 (20%) and 88 (11%) d after TAI. Relative PAG levels in both milk and serum were negatively correlated (P < 0.01) with milk production in multiparous but not primiparous cows at 53 and 60 d after TAI when relative PAG levels were at their nadir. We conclude that low relative PAG levels in both milk and serum resulted in NP and RC outcomes in pregnant cows using these assays and that both parity and milk production affected relative PAG levels in milk and serum. *Supported by Hatch project WIS01171.*

Key Words: pregnancy diagnosis, pregnancy associated glycoprotein, milk

1406 (T216) Comparison of two gonadorelin formulations and two luteolytic agents on pregnancy rates in beef cattle synchronized with a 5-d CO-Synch + CIDR program.

S. Bas[*1], T. A. Brick[1], G. Starkey[1], G. Messerschmidt[1], A. A. Barragan[1], G. M. Schuenemann[1], and M. L. Day[2], *[1]Dep. of Veterinary Preventive Medicine, Ohio State University, Columbus, [2]Ohio State University, Columbus.*

The objective of the present study was to compare the effect of two gonadorelin formulations and two luteolytic agents (PGF) injected as part of a 5 d CO-Synch + CIDR program on fixed timed AI (FTAI) pregnancy rates (PR) in beef cattle. Postpartum beef cows (n = 473) and heifers (n = 78) from two herds received GnRH and a CIDR insert on d 0; 5 d later, at CIDR removal, animals received two doses of PGF. On d 8, cows and heifers received a second dose of GnRH and were FTAI. At the initiation of the breeding program, cows were blocked by age and d postpartum (DPP) and randomly assigned into one of two treatment groups. For animals in the control group (CON = 280), the hormones used for the synchronization program were gonadorelin diacetate tetrahydrate (100 μg; Cystorelin) and dinoprost tromethamine [50 mg (two 25 mg doses); Lutalyse]; while animals in the Parnell group (PAR = 271) received gonadorelin acetate (100 μg; GONAbreed) and Cloprostenol sodium [1000 μg (two 500 μg doses); estroPLAN]. Determination of pregnancy status was performed by transrectal ultrasonography at 35 to 45 d after FTAI and after the conclusion of the breeding season. Age (CON = 4.8 ± 0.2; PAR = 4.6 ± 0.2), DPP (CON = 73.8 ± 1.6; PAR = 75.9 ± 1.5), and body condition score (CON = 6.6 ± 0.9; PAR = 6.6 ± 0.1) were not different (P > 0.05) between treatments. No difference (P > 0.05) in PR at FTAI was observed for the

CON (54.9%) and PAR (55.9%) treatment groups. Similarly, no difference ($P > 0.05$) in PR was observed between treatments for cows [CON ($n = 236$) = 55.1%; PAR ($n = 243$) = 56.9%] and heifers [CON ($n = 37$) = 54%; PAR ($n = 35$) = 51.4%]. Breeding season PR (89.8%) did not differ ($P > 0.05$) between treatments. In conclusion, the use of gonadorelin diacetate tetrahydrate plus dinoprost tromethamine (CON) resulted in similar FTAI PR when compared to gonadorelin acetate plus cloprostenol sodium (PAR).

Key Words: beef, GnRH, prostaglandin

1407 (T217) Rams treated with testosterone induce sexual activity in anovulatory dorper adult sheep.

L. M. Tejada*, *Universidad Autónoma Agraria Antonio Narro, Torreón, México.*

The aim of this study was to determine whether rams treated with testosterone induce estrus in multiparous anovulatory ewes in northern México. On April 15, Dorper multiparous ewes ($n = 60$) were randomly distributed to two experimental groups; all females received daily 30 mg i.m. of progesterone from d −8 and d −4 before contact with males. On April 20, while one group (GMT, $n = 31$) was exposed to three males treated with testosterone (25 mg i.m., every 3 d × 2 wk before mating), the other group (GMC, $n = 29$) was exposed to three non-testosterone treated males. Estrous response was evaluated in two periods. The first period from d 0 to 14 while the second period from 15 to 25 d after male introduction (twice daily, during 1 h). On d 10 and 25 of the experimental period, ovulation rate was assessed throughout ultrasonographic scanning. Estrus activity was compared using chi2 (SYSTAT program 12). During the first 14 d after male introduction, 87% of the GMT-ewes (27/31) ovulated but only 9.6% (3/31) showed estrus activity, whereas 68% of the GMC-females (20/29) ovulated and 3.4% (1/29) showed estrous activity. After 15 d post-male introduction, 83% of the GMT-females(26/31) ovulated, with 80% of the ewes showing signs of estrus (25/31). Regarding the GMC-females, 51% (15/29) ovulated, and 68% (13/29) showed signs of estrus activity. Results of this study confirm that males treated with testosterone are more effective to induce ovulation and estrus activity during the second phase of the experimental period (15 to 25 d after male introduction) in Dorper adult ewes, regarding the untreated-males.

Key Words: testosterone, sheep, anestrus, estrus activity

Table 1407. Sexual response in sheep exposed to male control group (GC) or treated with testosterone (GT)

	Response 0 to 14 d after introduction of males		Response 15 to 25 d after introduction of males	
	Ovulation	Estrous	Ovulation	Estrous
GT	87% (27/31)a	9.6% (3/31)a	83%(26/31)a	80%(25/31)a
GC	68%(20/29)a	3.4%(1/29)a	51%(15/29)b	68%(13/29)b

Different letters in columns indicate different statistical differences $P > 0.05$.

1408 (T218) Regulation in vivo and in vitro of G protein-coupled receptor 34 (GPR34) mRNA in ovarian granulosa cells of cattle and its role in steroidogenesis.

L. J. Spicer*[1], J. A. Williams[1], L. F. Schutz[1], M. L. Totty[1], N. B. Schreiber[1], and J. Gilliam[2], *[1]Oklahoma State University, Stillwater, [2]Oklahoma State University Center for Veterinary Health Sciences, Stillwater.*

Abundance of *G* protein-coupled receptor 34 (GPR34) mRNA is greater in granulosa cells (GC) of cystic follicles *vs*. normal dominant follicles of cattle. The present experiments were designed to determine if: 1) GPR34 expression in GC changes during normal follicular development in estrogen-active (EA) and estrogen-inactive (EI) follicles of cattle, 2) hormones that have been shown to influence steroidogenesis such as IGF-I and FSH regulate expression of GPR34 mRNA, and 3) GPR34 ligands function to regulate GC function. In Exp 1, estrous cycles of non-lactating Holstein cows were synchronized and ovariectomized on either Day 3 or 6 after ovulation; a 2 × 2 factorial ANOVA (Day 3 vs. 6; EA vs. EI) indicated that GPR34 mRNA abundance in GC increased ($P < 0.05$) from 6.1 to 14.1 ± 4.3 relative mRNA units between Day 3 ($n = 5$ cows) and 6 ($n = 5$ cows) post-ovulation but did not differ ($P > 0.10$) between EA ($n = 15$) and EI ($n = 23$) follicles. In Exp 2, ovaries were collected at a local slaughterhouse and GC were isolated and treatments applied in vitro for 24 h; a 2 × 2 factorial ANOVA (± IGF-I with ± tumor necrosis factor (TNF)-α) indicated that IGF-I increased ($P < 0.05$) GPR34 expression from 3.5 to 7.8 ± 0.3 relative mRNA units and TNFα decreased ($P < 0.05$) the IGF-I-induced GPR34 mRNA abundance to 6.0 ± 0.4 relative mRNA units in small-follicle (1–5 mm) GC ($n = 3$ replicates and GC pools/treatment). Also in Exp 2, IGF-I and TNFα decreased ($P < 0.05$) GPR34 expression from 17.1 to 9.4 and 2.2 relative mRNA units, respectively, in large-follicle (8–22 mm) GC, indicating a change in GPR34 responsiveness occurs during follicle development. Other in vitro experiments (Exp 3–7; $n = 3$ replicates) revealed that treatment with IL-2, prostaglandin E2 and angiogenin decreased ($P < 0.05$) GPR34 expression by 62, 19, and 21%, respectively, whereas FSH, IL-6 and cortisol did not affect ($P > 0.10$) *GPR34* expression in small-follicle GC. In Exp 8, the presumed ligand of GPR34, L-a-lysophosphatidyserine (LPPS), increased GC numbers by 1.74-fold and estradiol production by 5.4-fold (0.19 vs. 1.03 ng/10^5 cells/24 h) in small-follicle GC ($n = 3$ replicates). For the first time, we have identified the lysophosphatidylserine receptor GPR34 as a developmentally and hormonally regulated gene in GC, the ligand of which enhances GC proliferation and estradiol production.

Key Words: G protein coupled receptor, granulosa cell, cattle

1409 (T219) Interaction between a mammary immune response to lipopolysaccharide and luteal function in lactating dairy cows. J. Luettgenau[1], O. Wellnitz*[1,2], R. M. Bruckmaier[2], and H. Bollwein[1], *[1]Clinic of Reproductive Medicine, Vetsuisse Faculty University of Zurich, Switzerland, [2]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Switzerland.*

In a previous study we observed negative effects of an intravenous injection of *Escherichia coli* lipopolysaccharide (LPS) on luteal size and blood flow (LBF) as well as on plasma P4 concentrations. Because there are several reports about negative effects of mastitis on fertility of dairy cows, the objective of the present study was to investigate if LPS applied into the mammary gland could also suppress luteal function. Each of 8 lactating dairy cows received once 200µg LPS into one quarter of the mammary gland on d 9 of the estrous cycle (d 1 = ovulation). Plasma cortisol (stress hormone) and haptoglobin (acute phase protein), both indicating a systemic immune response, as well as P4 were determined immediately before (0h), hourly until 9, 12, and 24 h after administration of LPS. Luteal size and LBF were measured 0, 3, 6, 9, 12, and 24 h after LPS-injection. Cows showed local and systemic symptoms (swelling of the udder, pyrexia, increased cardiac and respiratory frequencies), increased ($P \leq 0.02$) cortisol concentrations between 2 and 8 h, and a fivefold increase ($P = 0.02$) of haptoglobin between 0 and 24 h after treatment. Plasma P4 increased between h 2 and 4, and decreased between h 4 and 6 after LPS exposure. There was no effect ($P > 0.05$) of treatment on luteal size, but LBF increased ($P = 0.05$) during the first 3 h after LPS-injection, remained constant ($P > 0.05$) between h 3 and 6, and decreased ($P < 0.0001$) between h 6 and 12. Results indicate that in contrast to an intravenous injection the application of LPS into the mammary gland does not show an obvious suppression of luteal function, although inducing systemic effects.

Key Words: mastitis, corpus luteum

1410 (T220) Influence of maternal nutrient restriction and realimentation on vascularity of bovine placentomes. B. R. Mordhorst*[1], L. E. Camacho[2], C. O. Lemley[3], P. P. Borowicz[1], D. A. Redmer[1], K. C. Swanson[1], and K. A. Vonnahme[1], *[1]North Dakota State University, Fargo, [2]University of Arizona, Tucson, [3]Mississippi State University, Starkville.*

To investigate maternal global nutrient restriction and realimentation impacts on placentome vascularity and mRNA expression for angiogenic and vasoactive factors in cotyledonary (COT) and caruncular (CAR) tissues, multiparous beef cows were randomly assigned to either 100% (CON; $n = 18$) or 60% NRC requirements for all nutrients (RES; $n = 28$) on d 30 of gestation. On d 85, tissues were collected, or cows remained on CON or RES diets, or were realimented to CON. On d 140, tissues were collected and all remaining cows were placed on CON diets until d 254 where all remaining cows were slaughtered to collect tissues. At tissue collection, placentomes were separated and portions snap frozen until qPCR analyses for mRNA expression of platelet endothelial cell adhesion molecule-1 (PECAM-1), soluble guanylate cyclase-β, endothelial nitric oxide synthase, vascular endothelial growth factor, fms-like tyrosine kinase, and kinase insert domain containing receptor were performed with all normalized to 18S. Vascularity measurements in CAR and COT were stained for PECAM-1, Rhodamine labeled lectin, and DAPI, and micrographs analyzed with Image-Pro Premiere. Treatment did not affect ($P \geq 0.06$) mRNA expression in any tissue on any day. Data from d 85 was presented previously where COT capillary size was smaller in RES vs. CON (465 vs. 764 ± 91 μm^2). Treatment did not affect any CAR or COT measurements d 140 or 254. In CON cows, CAR tissue area decreased ($P = 0.02$) and capillary number density increased ($P < 0.01$) from d 85 to 254 (0.76 vs. 0.59 ± 0.05 mm^2; 114 vs. 301 ± 26 number/μm^2). In COT, tissue area increased ($P = 0.02$) from d 85 to 254 (2.66 vs. 2.84 ± 0.05 mm^2). Capillary area and surface densities were similar ($P \geq 0.19$) on d 85 and 140 and increased ($P \leq 0.04$) by d 254. Capillary size decreased ($P < 0.01$) from d 85 to 140 and were similar ($P = 0.14$) from d 140 to 254. Capillary number density increased ($P < 0.03$) throughout gestation (45.6, 66.6, vs. 162.6 ± 6.5 number/μm^2). Capillary changes throughout gestation are more prevalent in COT vs. CAR. While we have previously reported that realimentation can augment uterine blood flow and placental arteriole vasoreactivity, the histologic and mRNA expression for angiogenic/vasoactive factors do not appear to be altered by maternal dietary intake. *Supported partly by AFRI Competitive Grant no. 2009–65203–05812 from the USDA-NIFA.*

Key Words: cow, placenta, vascularity

1411 (T221) Lysophosphatidic acid (LPA) activates ERK1/2-P90RSK signaling in porcine trophoblast cells. J. Kim*, J. Lee, S. Jung, H. Bang, Y. Sung, Y. Choi, and J. Kim, *Dankook University, Cheonan, South Korea.*

LPA (lysophosphatidic acid) is a phospholipid having diverse biological effects on various types of tissues. Recently, we indicated that LPA and their specific G protein-coupled receptors appear to play a lipid regulator during implantation and establishment of pregnancy in a human, mice and pig. In pig, LPA with various fatty acyl groups and receptors (LPA_{1-3}) were expressed in the uterine endometrium and conceptus during pregnancy. The extracellular-signal-regulated kinase (ERK1/2) pathway has emerged as one of the critical components in LPA signaling cascades. However, little is known of the biological role of LPA in the porcine conceptus during implantation. Therefore, this study examined LPA and the ERK1/2 signal transduction pathway in porcine conceptuses

during early pregnancy. The effects of LPA on the ERK1/2 signaling pathway were studied using established porcine trophectoderm cells (PTr) isolated from Day 12 pig conceptuses. The pTr cells were serum starved for 24 h and then treated with LPA (0–20 uM) for 30 min. LPA dose dependently increased ERK1/2 phosphorylation. Western blot analyses of whole cell extracts with antibodies to target proteins also found that LPA increased levels of pERK1/2 and pP90RSK (ribosomal protein S6 kinase, 90 kDa) by 2.3- and 1.6-fold, respectively, within 15 min which was maintained for up to 90 min. MEK inhibitor U0126 and LPA_3 receptor blocker significantly decreased LPA-induced ERK and P90RSK activity. Collectively, these results indicate that LPA coordinately activates ERK1/2, P90RSK in pTr cells and supports the hypothesis that LPA is a critical regulator of trophoblast survival, growth and differentiation during early pregnancy.

Key Words: LPA, pig trophoblast, ERK1/2

1412 (T222) Relationship between dry-matter intake and subclinical endometritis in healthy postpartum dairy cows.

A. H. Souza*[1], P. D. Carvalho[2], A. R. Dresch[3], L. M. Vieira[4], K. S. Hackbart[3], R. D. Shaver[2], and M. C. Wiltbank[2], *[1]University of California Cooperative Extension, Tulare, [2]University of Wisconsin, Madison, [3]Dep. of Dairy Science, University of Wisconsin—Madison, Madison, [4]University of Sao Paulo-VRA, Brazil.*

The main objective was to study the relationship between dry matter intake (DMI) and subclinical endometritis of postpartum dairy cows. A secondary objective was to evaluate whether colostrum quality at calving was associated with subclinical endometritis. Postpartum Holstein cows (n = 70 total; primiparous = 28; multiparous = 42), were milked twice daily and housed and fed individually in tie-stalls. Dry matter intake was measured daily from individual cows from calving to 10 wk postpartum. Four cows that were evidently sick in the first wk after calving with depressed DMI for over 3 d and/or detected with fever were removed from further analysis. Colostrum was collected from the first milking and frozen for later quality analysis (digital Brix refractometer, 0 to 53% scale). To measure level of subclinical endometritis, uterine swabs were performed at 40 ± 3 d postpartum and a single treatment-blind technician evaluated all the slides by counting a minimum of 100 cells at 400x magnification and determined the number and percentage of polymorphonuclear cells (PMN) in the endometrial smear. The statistical analyses were performed with PROC CORR and PROC GLIMMIX of SAS. Dry matter intake averaged 18.5 ± 0.3 kg/d and 23.6 ± 0.4 kg/d, for primiparous and multiparous, respectively. There was no significant association between proportion of uterine PMN cells and average DMI (r = 0.16; P = 0.20), with no significant interactions with parity. In a further retrospective analysis, cows were divided in three classes of subclinical endometritis [0% PMN (n = 22); 1 to 20% PMN (n = 32); or > 20% PMN (n = 16)]. Similarly, the repeated measures comparison indicated no effects (P = 0.42) of subclinical endometritis on DMI. Interestingly, greater colostrum quality at calving was associated with greater DMI in multiparous (r = 0.40; P = 0.01), but not in primiparous cows (r = -0.08; P = 0.69). Further, colostrum quality was not associated with subclinical endometritis in older cows (r = 0.19; P = 0.25); but surprisingly, greater colostrum quality was associated with lower subclinical endometritis in primiparous cows (r = -0.37; P = 0.05). In conclusion, healthy postpartum cows with lower DMI had similar incidence of subclinical endometritis as compared to cows with greater intake levels. Associations between colostrum quality at calving and DMI and/or proportion of subclinical endometritis need further examination, but could represent an interesting tool to predict postpartum performance. *Support: USDA Grant 2010–85122–20612.*

Key Words: dairy cows, postpartum, dry matter intake, subclinical endometritis

---

1413 (T223) The effect of the initial GnRH and dose of PGF2α on pregnancy rate to TAI in beef heifers submitted to the 5-d CO-Synch + CIDR program.

L. H. Cruppe*[1], S. L. Lake[2], F. M. Abreu[1], S. G. Kruse[3], S. L. Bird[3], K. Heaton[4], B. R. Harstine[1], M. L. Day[1], and G. A. Bridges[3], *[1]Ohio State University, Columbus, [2]University of Wyoming, Laramie, [3]University of Minnesota, Grand Rapids, [4]Utah State University, Logan.*

The objective was to determine the effects of GnRH (Factrel) at CIDR insertion and number of doses of $PGF_{2\alpha}$ (PGF; Lutalyse) at CIDR removal in a 2 × 2 factorial on pregnancy rates to timed AI (TAI) in beef heifers enrolled in a 5-d CO-Synch + CIDR program. Yearling beef heifers (n = 1105) in seven locations (Ohio [2 locations; n = 149 and n = 116; Angus x Simmental], Utah [n = 274; Angus x Hereford], Wyoming [n = 156; Angus] and Minnesota [3 locations; n = 150, n = 150 and n = 110; Crossbred]) were enrolled in the 5-d CO-Synch + CIDR protocol and randomly assigned to either receive 100 µg GnRH (G+, n = 547) or not to receive GnRH (G-, n = 558) at CIDR insertion (d 0 of the experiment). At CIDR removal (d 5), heifers within G+ and G- groups were randomly assigned to receive either a single 25 mg PGF (PGF1) or two 25 mg PGF 6 ± 2 h apart (PGF2), resulting in four distinct treatments (G+PGF1, n = 272; G+PGF2, n = 275; G-PGF1, n = 277; G-PGF2, n = 281). All heifers received either tail paint or Estrotectpatches at CIDR removal to determine estrus response and were inseminated by TAI concomitant with 100 µg GnRH at 60 h after CIDR removal. Pregnancy diagnosis was performed between 32 and 36 d after TAI. Estrus response, as determined by estrous detection aids, did not differ among treatments. Pregnancy rate to TAI averaged 55.5% and was similar among treatments (G+PGF1, 53.3%; G+PGF2,

57.4%; G-PGF1, 55.2%; G-PGF2, 55.9%). Heifers classified as having been in estrus before TAI had a greater ($P < 0.05$) pregnancy rate to TAI (64.6%; 277/429) than either heifers with minimal (49.8%; 150/301) or no (48.7%; 172/353) evidence of estrus before TAI. In conclusion, omission of the initial GnRH treatment in the 5-d CO-synch + CIDR program did not influence TAI pregnancy rate in yearling beef heifers. Moreover, an additional dose of PGF at CIDR removal did not improved fertility in these yearling beef heifers, regardless of whether or not the initial GnRH treatment was given.

Key Words: GnRH, PGF, yearling beef heifers

1414 (T224) Use of a CIDR in the 5-d CO-synch estrous synchronization protocol improves pregnancy rates to timed artificial insemination. G. A. Bridges[1], R. P. Lemenager[2], E. Taylor[3], and P. J. Gunn[*4], *[1]University of Minnesota, Grand Rapids, [2]Purdue University, West Lafayette, IN, [3]Purdue University, Lafayette, IN, [4]Iowa State University, Ames.*

The objective of this experiment was to compare timed-AI (TAI) pregnancy rates in suckled beef cows synchronized with the 5-d CO-Synch protocol with (5CIDR) or without (5NoCIDR) the inclusion of an EAZI-BREED CIDR insert (CIDR). The experiment was conducted in 879 cows over 2 yr, and at three locations with a total of five replications. Cows were assigned to either the 5CIDR ($n = 438$) or 5NoCIDR ($n = 436$) protocol by breed, age, and days postpartum. Blood samples were collected to determine estrous cyclicity status for four of five replications. On d 0 all cows received GnRH (100 μg) and cows in the 5CIDR treatment received a CIDR. On d 5 CIDR were removed (5CIDR) and all cows received two separate doses of $PGF_{2\alpha}$ (25 mg/dose) between 2 and 10 h apart. Cows were TAI 72 h after CIDR removal (d 8), concurrent with GnRH (100 μg). Timed-AI and breeding season pregnancy rates were determined via ultrasonography 32 to 38 d after TAI and end of the breeding season, respectively. Data were analyzed with the GLMIIX procedure of SAS. There were no significant treatment-based interactions with year, age, or cyclic status; therefore data were pooled across year and cyclic status. In reps that had cyclicity determined, the proportion of cyclic cows was 89.3% (583/653). Timed-AI pregnancy rates were greater ($P = 0.0002$) in 5CIDR (62.3%, $n = 438$) than 5NoCIDR (50.7%, $n = 436$) treatment. Age classification, year, and cyclicity did not affect TAI pregnancy rates ($P \geq 0.33$). In conclusion, to optimize TAI pregnancy rates in beef cows synchronized with the 5 d CO-Synch protocol, the inclusion of a CIDR is recommended.

Key Words: 5-d CO-synch, beef cow, CIDR

1415 (T225) Incidence of ovulation to GnRH at onset of 5-d CO-synch + CIDR and impact on reproductive responses. H. P. Dias[*1], S. G. Kruse[2], S. L. Bird[2], B. J. Funnell[2], T. C. Geppert[3], E. L. Lundy[3], P. J. Gunn[3], and G. A. Bridges[2], *[1]Aluno do Programa de Pós Graduação em Zootecnia, FMVZ-UNESP-Botucatu, Brazil, [2]University of Minnesota, Grand Rapids, [3]Iowa State University, Ames.*

The objective of this study was to determine how response to GnRH at the onset of the 5-d CO-Synch + CIDR protocol (5dCO) affected estrous response, follicular dynamics, and pregnancy success to timed-AI (TAI) in beef cows. Suckled primiparous ($n = 95$) and multiparous ($n = 264$) beef cows at four locations (1; $n = 126$, 2; $n = 121$, 3; $n = 73$, 4; $n = 39$) were enrolled in the 5dCO that consisted of GnRH (GnRH-1) and CIDR insertion on d −8, CIDR removal and two 25-mg doses of $PGF_{2\alpha}$ given concurrently on d -3, and TAI on d 0 concurrent with GnRH (GnRH-2). Estrus was detected twice daily from d -3 to 0. Estrous cyclicity (70.6%) was determined at locations 1 and 2 via assessment of circulating progesterone concentrations. Ovarian ultrasound was conducted on d −8, -3, 0, and 2. Ovulation to GnRH-1 was defined by the disappearance of a dominant follicle observed on d −8 and development of a new corpus luteum on d -3. Follicle diameter at GnRH-2 (d 0) was assessed and ovulation confirmed on d 2 via ultrasonography. Pregnancy to TAI was determined approximately 30 d after TAI via ultrasonography. Cows were classified as having ovulated (OV; $n = 196$) or not ovulated (NoOV; $n = 163$) to GnRH-1. Statistical analyses were conducted using the MIXED and GLIMMIX procedures of SAS with location included as a random variable. Response to GnRH-1 (54.6%) was not influenced by parity (multiparous versus primiparous) or estrous cyclicity status. Estrus before TAI was greater ($P < 0.05$) in NoOV (47.6%) than OV (40.8%) cows. In cows that displayed estrus, interval from CIDR removal to estrus tended to be greater ($P = 0.07$) in OV (64.4 ± 0.9 h) than NoOV (60.6 ± 1.0 h), and was greater ($P < 0.01$) in multiparous (64.4 ± 0.8 h) than primiparous (58.3 ± 1.4 h) cows. Ovulation to GnRH-1 did not impact follicle diameter at GnRH-2. Pregnancy rate to TAI was greater ($P < 0.05$) in NoOV (65.0%) than OV (51.5%), primiparous (68.4%) than multiparous (53.8%) cows, and those cows that did (63.9%) than did not (52.7%) exhibit estrous. In summary, ovulation in response to GnRH-1 at the onset of the 5dCO protocol reduced estrous response and TAI pregnancy rates in suckled beef cows.

Key Words: timed-AI, beef cow, 5-d CO-synch + CIDR, GnRH

1416 (T226) The use of 5-d CO-synch+CIDR and 7-d EB+CIDR synchronization programs in Nellore females. M. V. C. Ferraz Jr.[*1], A. V. Pires[2], M. V. Biehl[2], R. Sartori[2], J. R. S. Gonçalves[3], E. M. Moreira[1], M. H. Dos Santos[1], L. H. Cruppe[4], and M. L. Day[4], *[1]University of São Paulo– FMVZ/USP, Pirassununga, Brazil, [2]University of São Paulo–ESALQ/USP, Piracicaba, Brazil, [3]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, Brazil, [4] Ohio State University, Columbus.*

Reproductive performance of heifers and cows submitted to either the 5-d CO-Synch+CIDR or 7-d EB+CIDR program was evaluated. Nellore females (n = 411) were used (nulliparous, n = 198; primiparous, n = 80; multiparous, n = 133). The 5-d CO-Synch+CIDR program consisted of insertion of a CIDR and 100 μg of GnRH (Fertagyl) on d 0. On d 5, CIDR was removed and two doses of 25 mg $PGF_{2\alpha}$ (PGF; Lutalyse) were administered 6 h apart. Timed-AI was performed on d 8 (72 h after CIDR removal). The 7-d EB+CIDR program consisted of insertion of a CIDR and 2 mg estradiol benzoate (EB) on d 0. On d 7, CIDR was removed and 25 mg of PGF, 0.6 mg of estradiol cypionate (ECP) and 150 IU of eCG (Novormon) administered. Timed-AI was performed 55 h after CIDR removal. Estrotect patches were applied at CIDR removal and visual estrus detection performed on a 12 h interval for the following 96 h. Blood samples for progesterone (P4) analysis were collected 10 d after AI to confirm ovulation. Concentration of P4 was assessed by chemiluminescent immunoassay. Data were analyzed using the GLIMMIX and PROC MIXEDs of SAS. Estrus response was greater (P < 0.05) in 7-d EB+CIDR than the 5-d CO- Synch+CIDR program (nulliparous, 95.8 vs. 66.0%; primiparous, 48.7 vs. 0.0%; and multiparous, 76.9 vs. 13.4%, respectively). In contrast, ovulation rate (89.8%) was similar between programs. Concentration of P4 10 d post AI was greater (P < 0.05) in primiparous and multiparous cows in the 7-d EB+CIDR than 5-d CO-Synch+CIDR program (6.8 vs. 4.9 ng/mL; and 6.9 vs.5.8 ng/mL, respectively); but did not differ between treatments in nulliparous females (4.4 ± 0.14 ng/mL). Timed-AI pregnancy rate was greater (P < 0.05) in multiparous cows (58.4 vs. 32.8%), but did not differ for nulliparous (51.0 vs. 41.0%) and primiparous, (25.6 vs. 31.7%) for the 7-d and 5-d program, respectively). The 7-d EB+CIDR program resulted in a greater number of females in estrus, and either greater or similar P4 on the subsequent estrous cycle and timed-AI pregnancy rates. In conclusion, reproductive performance seems to be enhanced with the 7-d EB + CIDR in comparison to the 5-d CO-Synch+CIDR program in Nellore females.

Key Words: Nellore, 7-d EB-P4, 5-d CO-synch

1417 (T227) The efficacy of different PGF2α treatments to promote luteolysis on D 7 or D 9 of the estrous cycle in nonlactating Nellore cows. M. V. Biehl[*1], A. V. Pires[1], L. H. Cruppe[2], M. V. C. Ferraz Jr.[3], R. Sartori[1], A. D. B. Ribeiro[3], J. A. Faleiro Neto[3], J. R. S. Gonçalves[4], and M. L. Day[2], *[1]University of São Paulo– ESALQ/USP, Piracicaba, Brazil, [2]Ohio State University, Columbus, [3]University of São Paulo–FMVZ/USP, Pirassununga, Brazil, [4]Experimental Station Hildegard Georgina Von Pritzelwitz, Londrina, Brazil.*

The objective was to evaluate the luteolytic competence of different PGF2α (PGF, Lutalyse) treatments on d 7 and 9 of the estrous cycle. Nonlactating Nellore cows (n = 270) were synchronized with the 7-d EB + CIDR program. Cows received Estrotect patches at CIDR removal to determine estrus response. Presence of an ovulatory follicle and its disappearance were confirmed 48 and 72 h after CIDR removal, respectively. Cows detected in estrus within 48 h and with confirmed ovulation 72 h after CIDR removal remained in the study (n = 225). Cows were assigned to treatments according to BW (389 ± 3.1) and BCS (2.7 ± 0.01, scale 1 to 5). One of four PGF treatments were administered either 7 or 9 d after confirmed ovulation (a single 12.5-, 25- or 50-mg dose or two 25-mg doses 8 h apart), in a 2 × 4 factorial. Presence of a corpus luteum was determined by ultrasound and progesterone (P4) analyses (P4 ≥ 1 ng/ml) on either d 7 (h 0) or d 9 (h 0) of the estrous cycle. Blood samples were collected at h 24, 48, and 72 after PGF treatment to assess the incidence of luteal regression (defined as concentrations of P4 < 1 ng/ml at 48 and 72 h after PGF). Serum P4 concentrations were quantified using a chemiluminescent immunoassay. Cows received a new Estrotect patch at PGF and were observed for estrus twice daily for 5 d. The incidence of luteal regression was greater (P < 0.05) in cows receiving either a single 50-mg (89.3%; 50/56), or two 25-mg doses of PGF (89.5%; 51/57) compared to cows receiving 12.5-mg (67.9%; 38/56) or one 25-mg PGF dose (66.1%; 37/56). Moreover, estrus response was greater (P < 0.05) for cows receiving the single 50-mg or two 25-mg doses of PGF (80.4 and 78.9%, respectively) compared to cows receiving 12 mg (55.4%); cows that received a single 25-mg dose were intermediate (66.1%) and did not differ from other treatments. Neither day of estrous cycle (7 or 9) nor its interaction with PGF treatment influenced luteal regression and estrus response. In conclusion, luteal regression and estrus response were greater in nonlactating cycling Nellore cows treated with 50 mg of PGF either in a single or split dose injection on d 7 or 9 of a synchronized estrous cycle.

Key Words: beef cows, luteolysis, PGF

1418 (T228) Effect of timing of artificial insemination and estrus expression using sexed semen on pregnancy rates in Holstein dairy cows.
S. E. Crego*, E. L. Larimore, and G. A. Perry, *South Dakota State University, Brookings.*

The use of sexed semen has become important in dairy herds across the United States, but reported lower conception rates have limited the adaptation in some herds. The objective of this study was to determine if timing of AI and expression of estrus impacted fixed-time AI pregnancy success with sexed semen. Primiparous and multiparous lactating Holstein cows (n = 130) were synchronized with a Presynch-Ovsynch protocol (PGF d -29; PGF d -19; GnRH and CIDR insertion d −9; PGF and CIDR removal d -2; GnRH d 0) starting at 35 DIM. The cows were allotted into a 2x2 factorial randomized block (lactation) design with 1) sexed (n = 68) versus conventional (n = 62) semen, and 2) insemination at second GnRH (n = 54) versus 16 h later (n = 76). Follicle size was determined in all cows by transrectal ultrasonography at GnRH and ovulation was confirmed on d −5 and 4. Only those cows that ovulated after AI were utilized in the analysis (n = 130). Estrus detection was determined by visual observation with the aid of tail chalk. Blood samples were collected on d -16, −9, -2, 0, and 4 to determine circulating concentrations of progesterone and estradiol by RIA. Data were analyzed using the GLIMMIX procedures of SAS. There was a significant effect of time of insemination (P = 0.04) and estrus expression (P = 0.02) on pregnancy success. Cows inseminated 16 h after GnRH had greater pregnancy success compared to cows bred at time of second GnRH (53 vs. 35%, respectively), and cows expressing estrus had greater pregnancy success compared to cows not expressing estrus (54 vs. 34%, respectively). However, there was no effect of semen (P = 0.20; 50 vs. 38% for conventional and sexed, respectively) or any interaction of semen by estrus (P = 0.55); semen by time (P = 0.47); or time by estrus (P = 0.23) on pregnancy success. There was no difference between treatments (P = 0.62) or between cows that became pregnant and cows that did not (P = 0.45) for follicle size at the second GnRH injection, but cows that expressed estrus had larger (P < 0.01) follicles than cows that did not express estrus. In conclusion, pregnancy success was significantly influenced by time of insemination and estrus expression, but was not influenced by semen, or any interactions.

Key Words: fixed-time AI, sexed semen, estrus

1419 (T229) Evaluation of the hypothalamic kisspeptin system throughout the estrous cycle in gilts.
E. S. Jolitz*, and J. A. Clapper, *South Dakota State University, Brookings.*

Kisspeptin has been demonstrated to increase peripheral concentrations of LH in pigs, presumably by its actions on GnRH, as has been demonstrated in other species. To determine if hypothalamic expression of kisspeptin (Kiss1), kisspeptin receptor (Kiss1R), estrogen receptor α (ER-α), and estrogen receptor β (ER-β) varies throughout the estrous cycle, the following experiment was performed. Forty crossbred prepubertal gilts of similar age (191 d) and weight (121 kg) were administered an intramuscular injection of PG600 (200 IU human chorionic gonadotropin and 400 IU equine chorionic gonadotropin). Twelve days after the administration of PG600, gilts were fed 15 mg of altrenogest (Matrix) daily for 15 d to synchronize estrus. Estrus detection was performed by exposing gilts to a mature boar beginning 4 d after the cessation of altrenogest and continuing for 4 d. The first day gilts stood immobile was denoted d 1 of the estrous cycle. Blood samples were collected via jugular venipuncture on d 1, 4, 7, 10, 13, 16, 19, and 21 of the estrous cycle. Ten animals were slaughtered on d 1, 9, 14, and 21 of the estrous cycle, when hypothalami, anterior pituitary glands, and blood were collected. Relative expression of hypothalamic Kiss1, Kiss1R, ER-α, ER-β, and β-actin was determined using real-time reverse transcriptase PCR. Fold changes in relative expression were determined using the Relative Expression Software Tool. Relative expression is based on the expression ratio of a target gene versus a reference gene. The expression ratio results of the investigated transcripts were tested for significance by a Pair Wise Fixed Reallocation Randomized Test with day compared as independent time effects. Relative expression of Kiss1 was increased (P < 0.05) 3.2-fold on d 1 vs. d 21 and 2.3-fold on d 9 versus d 21 of the estrous cycle. Relative expression of Kiss1 was not different (P > 0.05) among the remaining days. Relative expression of ER-β was decreased (P < 0.05) 0.8-fold on d 9 versus d 21 and 0.7-fold on d 14 vs. d 21. Relative expression of ER-β was not different (P > 0.05) when comparing the remaining slaughter days. Relative expression of Kiss1R and ER-α were each not different (P > 0.05) among days. These data provide preliminary evidence that hypothalamic expression of kisspeptin varies throughout the porcine estrous cycle, which may modulate the subsequent release of GnRH.

Key Words: kisspeptin; hypothalamus; pig

1420 (T230) Levels of IGF-1, thyroxine, triiodothyronine and cortisol in yearling bulls in feedlot or silvopastoral system.
M. E. Romero*[1], J. A. Ramírez-Godínez[1], G. Corral-Flores[1], A. Flores-Mariñelarena[1], C. Rodríguez-Muela[1], P. F. Mancillas[1], J. A. Gutierrez[1], and A. Ayala[2], *[1]Universidad Autónoma de Chihuahua, México, [2]Universidad Autónoma de Yucatán, Mérida, México.*

The aim of this research was to compare serum levels of Insulin-like growth factor (IGF-1), triiodothyronine (T3), thyroxine (T4) and Cortisol (C) in 80 yearling bulls from two genetic groups, Brahman x Charolais (40 BhXCH) and Brahman x Brown Swiss (40 BhXBS), which were randomly assigned to the feeding system in the dry tropic region in Michoacan,

México; feedlot (F) or intensive silvopastoral (ISPS). Animals were bled from the jugular vein at 0, 71, 132, and 195 d to quantify serum hormones by radioimmunoassay. Effects of feeding system and genetic group across time were analyzed using mixed models from SAS with time repeated measures. Differences were found for IGF-1, T3 and C by feeding system ($P < 0.05$). Means were higher in IGF-1 (201.36 ± 8.25; 117.74 ± 7.74 ng mL^{-1}).T3 of F was higher ($P < 0.05$) than ISPS (1.15 ± 0.03; 0.99 ± 0.03 ng mL^{-1}). C of F was lower ($P < 0.05$) than ISPS (19.13 ± 1.80; 25.30 ± 1.71 ng mL^{-1}), respectively. Genetic group had no effect ($P > 0.05$) on T3, T4 and C concentration; however, effect on IGF-1 was found ($P < 0.05$). T4 was similar ($P > 0.05$) between systems. It was conclude that IGF-1 and T3 were higher in F than in ISPS. Genetic group only had effect on IGF-1. Handling of ISPS animals were more susceptible to stress than F, since the values for C were higher but decreased with time.

Key Words: silvopastoral, IGF-1, thyroid hormones, bovine.

1421 (T231) Meta-analysis of the effect of estrus expression before fixed-time AI on conception rates in beef cattle. B. N. Richardson*[1], S. L. Hill[2], J. S. Stevenson[2], G. D. Djira[1], and G. A. Perry[1], *[1]South Dakota State University, Brookings, [2]Kansas State University, Manhattan.*

Expression of estrus after PGF and before fixed-time AI has been reported to change the uterine environment, increase fertilization rates, accessory sperm numbers, and overall embryo survival. Thus, expression of estrus can strongly impact overall pregnancy success. Because of variation in percentage of beef animals exhibiting estrus and number of animals per study, it can be difficult to detect a significant effect of estrus on pregnancy success. Thus, a meta-analysis was conducted using data from 6981 animals in 20 studies that utilized variations of the 5 most common fixed-time AI protocols (CO-Synch, CO-Synch+CIDR, 5-d CIDR, PG 6-d CIDR, and the 14-d CIDR protocols) to examine the effect estrus had on conception rates. A random-effects model was used to combine the studies. The overall model indicated a positive effect of estrus on conception rates with cows expressing estrus before fixed-time AI having a 27% greater conception rate compared with those not exhibiting estrus ($P < 0.05$; 95% CI = 22% to 32%). Next we determined factors that influenced expression of estrus. Data were available on 547 cows synchronized with one of the CIDR based fixed-time AI protocols and observed for estrus for 2 to 4 yr. Analysis of these cows indicated that days postpartum ($P = 0.22$) did not impact estrus expression. In contrast, BCS influenced estrus expression ($P = 0.04$) with cows in a BCS of ≤ 4 (51 ± 5%) having decreased expression of estrus compared to those with a BCS > 4 ($\geq$ 70 ± 4%). Initiation of estrous cycles before the breeding season also influenced estrus expression ($P = 0.03$), with anestrous cows having greater expression of estrus compared with estrus-cycling cows (78 ± 5% versus 70 ± 5%, respectively). In conclusion, among all currently recommended fixed-time AI protocols, cows expressing estrus before fixed-time AI improved conception rates, and BCS and estrus-cycling status had the greatest influence on expression of estrus.

Key Words: fixed-time AI, estrus, pregnancy success

1422 (T232) Comparison of estrus parameters in nulliparous heifers by two automated activity monitoring systems. B. F. Silper*, A. M. L. Madureira, T. A. Burnett, M. Kaur, E. L. Drago Filho, A. M. de Passillé, J. Rushen, and R. L. A. Cerri, *Faculty of Land and Food Systems, University of British Columbia, Vancouver, Canada.*

The aim of this study was to compare a commercial (Heatime, SCR Engineers, Israel) and a research based (IceTag, IceRobotics, Scotland) activity monitoring system on their ability to measure estrus episodes in nulliparous heifers (n = 57; 119 estrus episodes) starting at 12 mo old. Only heifers detected by Heatime system were evaluated, therefore only the sensitivity of the systems could be measured for accuracy. Ultrasound scanning to describe ovarian structures and blood sampling for estradiol were performed at each estrus episode and later used to determine heat detection precision. Secondary signs of estrus (mucus, uterine tonus, and visual mounting and standing) were also recorded. Heifers were housed in dynamic groups of 24 animals in a free stall barn from May 2012 to August 2013. Data was analyzed using ANOVA and Pearson correlations using proc GLM, CORR and REG of SAS. Sensitivity of Heatime system was 84.7% (94/111), whereas IceTag had 98.7% (74/75) sensitivity. Estrus episodes lasted 12.7 ± 5.6 h on Heatime and 15.0 ± 3.9 h on IceTag and were highly correlated between them ($r = 0.60$; $P < 0.01$). Mean time difference of estrus initiation and end was 3.5 ± 4.3 h and 2.9 ± 4.9 h (IceTag as reference). Peak activity was also positively correlated ($r = 0.62$; $P < 0.01$) between systems and was 76.6 ± 19.9 index value and 4.6 ± 1.7 times increase related to baseline on Heatime and IceTag, respectively. Duration and peak activity were highly correlated for Heatime ($r = 0.63$; $P < 0.01$), but not significant when using the IceTags ($r = 0.13$; $P = 0.26$). Diameter of preovulatory follicle (15.7 ± 2.6 mm; mean ± SD) had no correlation with duration or peak activity as measured by both sensors. However, concentrations of estradiol in plasma were correlated with both duration ($r = 0.47$) and peak activity ($r = 0.36$; $P < 0.01$) measured only by the Heatime system. Number of baseline steps/h measured by the IceTag system had a strong negative correlation ($P < 0.01$) with peak activity in both sensors (r = -0.37 and -0.70). Heifers with more than one secondary sign of estrus had great peak activity and duration ($P < 0.05$) on the Heatime system, but not on the IceTag sensor. Secondary signs were not affected by follicle diameter and concentration of estradiol. Re-

sults indicate that both activity monitoring systems identified estrus with high sensitivity and that major measurements (i.e., episodes, duration, peak/intensity, initiation of estrus) were mostly correlated. However, some variables such as concentration of estradiol and secondary signs of estrus should be analyzed independently for research purposes.

Key Words: automated monitoring system, dairy cows, estrus detection

---

1423 (T233) Cryopreserved sperm quality in young Brangus bulls raised on pasture and supplemented with vitamin E.

P. P. Tsuneda*, L. K. Hatamoto-Zervoudakis, R. D. Almeida, W. A. D. S. Marinho, J. T. Zervoudakis, B. H. Tsuneda, F. A. D. P. D. B. Arguello, M. F. Duarte, Jr., and T. B. Castaldeli, *Federal University of Mato Grosso, Cuiaba, Brazil.*

Vitamin E (or tochopherol) is a fat-soluble antioxidant that inhibits propagation of chain reactions induced by reactive oxygen (ROS) species in biological membranes, being an important defense mechanism against oxidative damage caused to sperm membrane, and reducing lipid peroxidation of membranes. The objective of this study was to evaluate semen characteristics and semen quality after freezing of young bulls raised on pasture and supplemented with vitamin E (α-tochopherol acetate). Sixteen Brangus bulls with 24 mo of average age and 462.2 kg of body weight mean, were randomly assigned to two treatments. Treatments were control group (CG, without supplementation) and group supplemented with vitamin E (GE- 400 IU of vitamin E/day added into concentrate). Each group was kept in separate paddocks formed by Panicum maximum cv. Mombaça and received 4.5 kg concentrate/animal/day. Animals received vitamin E supplementation for 60 d. Semen was collected by electroejaculation and diluted in TRIS–egg-yolk citrate extender with 4% of glycerol and were manually frozen. Cryopreserved semen was thawed in a water bath at 360°C for 30 sec. Immediately after thawing were evaluated sperm motility (percentage of mobile sperm), sperm vigor (intensity of motility, 1–5), sperm viability (percentage of live sperm), acrosome integrity (percentage of acrosome membrane integrity), sperm integrity (percentage of sperm with membrane integrity), and occurrence of acrosome reaction (percentage). The experiment was a completely randomized design with repeated measures and data were analyzed by ANOVA with a significance level of 5%. Supplementation with vitamin E improved the sperm viability ($P = 0.0225$) post-thaw (76.83 ± 2.07 vs. 81.91 ± 2.56). None effects of supplementation ($P > 0.05$) was observed in other traits. Based on parameters evaluated and results obtained from supplemented animals, it is concluded that this level of supplementation was beneficial for semen subjected to cryopreservation process indicating a better protection of the sperm membrane to membrane damage caused by freezing semen, justified by increased percentage of viable cells found in the supplemented group compared with control group.

Key Words: cryopreservation, oxidative stress, sperm viability

---

1424 (T234) Addition of vitamin C extender and post-cryopreservation semen quality in bulls.

A. L. Cândida de Resende Fraga, L. K. Hatamoto-Zervoudakis, T. B. Castaldeli*, R. A. Minozzo, J. T. Zervoudakis, P. P. Tsuneda, F. M. Wingert, and R. D. Almeida, *Federal University of Mato Grosso, Cuiaba, Brazil.*

The process of spermatozoa freezing provides a resting state of cell while preserving cellular structure and fertilizing capacity of sperm. However, after thawing, semen quality is reduced compared to fresh semen. Sperm cell is able to generate and degrade reactive oxygen species (ROS) necessary for cell functioning, and oxidative stress is a cellular damage caused by imbalance between increased ROS and decreased antioxidant mechanisms. During cryopreservation can occur an increase in oxidative stress due deficiency of intra and extra cellular antioxidant defense system. Vitamin C is considered a great antioxidant of extracellular fluid, working mainly preventing formation of lipid hydroperoxide in plasma lipoproteins and protecting phospholipids in cell membranes. Thus, this study aimed to evaluate the use of vitamin C in cryopreservation extender medium of bull semen to reduce damage caused by cryopreservation process. Sixteen Brangus bulls in reproductive age were used. Ejaculate was collected by electrostimulation. After analyzed, samples were diluted in a extender (TRIS-citrate-egg-yolk with 4% of glycerol), divided into two treatments: the control group (without additive, CG) and other group supplemented with vitamin C (0.45 mg/mL, GS). Thawing was performed in water bath at 37°C for 30 sec. After that aliquots were evaluated to: sperm motility, sperm vigor, sperm viability and sperm membrane integrity. Data were analyzed by analysis of variance with a significance level of 5%. Vitamin C did not improved sperm motility after cryopreservation ($P > 0.005$, CG 45.06 ± 5.51 vs. SG 43.18 ± 4.04). Sperm vigor on GC (0.93 ± 0.85) not differ ($P > 0.05$) of SG (1.00 ± 0.89). Sperm viability in GC (51.71 ± 9.70) was not different ($P > 0.05$) to SG (49.99 ± 6.46). Sperm membrane integrity was not affected by supplementation ($P > 0.05$). Medium supplementation with vitamin C did not affect seminal parameters evaluated, demonstrating that supplementation was not effective in reducing damage caused by cryopreservation in bovine semen.

Key Words: antioxidant, sperm viability, oxidative stress

1425 (T235) Concentrations of progesterone during early follicular development and pregnancy rate to AI in beef cows. F. M. Abreu*[1], M. L. Day[1], M. A. Coutinho da Silva[1], C. A. Madsen[2], T. Martins[2], L. H. Cruppe[1], B. R. Harstine[1], G. A. Bridges[3], and T. W. Geary[2], *[1]Ohio State University, Columbus, [2]USDA ARS Fort Keogh, Miles City, MT, [3]University of Minnesota, Grand Rapids.*

The objective was to investigate if decreased progesterone (P4) concentrations earlier during follicular growth would impact fertility in beef cows. Crossbred (Angus x Hereford) cows (n = 261) received estradiol benzoate (EB; 1 mg, i.m.) and a previously used CIDR on d −7, to induce emergence of a new follicular wave approximately 3 d later (d −4). On d 0, all cows received 100 µg GnRH and were randomly assigned to one of the two treatments. In the high P4 (H; n = 131) treatment, the previously inserted CIDR was replaced with a new CIDR on d 0. In the low P4 (L; n = 130) treatment, 25 mg PGF was administered on d 0, and the CIDR previously inserted on d −7 remained. On d 5, blood samples to determine P4 concentrations were collected, all cows received two 25 mg PGF doses and CIDRs were removed. Estrous detection coupled with artificial insemination (AI) 12 h later (Estrus-AI) was performed for 60 h after PGF. Cows not detected in estrus within this period were bred by timed-AI (TAI) and received 100µg GnRH at 72 h. Pregnancy diagnosis was performed approximately 40 d after AI. P4 concentrations at CIDR withdrawal (d 5) were greater ($P < 0.01$) in the H (2.81 ± 0.10 ng/ml) than in the L (1.73 ± 0.05 ng/ml) treatment. Within the first 60 h after PGF, estrus response (82% vs. 85%) and estrus distribution (56.1 ± 0.7 h vs. 54.0 ± 0.7 h) did not differ between H and L treatments, respectively. Synchronized pregnancy rate was similar between H (77.1%) and L (82.3%) treatments. Across treatments, pregnancy rates were greater ($P < 0.01$) with Estrus-AI (82.9%) than TAI (63.6%). Concentrations of P4 on d 5 were negatively related ($P < 0.01$) with estrus response and time to estrus; across treatments. In conclusion, P4 concentrations during early follicular development did not influence synchronized pregnancy rate in beef cows.

Key Words: beef cattle, progesterone, pregnancy rate

1426 (T236) Tocopherol in bovine semen cryopreservation extender: Fertility and oxidative stress. L. K. Hatamoto-Zervoudakis*, L. Soares, J. T. Zervoudakis, F. M. Wingert, P. P. Tsuneda, M. F. Duarte Junior, and L. E. S. Silva*, Federal University of Mato Grosso, Cuiaba, Brazil.*

The study was conducted to evaluate effects of supplementation with tocoferol (α-tocopherol acetate) in bovine semen extender for cryopreservation on sperm quality and oxidative stress. Thirty-eight Nellore bulls with average age of 36 mo and average body weight of 490 kg were used. Ejaculate was obtained by electroejaculation and semen was diluted in lactose–egg yolk extender with 4% of glycerol. After semen + extender were divided in four fractions and subjected to four concentrations of vitamin E: TC, Control treatment, without supplementation medium; T10, 10 mmol mL of tocopherol supplementation/mL; T30, 30 mmol of tocopherol supplementation/mL; T50, 50 mmol of tocopherol/mL. Semen were frozen with a concentration of 45 million sperm per straw. Straws were thawed at 36°C for 30 sec, and evaluated for sperm motility, sperm viability, and oxidative stress. The experiment was a completely randomized design and data were analyzed using ANOVA and SNK test (Student- Newman-Keuls) with a significance level of 5%. Treatment control afforded less decrease in progressive motility rectilinear (P = 0.0135) after thawing (13.31 ± 2.34%) compared to the other experimental groups (T10: 5.36 ± 0.92%; T30: 8.15 ± 1.80%; and T50: 27.90 ± 3.89%). Oxidative stress on sperm in T10, T30 and T50 treatments (50.91 ± 7.22, 65.88 ± 2.58, 84.22 ± 11.68 ng/mL respectively) were higher (P = 0.0001) shown in the TC control treatment (13.07 ± 1.87 ng/ml). However, the treatment T10 provided a higher sperm viability (P = 0.0001, 73.91% ± 3.72) compared to supplementation levels (54.29% ± 4.20 T30, T50 46.41% ± 5.49), but was not superior to CT (68.95% ± 3.88). It can be concluded that use of antioxidants in bovine semen extender for cryopreservation did not protect sperm plasma membrane of lipid peroxidation, or against damage caused by cryopreservation, and the levels used in this work were detrimental to sperm fertility.

Key Words: TBARS, fertility, antioxidant

1427 (T237) Embryonic growth between d 33 and 45 of pregnancy in lactating dairy cows differing in hormone and metabolite concentrations. T. J. Stratman*[1], S. E. Poock[2], S. L. Murphy[1], A. Thomas[1], D. Bouhan[1], D. H. Keisler[1], and M. C. Lucy[1], *[1]University of Missouri, Division of Animal Sciences, Columbia, [2]University of Missouri, College of Veterinary Medicine, Columbia.*

Embryonic loss in dairy cows continues to occur into the 5 and 6 wk of pregnancy, and there is an association between slower embryonic growth and pregnancy loss during this period. Individual differences in hormone and metabolite concentrations may affect the growth of the embryo via endocrine mechanisms or by affecting nutrient flux across the placenta. The objective was to examine the relationship between postpartum hormones/metabolites and embryonic growth from d 33 to 45 of pregnancy. Holstein cows (n = 56; 86 ± 17 d postpartum at AI) were examined by transrectal ultrasonography on d 33, 35, 38, 40, 42, and 45 of pregnancy. Length (l) and width (w) of the embryo and amnionic vesicle were measured and the volumes for the embryo (e_vol) and amnionic vesicle (a_vol) were calculated [volume = 4/3*π*(0.5*l)*(0.5*w)*(0.5*w)]. There was an effect of day of pregnancy ($P < 0.001$) because

e_vol and a_vol increased from d 33 to d 45 (0.14 ± 0.01 cm^3 vs. 0.60 ± 0.06 cm^3; and 1.52 ± 0.05 cm^3 vs. 10.57 ± 0.59 cm^3, respectively). Across all days, the a_vol of male embryos was larger than female (4.25 ± 0.20 vs. 3.70 ± 0.20 cm^3) but e_vol was similar for male vs. female. Blood was collected on the d of ultrasound and plasma analyzed for glucose, progesterone (*P*4), growth hormone (GH), IGF1, and insulin (INS). Plasma hormone and metabolite concentrations were not affected by day of pregnancy ($P > 0.1$) but differed for individual cows ($P < 0.001$; range = 51 to 82 mg/dL for glucose, 4.7 to 13.5 ng/mL for P4, 2.3 to 13.4 ng/mL for GH, 50 to 131 ng/mL for IGF1, and 0.2 to 0.7 ng/mL for INS). Individual cows were categorized as being above or below the median for each blood hormone/metabolite concentration. Cows that were above or below the median for glucose, P4, GH, or INS were similar for e_vol and a_vol ($P > 0.1$). There was a category by day interaction ($P < 0.05$) for IGF1, however, because cows with IGF1 above the median (mean = 102.4 ± 16.4 ng/ml) had greater e_vol on d 42 compared with low IGF1 cows (mean = 69.9 ± 13.0 ng/mL) (1.11 ± 0.04 vs. 0.98 ± 0.04 cm^3; above vs. below). A_vol was not affected by IGF1 category. Conclusions were that male embryos have greater amnion vesicle volume from d 33 to 45 of pregnancy. Plasma concentrations of IGF1 were positively associated with a larger embryo on d 42. Chronically low IGF1 concentrations in lactating cows may lead to embryonic loss via slower embryo growth.

Key Words: bovine, embryo, metabolites

1428 (T238) Altered ovarian dynamics in lactating dairy cows undergoing embryonic mortality. *R*. Wijma*[1], M. L. Stangaferro[1], J. R. Branen[2], J. M. Howard[2], and J. O. Giordano[1], *[1]Dep. of Animal Science, Cornell University, Ithaca, NY, [2]Biotracking LLC, Moscow, GA.*

Our objective was to characterize ovarian dynamics in lactating dairy cows undergoing embryonic mortality. Cows ($n = 62$) received timed AI at 60 to 79 DIM after Presynch-Ovsynch. At AI, cows were blocked by parity (primiparous vs. multiparous) and randomly assigned to AI with regular semen ($n = 52$) or extender only ($n = 10$; Cycling; CY). Blood was collected every 48 h from 14 to 42 d after AI to determine concentrations of progesterone (P4) and pregnancy specific protein B (PSPB). Transrectal ultrasound was performed daily to assess ovarian dynamics. Cows were considered: 1) pregnant (PG; $n = 18$) if a viable embryo with a heartbeat was observed, 2) embryonic mortality (EM; $n = 6$) when a viable embryo or its heartbeat was no longer observed, and/or PSPB concentrations were initially above and then below 0.8 ng/mL, and 3) Non-pregnant (NP; $n = 28$) when no viable embryo was observed and PSPB concentrations remained below 0.8 ng/mL. Pregnant and EM cows had greater ($P < 0.01$) PSPB concentrations than NP and CY cows beginning 24 d after AI. Percentage of cows with complete luteal regression (CLR) was affected ($P = 0.02$) by group (CY and NP = 100 vs. 66.7% for EM) and occurred later ($P < 0.01$) in EM (39.5 ± 2.1) than in CY and NP cows (20.2 ± 1.3 and 22.9 ± 0.8). At 18 d after AI, NP cows had greater ($P < 0.05$) P4 than CY cows, whereas EM and PG cows had greater ($P < 0.05$) P4 concentrations than CY and NP cows. Among cows with CLR, the percentage ovulating was similar ($P = 0.21$) for CY, NP, and EM (90.0, 85.7, and 50.0%) cows. The interovulatory interval (IOI) was affected by group ($P < 0.01$). Cycling cows had the fewest days to ovulation (22.9 ± 0.96) followed by NP cows (25.8 ± 0.6) whereas EM cows had the longest interval to ovulation (40.0 ± 2.0 d). Days from CLR to ovulation was similar ($P = 0.52$) for CY (5.0 ± 0.9), NP (6.0 ± 0.6), and EM (7.0 ± 1.9) cows. Ovulatory follicle growth rate for the 5 d preceding ovulation was similar ($P = 0.28$) for all groups (CY = 1.6 ± 0.2, NP = 1.5 ± 0.1 and EM = 0.8 ± 0.5 mm/day). Likewise, diameter at ovulation was similar ($P = 0.77$) for all groups (CY = 22.7 ± 1.1, NP = 23.9 ± 1.8 and EM = 24.8 ± 3.8 mm). Thus, cows with EM were less likely to undergo complete luteal regression, and had extended IOI. The observed differences in IOI were due to delayed luteal regression rather than alterations in follicular wave dynamics. The longer IOI for NP than CY cows may have been caused by undetected EM. *Supported by Hatch project NYC127813.*

Key Words: ovarian dynamics, embryonic mortality, dairy cow

PHYSIOLOGY AND ENDOCRINOLOGY III

1429 (W189) Estimated energy balance of periparturient ewes grazing in rangelands. E. González-García[*1], D. Tagliatella[2], M. Jouven[3], and F. Bocquier[3], *[1]INRA UMR868 Systèmes d'Elevage Méditerranées et Tropicaux (SELMET), Montpellier, France, [2]Universidade Estadual de Londrina (UEL), Rodovia Celso Garcia Cid, Campus Universitário, Londrina, Brazil, [3]Montpellier Supagro, Sciences Animales, UMR868 Systèmes d'Elevage Méditerranées et Tropicaux (SELMET), Montpellier, France.*

In a previous work we demonstrated that efficiency in body reserves (BR) mobilization/accretion was affected by parity [multiparous (MULT) ewes being more flexible than primiparous], litter size and physiological stage (peaks of BR mobilization attained around lambing and 1 mo after mating). The objective of this study was to estimate the dynamic individual energy balance of periparturient MULT Romane grazing ewes, from 15 d before until 15 d after lambing. A group of MULT ewes (n = 20), allocated according to litter size (lambing and suckling singletons, SING-n = 10-, or twins, TWIN-n = 10) was used. Details on management and feeding were reported by González-García et al. (2014). At late pregnancy, ewes were in rotational grazing of native rangeland and supplemented with 0.7, 2.0 and 0.8 kg/d of hay (*Dactylus glomerata* and alfalfa), silage (*Lolium perenne* and alfalfa) and barley, respectively. After lambing, ewes were fed on fertilized paddocks without supplementation. Individual progression of BW, BCS, plasma NEFA as well as ADG of lambs was considered for energy balance interpretation. Some estimation is established based on NRC (2007) recommendations. Data were analyzed using the PROC MIXED of SAS (2007) with repeated measures. During the last 4 wk of gestation, one 50 kg ewe from this flock is estimated to display a daily consumption of around 1.6 kg of DM (3.2% BW) to support around 180 g of BW gain, requiring 3.4 mcal of ME. During the first 6–8 wk lactation, feed intake is affected by litter size (NRC, 2007; 2.1 or 2.4 kg of DM/d for ewes suckling SING or TWIN; 4.2 or 4.8% BW, respectively) with an increase in energy requirement of 4.9 or 5.6 mcal of ME for SING or TWIN, respectively. At late pregnancy, a positive energy balance of > 1.1 mcal/d was observed (4.7 mcal of ME vs. 3.6 of ME requirements) due to the advantageous supplementation regime established in the farm. Paradoxically, at this stage (late pregnancy) NEFA values showed a peak in BR mobilization. After lambing, ewes suckling SING and TWIN were both required to mobilize their BR to meet energy requirement despite the high quality of the fertilized paddocks and the BW increase. More precise and targeted studies are required to better address the combined anabolic and catabolic phases experimented under the conditions of this experiment in periparturient ewes. Reference: González-García E. et al. (2014). Domestic Animal Endocrinology 46:37–48.

Key Words: periparturient ewes, rangelands, energy balance, body reserves

1430 (W190) Effects of adsorbent on milk aflatoxin M1 and lactation performance of dairy cows exposed to long-term challenge of aflatoxin B1. J. L. Xiong[1], Y. M. Wang[*2], W. M. Huang[1], Y. Zhang[1], H. M. Guo[1], and J. X. Liu[3], *[1]Institute of Dairy Science, Zhejiang University, Hangzhou, China, [2]Novus International Trading Co., Ltd, Shanghai, China, [3]Zhejiang University, Hangzhou, China.*

The objective of the study was to evaluate the effects of adsorbent on milk aflatoxin (AF) M1 and lactation performance of dairy cows exposed to long-term challenge of AFB1. Forty dairy cows were blocked based on days in milk (33 ± 7; mean ± SD) and milk production (33.9 ± 3.1 kg; mean ± SD), and were randomly assigned to one of four treatments in a 2 × 2 factorial arrangements with AFB1 (0 or 20 μg/kgDM) and Solis Mos (Novus International Inc., 0 or 0.25% of DM). The experiment lasted 9 wk, with the first week for adaptation. Milk yield and milk composition were recorded weekly, and serum concentrations of biochemical and antioxidant variables were analyzed in the first and the last week of the experiment. Milk AFM1 was analyzed by HPLC-MS/MS. Variables of data were analyzed using the PROC MIXED of SAS. Dry matter intake, milk yield, contents of milk protein and milk fat, and linear somatic cell count averaged 23.9 kg/d, 35.5 kg/d, 2.9%, 3.6%, and 5.1, respectively and were not affected (P > 0.05) by either AFB1 or Solis Mos supplement. Addition of Solis Mos in AFB1-contaminated diet significantly reduced (P < 0.01) milk AFM1 concentration (0.19 vs. 0.13 μg/kg) and transfer rates (1.38 vs. 0.89%). Dairy cows fed AFB1-contaminated diet had lower level of superoxide dismutase activity, total antioxidant capacity, glutathione peroxidase, IgG and IgA (P < 0.05), and higher level of malondialdehyde in plasma (P < 0.05). Inclusion of Solis Mos into diets increased the plasma superoxide dismutase activity, total antioxidant capacity, and IgG, while deceased malondialdehyde (P < 0.05). Neither AFB1 nor Solis Mos affected (P > 0.05) the plasma levels of alanine transaminase, aspartate aminotransferase, and alkaline phosphatase and IgM. It is concluded that inclusion of Solis Mos did not affect lactation performance, but reduced milk AFM1 concentration and transfer rate, and increased antioxidant capacity and immunity in early-lactating dairy cows exposed to long-term challenge of AFB1.

Key Words: adsorbent, aflatoxin, transfer

1431 (W191) Effects of excessive energy intake and supplementation with chromium propionate on insulin resistance parameters in lactating dairy cows: II. Glucose tolerance tests and follicular flushing. T. Leiva[1], R. F. Cooke[2], F. N. Correa[1], A. C. Aboin[1], A. P. Brandao[1], H. F. Soares[1], M. B. Piccolo[1], and J. L. M. Vasconcelos[*1], *[1]UNESP-FMVZ, Botucatu, Brazil, [2]Oregon State University-EOARC Burns, Burns.*

The objective of this experiment was to compare insulin resistance parameters and reproductive outcomes in lactating dairy cows with adequate or excessive energy intake, as well as in lactating dairy cows with excessive energy intake receiving Cr-propionate supplementation. Seventeen primiparous and multiparous, lactating Holstein cows were ranked by parity, BW, and BCS, and assigned to 1 of 3 dietary treatments on d 0: 1) diet to meet their NE_l requirements without Cr supplementation (MAN; $n = 5$), 2) diet to exceed their NE_l requirements without Cr supplementation (HIGH; $n = 6$), and 3) HIGH with 2.5 g/d of Cr-propionate (HIGHCR; $n = 8$, with 10 mg of Cr/cow daily). Cows were maintained in a single group and offered corn silage for ad libitum consumption, but received a corn-based concentrate twice daily via individual self-locking head gates from d 0 to 210. Concentrate intake was formulated to provide 100% of daily NE_l requirements of MAN and 160% of daily NE_l requirements of HIGH and HIGHCR cows. Glucose tolerance tests (GTT) were performed on d 40, 82, 124, 166, and 208 by infusing cows with 0.5 g of glucose/kg of BW, whereas blood samples were collected at -15, 0, 10, 20, 30, 45, 60, 90, and 120 min relative to infusion for determination of serum insulin and glucose. Follicle aspiration for in vitro embryo production was performed 2 d after each GTT. No treatment effects were detected ($P = 0.53$) for serum glucose concentrations. Treatment x min interactions ($P < 0.01$) were detected for serum insulin and insulin:glucose ratio, given that these parameters were greater ($P \leq 0.05$) for HIGH compared with HIGHCR and MAN from 10 to 60 min relative to glucose infusion, but always similar between HIGHCR and MAN ($P \geq 0.25$). A treatment x parity interaction was detected for oocyte collection ($P = 0.05$). Within multiparous cows, HIGHCR had greater ($P \leq 0.03$) number of viable oocytes collected compared with HIGH and MAN, whereas the same outcome was not detected ($P \geq 0.36$) within primiparous cows. No treatment effects were detected ($P \geq 0.33$) for number of embryos produced, or oocyte collected:embryo produced ratio. In conclusion, Cr-propionate supplementation prevented the increase in insulin resistance caused by excessive energy intake in lactating dairy cows during a GTT, and increased the number of viable oocytes collected during follicle aspiration for in vitro embryo production.

Key Words: chromium, dairy cows, energy, insulin resistance

1432 (W192) Deuterium enrichment in plasma, rumen fluid and urine of growing sheep dosed with D_2O intravenously and intraruminally does not differ. C. C. Metges[*1], S. Görs[1], H. M. Hammon[1], U. Agarwal[2], and B. J. Bequette[2], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]Dep. of Animal and Avian Sciences, University of Maryland, College Park.*

The D_2O method has been used in humans to measure fractional gluconeogenesis. The advantage of this method is that all contributions of gluconeogenic substrates are considered. In ruminants, we aimed to determine whether the route of D_2O administration affects equilibration of deuterium with protons from water in various body water pools. Four sheep (23.5 ± 1 kg BW), equipped with a rumen fistula and a jugular vein catheter, were fed a pelleted ration (35 g/kg BW and d; 9 MJ ME/d) at 2-h intervals. Water was offered ad lib. To label body water, sheep were given two boli of 7 g D_2O/kg BW (99.2 atom% D) at 800 and 1200 h either into the rumen (IR) or into the jugular vein (IV) in a balanced crossover design. Two weeks separated each site of administration. Plasma was sampled before and hourly for 11 h following the first bolus whereas rumen fluid and urine were collected before and at 3, 6, 9, and 11 h. Samples were diluted and D_2O enrichments were measured by isotope ratio mass spectrometry. Paired *t* test was used to evaluate route effect. D_2O enrichments did not differ with route of tracer administration. A quasi-plateau in D2O enrichment was reached 2 h after the first bolus (IR: 0.76; IV: 0.78 atom% excess (APE)) with a further increase to a second plateau 2 h after the second bolus (IR: 1.48; IV: 1.47 APE; $P > 0.1$). Urine D_2O enrichment 3 h after the initial IR dose tended ($P = 0.09$) to be lower than with the IV route (IR: 0.47; IV: 0.78 APE), however, both routes of dosing lead to a similar maximum enrichment 9 to 11 h after the initial bolus (IR: 1.51; IV: 1.52 APE; $P > 0.1$). Rumen fluid D_2O enrichment attained a plateau 6 h after the initial bolus (IR: 1.51; IV: 1.43 APE; $P > 0.1$). This study verified that for measurement of fractional gluconeogenesis using the D_2O method, the kinetics of D_2O labelling are similar with the IR and IV routes of administration, and that either approach can be employed in ruminants.

Key Words: gluconeogenesis, deuterium oxide, rumen

1433 (W193) Manipulated plasma insulin, glucose, and BHBA affect immune factors in somatic cells in milk with and without intramammary LPS challenge in dairy cows. M. Zarrin[*1,2,3], R. M. Bruckmaier[1], and O. Wellnitz[1], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Switzerland, [2]Dep. of Animal Science, Yasouj University, Iran, [3]Graduate School for Cellular and Biomedical Sciences, University of Bern, Switzerland.*

Changes of plasma hormones and metabolites affect mammary immunity during onset of lactation. Somatic cells are important for the initial udder defense and they are additionally recruited into milk during the immune response. This study aimed to investigate effects of long term (56 h) elevated insulin at simultaneous hypoglycemia or euglycemia, and elevated β-hydroxybutyrate (BHBA) concentrations, and additional intramammary LPS challenge on mRNA abundance of immune factors in somatic cells in milk. Animals were subjected to four intravenous treatment groups: an insulin infusion (HypoG, $n = 5$) to decrease plasma glucose concentration to 2.5 ± 0.1 mmol/L, a hyperinsulinemic euglycemic clamp to maintain plasma glucose concentration at pre-infusion level (EuG, $n = 6$), a BHBA infusion (HyperB, $n = 5$), and a 0.9% NaCl infusion (Control, $n = 8$). Two udder quarters were challenged with 200 µg *E.coli* LPS at 48 h of infusions. Cells were extracted from milk of control and treated quarters obtained before, after 48 h, and at the end of infusion with a quarter milking device. The mRNA abundances of immune factors were measured by RT-qPCR. Changes of mRNA abundance between before and after 48 h of infusions, and before and after LPS challenge were evaluated by analysis of variance with treatments as fixed effect. In HypoG mRNA abundance of interleukin (IL)-1β and RANTES (regulated on activation, normal T cell expressed and secreted) decreased ($P < 0.05$) during 48 h. In HyperB the mRNA abundance of IL-1β, IL-8, and RANTES tended to increase ($P < 0.1$) during 48 h. Intramammary LPS challenge up-regulated mRNA abundance of IL-1b, IL-8, and nuclear factor kappa-light-chain-enhancer of activated B cells after 8 h in all treatment groups ($P < 0.05$), and tumor necrosis factor-α in HypoG ($P < 0.05$). The mRNA abundance of IL-1β and IL-8 was up-regulated in HypoG ($P < 0.05$), and IL-1β, IL-8, and RANTES was downregulated in control quarters of HyperB ($P < 0.05$) 8 h after LPS challenge. Results demonstrate that intravenous insulin infusion downregulates the expression of immune factors in somatic cells in milk during hypoglycemia, whereas induced hyperketonemia seems to up-regulate some of these factors during 48 h. It can be speculated that the downregulation of immune factors in HypoG is related to a lack of energy (glucose) for the immune system, while BHBA is an alternative energy source for the immune system during immune response. Up-regulation of immune factors after LPS challenge was predictable, whereas mechanisms of downregulation in control quarters after LPS challenge are unclear.

Key Words: immunity, metabolite, LPS

1434 (W194) Effects of road transportation on metabolic and immunological responses in dairy heifers. M. Baik[*1], H. J. Kang[1], I. K. Lee[1], M. Y. Piao[1], C. W. Kwak[1], M. J. Gu[1], C. H. Yun[1], H. J. Kim[1], G. H. Kim[2], S. K. Kim[2], and J. K. Ha[1], *[1]Dep. of Agricultural Biotechnology, College of Agriculture and Life Sciences, Seoul National University, Seoul, South Korea, [2]Dep. of Animal Science and Technology, Konkuk University, Seoul, South Korea.*

This study was performed to determine the effects of road transportation on metabolic responses in dairy heifers. Twenty-two Holstein heifers (average 17.6 mo of age, 440 kg of average body weight) were divided into non-transported (NT; $n = 8$) and transported (T; $n = 14$) groups. Feed and water in the NT heifers were restricted the same amount as the T heifers. The heifers were acclimated in stanchion barn. All heifers were restrained with a halter in a stanchion, and blood was collected using vaccutainer by jugular venipuncture. The NT heifers In the T group, blood was collected before transportation (BT), after 100 km (T1) and 200 km transportation (T2), and at 24 h after transportation (AT). In the NT group, blood was collected at same time as the T group. The T heifers showed higher ($P < 0.001$) blood cortisol concentrations after T1 and T2 than the NT heifers. The T heifers showed higher ($P < 0.01$) serum non-esterified fatty acid (NEFA) concentrations after T1 and T2 than the NT heifers. In contrast, the T heifers showed lower serum triglyceride (TG) concentrations after T1 ($P = 0.01$) and T2 ($P < 0.001$) than the NT heifers. Serum concentrations of cortisol, NEFA, and TG at 24 h AT were returned ($P > 0.05$) to those of the BT in the T heifers. Other serum lipid concentrations, including phospholipid ($P = 0.02$), high density lipoprotein ($P = 0.03$), low density lipoprotein ($P = 0.01$), and cholesterol ($P = 0.04$) were lower in the T heifers after T2 than the NT heifers. Serum glucose concentrations were not changed by T1 and T2. The ratio of granulocytes to lymphocytes ($P < 0.001$) and the percentage of monocytes ($P < 0.05$) were shown higher after T2 in the T heifers when compared to those of the NT heifers, suggesting increased number of innate immune cells on transportation stress. In conclusion, short transportation increases cortisol secretion, which was coincident with induction of metabolic responses and up-regulation of peripheral innate immune cells in dairy heifers.

Key Words: transportation, stress, metabolic responses, dairy heifers

1435 (W195) Differences in mitochondrial DNA copy numbers in various subcutaneous and visceral fat depots of overconditioned cows. L. Laubenthal[*1], L. Locher[2], J. Winkler[3], U. Meyer[3], J. Rehage[2], S. Dänicke[3], H. Sauerwein[1] and S. Häussler[1], *[1]University of Bonn, Institute of Animal Science, Germany, [2]University for Veterinary Medicine Foundation, Hannover, Germany, [3]Institute of Animal Nutrition, Friedrich Loeffler Institute (FLI), Braunschweig, Germany.*

In dairy cows, adipose tissue (AT) is mobilized during early lactation to meet the increased energy demands through lactation. Overconditioned cows are more prone to metabolic disorders during this period than lean cows. Just like in other tissues, mitochondria are the main site of energy production within AT. Different energy demands may lead to changes of mitochondrial DNA (mtDNA), which reflects the abundance of mitochondria in a cell. Different bovine AT depots differentiated into visceral (vc) and subcutaneous (sc) regions, might present different mtDNA contents, due to diverse metabolic functions. Therefore, we aimed to compare the number of mtDNA copies per cell between various sc and vcAT depots from overconditioned cows. Eight non-lactating, non-pregnant German Holstein cows (age 4 to 6 yr) received diets with increasing proportions of concentrate feed during the first 6 wk of the trial until 60% were reached. This diet was maintained for 10 wk and cows had an average body weight (BW) gain of 243 ± 33.3 kg within this period. Animals were slaughtered at the end of the experiment and tissue samples from sc (sternum, withers and tailhead) and vc (mesenterial, omental and retroperitoneal) AT were collected and snap frozen for genomic DNA isolation. The number of mtDNA copies/cell was quantified by multiplex quantitative PCR using β-globin as reference gene. Data (mean ± SEM) were analyzed using Mann–Whitney-U-test and the Spearman (r) correlation coefficient (SPSS). The number of mtDNA copies/cell was 2.6-fold higher in all vc compared to all sc ($P < 0.001$) AT. Retroperitoneal AT exhibits greatest mtDNA copies/cell (3488 ± 190) compared to all other AT depots. The mtDNA copy number/cell in mesenterial and omental AT were 3058 ± 405 and 2921 ± 235, respectively. In tailhead and sternum AT mtDNA copy number/cell was three-fold and in withers AT two-fold lower compared to retroperitoneal. Different amounts of mtDNA copies/cell might reflect individual energy demands and metabolic functions in different sc and vcAT depots. In this study, mtDNA was isolated from whole AT including both adipocytes and the cells belonging to the stromal vascular cell fraction (SVF). Therefore, lower values of mtDNA copies in scAT might be due to an increased SVF, which contains significantly less mtDNA copy numbers. Higher amounts of mtDNA copies per cell in vcAT compared to scAT are in accordance to the higher metabolic activity of vcAT, particularly the retroperitoneal AT depot.

Key Words: adipose tissue, mtDNA copy number, cows

1436 (W196) In vitro insulin sensitivity of subcutaneous and omental adipocytes of precalving dairy cows across a range of BCS. J. De Koster[*1], L. Hulpio[1], V. Fievez[2], W. Van den Broeck[3], and G. Opsomer[1], *[1]Dep. of Reproduction, Obstetrics and Herd Health, Faculty of Veterinary Medicine, Ghent University, Belgium, [2]Dep. of Animal Production, Faculty of Bioscience Engineering, Ghent University, Belgium, [3]Dep. of Morphology, Faculty of Veterinary Medicine, Ghent University, Belgium.*

The adipose tissue of dairy cows plays an important role during the transition period. Recent research indicates a selective mobilization of adipose depots during negative energy balance. In the present study, we investigated the effect of the size of the adipocytes and type of adipose depot (omental versus subcutaneous) on insulin sensitivity of the lipolytic activity of adipocytes from precalving dairy cows. Ten pregnant dairy cows (BCS 2.75–5) were euthanized and samples of subcutaneous (at the tail base) and omental adipose tissue were transferred to sterile falcon tubes containing medium (Krebs ringer bicarbonate hepes + 3% BSA). Adipose tissue fragments were minced and approximately 100 mg adipose tissue explants were incubated in 3 mL medium at 38°C on a shaker. Five different culture conditions were tested in duplicate: lipolytic activity in all the plates was stimulated with 10^{-6} mol/l isoproterenol and five different insulin concentrations (0; 1; 10; 200; 1000 μU/ml) were added. After 3 h of incubation, media were sampled for glycerol analysis. Results are expressed as nmol glycerol release per 3 h per million adipocytes. The number and volume of adipocytes were determined as described by DiGirolamo et al. (1971). Insulin decreased glycerol release and insulin sensitivity was expressed as percentage decrease of the maximal glycerol release (10^{-6} mol/l isoproterenol; 0 μU/ml insulin). Dose response curves were created using PROC NLIN in SAS to determine maximal effect and insulin dose needed to elicit halfmaximal effect (logED50). Effects on both parameters were analyzed using PROC MIXED in SAS with cow as random factor, adipose depot and volume of adipocytes as fixed factors. One cow was excluded because insulin failed to inhibit lipolytic activity. The maximal effect and logED50 for the insulin sensitivity were 0.32 ± 0.1279% and -0.22 ± 0.415 μU/ml, respectively in subcutaneous adipocytes and 0.23 ± 0.148% and 0.15 ± 0.849 μU/ml in omental adipocytes (mean ± stdev), respectively. Statistical analysis revealed negative effects of volume of the adipocytes (β = -0.2569; $P < 0.05$) and adipose depot (β = -0.2145; $0.1 < P < 0.05$, subcutaneous depot as reference) on the maximal effect while no significant effects were found on the logED50. Insulin sensitivity of the lipolytic activity of adipocytes in precalving dairy cows is influenced by the size of the adipocytes and the adipose depot with a lower maxi-

mal effect in omental adipocytes and lower maximal effect in larger adipocytes. The dose to elicit halfmaximal effect is not influenced by adipocyte size or adipose depot.

Key Words: in vitro insulin sensitivity, adipose depot, dairy cow

1437 (W197) Dietary melatonin supplementation during late gestation alters concentrations of progesterone and milk yield in Holstein heifers. C. O. Lemley*, K. E. Brockus, C. G. Hart, and S. H. Ward*, Mississippi State University, Starkville.*

The objective was to examine the effects of supplementing dietary melatonin during late gestation Holstein heifers on maternal concentrations of progesterone and estradiol-17β as well as subsequent milk yield during the first 30 d of lactation. On d 190 of gestation, heifers (n = 20) were blocked by body weight and then randomly assigned to one of two dietary treatments: 1) 20 mg of dietary melatonin per day (MEL) or 2) no melatonin supplementation (CON). At 0800 h, MEL heifers received 0.7 kg of grain top dressed with 2 mL of 10 mg/mL melatonin in ethanol while CON heifers received 0.7 kg of grain top dressed with 2 mL of ethanol alone. A TMR was provided after grain consumption. Supplementation ceased on d 262 of gestation for both treatment groups. Blood samples were collected on d 180 (baseline), 210, 240, and 262 of gestation. Serum concentrations of progesterone and estradiol-17β were determined via radioimmunoassay. Milk yield was recorded for the first 30 d of lactation. Dependent variables were analyzed using repeated-measures ANOVA of the PROC MIXED of SAS with the model statement containing dietary treatment, day, and their respective interaction. Main effects of dietary treatment or day are discussed in the absence of significant ($P < 0.05$) treatment by day interactions. Serum progesterone was decreased ($P < 0.05$) by 12% in MEL vs. CON heifers. Moreover, concentrations of progesterone were decreased ($P < 0.0001$) on d 262 of gestation vs. d 180, 210, and 240. Serum estradiol-17β tended to be decreased ($P = 0.06$) by 19% in MEL vs. CON heifers. Concentrations of estradiol-17β increased ($P < 0.0001$) as gestation proceeded. Gestation length was not different ($P > 0.50$) between treatments and averaged 275 ± 2 d. Daily milk yield showed a treatment by day interaction ($P < 0.01$), whereby milk yield was increased by 41% and 33% on d 2 and 3 of lactation in MEL vs. CON heifers, respectively. Dietary melatonin supplementation during late pregnancy altered steroid synthesis and/or clearance. In addition, the decreased concentrations of steroids during late gestation in MEL heifers had no adverse effects on subsequent milk yield during early lactation.

Key Words: melatonin, pregnancy, progesterone

1438 (W198) Dry-matter intake level and its effects on follicle growth and circulating progesterone in Nellore (*Bos indicus*) and Holstein (*Bos taurus*) heifers. E. O. S. Batista*[1], R. V. Sala[1], M. D. D. V. Ortolan[1], E. F. Jesus[2], T. A. D. Vale[3], G. G. Macedo[1], F. P. Rennó[3], A. H. Souza[4], and P. S. Baruselli[5], *[1]USP, São Paulo, Brazil, [2]School of Agricultural and Veterinary Sciences of UNESP, Jaboticabal, Brazil, [3]USP, Pirassununga, Brazil, [4]University of California–Davis, Davis, [5]University of Sao Paulo-VRA, Brazil.*

The aim of this study was to evaluate circulating progesterone concentration (P4) and ovarian follicular dynamics in *Bos indicus* and *Bos taurus* heifers under high (HDM; weight gain of 900 g per d) and low (LDM; maintenance, NRC 2001) consumption of dry matter. Cycling Holstein (n = 16) and Nellore (n = 16) heifers were used in a 2 × 2 factorial arrangement (crossover). The experimental diet was given during 32 d (15 d before and 17 d during the hormonal protocol). The animals were pre-synchronized with two applications of cloprostenol (0.53mg, i.m. $PGF_{2\alpha}$, Sincrocio, Ourofino Agronegócio) 12 d apart and 18 and 12 h before device insertion. At onset of synchronization protocol (d 0), heifers received a new intravaginal P4 device (CIDR, Zoetis Brasil), 2 mg of estradiol benzoate i.m. (BE, Sincrodiol, Ourofino Agronegócio) and a dose of $PGF_{2\alpha}$. After 8 d, the P4 device was removed and 1 mg of BE was administered 24 h later. Ultrasonographic exams were performed every 24 h during P4 device treatment (d 0 to 8), and at every 12 h from P4 device removal to ovulation. Blood samples were collected daily from d 0 to 10. The results were analyzed using PROC MIXED of SAS 9.2 and presented as mean ± standard error. An interaction (genetic group*d, $P < 0.0001$; diet*d, $P = 0.03$) was observed between genetic group, diet and d of the hormonal protocol on the diameter of the dominant follicle (DDF). The effect of diet on the DDF during hormonal protocol was observed as soon as two d after follicular wave emergence (d 5 to 10 of the hormonal protocol, $P < 0.05$). However, the effect of genetic group was observed only towards the end of the protocol (d 8 to 10, $P < 0.05$). Regardless of the diet, the DDF on d 8 ($P = 0.04$) and d 10 ($P = 0.01$) of the hormonal protocol were larger in Holstein (11.6 ± 0.4 and 14.4 ± 0.4) than Nellore (10.3 ± 0.4 and 12.2 ± 0.4) heifers. Independently from genetic group, the DDF on d 8 ($P < 0.0001$) and d 10 ($P = 0.01$) of the hormonal protocol was larger in heifers receiving to HDM (12.2 ± 0.4 and 14.3 ± 0.4) than LDM (9.6 ± 0.4 and 12.2 ± 0.4). Curiously, lowering DM intake caused a greater increase in circulating P4 in Nellore than in Holsteins (genetic group*diet*d, $P = 0.05$). In conclusion, heifer breed had a market effect in hormonal profile and follicle growth during synchronization programs, but increasing DM intake greatly influenced ovarian dynamics and circulating P4. *Acknowledgements: FAPESP, CNPq.*

Key Words: *Bos indicus, Bos taurus*, progesterone

1439 (W199) Association between insulin signaling and oxidative stress in serum and subcutaneous adipose tissue of overconditioned cows. S. Häussler[*1], L. Locher[2], L. Laubenthal[1], S. P. Singh[1], U. Meyer[3], J. Rehage[2], S. Dänicke[3], and H. Sauerwein[1], *[1]University of Bonn, Institute of Animal Science, Germany, [2]University for Veterinary Medicine Foundation, Hannover, Germany, [3]Institute of Animal Nutrition, Friedrich Loeffler Institute, Braunschweig, Germany.*

Cows with higher BCS or greater BCS loss in early lactation have more problems to adapt to the needs of lactation and are more sensitive to oxidative stress. Mitochondrial (mt)DNA copy numbers, reflecting the abundance of mitochondria in a cell, can increase to compensate mtDNA damage. Moreover, reactive oxygen species produced through lipid-induced mitochondrial dysfunction impair insulin signaling. We hypothesized that decreasing insulin sensitivity in overconditioned cows will be associated with oxidative stress concomitant with increased numbers of mitochondria. Therefore, we aimed to investigate the association between oxidative stress (assessed by quantifying derivates of reactive oxygen species (dROM)) and mtDNA copies/cell in subcutaneous (sc) adipose tissue (AT) with variables describing insulin sensitivity (IS) in overconditioned cows independently from homeorhetic processes. Non-pregnant, non-lactating German Holstein cows (n = 8) were gradually adapted to a high-energy ration (corn-grass-silage with increasing portion of corn-silage and increasing concentrate feed from 0% up to 60% of total dry matter intake). Over a period of 15 wk, the average weight gain of the animals was 243 ± 33.3 kg. Blood samples were collected once per month and were analyzed for insulin, glucose and NEFA to calculate a surrogate marker for IS (RQUICKI). Adiponectin was measured in serum using an in-house developed ELISA. Derivates of reactive oxygen metabolites (dROM) were indirectly measured in serum using a photometric method with N,N,diethyl-1,4-phenylendiamine as chromogen. Every 8 wk, scAT from tailhead was biopsied and snap frozen for genomic DNA isolation. The number of mtDNA copies/cell was measured by multiplex qPCR. Data (mean ± SEM) were analyzed using repeated measures ANOVA and Spearman correlations (SPSS). Decreasing insulin sensitivity throughout the experiment, indicated by decreasing RQUICKI values (P = 0.001), were negatively correlated with dROM (r = -0.543, P = 0.007) and mtDNA copies (r = -0.568, P = 0.005). Moreover, adiponectin concentrations were decreased throughout the experiment (P < 0.05) and tended to be negatively correlated (r = -0.381, P = 0.067) with mtDNA copies. Increased oxidative stress seems to enhance insulin resistance. However, dROM was not associated with serum adiponectin which is known for its insulin sensitizing and lipolysis inhibiting effects. In contrast to reports about insulin resistance being related to reduced mitochondrial content in humans, increasing mtDNA copies in the present study seem to compensate mitochondrial damage caused by enhanced dROM.

Key Words: insulin resistance, oxidative stress, mtDNA

1440 (W200) Serum apelin concentrations in dairy cows receiving different amounts of concentrate and a nicotinic acid supplement. M. Weber[1], L. Locher[2], K. Huber[3], J. Rehage[2], R. Tienken[4], U. Meyer[4], S. Dänicke[4], U. Müller[5], H. Sauerwein[*5], and M. Mielenz[6], *[1]Institute of Animal Science, Physiology and Hygiene Unit, University of Bonn, Germany, [2]University for Veterinary Medicine Foundation, Hannover, Germany, [3]University of Hannover, Germany, [4]Institute of Animal Nutrition, Friedrich Loeffler Institute, Braunschweig, Germany, [5]University of Bonn, Institute of Animal Science, Germany, [6]Leibniz Institute for Farm Animal Biology, Institute of Nutritional Physiology, Dummerstorf, Germany.*

Apelin, a 77 amino acid preproprotein, which is also known as an adipokine, is suggested to play a physiological role in glucose metabolism. It stimulates glucose uptake by adipose tissue in humans and mice, whereas lipolysis in humans is not affected. This might lead to a decreasing lipolysis during the transition period in cattle and may prevent lipid-related disorders. Nicotinic acid (NA), a known antilipolytic agent, might decrease plasma NEFA concentrations and enhances the response to insulin. As plasma apelin concentrations are decreased by a hypochaloric diet, we hypothesized, that different levels of concentrate in the diet combined with NA supplementation would affect the serum apelin concentrations in dairy cows. Thus the objectives of the present study were to quantify apelin in bovine serum samples and to examine the impact of different levels of concentrate in combination with a NA supplementation on apelin serum concentrations. Serum samples were obtained from 20 pluriparous Holstein-Friesian cows at d −42, −14, 1, 7, 14, 21, 42 and d 100 relative to calving. Until d −42 all cows were fed the same silage-based diet. Between d −42 and d −1 10 animals each were assigned to either a high-concentrate (HC, 60:40 concentrate:roughage) or a low concentrate group (LC, 30:70 concentrate:roughage). Both groups were further subdivided into a control and a niacin group (n = 5), the latter receiving 24 g/d NA (Lonza, Basel, Switzerland) until d 24. Serum apelin concentrations were measured using a commercially available ELISA kit (*P*hoenix Pharmaceuticals, Burlingame, CA) validated for bovine samples. Statistical analysis was done using Mixed-Model procedure followed by Bonferroni correction (SPSS 22); d −42 values were considered as covariate. The serum apelin concentrations were not affected by treatment and time (P > 0.05) and remained on a constant concentration (mean 1.21 ± 0.08 ng/ml). The results of this study indicate that serum apelin concentrations are independent of the prepartum feeding regimen as well as of the stage of lactation.

Key Words: apelin, nicotinic acid, dairy cow

1441 (W201) Nuclear related factor-E2 is downregulated by hyperinsulinemic euglycemia in dairy cows.

M. Zarrin[*1,2,3], O. Wellnitz[1], and R. M. Bruckmaier[1], *[1]Veterinary Physiology, Vetsuisse Faculty, University of Bern, Switzerland, [2]Dep. of Animal Science, Yasouj University, Iran, [3]Graduate School for Cellular and Biomedical Sciences, University of Bern, Switzerland*.

At the onset of lactation the liver undergoes a high load to provide metabolites for milk synthesis in dairy cows. The endocrine and metabolic changes induce inflammation that impairs liver function. The liver is protected by nuclear factor E2-related factor 2 (Nrf2), which is activated by inflammatory signals such as reactive oxygen species (ROS), and has anti-oxidative effects, diminishes inflammatory damage, neutralizes ROS, and suppresses pro-inflammatory signaling. We have studied hepatic mRNA abundance of Nrf2 as a response to long-term (48 h) insulin and β-hydroxybutyrate (BHBA) infusion in mid-lactation dairy cows. Twenty four Holstein dairy cows were randomly assigned to four intravenous treatment groups including an hyperinsulinemic clamp infusion to decrease plasma glucose concentration to 2.5 ± 0.1 mmol/L (HypoG, n = 5), a hyperinsulinemic euglycemic clamp to maintain plasma glucose concentration at pre-infusion level (EUG, n = 6), a BHBA infusion (HyperB, n = 5), and a 0.9% NaCl infusion (Control, n = 8). Liver tissue samples were taken 1 wk before and 48 h after the start of infusion. Changes of hepatic mRNA abundance (RT-qPCR) of several acute-phase proteins and of Nrf2 between before and after 48 h infusions were evaluated by analysis of variance with treatment as fixed effect. SAA and Hp mRNA was up-regulated in all treatment groups ($P < 0.05$) during 48 h infusions. The mRNA of glutathione peroxidase 3 (GPX3), metallothionein (MT) 1A, MT1E, and MT2A was up-regulated after 48 h of infusions in Control ($P < 0.05$). Insulin infusion downregulated mRNA abundance of microsomal glutathione S-transferase 3 (MGST3), MT1E, MT2A, NAD (P) H dehydrogenase, quinone 1 (NQO1), and superoxide dismutase 1 (SOD1) ($P < 0.05$). Changes of GPX3, MGST3, MT1A, MT1E, MT2A, and SOD1 mRNA abundance during 48 h of infusion differed significantly between EUG and Control ($P < 0.05$). Change of mRNA abundance of NQO1 after 48 h of infusions differed significantly between EUG and HyperB ($P < 0.05$). Results show that infusions and experimental condition up-regulated mRNA abundance of APP in all treatments, and up-regulated some of Nrf2 in control, whereas induced hyperinsulinemic euglycemic clamp downregulated most of Nrf2 factors in EUG. It seems that the up-regulation of these factors in Control occurs despite unchanged metabolites during the infusion. Although insulin has an anti-inflammatory role different results observed in both HypoG and EUG. It can be assumed that downregulation of Nrf2 mRNA factors in EUG is related to a decrease of hepatic gluconeogenesis through the decline in glucagon secretion.

Key Words: liver, immune response, cow

1442 (W202) Bovine oocytes in vitro matured in the presence of antioxidants: Implications for intracellular levels of glutathione and reactive oxygen species and blastocyst development.

N. A. D. S. Rocha Frigoni[*1], B. C. D. S. Leão[1], P. C. Dall'Acqua[1], L. Rigon[1], Nogueira[2], and G. Z. Mingoti[1], *[1]University of Sao Paulo State (UNESP), Araçatuba, Brazil, [2]EMBRAPA Pantanal, Corumbá, Brazil.*

Production of reactive oxygen species (ROS) is a physiological process that occurs mainly on mitochondrial metabolism. Some, in vitro culture conditions can lead an increase in ROS production, making the oocytes more susceptible to oxidative stress damage. This study was conducted with the main objective to assess the effects of supplementation of in vitro maturation (IVM) medium with intracellular (cysteine and cysteamine) and extracellular (catalase) antioxidants on the intracellular levels of glutathione (GSH) and ROS in bovine oocytes and its implications on the subsequently embryonic development. *Cumulus*-oocyte complexes were matured in TCM-199 with bicarbonate, hormones and 10% FCS without supplementation (Control group) or supplemented with 0.6 mM cysteine associated with 100 µM cysteamine (C+C group), 100 UI catalase (CAT group) or 0.6 mM cysteine associated with 100 µM cysteamine and 100 UI catalase (C+C+CAT group) for 22 h at 38.5°C in 5% CO_2 in air. A sample of matured and immature oocytes (0 h) were stained (n = 192) with 5 µM of the fluorescent probe 6-carboxy-2'7'-dichlorodihydrofluorescein diacetate (H_2DCFDA; Molecular Probes, Invitrogen, Oakville, Canadá) or stained (n = 246) with ThiolTracker Violet (Glutathione Detection Reagent; Molecular probes, Invitrogen, Oregon) to evaluate ROS and GSH, respectively. Stained oocytes were evaluated immediately under an epifluorescence inverted microscope (excitation 495/510–550 nm and emission 404/526 nm, respectively for H_2DCFDA and ThiolTracker™) and the images were analyzed by Q-Capture Pro image software for determining the fluorescent intensity. Other oocytes were submitted to IVF and the presumptive zygotes were IVC in SOF medium, at 38.5°C in 5% CO_2 in air, for 7 d. The cleavage rates and embryonic development were evaluated, respectively, at 72 and 168 hpi. The differences of fluorescent intensity among groups was compared by ANOVA followed by Tukey's test and embryonic development was analyzed by Chi-square test ($P < 0.05$). The fluorescent intensity for ROS quantification was 1.00 ± 0.12^{a} (0 h), 1.91 ± 0.10^{c} (Control), 1.11 ± 0.04^{a} (C+C), 1.45 ± 0.08^{b} (CAT) and 1.07 ± 0.04^{a} (C+C+CAT). The fluorescent intensity for GSH quantification was 1.00 ± 0.4^{a} (0 h), 0.21 ± 0.01^{bd} (Control), 0.47 ± 0.02^{c} (C+C), 0.32 ± 0.01^{b}

(C+C+CAT) and 0.15 ± 0.01[d] (CAT). The cleavage rates were 73.5[a] (Control), 75.7[a] (C+C), 75.4[a] (CAT) and 73.1[a] (C+C+-CAT). The blastocyst rates were 28.2%[a] (Control), 31.1%[a] (C+C), 33.3%[a] (CAT) and 46.2%[b] (C+C+CAT). In conclusion, supplementation with cysteine, cysteamine and catalase during IVM reduced intracellular ROS levels and improved the embryonic development; however, such improvement was not due to an increase on intracellular amounts of GSH.

Key Words: antioxidants, in vitro maturation, ROS, GSH, blastocyst

---

1443 (W203) Heat stress alters adipose adrenergic signaling in lactating dairy cows. G. Xie*[1], L. W. Hall[2], M. Nearing[2], L. C. Cole[2], D. M. Spurlock[3], L. H. Baumgard[3], and R. P. Rhoads[1], *[1]Virginia Tech, Blacksburg, [2]University of Arizona, Tucson, [3]Iowa State University, Ames.*

Malnourished animals mobilize adipose tissue to alleviate the impact of energy deficiency on galactopoiesis, but heat-stressed (HS) lactating cows lessen their dependence on this strategy. One possibility is that lipolytic response becomes refractory to adrenergic signaling. To test this hypothesis, multiparous dairy cows (n = 6; parity = 4 ± 0.9; 436 ± 93 DIM; 721 ± 39 kg BW) housed in climate chambers were fed a TMR consisting primarily of alfalfa hay and steam-flaked corn and subjected to 2 experimental periods: 1) thermoneutral conditions (TN; 18°C, 20% humidity) with ad libitum intake for 9 d and 2) HS conditions (cyclical temperature 31 to 40°C, 20% humidity: min THI = 73, max THI = 86) with ad libitum intake for 9 d. Rectal temperature (Tre) was measured thrice daily at 0600, 1400, and 1800 h. During each period, cows were administered epinephrine intramuscularly (0.02 mg/kg) twice daily from d 6 to 9. Before and after epinephrine treatment, adipose biopsies were obtained from contralateral tailhead areas. Adipose lipolysis and lipogenic-related proteins were measured by western immunoblotting. During period 2, HS caused a 1.3°C increase in Tre compared with TN (P < 0.001). Heat stress reduced DMI by 18% (P < 0.001) and milk yield by 10% (P < 0.01). Epinephrine increased 5' adenosine monophosphate (AMP)-activated protein kinase (AMPK) (P < 0.1), cyclic-AMP response element-binding protein (CREB) (P < 0.05) and hormone sensitive lipase (HSL) (P < 0.05) phosphorylation abundance during TN but not in HS. Beta2 adrenergic receptor (BAR2) abundance was stable in all periods and treatments. Adipose triglyceride lipase (ATGL) protein expression was blunted (P < 0.05) by epinephrine in TN and HS. Fatty acid synthase (FAS), acetyl-CoA carboxylase (ACC) and phosphorylated ACC protein abundance were decreased (P < 0.05) by HS but did not respond to epinephrine challenge. In contrast, insulin receptor (IR) increased (P < 0.05) in HS regardless of epinephrine administration. Protein kinase B (AKT) phosphorylation tended to increase (P < 0.1) in response to epinephrine during HS. These observations indicate HS may alter adrenergic signaling by blunting lipolytic response in lactating cows. Potential cross talk between epinephrine and insulin may underlie HS adaptation.

Key Words: heat stress, lactation, catecholamine

1444 (W204) Effect of vitamin C supplementation on biochemical parameters and haemagglutination potential of Giant African Land Snail (*Archachatina marginata*) haemolymph. J. A. Abiona*, A. O. Ladokun, J. O. Daramola, D. M. Abioja, E. O. Oke, and O. M. Onagbesan, *Federal University of Agriculture, Abeokuta, Nigeria.*

A study was conducted on the effect of vitamin C on biochemical parameters and haemagglutination potential of Giant African Land Snail's haemolymph (*Archachatina marginata)*. Thirty-two snails with weight range of 100 to 180 g were used for this study. Eight snails were subjected to each of the four treatments which included: concentrate only, concentrate + 50 mg vitamin C, concentrate + 100 mg vitamin C and concentrate + 150 mg vitamin C. After 9 wk, haemolymph was collected from the mantle cavity from all the snails. Parameters monitored were: haemolymph total protein, albumin, globulin, cholesterol, glucose and haemagglutination titre. The result showed that haemolymph albumin, total protein, glucose, and cholesterol were not significantly affected (P > 0.05) by the treatment. However, the different levels of vitamin C with concentrate had significant effect (P < 0.05) on globulin. Snails fed concentrate + 150 mg of vitamin C had the highest least square mean (29.46 ± 1.47). For the haemagglutination test, 100 mg and 150 mg of vitamin C with concentrate for 120 min and 150 min had better haemagglutination titre (strength). It was however recommended that Inclusion of vitamin C in concentrate feed of snails should be encouraged with levels not less than 200 mg/kg of feed.

Key Words: vitamin C, biochemical parameters, haemagglutination potential

---

1445 (W205) Effects of grape seed supplementation on blood metabolic profile, immunity and milk production traits of dairy ewes. F. Correddu[1], A. Marzano[1], P. Bonelli[2], P. Nicolussi[2], and A. Nudda*[1], *[1]Dipartimento di Agraria, University of Sassari, Italy, [2]Istituto Zooprofilattico della Sardegna, Sassari, Italy.*

Grapes (*Vitis vinifera*) are rich in polyphenols with approximately 60 to 70% of these being in the seeds. The grape seeds (GS) are rich in proanthocyanidins that exert anti-oxidant and anti-inflammatory activities. The aim of this work was to study the effect of GS by-products in lactating sheep diet on milk production, blood metabolic profile and immune function. Twelve Sarda ewes in the first part of lactation, were divided in two isoproductive groups (1.7 kg/head/d): a control group (CON) and a treated group supplemented with 300 g/d

of grape seed (GS). Milk yield was measured weekly. Blood samples were collected every 2 wk and analyzed for total bilirubin, creatinine, aspartate transaminase (AST), alanine transaminase (ALT), γ glutamyl transpeptidase (GGT), alkaline phosphatase (ALP), total protein and urea nitrogen (BUN). Plasma samples were used to perform ELISA to evaluate the anti-OVA IgG titers, CD4 and CD8 cells. Lymphocyte proliferation was determined in vivo in each ewe by the measurement of changes in skin-fold thickness. Milk yield not affected by GS supplementation. All kidney and liver function biomarkers in serum did not differ between dietary groups. A slight suppressing effect of GS on immune activities was evidenced by the reduction of skin-fold thickness, IgG titers, Cd4/Cd8 ratio compared to CON. Grape seed by-product can be supplemented to lactating ewes for 2 mo without altering the immunity and the hepatic and renal metabolism status. *Acknowledgements: Research supported by Cargill–Animal Nutrition Division, Milan, Italy.*

Key Words: grape seeds byproduct, sheep, Immunity

1446 (W206) Determination of glucose metabolism and TCA cycle activity of early antral and late antral feline cat follicles employing [$^{13}C_6$]glucose and mass spectrometry. J. L. Colvin[1], N. Songsasen[2], C. L. Keefer[1], and B. J. Bequette[*1], *[1]Dep. of Animal and Avian Sciences, University of Maryland, College Park, [2]Center for Species Survival, Smithsonian Conservation Biology Institute, Front Royal, VA.*

Improving in vitro culture systems for follicles and oocytes requires knowledge of their metabolism. Thus, our objectives were to establish glycolytic and TCA cycle activity in feline follicles at two developmental stages, and after 13 d of in vitro culture. Paired feline ovaries from sexually mature cats ($\geq$ 1 yr) were acquired from a clinic. Morphologically healthy early (< 0.5 mm o.d.) and late (> 2 mm o.d.) antral follicles with a visible antrum were isolated. Early (n = 10 per cat, n = 9 cats) and late (n = 1 per cat, n = 9 cats) antral follicles were placed into individual wells with culture media (0.5 mL, DMEM containing glutamine and pyruvate plus a 50:50 mix of unlabeled and [$^{13}C_6$]glucose) and incubated for 24 h (5% CO_2) at 38.5°C. To determine whether in vitro culture of early antral follicles leads to acquisition of a late antral metabolism, a group of early antral follicles (n = 10 per cat, n = 9 cats) were encapsulated in 0.5% alginate hydrogel and cultured individually for 13 d with media containing [$^{13}C_6$]glucose the last 24 h. Following incubation, in vivo derived and in vitro cultured early antral follicles were pooled separately by cat for analysis, while late antral follicles were analyzed individually. Metabolites from follicles were extracted, and ^{13}C-isotopomer enrichments of metabolites determined by gas chromatography-mass spectrometry. The TCA cycle intermediate equilibrium partners alanine (pyruvate) and glutamate (α-ketoglutarate) were monitored for calculation of glycolytic and TCA cycle fluxes. Data were analyzed as a mixed model ANOVA with cat and cat age as blocking factors. A greater proportion of pyruvate flux derived from glucose metabolism in late (56%) compared to early (33%) antral follicles, indicating higher rates of glycolysis by late antral follicles. For both early and late antral follicles, only 2% of acetyl-CoA flux derived from glucose, indicating that TCA cycle oxidative metabolism relies on other substrates. Early antral follicles cultured in vitro for 13 d metabolized glucose and had TCA cycle flux activity similar to that of the early antral follicles cultured for 1 d. Thus, in vitro culture of early antral follicles for 13 d did not result in these follicles acquiring a similar metabolism as late antral follicles. The current research demonstrates a metabolic shift between early and late antral follicles derived in vivo, as well as a limited ability of early antral follicles to acquire a late antral metabolism after in vitro culture for 13 d.

Key Words: feline, follicle, metabolism

1447 (W207) Interrelationships between methods of blood mineral measurement in early postpartum dairy cows. B. M. Sweeney[*1], E. M. Martens[1], K. P. Zanzalari[2], J. C. Lawrence[3], and T. R. Overton[1], *[1]Cornell University, Dep. of Animal Science, Ithaca, NY, [2]Prince Agri Products, Inc., Franklin, IN, [3]IDEXX Laboratories, Inc., Westbrook, ME.*

The objective of this study was to determine the relationship between blood minerals measured by different methods and to determine the relationship between blood total (tCa) and ionized calcium (iCa) measured on samples taken from early postpartum dairy cows, as well as the agreement of tCa and iCa for diagnosis of subclinical hypocalcemia (SCH). Seventeen multiparous Holstein dairy cows were sampled 2× in the 24 h period postpartum and 1×/d for the following 4 d. Whole blood was analyzed immediately after collection for iCa by an iSTAT Portable Clinical Analyzer (*P*CA), and serum was analyzed for tCa, Mg and P using both the IDEXX VetTest (VT) and colorimetric methods at a veterinary diagnostic laboratory (DL). Serum total minerals measured by VT vs. DL were highly correlated (tCa $r = 0.95$,$P < 0.0001$;Mg $r = 0.91$,$P < 0.0001$;P $r = 0.97$,$P < 0.0001$). A VT tCa cutpoint with the highest combined sensitivity (96%) and specificity (85%) for diagnosing SCH (defined as DL tCa $\leq$ 8.0 mg/dL) was found to be 8.9 mg/dL as determined by receiver operator characteristic (ROC) analysis. The correlation between tCa measured by DL and iCa measured by PCA was high ($r = 0.89$,$P < 0.0001$). Generally when iCa is used to diagnose SCH, a cutpoint of 4.0 mg/dL iCa is used based on the assumption that iCa constitutes 50% of tCa. Using this assumption, agreement (as determined by McNemar's Test) for diagnosis of SCH ($\leq$ 8.0 mg/dL tCa, $\leq$ 4.0 mg/dL iCa) was poor (Exact $P = 0.06$; Kappa = 0.45, $P < 0.05$). Based on the two samples taken postpartum [7(± 4) h and 20(± 4) h postpartum], this data showed that iCa constituted 58% of tCa in the 24 h postpartum. The iCa cutpoint

with the greatest combined sensitivity (91%) and specificity (87%) for diagnosing SCH was determined by ROC analysis and found to be 4.68 mg/dL. Overall, serum minerals (tCa, Mg and P) measured by standard laboratory techniques are highly correlated with minerals measured by the VT and different cut-points can be used to accurately diagnose SCH with tCa measured by the VT. The relationship between iCa and tCa in the period immediately postpartum must be better characterized before iCa can be used for diagnosis of SCH.

Key Words: ionized calcium, subclinical hypocalcemia, serum minerals

---

1448 (W208) Development of a multiplex assay for simultaneous quantification of endocrine analytes.

E. A. Benavides*[1], K. D. Wells[1], and D. H. Keisler[2], *[1]University of Missouri–Division of Animal Sciences, Columbia, [2]University of Missouri–Division of Animal Sciences, Columbia.*

Since the advent of the radioimmunoassay in the 1950s, numerous immunologically-based methods have evolved for sample analysis. Although each immunological method possesses unique assets and liabilities, all share limited abilities in range of detection and the number of analytes resolvable simultaneously; most procedures are limited to one analyte determined per replicate per sample. The objective of this study was to adapt technology evolving from the genomics revolution for multiplexed hormonal analysis in livestock. We sought to complete this objective using sequencing technologies and tools: Illumina BeadXpress, Luminex xMAP, and quantitative immuno-PCR. The Illumina BeadXpress and Luminex xMAP both share similar characteristics; each platform consists of a laser spectrum analyzer and a bead-set. Each bead-set contains microscopic beads; each set with unique identifying signatures. As a test of proof of concept, the surface of a bead set was conjugated to an LH antibody. Using these technologies, we were able to establish an assay for LH on the Luminex platform, but not on the Illumina platform. The proprietary nature of both the Luminex and Illumina platforms however, greatly limited assay flexibility. Therefore, we chose to establish an assay for LH using quantitative immuno-PCR. Quantitative immuno-PCR exploits PCR amplification with antibody detection. Briefly, a sandwich immunoassay is performed with capture antibody immobilized to a PCR plate. A second detection antibody is conjugated to an oligonucleotide and after a series of washes, the plate is subjected to quantitative PCR (qPCR). Detection of LH was achieved, but background binding was a problem. Subsequently, to simplify the design and demonstrate proof of concept, a biotinylated oligonucleotide was incubated with streptavidin coated PCR plates and subjected to qPCR. The results of this latter experiment suggested that the assay performed well with over six orders of magnitude linearity. In conclusion, background binding was found to be a major problem with quantitative immuno-PCR but one that is believed to be resolvable. Moreover, our observations suggest that immuno-PCR has the potential to improve detection capabilities of hormonal assays with six orders of magnitude sensitivity, reproducibility, and ultimately in a multiplex capacity with the oligonucleotide serving as both a label and as a barcode for identifying the analyte. The technological leap in capabilities provided by successful multiplexing can be used for understanding the complex interaction of endocrine and metabolic signals in the dynamically changing animal.

Key Words: multiplexing, endocrine profiling, immuno-PCR

1449 (W209) Effect of periconceptual growth hormone injection on feed intake and early fetal development in ewes.

C. H. Pereira*[1,2,3], K. C. Swanson[3], H. O. Patino[4], F. E. Doscher[3], V. C. Kennedy[3], B. R. Mordhorst[3], J. D. Kirsch[3], and K. A. Vonnahme[3], *[1]Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil, [2]North Dakota State University, Fargo, [3]North Dakota State University, Fargo, [4]Universidade Federal do Rio Grande Do Sul, Porto Alegre, Brazil.*

Researchers have reported improved birth weight and numbers of lambs from ewes treated with growth hormone (GH) at the time of breeding. Therefore, our hypothesis was that the administration of GH at time of breeding could increase DMI which consequently could result in greater early development of the fetus. Thirteen individually-penned ewes (mean BW = 69.8 ± 3.14 kg and BCS = 3.2 ± 0.13 [1-to-5 scale]) were fed a pelleted diet (CP 12.88%, ash 6.48%, fat 1.69%, NDF 37.86%, ADF 23.83% of DM) for ad libitum intake. Estrus was synchronized by administering 2 doses of prostaglandin $F_{2\alpha}$(*P*GF) 11 d apart. At the second dose of PGF, six ewes were injected IM with GH (500 mg) and seven ewes with saline solution (control). The ewes in both treatments were exposed to the same ram at 0700 and 1900 h and allowed to breed. Doppler ultrasound measurements were taken on d 25, 30, 40, and 50 of gestation for fetal length, fetal width, kidney length, kidney width, placentome size, biparietal distance and umbilical blood flow (BF; at d 50 of gestation). Data were analyzed in PROC MIXED (SAS; 2011) to test for the effects of treatment, day and treatment × day. No differences between treatments were observed for BW ($P = 0.16$), BCS ($P = 0.54$) and DMI ($P = 0.84$) after injection of GH. There was a day effect ($P < 0.05$) for fetal length, fetal width, kidney length, placentome size, and biparietal distance with all increasing as gestation advanced. No difference ($P > 0.05$) was observed between treatments for any ultrasound measurements. Growth hormone administration did not influence DMI or conceptus development as measured using ultrasonography. It is still unknown how periconceptual GH treatment could enhance growth and

development of the conceptus, or umbilical BF, after d 50 of gestation when exponential growth of the fetus occurs.

Key Words: ewe, growth hormone, ultrasound

1450 (W210) Relationship between plasma concentrations of thyroid hormones and physiological state of beef cow/calf pairs.

B. H. Boehmer*, M. R. Davis, and R. P. Wettemann, *Oklahoma Agricultural Experiment Station, Stillwater.*

Triiodothyronine (T_3) and thyroxine (T_4) are important mediators of energy expenditure, growth, and thermogenesis. The prohormone T_4 is converted to the biologically active form, T_3. Relationships between concentrations of T_3 and T_4 in cows and their offspring have not been defined. Spring calving, Angus cow/calf pairs (n = 27) were used to evaluate the relationship between plasma concentrations of T_3, T_4, and T_4:T_3 in cattle of different physiological ages. Calves were weighed at birth and bulls were castrated by banding. Weights of cows and calves were recorded at 48 and 97 d post partum and blood samples were collected at 97 d postpartum. Plasma concentrations of T_3 and T_4 were quantified by RIA. Triiodothyronine, T_4, and the ratio of T_4 to T_3 (T_4: T_3) were analyzed with PROC CORR and PROC MIXED (SAS Inst. Inc.). Plasma concentrations of T_4 did not differ between cows (P = 0.17, 40.5 ± 7.4 ng/ml) and calves (59.2 ± 7.4 ng/ml). Concentrations of T_4 in cows and their calves were not correlated (P = 0.40). Concentrations of T_3 tended to be greater in calves (P = 0.06; 1.99 ± 0.17 ng/ml) compared with cows (0.88 ± 0.17 ng/ml). Concentrations of T_3 in plasma were correlated (r = -0.43, P = 0.03) between cows and their calves. Plasma concentrations of T_4:T_3 in cows were greater (P < 0.001; 49.0 ± 9.3) compared with calves (31.3 ± 9.3) and T_4:T_3 was not correlated between cows and their calves (P = 0.83). The T_4: T_3 in calves was correlated with T_3 (r = 0.45, P = 0.02) in their dams and tended to be positively correlated with T_4 (r = 0.38, P = 0.06) in their dams. Concentrations of T_4 in calves and T_3 in cows were not correlated (P = 0.87). Average daily gain of calves was not correlated with T_4, T_3, or T_4: T_3 in cows or calves ($P \geq 0.12$). Concentrations of T_3 tended to be greater in calves compared with their dams; however, concentrations of T_4 were similar. These results indicate thyroid function in cows and their calves was related as plasma concentrations of T_3 were negatively correlated. Production efficiency of beef cows and calves may be enhanced by identifying individuals with greater metabolic efficiency.

Key Words: thyriod hormone, beef cattle, metabolism

1451 (W211) Follicle-stimulating hormone converges with canonical WNT signaling to enhance Cyp19a1 promoter activity in granulosa cells.

B. I. Gomez*[1], J. O. E.[1], C. A. Gifford[1], D. M. Hallford[2], and J. Hernandez Gifford[1], *[1]Oklahoma State University, Stillwater, [2]New Mexico State University, Las Cruces.*

Biosynthesis of estradiol in the adult ovary requires activation of the tissue specific cytochrome P450 aromatase (*Cyp19a1*) type II promoter (*PII*) by FSH. Canonical wingless-type mammary tumor virus integration-site (WNT) signaling has been recognized to contribute to ovarian regulation of steroidogenesis by increasing the transcriptional co-factor, β-catenin. Recent data suggest WNT3A is inhibitory on FSH mediated mRNA induction of key steroidogenic enzymes and steroid biosynthesis; however, the mechanism by which WNT3A negatively regulates FSH remains to be determined. Therefore, the objective of this study was to investigate the inhibitory effects of WNT3A on FSH-mediated *Cyp19a1* activity. Immunofluorescence was performed on primary rat granulosa cells treated with WNT3A (500 ng/mL) in the presence or absence of FSH (100 ng/mL) for 24 h (n = 4) to determine if FSH prevents WNT3A translocation of β-catenin. Treatment with WNT3A and WNT3A+FSH resulted in nuclear accumulation of β-catenin, while FSH treated cells resembled control groups with the majority of β-catenin remaining at cell membrane. To identify if WNT3A+FSH prevents β-catenin ability to bind the *Cyp19a1 PII*, a 516 bp fragment of the *Cyp19a1 PII* (516-*Cyp19a1 PII*) was transfected into primary cultures of rat granulosa cells, treated with vehicle or WNT3A (500 ng/mL) for 24 h, then co-cultured with or without FSH (100 ng/mL) for an additional 24 h (n = 4). Promoter activity was measured by the luciferase reporter assay and statistical differences for treatment interaction were quantified using one-way ANOVA procedure of SAS. Activity of *Cyp19a1 PII* with WNT3A alone was similar to controls, while FSH treatment increased (P = 0.01) *Cyp19a1 PII* activity 6.65-fold when compared to controls. Co-incubation of FSH and WNT3A was synergistic resulting in a 16.09-fold increase in *Cyp19a1 PII* activity (P = 0.01; n = 4). To evaluate if regions upstream of the 516 bp *Cyp19a1 PII* fragment are responsible for the inhibition of estradiol biosynthesis, the full length *Cyp19a1 PII* (full-*Cyp19a1 PII*) and 2000 bp (2000-*Cyp19a1 Promoter*) upstream of the ATG site on *Cyp19a1* was cloned into a luciferase reporter. Preliminary data suggest *full-Cyp19a1 PII* and *2,000-Cyp19a1 promoter*activity is not synergistic (n = 2) with co-incubation of WNT3A+FSH. Future studies are needed to determine the regions on the promoter responsible for WNT3A inhibition on FSH signaling.

Key Words: Cyp19a1, granulosa cells, WNT

1452 (W212) Effects of various doses of gonadotropin stimulation on reproductive performance of seasonally anestrous ewes. S. L. Rastle-Simpson*, K. N. D'Souza, A. K. Redhead, C. D. Paul, E. N. Keller, and M. Knights, *West Virginia Univeristy, Morgantown.*

The use of exogenous gonadotropins as part of an estrous induction protocol can have beneficial effects on fertility in ewes bred out-of-season. Few studies have evaluated the ability of a mixture of eCG (FSH-like) and hCG (LH-like) (*P*.G. 600, Intervet, Millsboro, DE) to increase fertility in ewes bred out-of-season, specifically following the pre-treatment with progesterone delivered via CIDR devices. Previously, our lab found that administering 3 mL of the gonadotropin mixture 1 d before CIDR removal increased conception rate, pregnancy to first service, lambing rate and the overall percentage of ewes that lambed. The objective of this study was to evaluate the dose effects of a gonadotropin mixture on reproductive performance of seasonally anestrous ewes. Crossbred ewes (n = 200) from three farms in West Virginia and Pennsylvania received CIDR inserts (between the months of May and July) 5 d before introduction of rams. At insert removal, all ewes were assigned randomly to receive a 5-mL injection (i.m., 400 IU eCG, 200 IU hCG) of P.G. 600, a 3-mL injection (i.m., 240 IU eCG, 120 IU hCG) of P.G. 600, or receive no further treatment. The reproductive performance parameters that were measured include pregnancy rate, prolificacy, pregnancy retention, and lambing rate. Analysis of variance was conducted using the GLM procedures of SAS, and least squares means were computed. None of measured reproductive performance parameters was significantly affected by the different doses of gonadotropin stimulation ($P > 0.05$). It is possible that no effect of the gonadotropin stimulation may be due to the high reproductive performance observed in the control ewes. In conclusion, administration of various doses of a gonadotropin mixture at progesterone withdrawal had no effect on reproductive performance of ewes bred outside their normal breeding season.

Key Words: gonadotropin stimulation, anestrus, ewe

1453 (W213) Effect of methionine supplementation on methylation and lipid accumulation of the preimplantation embryo in dairy cows. D. A. Velasco Acosta*[1,2], A. C. Denicol[3], C. S. Skenandore[1], Z. Zhou[1], M. Nunes Corrêa[2], D. N. Luchini[4], P. J. Hansen[3], J. J. Loor[1], and F. C. Cardoso[1], *[1]University of Illinois, Urbana, [2]Federal University of Pelotas, Brazil, [3]Dep. of Animal Sciences, University of Florida, Gainesville, [4]Adisseo S.A.S., Alpharetta, GA.*

The lipid profile of oocytes and early embryo can be influenced by the environment of the cow. Our objective was to determine effect of supplementing rumen-protected methionine on DNA methylation and lipid accumulation in preimplantation embryos of dairy cows. Lactating Holsteins entering their second or greater lactation were randomly assigned to two treatments from 30 ± 2 DIM to 72 ± 2 DIM; Control (CON; n = 5, fed a basal diet with a 3.4:1 Lys:Met) and Methionine (MET; n = 5, fed the basal diet plus Smartamine M to a 2.9:1 Lys:Met). On d 60, dominant follicles greater than 5 mm were aspirated using an ultrasound-guided transvaginal approach. A CIDR device was inserted in all cows after follicular aspiration (d 60) and superovulation began at d 61.5 using FSH treatment equivalent to 400 mg of NIHFSH-P1 (Folltropin) in 8 decreasing doses at 12-h intervals over a 4-d period. During the superovulatory period, all cows received two PGF2α injections at d 63 and 64 (concomitant with the fifth and seventh FSH injections), and CIDR was withdrawn at d 65. Twenty-four h after CIDR withdrawal, ovulation was induced with GnRH. Cows were artificially inseminated at 12 and 24 h after GnRH using a high-fertility sire. Embryos were flushed 6.5 d after artificial insemination. Embryos with stage of development 4 or greater were used for analysis. Methylation was assessed by immunofluorescent labeling with anti-5-methylcytosine while lipid accumulation was assessed by staining with Nile Red. ImageJ software was used for image analysis to determine intensity of labeling. For methylation, fluorescence intensity of nuclear 5-methylcytosine labeling was expressed as a ratio of labeling for DNA using propidium iodide. For lipids, fluorescence intensity of Nile Red staining was compared against a negative control embryo (subtraction of background). Nuclear staining (propidium iodide or Hoescht 33342) was used to count the total number of cells/embryo. A total of 37 embryos were harvested from cows (MET = 16; CON = 21). Statistical analysis was performed using the PROC MIXED of SAS. Cows receiving MET (1661) had greater ($P = 0.021$) lipid accumulation when compared with cows receiving CON (1033). There were no treatment effects ($P > 0.511$) on number of cells or stage of development. In conclusion, cows supplemented with methionine produced embryos with higher lipid concentration when compared to CON which could potentially serve as an important source of energy for the early embryo.

Key Words: methionine, embryo, methylation, lipid

1454 (W214) Expression of Foxp3 in peripheral blood mononuclear cells of pregnant cows. M. A. Paibomesai*[1], R. Machado Ferreira Saran[2], R. da Silva Nunes Barreto[2], F. V. Meirelles[2], and L. J. Oliveira[3], *[1]University of Guelph, ON, Canada, [2]Universidade de São Paulo, Pirassununga, Brazil, [3]Michigan State University, East Lansing.*

Pregnancy has been shown to have great influence over the immune system through the modulation of immune cell types, dampening of the immune response, and display of overall immunodysfunction. It is a period through which the maternal immune response must tolerate long periods of exposure to

foreign antigens produced by the growing fetus throughout gestation. To prevent loss of the fetus the maternal immune system will downregulate specific receptors, such as MHC, and push the system towards to tolerogenic state, as shown in mouse and woman studies. One of these strategies includes the increase in T-regulatory cells, which express the transcription factor FoxP3 and downregulate the immune response after activation. It has been previously shown in mice and woman that as gestation time lengthens the presence of T-regulatory cells increases both locally and systemically. However, this increase in T-regulatory cells has not been well defined in bovine pregnancy. The objective of this study is to determine the expression of FoxP3 transcription factor in $CD4^+$ T cells isolated from pregnant cows (n = 5) and non-pregnant (n = 5) at Day 30 after AI; periparturient (n = 5; 2 to 4 d before parturition) and nonpregnant (n = 5) n lactating cows. $CD4^+$ T cells were isolated by magnetic sorting from selected cows and snap-frozen for RNA extraction and reserve transcription. Gene expression of FoxP3 and PXT-3 were determined by quantitative RT-PCR. Preliminary results show that there is a tendency (P = 0.12) for decreased expression of FoxP3 on pregnant cows at d 30 compared to cow close to parturition. The absence of difference in expression of FoxP3 between pregnant and non-pregnant cows could be due to sample time as well as small group sizes. Additionally, PTX-3 expression is downregulated (P = 0.34) in the periparturient cows, although this was not significant. The decreased expression of PTX3 confirms that peripartum period represents a period of overall immunodysfunction as compared to early gestation. Overall, this study has the potential to identify cows that have higher conception rates due to an immunological system geared towards fetus tolerance.

Key Words: pregnancy, regulatory immune responses, dairy cows

1455 (W215) Luteinizing hormone (LH) profiles after either porcine LH or GnRH treatment in Holstein cows with or without FSH-stimulation.

A. Behrouzi*[1], M. Fakheri[1], R. Salehi[1], M. G. Colazo[2], and D. J. Ambrose[1,2], *[1]Dep. of Agricultural, Food and Nutritional Science, University of Alberta, EdmontonCanada, [2]Alberta Agriculture and Rural Development, Livestock Research Branch, Edmonton, AB, Canada.*

Using porcine LH (*P*LH) in lieu of GnRH for synchronizing ovulation in non-stimulated dairy cows resulted in a prolonged and elevated LH profile which favourably altered the expression of intrafollicular proteins associated with improved oocyte competence, and increased pregnancy rates. The wide variability in superovulatory responses and embryo yield in FSH-stimulated cows could potentially be reduced using pLH if the altered (i.e., prolonged and elevated) LH profile attained in non-stimulated cows could be established in superovulated cows. As a first step, our objective was to characterize LH profiles after giving pLH or GnRH in non-lactating Holstein cows subjected to different levels of ovarian stimulation. Cows (n = 13) assigned to no ovarian stimulation (NS; 0 mg FSH) received 100 μg GnRH followed by 500 μg cloprostenol (*P*GF) 7 d later. In ovarian-stimulated groups, cows received decreasing doses of FSH, twice daily over 4-d, with PGF treatments given with the sixth and seventh FSH, to attain either partial stimulation (PS; n = 8, 200 mg FSH) or full stimulation (FS; n = 12, 400 mg FSH). Cows received either 100 μg GnRH or 25 mg pLH 2 d after PGF in NS and 1 d after last FSH in PS and FS groups. Blood samples were collected to determine LH concentrations from 30 min before GnRH- or pLH- treatment, up to 20 h post-treatment and plasma LH concentrations were measured by radioimmunoassay using an anti-bovine LH monoclonal antibody. In GnRH-treated cows, mean (± SE) plasma LH (ng/mL) increased from 0.3 ± 0.1 to a peak of 14.3 ± 1.3 (NS), 6.3 ± 0.8 (PS) and 17.0 ± 2.6 (FS) by 1.5 h, remained elevated for up to 4 h after GnRH treatment ($P \leq 0.01$) returning to baseline by 8 h after treatment in all three groups. In pLH-treated NS and FS cows, plasma LH increased from 0.2 ± 0.2 to a mean peak of 2.1 ± 0.2 and 1.1 ± 0.1 by 1.5 h, and maintained above-basal concentrations ($P < 0.0001$) up to 20 h after treatment, respectively. In pLH-treated PS cows, however, LH concentrations increased from 0.1 ± 0.2 to a mean peak of 1.3 ± 0.2 ng/ml by 3 h, and remained above basal concentrations for up to 10 h post-treatment (0.5 ± 0.2; $P < 0.01$). In summary, LH concentrations in non- and FSH-stimulated cows given pLH remained elevated for a longer period than in cows given GnRH. Whether giving pLH to superovulated cows will reduce variability in ovarian response and improve embryo quality remains to be seen.

Key Words: LH, porcine LH, GnRH, dairy cow

PRODUCTION, MANAGEMENT, AND THE ENVIRONMENT: **INFLUENCE OF DIET AND MANAGEMENT ON HEALTH AND PERFORMANCE**

1456 (M217) A 6-yr study evaluating health, milk and milk quality in 427 dairy herds fed OmniGen-AF to dry and lactating cows. O. Bewley[1], T. Boyle[1], M. Brady[1], K. Brubaker[1], J. D. Chapman[*1], T. Elliott[1], L. O. Ely[2], S. Fitzner[1], A. E. Holland[1], D. Larson[1], R. Shaw[1], and J. Ydstie[1], *[1]Prince Agri Products, Inc., Quincy, IL, [2]University of Georgia, Athens.*

From 2007 through 2012, 427 U.S. dairy herds totaling 273,796 cows were enrolled in a study to evaluate health and production records collected from 90-dperiods before and during the feeding of OmniGen-AF (Prince Agri Products, Inc., Quincy, IL). Herd sizes ranged from 68 to 6700 cows with dairies starting the studies throughout the year (Januaury to March, $n = 158$, April to June, $n = 98$, July to September, $n = 84$, October to December, $n = 87$). All dry and lactating cows were fed OmniGen-AF (OG) at 56 g/hd/d for 90 d. Health events, milk quality and milk yields were collected from DC305, DRMS and PCDART systems. Data were analyzed using paired *t* test (SAS, Statistical Analysis System) comparing number of health events and production recorded during the 90 d OG was fed (post-OG) to those occurring in the 90 d before feeding OG (*P*re-OG). The resulting data were sorted and analyzed by all herds ($n = 427$), herd size (< 100 hd, $n = 68$: 101–500 hd, $n = 198$: 501–999 hd, $n = 76$: > 1000 hd, $n = 85$), and pre-OG somatic cell count (SCC) cells/ml (< 200k, $n = 103$: 201k-300k, $n = 127$: 301k-400k, $n = 72$: > 401k, $n = 62$). Significance was declared at $P < 0.05$. Reductions in mastitis cases/mo. (-24.3%), late term abortions/mo. (-28.6%), hospital pen cows/d (-16.7%) and dead cows/mo. (-33%) expressed as a % of total herd cows differed ($P < 0.001$) between the pre-OG to post-OG 90-d periods. Although incidence rates of health events varied across herd sizes and among herds grouped by SCC, common to all were significant differences detected in metritis and dead cows between pre-OG and post-OG. The average pre-OG SCC for all herds was 288,953 with an average of > 70% of herds reporting a reduction in SCC. Changes in SCC from pre-OG to post-OG were proportional to the pre-OG SCC. Herds with a pre-OG SCC of between 201k to 300k and 301k to 400k or > 400k were observed to have post-OG SCC reductions of 23,102; 56,463 and 127,911 cells/ml, respectively ($P < 0.001$). Milk production was reported in 208 herds with an average change from pre-OG to post-OG of 0.45kg/hd/d ($P < 0.05$); however, only herds of < 100 hd ($P < 0.05$) and herds with a SCC of 201k to 300k ($P < 0.001$) showed significant milk improvements. Results from this study suggest a nutritional strategy that includes feeding OG as part of a best-management practice program for dry and lactating cows can influence health, milk yield and milk quality in commercial dairies.

Key Words: health, milk quality, OmniGen-AF

1457 (M218) Crude glycerin as a replacement for dry ground corn in finishing diets for beef cattle: Economic analysis. P. Del Bianco Benedeti[*1,2], P. V. R. Paulino[3], M. I. Marcondes[1], A. Faciola[2], I. França *S*mith Maciel[1], and M. Custódio da Silva[1], *[1]Federal University of Viçosa, Brazil, [2]University of Nevada, Reno, [3]Nutron Alimentos Ltda., Campinas, Brazil.*

The objective of this study was to evaluate the effects of replacing dry ground corn (DGC) with crude glycerin (CG) on production costs of finishing beef bulls. A complete randomized design experiment with 25 d for adaptation and 95 d for sampling collection was conducted, in which 3640 Nellore bulls (367 ± 37 kg) were blocked by BW and assigned to 20 pens. Animals were randomly assigned to one of four treatments: 0, 5, 10, and 15% (DM basis) CG in diet. All diets contained 15% roughage and 85% concentrate and were formulated to meet NRC (2000) recommendations. Diets were isoenergetic, isonitrogenous, and allowed 1.4 kg/d BWG. Initially, twenty animals were slaughtered to serve as reference to estimate initial empty BW, which allowed carcass gain calculation. Sensitivity analysis was performed according to Diniz et al., 2010 (Asian-Aust. J. Anim. Sci. 23:1308–1318) to determine which diet was more economical according to current CG prices as a function of DGC prices. Data presented in Table 1457 shows the cost of each diet tested in this work during the period of August to November 2012. Treatment without CG had the lowest diet cost, followed by treatments with 5, 15, and 10% of CG inclusion, respectively. Sensitive analysis indicated that the treatment that provided the lowest cost per kg of carcass produced changes depending on the CG:DGC price relationship. When CG price was up to 110% of DGC price, the treatment that provided the lowest price per kg of carcass produced was 15% CG inclusion. When CG price was 120% or more of DGC price, the diet without CG was the most economical treatment. Data from this sensitive analysis indicates that CG may be an economical alternative to DGC for beef cattle feedlots in Brazil.

Key Words: economic analysis, feedlot, glycerin

Table 1457.

	Crude Glycerin (%)			
	0	5	10	15
Diet cost, $/kg DM	0.21	0.22	0.23	0.24
DMI, kg/d	10.5	10.1	10.2	9.6
Diet cost, $/animal/d	2.22	2.23	2.32	2.27
Carcass gain, kg/animal/d	0.89	0.85	0.84	0.83
Diet cost, $/kg carcass	2.49	2.62	2.76	2.72
Crude Glycerin price, kg (% of price of DGC kg)	———— $/kg carcass ————			
90	2.49	2.51	2.54	2.41
100	2.49	2.52	2.56	2.44
110	2.49	2.54	2.59	2.48
120	2.49	2.55	2.62	2.52
130	2.49	2.56	2.64	2.55
140	2.49	2.58	2.67	2.59

1458 (M219) Inhibition of rumen methanogenesis induced by Bioflavex and its pure flavonoid components under in vitro fermentation using rumen fluid from steers fed high concentrate diets. A. R. Seradj[1], J. Crespo[*2], D. Villalba[1], and J. Balcells[1], *[1]University of Lleida, Spain, [2]Interquim |S. A.* (*Ferrer Health Tech), Barcelona, Spain.*

Four separated incubation series were performed in a complete randomized blocks design to determine the effect of a citrus extract rich in flavonoids (Bioflavex) and its main components on methane mitigation under in vitro condition. Rumen liquor from four rumen cannulated growing steers fed a high concentrate diet (90:10 commercial concentrate:barley straw) was used as inoculum. Bottles of 120 mL were prepared under the CO_2 stream and filled with incubation solution and a mixture of concentrate:barley straw (600:60 mg/bottle) was used as substrate. Bioflavex (BF) was added to the incubation media and its effect compared against its pure flavonoid components (Hesperidine [HS]; Isonaringine [IN]; Naringine [NG]; Neoeriocitrine [NE]; Neohesperidine [NH] and Poncirine [PC]) at 200µg/g dry matter (DM), and the substrate without flavonoids was also included as a control (CTR). Bottles were sealed and incubated at 39 ± 1°C for 72 h. The head space pressure was measured at intervals of 2 h, started from 2 to 12 h then 24, 48, and 72 h. Values (mbar) converted to volume (ml) by a linear regression. Since 12 h post incubation, a sample (0.1 mL) from head space gas was analyzed for methane concentration using GC. The pattern of cumulative gas production (y) was fitted to the model: $y = a(1\text{-}e^{-b(t-c)})$, being a the potential cumulative gas production (ml); b the production rate (ml/h) and c is the lag time (h). The addition of BF or any of its components reduced the cumulative gas ($P < 0.01$) and methane production (mmol/g DM) ($P < 0.01$) except for NE and PC, that did not differ from the CTR values. However, reduction in CH_4 production was more pronounced than it was in gas production ($P < 0.01$). No changes were observed in the gas (ml/h) and methane production rate (mmol/h) in relation to CTR. The addition of flavonoids in the in vitro culture media reduced gas production and it would reflect the activity of bioflavex and its main components against the fermentative activity of the rumen liquor although our result also showed specific activity against methanogenic archaea.

Key Words: in vitro incubation, methanogenesis, pure flavonoids

1459 (M220) Effects of trace mineral-fortified, limit-fed creep supplements on performance of beef calves (pre-weaning). A. Saran Neto[1], L. S. Caramalac[2], P. G. M. D. A. Martins[2], P. Moriel[2], H. J. Fernandes[3], and J. D. Arthington[*2], *[1]University of São Paulo, Pirassununga, Brazil, [2]UF/IFAS Range Cattle Research and Education Center, Ona, FL, [3]State University of Mato Grosso do Sul, Aquidauana, Brazil.*

To assess the effects of limit-fed creep supplements, with or without trace mineral (TM) fortification, 30 cow/calf pairs were stratified by birth date and randomly allocated to 1 of 15 bahiagrass pastures (1 heifer and 1 steer cow-calf pair/pasture). Calves were approximately 5 mo of age at the start of the study. Four treatments were randomly assigned to pastures, including, (1) limit-fed creep fortified with hydroxy-Cu, Zn, and Mn, (2) limit-fed creep fortified with Cu- and Zn-sulfate and Mn-oxide (sulfate/oxide), (3) limit-fed creep without TM fortification, and (4) no limit-fed creep (n = 3, 3, 4, and 5 pastures, respectively). Creep supplements for treatments 1 and 2 were also fortified with Co carbonate, Na selenite, and I (via EDDI). All pastures were provided free-choice access to salt with no mineral fortification. Supplements were offered 3 times weekly for 89 d (265 g/calf on Monday, Wednesday, and Friday) which targeted a maximum intake of 114 g/d. Calf BW was measured on d 0, 45 and 89 (weaning). Calf TM status was assessed in liver biopsy samples collected at weaning. Limit-creep intake increased over time ($P < 0.001$) and total limit-creep intake tended to be greater ($P = 0.10$) for hydroxy- vs. sulfate/oxide-formulated supplements (7.6 and 5.1 kg; SEM = 0.97). Limit-creep had no effect ($P = 0.22$) on pre-weaning BW gain (80.0 and 73.5 kg for limit-creep and no limit-creep, respectively; SEM = 5.44); however, BW gain tended ($P = 0.09$) to be greater for calves consuming hydroxy- vs. sulfate/oxide-formulated supplements (87.1 and 74.4 kg, respectively; SEM = 5.44). Efficiency of added BW gain did not differ ($P \geq 0.13$) among treatments (G:F = 1.94, 0.64, and 1.60 kg/kg for hydroxy, sulfate/oxide, and no TM fortification limit-creep feed, respectively; SEM = 0.850). The cost of added calf gain was $0.27, $1.98, and $0.60/kg for hydroxy-, sulfate/oxide-, and no-TM fortification limit-creep, respectively. Calves consuming TM-fortified, limit-creep, irrespective of source, had greater ($P \leq 0.02$) liver concentrations of Co, Cu, and Se compared to calves consuming no limit-creep or limit-creep without TM fortification. These results imply that the consumption of TM-fortified limit-creep increases the mineral status of calves and the use of hydroxy sources of Cu, Zn, and Mn may result in greater intake acceptability with a favorable cost of gain compared to sulfate/oxide alternatives.

Key Words: calves, creep feeding, trace minerals

1460 (M221) The effect of a maternal dietary yeast cell wall supplement during gestation on cow performance and calf growth and immunity.

M. C. Roberts*[1], S. E. Schmidt[2], D. A. Neuendorff[3], R. C. Vann[4], N. C. Burdick Sanchez[5], J. R. Corley[6], J. A. Carroll[7], T. H. Welsh, Jr.[8], and R. D. Randel[1], *[1]Texas A&M AgriLife Research, Overton, [2]Texas A&M University, College Station, [3]Texas A&M Agrilife Research, Overton, [4]MAFES– Brown Loam Experiment Station, Mississippi State University, Raymond, [5]USDA-ARS, Lubbock, TX, [6]Lesaffre Feed Additives, Milwaukee, WI, [7]USDA-ARS, Livestock Issues Research Unit, Lubbock, TX, [8]Texas A&M University Dep. of Animal Science, College Station.*

The objective of this study was to determine if feeding of yeast cell wall (YCW) to pregnant cows influences cow performance as well as postnatal calf growth and immunity. Multiparous cows were assigned by predicted calving date into either the control (C; n = 24) or supplemented (Y; n = 24) groups. The Y cows were fed 4 g of YCW in 230 g of ground corn top-dressed on 1.81 kg of corn gluten and soybean meal (4:1) from approximately 90 d prepartum through 28 d postpartum. Weight and body condition score (BCS) were taken at 28-d intervals prepartum and postpartum. Within 24 hof parturition, the BW and BCS of cows and BW of calves were recorded, and blood samples from calves were obtained to determine white blood cell numbers. These procedures were repeated on d 14 and 28 postpartum, and continued at 28-d intervals through weaning. Weaning weights were adjusted to 180 d of age. Cows were observed for estrus twice daily starting d 28 postpartum through first estrus. Data were analyzed using the PROC MIXED in SAS. Yeast supplementation did not affect cow prepartum BW (P = 0.39) or BCS (P = 0.14), postpartum BW (P = 0.97) or BCS (P = 0.89), or the postpartum interval (P = 0.98; C = 56.2 ± 3.3, Y = 56.3 ± 3.2 d). Calf weight was not different at birth; however, on d 14 and at weaning, C males tended to be heavier than Y group males as well as females from the C and Y groups (P = 0.08, 0.07, respectively). At d 28 C males were heavier than Y males or females (P = 0.02). There was a tendency for 180-d adjusted weaning weight to be heavier for C males than either Y males or C and Y females (P = 0.0563). There was also a treatment by day interaction in which C calves were heavier than Y calves (P = 0.01) and a calf sex by day interaction with males being heavier than females preweaning (P = 0.01). Treatment did not affect the white blood cell profile of calves on d 0 or 28 as C and Y calves had similar percentages (P > 0.2) of lymphocytes, monocytes, segmented neutrophils, banded neutrophils and eosinophils. The C males demonstrated a greater growth rate than prenatally supplemented calves in the neonatal and preweaning periods. These data suggest that prenatal YCW supplementation to healthy mature cows in a low stress environment does not benefit cow or calf performance.

Key Words: yeast cell wall, calf performance, cow performance

1461 (M222) Effect of restricted feeding on body weight, some hematological and biochemical parameters in sheep and goats raised under semiarid conditions.

E. B. Abdalla*, *Faculty of Agriculture, Ain Shams University, Cairo, Egypt.*

A total of 10 Barki sheep and 10 Baladi goats were used in 4-mo experiment to investigate to what degree local sheep and goats can tolerate feed shortage under semiarid conditions and to compare sheep and goats for their ability to withstand these harsh conditions. Animals were divided into two groups according to feeding level (50 and 100% of maintenance energy requirements). Changes in live body weight and some biweekly hematological and blood biochemical parameters were examined. Restricted feeding level did not affect (P > 0.05) live body weight. In both sheep and goats, restricted diets showed a significant (P < 0.05) decrease in hemoglobin (Hb) and packed cell volume (PCV %). Reduction was shown in erythrocytes cell counts (RBCs) especially in goats (P < 0.05). Restricted feeding showed a significant decrease in white blood cells (WBCs) in both species, but the reduction was much greater in goats than in sheep (17.15 and 7.75%). Animals fed restricted diets show a significant decrease (P < 0.05) in total protein, globulin, and triglyceride, and a nonsignificant increase in albumin, albumin/globulin ratio, and total lipids in both species. While glucose and cholesterol increased in sheep, both parameters decreased in goats. Alanine transferase (ALT), aspartate transferase (AST), and γ glutamyl transferase (GGT) were increased in both species that received restricted diet. The increase in the three enzymes was significant only in sheep, and the GGT was only significant in goats. While alkaline phosphatase was significantly decreased in sheep, it was significantly increased in goats. Restricted feeding resulted in a significant increase in blood urea and a significant decrease in creatinine concentration in both species. In conclusion, results revealed that both sheep and goats are adapted to feed shortage with higher tolerance in sheep than in goats under semiarid conditions.

Key Words: sheep, goats, restricted feeding

1462 (M223) Effects of trace mineral-fortified, limit-fed creep supplements on performance of beef calves (post-weaning).

A. Saran Neto[1], L. S. Caramalac[2], P. G. M. D. A. Martins[2], P. Moriel[2], H. J. Fernandes[3], and J. D. Arthington*[2], *[1]University of São Paulo, Pirassununga, Brazil, [2]UF/IFAS Range Cattle Research and Education Center, Ona, FL, [3]State University of Mato Grosso do Sul, Aquidauana, Brazil.*

The effects of limit-fed creep supplements, with or without trace mineral (TM) fortification, on measures of performance

and stress in heifers following weaning were evaluated. Heifers were derived from an experiment involving 30 cow/calf pairs, stratified by birth date and randomly allocated to 1 of 15 pastures (2/pasture). Calves were approximately 5 mo of age at the start of the study. Four treatments were randomly assigned to pastures, including, (1) limit-fed creep fortified with hydroxy-Cu, Zn, and Mn, (2) limit-fed creep fortified with Cu- and Zn-sulfate and Mn-oxide, (3) limit-fed creep without TM fortification, and (4) no limit-fed creep (n = 3, 3, 4, and 5 pastures, respectively). Creep supplements for treatments 1 and 2 were also fortified with Co carbonate, Na selenite, and I (via EDDI). All cattle were provided access to salt with no TM fortification. Supplements were offered Monday, Wednesday, and Friday (265 g/calf) for 89 d prior to weaning, targeting a maximum intake of 114 g/d. At weaning, heifers consuming TM-fortified creep, irrespective of source, had greater ($P \leq 0.02$) liver Cu concentrations compared to heifers consuming no limit-creep or limit-creep without TM fortification. Following weaning, 15 heifers were individually provided free-choice access to a soybean hull-based feed and ground grass hay for 16 d. The acute phase protein response (APR) was assessed via plasma concentrations of the Cu-dependent protein, ceruloplasmin, on d 0, 2, 5, 9, and 16. Shrunk BW was measured on d 0 and d 17. Total DMI of calves provided TM-fortified, limit-creep supplements, irrespective of TM source, was less ($P = 0.03$) than calves not provided limit-creep or calves provided limit-creep without TM fortification (1.21 vs. 1.80% BW; SEM = 0.262). This response was mostly the result of less ($P = 0.056$) grain DMI among heifers provided TM-fortified, limit-creep vs. no limit-creep or limit-creep without TM-fortification (0.45 vs. 0.86% BW, respectively; SEM = 0.320). Heifers provided TM-fortified limit-creep had a greater ($P = 0.05$) increase in post-weaning plasma ceruloplasmin (8.02 and 5.04 mg/dL, respectively; SEM; 2.354) and less ($P = 0.03$) BW gain (7.9 vs. 17.6 kg; SEM = 9.26) compared to calves provided no limit-creep or limit-creep without TM-fortification. These results imply that TM-fortified limit-fed creep feed results in increased Cu status of weaned calves which corresponded to a heightened Cu-dependent APR and less post-weaning DMI and BW gain.

Key Words: calves, creep feeding, trace minerals

1463 (M224) Young beef calves preferentially consume supplements fortified with hydroxy vs. organic and sulfate sources of Cu, Zn, and Mn.

L. S. Caramalac*[1], H. J. Fernandes[2], and J. D. Arthington[1], [1]*UF/IFAS Range Cattle Research and Education Center, Ona, FL,* [2]*State University of Mato Grosso do Sul, Aquidauana, Brazil.*

Our objective was to evaluate the preferential intake of supplements fortified with Cu, Zn, and Mn from; (1) hydroxy, (2) organic, and (3) sulfate-sources. This was achieved in 4 individual feeding studies involving 8 pens of early-weaned calves (2 calves/pen; average age = 120 d; average BW = 115 kg). Each pen was provided free-choice access to a mixed concentrate ration and ground grass hay. On each study day at 10:00, all feed was withdrawn and calves were offered 3 different mineral fortified supplements, for a 4 h period, provided in three separate feeding containers. Supplements were created using a base mixture containing 52, 46, and 2% cottonseed meal, ground corn, and salt. Supplements were fortified with 2,000 mg/kg Zn (Exp. 1), 750 mg/kg Cu (Exp. 2), 3,000 mg/kg Mn (Exp. 3), and all 3 elements (Exp. 4). Preferential intake was measured over 7- (Exp. 1, 2, and 3) and 14-d (Exp. 4) evaluation periods. In Exp. 1 and 2, calves consumed more ($P < 0.001$) of the supplement offer containing hydroxy Cu (Exp. 1) and hydroxy Zn (Exp. 2) then sulfate and organic sources, while consumption of sulfate sources was greater ($P \leq 0.04$) than organic sources (81.9, 72.2, and 45.5%, and 48.1, 35.1, and 9.5% consumption of supplement offer for hydroxy, sulfate, and organic sources of Cu and Zn, respectively; SEM = 3.94 and 7.93). In Exp. 3, calves consumed more ($P < 0.001$) of the supplement offer containing hydroxy Mn than sulfate and organic sources, while there were no differences ($P = 0.97$) in preferential intake of supplements containing Mn sulfate or organic Mn. In Exp. 4, when all 3 elements were combined within a single supplement, calves almost exclusively selected ($P < 0.001$) the supplements containing hydroxy-source elements vs. supplements containing sulfate or organic sources (70.0, 12.5, and 8.0% consumption of supplement offer for hydroxy, sulfate, and organic sources, respectively; SEM = 3.16. When offered to young calves, these results reveal a lesser preferential intake of trace mineral concentrated supplements fortified with organic and sulfate sources of Cu, Zn, and Mn compared to the same supplements fortified with hydroxy sources of these elements.

Key Words: trace minerals, supplementation, calves

1464 (M225) Predicting dry matter intake of steers and heifers in the feedlot by using categorical and continuous variables.

O. Koskan*[1], H. Koknaroglu[1], D. D. Loy[2], and M. P. Hoffman[2], [1]*Suleyman Demirel University, Isparta, Turkey,* [2]*Iowa State University, Ames.*

Close-out information, submitted by Iowa cattle producers to the Iowa State University Feedlot Performance and Cost Monitoring Program, was used to develop dry matter intake prediction model for steers and heifers by considering categorical and continuous variables. Close-out information consisting of 1651 pens of steers and 601 pens of heifers included information on start and end dates, cattle per pen, sex, housing type, days on feed, initial and sale weight, feed conversion (FC), proportion of concentrate, average daily gain (ADG), percent death loss, feed cost and total cost per 45.35 kg gain, breakeven sale price, non-feed variable cost, non-feed fixed cost and corn price. Dry matter intake (DMI) was not provided but

was calculated as DMI = ADG x FC. In predicting DMI, categorical regression analysis (optimal scaling) was applied for steers and heifers separately. Independent variables used were starting date on feed (season) (1 = winter: December through February; 2 = spring: March through May; 3 = summer: June through August, and 4 = fall: September through November), number of cattle per pen (head), housing type (housing) (1 = confinement, 2 = partially open lot, 3 = open lot), days on feed (dof), initial weight (iw), proportion of concentrate (concentrate). When the model was applied separately for steers and heifers, DMI prediction for steers was found as DMI = 0.540*iw + 0.017*season +0.143*housing -0.062*head– 0.096*concentrate– 0.186*dof (R^2 = 0.433), whereas DMI prediction for heifers was found as DMI = 0.706*iw + 0.086*season + 0.085*housing + 0.186*dof -0.099*head– 0.084*concentrate (R^2 = 0.468). With this model, categorical variables such as housing type and season are included in the regression model and this may help professionals predict the DMI of their steers and heifers in the feedlot.

Key Words: dry matter intake prediction, categorical regression, feedlot

---

1465 (M226) Comparison of high-performance dairy cows fed concentrates vs. those fed no concentrates over a period of 10 yr. P. L. Kunz*[1], M. Buergisser[1], and M. Furger[2], *[1]Bern University of Applied Sciences, Zollikofen, Switzerland, [2]Agricultural Education and Advisory Centre Plantahof, Landquart, Switzerland.*

Milk prices in Switzerland have been falling for years. As a result, farmers seek to reduce production costs by feeding lower amounts of the most expensive feed component, i.e., concentrates, or cease feeding concentrates altogether. To clarify how high-performance dairy cows respond to a lack of concentrates in their rations, the high-performance herd (75 Brown Swiss cows) at the experimental farm of the Plantahof Agricultural Centre was divided into two groups: one herd (forage herd = FH, 37 cows) has not received concentrates since 2003, while the other herd (concentrate herd = CH, 38 cows) received the same roughage feed components as the FH and an additional 1500 kg concentrates per cow and lactation. The ration was composed of hay, dried grass and maize silage in winter, and hay, grass and maize silage in summer. Both herds were of equal genetic value, as the same bulls were used to sire progeny. Cows which left the herds were replaced by daughters originate from the same herd. Because not all results have been analysed up to now, the results shown are based on different times. The two feeding regimes resulted in differences between the two trial herds: Over the past 6 yr, feed intake in CH cows was higher (25.6 ± 3.3 kg DM/day) than in FH cows (21.5 ± 2.3 kg DM/day). Similarly, over the past 9 yr, milk yields of CH cows (10,323 ± 731 kg/Lactation) exceeded that of FH cows (8279 ± 341 kg/Lactation). There was no difference in milk fat and milk protein content. The CH cows suffered higher incidences of milk fever, acetonemia and ovarian cysts over a 4-yr period than the FH cows. None of these results were statistically significant. A total of 48 of the CH cows and only 27 of the FH cows had to be sent to slaughter due to infertility or illness over a 4-yr period. The economic analysis shows that in the Swiss cost environment the forage herd (FH) yielded a higher agricultural income than the concentrate herd (CH). This was primarily due to the higher feed costs for and inferior health of the CH.

Key Words: dairy cows, concentrates, costs of production

1466 (M227) Effect of *Leukonostoc citreum* SK2556 fermented korean aged garlic extract (KAGE) on feed intake, production performance, egg quality, odor gas emission from feces, excreta microbiota and hematological profiles in laying hens. D. Jung*, J. H. Cho, and I. H. Kim*, Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

The goal of this study was to investigate the impacts of dietary supplementation with Dorean aged garlic extract (KAGE) fermented by *Leukonostoc citreum* SK2556 on feed intake, production performance, egg quality, odor gas emission from feces, excreta microbiota and hematological profiles in laying hen. A total of 384, 54-wk (ISA- brown) laying hens were randomly assigned to 1 of 4 treatments with 8 replications per treatment and 12 adjacent cages as a replication (hens were caged individually). The experimental treatments were: 1) CON (Basal diet), 2) KAGE1 (CON + 0.05% Fermented Aged Garlic Feed Additive), 3) KAGE2 (CON + 0.1% Fermented Aged Garlic Feed Additive), and 4) KAGE3 (CON + 0.2% Fermented Aged Garlic Feed Additive). KAGE compounds were analysed by HPLC methods, IgG in the serum were then analysed using an automatic biochemistry blood analyser (HITACHI747, Tokyo, Japan), WBC, RBC and lymphocyte concentrations using an automatic blood analyser (ADVIA120, Bayer, Tarrytown, NY, USA) and fecal *Lactobacillus* and *E. coli* shedding were measured by using MacConkey agar plates and *lactobacilli* medium III agar plates. At 3 wk, laying hen fed with KAGE showed higher yolk height than CON (9.38, 9.47, 9.48 vs. 9.17 mm; $P < 0.05$). In the next week, KAGE3 proved better yolk height along with egg shell thickness compared to CON (9.47mm, 41.75mm^{-2} vs. 9.18mm, 40.26 mm^{-2}; $P < 0.05$). Likewise, 0.1 and 0.2% KAGE had meaningful higher value (96.23, 96.08 vs. 93.99; $P < 0.05$) on haugh unit than CON diets. In the last week of experiment, results showed that KAGE2 and KAGE3 treatment improved yolk height and egg shell thickness compared with basal diet (9.52, 9.52 vs. 9.25 mm; 41.89, 41.93 vs. 40.26 mm^{-2}; $P < 0.05$). Haugh unit was influenced by the 0.2% KAGE over CON (96.42 vs. 94.49; $P < 0.05$). However, laying hen feed with KAGE showed no significant result on feed intake, production performance, excreta gas production and microbiota

and blood composes in any level of experiment. In a nut shell, our findings demonstrated that the administration of KAGE at a level of 0.1% and/or 0.2% can improve yolk height, haugh unit and egg shell thickness in laying hen.

Key Words: aged garlic extract, laying hens, *Leukonostoc citreum* SK2556, haugh unit, gas emission

1467 (M228) Effects of probiotics supplementation on growth performance, nutrient digestibiliry, carcass characteristics, meat quality, intestinal microflora and fecal noxious gas emission in broilers. I. H. Kim*, Y. Lei, and S. Kim, *Dep. of Animal Science, Dankook University, Cheonan, South Korea.*

A total of 765 broilers (BW 36.77 ± 0.33 g; 1 d old) were used in a 35-d feeding trial to evaluate the effect of fermented plants on performance, carcass traits, blood profiles, nutrient digestibility, intestine microbial population and fecal noxious gas emission of broiler chicks. Broilers were randomly distributed into 1 of 5 treatments on the basis of BW (9 replicate pens per treatment with 17 broilers per pen). Dietary treatments were: 1) NC (basal diet); 2) PC (NC + 5ppm enramycin); 3) P1 (NC with 0.5% of CP reduced + 150ppm phytogenics; 4) P2 (NC + 0.1% probiotics); 5) P3 (NC + 0.2% probiotics). All nutrients in diets were formulated to meet or exceed the recommendation of NRC (1994) for broilers. The broilers were weighed and feed intake were recorded on d 1, 14, 28, and 35 for calculating BW gain (BWG), feed intake (FI), and feed conversion ratio (FCR). At d 35, fresh excreta samples were collected from each pen for the measurement of nutrient digestibility according to the procedures of AOAC (2003). All data were subjected to GLM procedures of SAS (1996) as a randomized complete block design, with pen as the experimental unit. Differences among treatments were separated by Duncan's multiple range test; $P < 0.05$ was considered statistically significant. Overall, broilers fed P3 diet had greater (1770 vs. 1681 g; $P < 0.05$) body weight gain (BWG), and lower (1.555 vs. 1.625; $P < 0.05$) feed conversion ratio (FCR) than those fed NC diet. The nutrient digestibility of dry matter (DM) and nitrogen (N) was increased (76.30 vs. 73.26%; 65.32 vs. 62.71%; $P < 0.05$) in P3 compared with NC. There was no difference ($P > 0.05$) in meat quality, relative organ weight and blood profiles. Addition of 0.2% probiotic enhanced the growth of *Lactobacillus*, but inhibited *Escherichia coli* in the small intestinal and large intestinal. Also, addition of 0.1% probiotic showed same result with P3 on the large intestinal microflora but no change in the number of *Lactobacillus* and *Escherichia coli* in small intestine. A significant increase in the rate of ammonia was observed in 1.0 g/kg and 2.0 g/kg probiotic-treated birds versus controls.

Key Words: broilers, growth performance, gas emission, nutrient digestibility, probiotic

1468 (M229) Effects of a synbiotic feed additive on milk quality and calving interval in Brazilian dairy herds. R. D. Sainz*[1], E. A. Filgueiras[2,3,4], C. U. Magnabosco[5], P. H. Medes[3], and K. S. Mendanha[2], *[1]University of California- Davis, Davis, CA, [2]Universidade Federal de Goiás, Goiânia-GO, Brazil, [3]Biofórmula Ltda, Goiânia-GO, Brazil, [4]CAPES, Brasília-DF, Brazil, [5]Embrapa Cerrados, Brasília, Brazil.*

Data on milk quality and reproduction were collected from 22 dairy herds in the Brazilian states of Paraná, Rio Grande do Sul, Minas Gerais and Goiás. These herds were selected because each one had used the synbiotic Biofórmula Leite (Biofórmula, Goiânia-GO, Brazil) at the minimum dose of 2 g·animal^{-1}·d^{-1}for a minimum of 1 yr and had records of milk yield and quality and herd reproduction for at least 1 yr before and 1 yr after the start of treatment. The synbiotic contained a mixture or probiotic microorganisms, prebiotics and fibrolytic enzymes. After data tabulation and verification, seven herds (total 189 cows) had sufficient information to study treatment effects on milk quality and three (total 115 cows) had enough for reproductive performance, all primarily Holsteins. The data for the 12 mo preceding treatment were considered as the control, and those for 12 mo following initiation of treatment as treated. Somatic cell count (SCC) data were log-transformed before analysis. These data were subjected to a meta-analysis using a mixed model considering herd as a random variable and treatment as a fixed effect nested within herd. There were no significant differences between treatments in milk yields and the concentrations of fat, protein and total milk solids in milk, but there were reductions in SCC (−41%, 654,963 vs. 386,473 SC/mL, $P < 0.001$) and in calving interval (−73 d, 446.3 vs. 373.4 d, $P < 0.01$) following initiation of treatment with the synbiotic. The synbiotic feed additive used in this study proved to be an effective tool in the reduction of somatic cells in milk as well as in improving the fertility of cows in commercial dairy herds, confirming results obtained under research conditions.

Key Words: dairy, somatic cells, reproduction

1469 (M230) Effects of injectable trace minerals at the start of the breeding season on attainment of pregnancy in commercial beef cows. J. D. Arthington[1], P. G. M. D. A. Martins[1], P. Moriel*[1], and L. Havenga[2], *[1]UF/IFAS Range Cattle Research and Education Center, Ona, FL, [2]MultiMin USA, Ft. Collins, CO.*

Our objective was to evaluate the effects of a single application of injectable trace minerals (ITM; MultiMin 90, MultiMin USA, Inc., Fort Collins, CO) on pregnancy attainment of lactating beef cows. Mature Brahman x British crossbred beef cows (n = 3750) were enrolled from 14 separate commercial cow/calf operations in central and southern Florida. Ranch breeding season ranged from 90 to 120 d with study

enrollment < 30 d after the start of the breeding season. During enrollment, cows were administered 5 mL of ITM or sterile saline subcutaneously in alternating order. The ITM contained 60, 10, 15, and 5 mg/mL of Zn, Mn, Cu, and Se, respectively. At the time of treatment administration, cow body condition score (BCS) was recorded and assigned a BCS category group (1 = low; 2 = moderate; 3 = high). In addition, samples of pasture forage and trace mineral supplement were collected. To estimate ranch trace mineral status, liver biopsy samples were collected from 10% (maximum of 16) of the enrolled cows. Treatment assignment was identified by an individual number and color coded ear tag. Tags were removed during pregnancy diagnosis. Overall tag loss was low and equally distributed between treatments (96.3 and 95.5% tag recovery for ITM and Saline, respectively) resulting in a total of 3597 collected tags for pregnancy analysis. Average Se and Cu were highly variable among ranches (Se, range = 0.39 to 4.36 and average = 1.14 ± 1.04 mg/kg DM; Cu, range = 65 to 307 and average = 158 ± 78 mg/kg DM). There were 5 and 3 ranches classified as Se and Cu deficient (liver concentrations < 0.60 and 100 mg/kg DM, respectively). There was no ranch x treatment interaction ($P = 0.50$) or overall treatment effect ($P = 0.19$) for pregnancy attainment (88.8 and 87.2% pregnant for ITM and Saline, respectively; SEM = 0.88). Attainment of pregnancy increased ($P < 0.001$) with increasing BCS category (83.9, 86.7, and 91.0 for low, medium and high BCS categories, respectively). Interestingly, although not statistically significant ($P = 0.62$), the numeric difference between the percentage pregnancy attainment due to ITM increased as cow BCS decreased (3.1, 1.8, and 0.1% for low, medium, and high BCS categories, respectively). Provided at the start of the breeding season, ITM injection did not significantly improve pregnancy outcome in the commercial cow/calf ranches enrolled in this study.

Key Words: injectable trace minerals, cow, pregnancy

1470 [Withdrawn]

1471 (M232) Cost analysis of feeding bermudagrass (*Cynodon dactylon*) or ryegrass (*Lolium multiflorum*) plus rye (*Secale cereale*) baleage based on nutrient composition and forage refusal of weaned crossbred beef calves. R. M. Martin*[1], R. J. Pruitt[2], B. Buttrey[3], and R. Walker[3], *[1]louisiana State University AgCenter, School of Animal Sciences, Baton Rouge, [2]Louisiana State University AgCenter, Agricultural Economics and Agribusiness, Baton Rouge, [3]Louisiana State University AgCenter, Hill Farm Research Station, Homer.*

In the Gulf Coast region, supplementation can be costly for weaned beef calves during the fall backgrounding period due to limited forage production and quality. A study was conducted evaluating performance of weaned Angus crossbred calves fed bermudagrass (*Cynodon dactylon*) or ryegrass (*Lolium multiflorum*) and rye (*Secale cereale*) baleage in hay rings during a 60-d fall backgrounding period. Four forage treatment comparisons included: early boot stage bermudagrass harvested for hay (BERH), early boot stage bermudagrass harvested for baleage (BERB), early boot stage ryegrass and rye harvested for baleage (ERRG), and bloom stage ryegrass and rye harvested for baleage (LRRG). Both BERH and BERB were harvested from the same hay field at the same time. Nutrient composition of forage treatments included 8.2% CP, 59.9% TDN, and 88.8% DM (BERH); 9.2% CP, 57.4% TDN, and 49.1% DM (BERB); 12.8% CP, 64.5% TDN, and 37.2% DM (ERRG); and 9.2% CP, 62.7% TDN, and 55.7% DM (LRRG). Forage refusal on a DM basis was estimated as amount of (kg) and percent of bale weight fed based on forage remaining outside of the hay ring. Cost estimates for each treatment were performed based on nutrient composition and forage refusal and were derived using standard performance assumptions associated with the tractor and implements used during harvesting of the forage and adjusted for the time needed to harvest forages for this study. Total costs of production were $293.92/ton DM (ERRG), $209.18/ton DM (LRRG), $128.33/ton DM (BERB), and $117.87/ton DM (BERH). On a cost per nutrient basis, ERRG had the greatest cost/lb of CP and TDN ($1.15 and $0.23) followed by LRRG ($1.14 and $0.17), BERB ($0.70 and $0.11), and BERH ($0.72 and $0.10), respectively. Forage refusal was greater ($P = 0.01$) for the BERH (115 kg and 10.0%) compared with BERB (27 kg and 3.4%), ERRG (26 kg and 5.0%), and LRRG (29kg and 3.7%) treatments, but similar among BERB, ERRG, and LRRG, respectively. Value associated with hay refusal measured outside the hay ring was $14.73/ton DM (ERRG), $7.66/ton DM (LRRG), $4.39/ton DM (BERB), and $11.74/ton DM (BERH). Production costs were lower for bermudagrass harvested as dry hay or baleage. While hay refusal was less outside the hay ring for all baleage treatments, the high value of hay refusal and production cost of the ERRB treatment was greatly associated with the high moisture content of the bales.

Key Words: baleage, economics, weaned beef calves

1472 (M233) Evaluation of three copper sources on measures of forage utilization and copper status in beef cattle. P. G. M. D. A. Martins[1], O. F. R. Cunha[1], G. P. Caputti[1], A. Saran Neto[2], J. M. B. Vendramini*[1], and J. D. Arthington[1], *[1]UF/IFAS Range Cattle Research and Education Center, Ona, FL, [2]University of São Paulo, Pirassununga, Brazil.*

We investigated the effect of Cu source on measures of subtropical forage utilization and Cu status in beef cattle. In Exp. 1, 24, 2-year old heifers (371 ± 48.1 kg) were individually fed limpograss hay and 2.1 kg/d of a molasses-based supplement (8.3 and 3.0 mg Cu/kg DM, respectively). Treatments were assigned to heifers consisting of, (1) no Cu, and 100 mg Cu/d

from (2) hydroxy Cu, (3) organic Cu, or (4) Cu sulfate. Forage DMI and liver Cu change was assessed over 33 d. In Exp. 2, forage DMI and DM, N, and NDF in situ ruminal disappearance was evaluated in 4 ruminally-fistulated steers using a 4 x 4 Latin square design with 4, 20-d periods with the same treatments as Exp. 1. Periods consisted of 10 d of no Cu, 7 d adaptation, and 5 d in situ bag incubation. Dried and ground bermudagrass (4 g) was placed into polyester bags and duplicate samples were incubated for 0, 3, 6, 9, 12, 24, 48, and 72 h. The non-linear model used was P=A+B [1-exp(-c x t)]. In Exp. 1, supplemental Cu had no effect ($P = 0.40$) on voluntary forage DMI; however, heifers provided hydroxy Cu tended ($P = 0.07$) to consume less hay than heifers consuming organic Cu (1.31 vs. 1.46% BW). All heifers experienced a decrease ($P < 0.001$) in liver Cu; however, heifers consuming no Cu tended ($P = 0.12$) to have a greater decrease vs. all other treatments, and heifers provided hydroxy Cu tended ($P = 0.14$) to have a lesser decrease than heifers consuming organic Cu (-94, -80, -64, and -44 mg/kg DM for no Cu, organic Cu, Cu sulfate, and hydroxy Cu, respectively). In Exp. 2, the DM, N, and NDF fractions were described as A, rapidly degradable; B, potentially degradable; and C, undegradable. There was no effect ($P \geq 0.15$) of treatment on forage DMI and in situ DM disappearance. Fraction A NDF and N did not differ among treatments; however, NDF fraction B tended ($P < 0.06$) to be greater for steers provided organic Cu vs. all other treatments (48.7 vs. 41.2%). Similarly, N fraction B was greater ($P = 0.03$) for steers receiving organic Cu vs. hydroxy Cu and No Cu (29.2 vs. 19.0%). These results imply that the organic Cu source utilized in these studies may positively influence the digestibility of subtropical forages.

Key Words: copper, digestibility, cattle

1473 (M234) Comparison of camelina meal and DDGS in the diet of replacement beef heifers. E. E. Grings, A. Sackey*, and G. A. Perry, *South Dakota State University, Brookings.*

The objective of this study was to evaluate the effect of supplementing beef heifers with either cold-pressed camelina meal or dried distillers grains with solubles (DDGS) for 75-d before breeding on weight gain and pregnancy rates. Heifers ($n = 110$) were blocked by weight (BW = 300 ± 1.1 kg) into five pens per treatment and assigned to one of two dietary treatments. Heifers fed camelina meal consumed an average of 5.3 kg/d millet hay, 0.7 kg/d camelina meal and 1.3 kg/d corn, whereas heifers fed DDGS consumed an average of 5.3 kg/d millet hay, 1.1 kg/d DDGS and 0.9 kg/d corn. Average nutrient composition of diets was 9.3% CP, 52.6% NDF and 29.5% ADF for the camelina diet and 9.6% CP, 54.7% NDF and 29.3% ADF for the DDGS diet. Supplements were placed in bunks each morning and millet hay fed after supplements had been consumed. Heifers were bred following a 5-d CO-synch + CIDR fixed time AI protocol and transported to pasture the next day. Fourteen d later, three clean-up bulls were placed in the pasture for 46 d. Pregnancy was determined by transrectal ultrasonography 96 d after AI. Weight and pregnancy data were analyzed using the GLM and GLIMMIX procedures of SAS, respectively. ADG (0.45 ± 0.08 kg/d; $P = 0.2$) and final BW (339 ± 1.26 kg; $P = 0.97$) did not differ between treatments during the 75-d treatment period. Similarly, no difference ($P = 0.35$) was detected for BCS (5.2 ± 0.04) at breeding between treatments. We noted no differences between treatments in conception to timed AI ($P = 0.57$) or in total pregnancy rate ($P = 0.35$). Our data suggests that camelina meal has the potential to serve as a feed resource for replacement heifers with no adverse effect on weight gain or pregnancy rates.

Key Words: beef heifers, protein supplement, reproduction

1474 (M235) Effects of prepartum evaporative cooling and vitamin E supplementation on immune function of Holstein cows during summer in Florida. G. C. Gomes*[1], J. E. Zuniga[1], E. Karakaya[1], L. F. Greco[1], L. D. P. Sinedino[1], N. Martinez[1], R. S. Bisinotto[1], E. S. Ribeiro[1], P. M. Leopoldo Junior[1], M. A. Engstrom[2], J. P. Driver[1], J. E. P. Santos[1], and C. R. Staples[1], *[1]Dep. of Animal Sciences, University of Florida, Gainesville, [2]DSM, Eden Prairie, MN.*

Objective was to evaluate the relationship of vitamin E (VitE) supplementation and prepartum environment on immunity of Holstein cows. Animals ($n = 70$) were blocked at 30 d prepartum by parity, milk yield, and body weight, and randomly assigned to treatments arranged in a 2 × 2 factorial. Cows were housed until parturition in either a free-stall barn equipped with fans and sprinklers (Cooling- C) or in an open lot providing only shade (No cooling- NC). After parturition, all cows were housed in a free-stall barn equipped with fans and sprinklers. All-rac-α-tocopherol (DSM, Parsippany, NJ) was top dressed daily at 1000 IU prepartum and 500 IU postpartum per cow for moderate VitE (M) or 3000 IU prepartum and 2000 IU postpartum per cow for high VitE (H). Blood samples were collected in the prepartum at d -30, and -14 relative to parturition. After calving, blood samples were obtained at d 3, 7, 14, 21, 28, 35, and 42. Analyses included phagocytosis and oxidative burst by neutrophils, percentage of lymphocytes positive for IL-10 and IFN-γ production after PMA/ionomycin stimulation, percentage of total, CD4(+), CD8(+), and γδ subtypes of T lymphocytes, concentrations of serum IgG against ovalbumin challenge at d -30, -14, and 3, and acute phase proteins. Data were analyzed by ANOVA for repeated measures with PROC GLIMMIX of SAS. Non -normally distributed data was appropriately transformed. Results from cytokines and neutrophil function analyses are presented as fold increase in percentage of positive cells or mean fluorescence intensity (MFI) relative to unstimulated

controls. Feeding more VitE increased ($P < 0.05$) the percentage of lymphocytes producing IFN-γ (10.0 vs. 5.4). Prepartum cooling tended ($P < 0.10$) to increase the percentage of T lymphocytes (31.0 vs. 23.4%) relative to total lymphocytes, CD4(+) subtype (12.4 vs. 7.4%), and IgG against ovalbumin (0.552 vs. 0.480 O.D.). Providing H vitE to NC cows tended to increase phagocytic activity (MFI) by neutrophils (4.83 vs. 4.25) whereas the reverse occurred when cows were cooled prepartum (4.52 vs. 5.20). Oxidative burst activity (MFI) of neutrophils from multiparous cows was enhanced when cows were cooled (8.72 vs. 6.59) whereas the opposite occurred for primiparous cows (4.84 vs. 5.84). VitE supplementation and prepartum cooling caused changes in adaptive immunity patterns. Additionally, prepartum cooling provided a conditional improvement of innate immunity depending on amount of vitE supplemented and parity, which might reflect differences in metabolic and oxidative stress status.

Key Words: cow, heat stress, vitamin E

1475 (M236) Forages used in high producing cow rations in CA. Y. Trillo[*1], A. Lago[2], and N. Silva-del-Rio[1], *[1]VMTRC, University of California, Tulare, [2]DairyExperts, Tulare, CA*

The objective of this study was to describe the forages included in the high cow ration of 16 California dairies ranging in size from 1000 to 6000 lactating cows. Records from a consecutive 12-mo period, starting from January to June 2012, were extracted from the feeding management software FeedWatch 7.0 (FW). Records from 16 high cow (HC) recipe and 13 high cow premix (HCP) recipe were used. Two dairies did not prepare premix and one dairy had sporadic premix records and records were not included in the final data set. Descriptive statistics were conducted with SAS 9.3. Across dairies, three to seven forage types were available to fed high producing cows. Most forages were directly included into the HC recipe. But some dairies included straw in the HCP recipe ($n = 5$). The median number of forages included daily in the HC recipe was two ($n = 7$), three ($n = 4$), four ($n = 4$), or five ($n = 1$). Throughout the 12-mo study period, the number of forages in the HC recipe varied within dairy in zero ($n = 1$), one ($n = 10$) or two ($n = 5$) forages. All dairies fed alfalfa hay, either for a twelve ($n = 14$) or seven ($n = 2$) month period. When alfalfa hay was not fed ($n = 2$), cows were fed green chop alfalfa. All dairies included corn silage in the HC recipe, but in some dairies it was only fed for 11 ($n = 3$), 9 ($n = 2$), 8 ($n = 1$), or 5 ($n = 1$) mo. BMR corn silage was fed ($n = 3$) in combination with conventional corn silage for 3 to 9 mo. High moisture earlage ($n = 5$) was fed for 2 to 6 mo in combination ($n = 4$) or not ($n = 1$) with corn silage. Other silages, such as wheat ($n = 5$), alfalfa ($n = 3$) or both ($n = 4$) were also included for 3 to 12 mo or 1 to 10 mo, respectively. Other crops were fed occasionally [sorghum silage ($n = 2$) and oat silage ($n = 1$)]. Some dairies fed straw for 6 to 12 mo ($n = 6$) while others for less than 2 mo ($n = 3$). Only 10 dairies had records of DM adjustments on FW. For corn silage, DM adjustments were made zero ($n = 4$), six ($n = 2$), eight ($n = 1$), nine ($n = 2$) or ten ($n = 1$) times in a year. Although corn silage and alfalfa hay are the most common forages used in California dairies, wheat silage, alfalfa silage and straw are other common roughage sources for high producing cows.

Key Words: dairy cow, forages, feeding management software

1476 (M237) Evaluating on-farm methods for measuring dry matter content of potatoes. R. J. Norell[*1], J. B. Glaze, Jr.[2], M. Chahine[2], and N. L. Olsen[3], *[1]University of Idaho, Idaho Falls, [2]University of Idaho, Twin Falls, [3]University of Idaho, Kimberly.*

Measuring dry matter content is critical for pricing cull potatoes and for effectively managing potato feeding rates on livestock operations. In this study, dry matter determinations from three on-farm methods (microwave, dehydrator, and Koster Moisture tester) were compared with a laboratory oven. Twenty lots of potatoes were obtained for the study (1 blue, 3 red, 3 yellow, and 14 burbank varieties). Ten potatoes from each lot were cleaned then sliced horizontally into 7mm thick slices. Duplicate 100-g subsamples were run with each drying method. Lab (L) samples were dried for 24 h at 55 C. Equipment for the on-farm methods included two 1000-W microwaves (M), four 500-W Nesco FD60 food dehydrators (D) set at 68 C, and two Koster Moisture Testers (K). Samples were weighed at specified time intervals during the drying process with the on-farm methods and a run was deemed complete when two identical weights were obtained. Drying time and dry matter (DM) data were analyzed as a completely randomized block design. Drying time differed significantly between on-farm methods ($P < 0.001$) and averaged 8.6, 248.5, and 428.6 min for M, K, and D, respectively. Mean DM was significantly higher ($P < 0.05$) for M (23.4%) and D (23.5%) than K (22.6%) or L (22.7%). A Bland-Altman assessment for agreement was used to compare difference in DM between each on-farm method and L. A range of agreement was defined as mean bias + or– 2 SD. The 95% limits of agreement between the lab oven and M, K, and D were: -0.7% to 1.5%; -1.6% to 1.4%; -1.0% to 1.6%, respectively. Overall, the three on-farm methods provided closely corresponding DM to L. The trend lines between Bland-Altman differences and oven DM were not statistically significant ($P > 0.75$) for D and K but was significant ($P < 0.05$) for M with a negative slope across the range of DM in the study. Drying potatoes with all three on-farm methods did not create objectionable odors and can therefore be conducted indoors if desired. This study indicates that the three on-farm methods are effective tools for measuring DM content of potatoes.

Key Words: potatoes, dry matter, on-farm testing

1477 (M238) Optimizing drying time of potatoes by food dehydrator and Koster Moisture Tester.

R. J. Norell*[1], J. B. Glaze Jr.[2], M. Chahine[2], and N. L. Olsen[3], *[1]University of Idaho, Idaho Falls, [2]University of Idaho, Twin Falls, [3]University of Idaho, Kimberly.*

Cull potatoes lose moisture over time when stacked outdoors in a pile. Measuring dry matter content on a frequent basis is therefore important for effectively managing potato feeding rates for cattle. In this study, different sample processing methods were compared for drying potatoes. In trial 1, drying time (DT) and dry matter content (DM) were evaluated for four potato sample sizes in food dehydrators and a lab oven 7-mm-thick horizontal slices (THICK), 3.5-mm-thick horizontal slices (THIN), 7-mm-square fries (LFF), and 3.5-mm-square fries (SFF). The dehydrators were 500-W, Nesco brand FD-60 with four trays, and each tray had a plastic insert to prevent sample movement between trays. Operating temperature was set at 68°C for the dehydrator and the lab oven was set at 55°C. Four lots of potatoes were used with a single lot analyzed each test day. Forty potatoes per lot were cleaned, and 10 were randomly selected for each processing method. A 100-g subsample from each processing method was then randomly assigned to an individual tray within dehydrator. Drying time was significantly different between potato processing methods ($P < 0.001$) with THICK requiring the longest time (459 min), LFF (264 min), SFF (225 min) and THIN (205 min). DM differed between processing methods with THICK slices having higher DM ($P < 0.053$) than the other three processing methods. DM was 0.8% lower ($P < 0.05$) in the lab oven than in dehydrator. In trial 2, DT and DM were evaluated for potatoes processed into THICK and LFF with two Koster Moisture Testers, lab oven, and eight potato lots. Twenty potatoes were cleaned from each lot, with 10 randomly assigned to each processing method. Three 100-g subsamples from each processed lot were randomly assigned to a Koster tester or lab oven. LFF reduced DT ($P < 0.001$) by 101 min compared to THICK. DM did not differ between the two processing methods ($P < 0.13$) nor between lab oven and Koster ($P < 0.16$). This study indicates that drying time is optimized by reducing potato particle size for both the food dehydrator and Koster Moisture Tester without reducing accuracy in estimating potato dry matter.

Key Words: potatoes, drying methods, sample processing

1478 [Withdrawn]

1479 (M240) Validating a refractometer to evaluate Immunoglobulin G concentration in Jersey colostrum and the impact of multiple freeze–thaw cycles on evaluating colostrum quality.

K. M. Morrill*[1], K. Hard[2], M. M. Spring[2], A. L. Robinson[2], and H. D. Tyler[2], *[1]Cornell University, Ithaca, NY, [2]Iowa State University, Ames.*

The objectives were: 1) validate an on farm method utilizing refractometry to rapidly and accurately determine immunoglobulin (IgG) concentration in Jersey colostrum and 2) evaluate the impact of freeze thaw (FT) cycles on radial immunodiffusion (RID) and refractometry to determine IgG concentration in bovine colostrum. Samples ($n = 58$; 3 L) of first-milking colostrum were collected from a single dairy in northwestern Iowa. Samples were analyzed within 2 h of collection for IgG concentration by RID, %Brix and refractive index (nD) by refractometer and an estimate of IgG concentration by colostrometer. Samples were then frozen, placed on dry ice and transported to the laboratory at Iowa State University (Ames). All samples arrived frozen and were placed in a -20°C manual defrost freezer until further analysis. On d 7 (1FT), 14 (2FT) and 1 yr (3FT), all samples were thawed, re-analyzed by RID, % Brix, nD and colostrometer and re-frozen. Fresh colostrum, had a mean IgG concentration, as determined by RID, of 72.91 mg/mL (SD = 3.30), mean % Brix of 21.21 (SD = 0.34) and mean nD of 1.3669 (SD = 0.0074). Immunoglobulin G concentration as determined by RID and IgG as estimated by colostrometer were impacted by the number of FT cycles. The estimates for IgG concentration by RID were greater in fresh and 1FT samples as compared to 2FT and 3FT samples (72.91, 75.38, 67.20 and 67.31 mg IgG/mL, respectively). The colostrometer reading was lower in 1FT samples compared to fresh and 2FT samples. There was no impact of multiple FT cycles on nD, or %Brix reading. In fresh samples, IgG concentration was moderately correlated with nD ($r = 0.79$), % Brix ($r = 0.79$) and colostrometer reading ($r = 0.79$). Diagnostic test characteristics utilizing the recommended cut-point of 1.34966 nD resulted in similar sensitivities for 1FT and 2FT samples (94.87 and 94.74%, respectively). Cut-points of 18, 19, 20, and 21% Brix were evaluated on Fresh samples. 18 and 19% Brix cut-points resulted in the greatest sensitivities (92.31 and 84.62%) and specificity (94.74 and 94.74%, respectively). Using the 18% cut-point resulted in 94.83% of the samples being correctly classified. This data supports the use of refractometry (nD and % Brix) to accurately and rapidly determine IgG concentration in fresh Jersey colostrum. Additionally the data suggests that IgG concentration as determined by RID is impacted by multiple FT cycles, whereas estimates obtained via refractometry are not impacted by multiple FT cycles.

Key Words: colostrum Jersey refractometer

PRODUCTION, MANAGEMENT, AND THE ENVIRONMENT: **MANAGEMENT AND HEAT STRESS**

1480 (T239) Concentrations of heavy metals in the whole raw milk of dairy cows under different management systems and country of origin: a meta-analytical study. G. Zwierzchowski and B. N. Ametaj*, *Dep. of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

The objective of this meta-analytical study was to investigate concentrations of toxic heavy metals including aluminium (Al), arsenic (As), cadmium (Cd), chromium (Cr), lead (Pb), nickel (Ni), and vanadium (Va) in whole raw bovine milk from different production systems (conventional vs. organic) and countries of origin. Data from 44 studies and 19 countries were used to create a dataset, which was used for statistical analyses. The average concentrations of Al, As, Cr, Va in the raw milk from the conventional system were greater (32.49, 0.27, 2.19, and 0.82, respectively) than those coming from ($P < 0.05$) organic farms (2.13, 0.14, 0.28, and 0.32 μmol/L, respectively). In addition, there were greater concentrations of Cd (0.25 μmol/L) and Pb (0.31 μmol/L) in the raw milk from conventional system vs. organic system (0.02 μmol/L and μmol/L 0.08, respectively) ($P < 0.05$). Lower amounts of Ni were reported for milk from conventional system (0.57 vs. 0.67 μmol/L; $P < 0.05$). Country of origin had significant effect on concentrations of toxic elements ($P < 0.05$). Turkey had greatest Al levels (283 μmol/L), whereas USA had the smallest means for this element (0.89 μmol/L) ($P < 0.05$). The lowermost concentrations of As were reported in Spain (0.01 μmol/L), whereas the greatest concentrations were found in Croatia (13.60 μmol/L) ($P < 0.05$). Average Cd level was 0.11 μmol/L; however, the greatest concentrations of Cd were reported in milk samples from Slovakia (6.49 μmol/L) ($P < 0.05$). In Nigeria concentrations of Cr in the milk were greater compared with other countries (38.04 μmol/L) ($P < 0.05$). Moreover, the greatest levels of lead (Pb) contamination were reported in milk samples from Egypt (4.63 μmol/L), whereas, the lowest means were observed in Poland (0.01 μmol/L) ($P < 0.05$). Regarding Ni, the lowest amounts were found in Brazil (0.03 μmol/L), whereas the greatest levels (50.25 μmol/L) were found in milk samples from Nigeria. Concentrations of Va varied from below 0.01 μmol/L (Spain) to 0.72 μmol/L (*P*oland). In conclusion, data from this meta-analytical study indicated that organic farms were characterized by lower concentrations of toxic heavy metals compared to the conventional system of management. This study also showed high variability in concentrations of heavy metals in raw milk with regards to the country of origin.

Key Words: whole raw milk, heavy metals, meta-analysis

1481 (T240) Macro- and microminerals in the whole raw milk of dairy cows from conventional and organic farms: A meta-analytical study. G. Zwierzchowski and B. N. Ametaj*, *Dep. of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, Canada.*

The objective of this meta-analytical study was to investigate selected macrominerals calcium (Ca), magnesium (Mg), phosphorous (P), potassium (K), and sodium (Na) and microminerals (copper (Cu), iodine (I), iron (Fe), manganese (Mn), selenium (Se), and zinc (Zn) in the bovine whole raw milk samples from two different management systems and 19 countries. An analytical dataset was constructed from 44 different studies and 19 countries with two types of production systems: conventional and organic. No differences in concentrations of Ca, Mg, and Na in the raw milk were observed when production systems were compared, whereas, concentrations of P and K were greater in the conventional production system ($P < 0.05$). The average concentrations of Cu, I, Fe, Mn, Se, and Zn in organic whole raw milk samples were 1.12, 1.77, 8.25, 0.47, 0.30, and 42.20 μmol/L respectively; and were lower ($P < 0.05$) compared with conventional milk (2.09, 2.37, 13.62, 1.97, 0.76, and 60.95 μmol/L respectively). The lowest concentrations of Cu (0.03 μmol/L), Se (0.17 μmol/L), and Zn (31.76 μmol/L) were reported in bovine raw milk samples from Italy, whereas Germany (Cu, 12.89 μmol/L) and Turkey (Se and zinc, 194.31, and 125.40 μmol/L respectively) had greater concentrations of those elements ($P < 0.05$). Raw milk samples from Polish and Czech dairy farms had greater concentrations of I (2.76 and 3.31 μmol/L respectively) compared to samples collected in Niger (0.17 μmol/L) and Germany (0.88 μmol/L). Iron levels varied from 3.47 μmol/L (USA) to 89.53 μmol/L (Pakistan) ($P < 0.05$). The lowest concentrations of Mn were observed in the milk samples from USA and Poland (0.38, and 0.48 μmol/L respectively), whereas the highest concentrations were reported in milk samples from China (5.89 μmol/L) and Republic of South Africa (3.62 μmol/L). In conclusion, data from this study indicate that concentrations of microelements in the samples of whole raw milk were lower in organic farms compared with the conventional production system. Moreover, milk samples originating from developed countries were characterized by normal concentrations of these minerals compared with other countries.

Key Words: whole raw milk, macro- and micro-minerals, production system

1482 (T241) Evaluating the accuracy of using reinforcing bar and an infrared thermometer versus long-stemmed thermometers in monitoring mortality compost pile temperature. E. Pacheco[1,2], A. Reyes[1,2], M. Negron[1,2], T. A. Gipson[2], and R. Merkel[*2], *[1]University of Puerto Rico, Mayaguez, [2]American Institute for Goat Research, Langston University, Langston, OK.*

Two mortality compost piles were constructed using a mixture of goat mortality and butcher waste with ground hay as the carbon source to compare core temperature recorded by long-stemmed thermometers (LST) vs. an infra-red thermometer (IR) to read temperature of a reinforcing bar (RB) thrust into the pile. One LST was inserted into the core of each pile along with a 3-m length of 0.95-cm-thick RB so that tips of both the RB and LST were in close proximity. For 30 d following pile construction, LST temperature was recorded daily between 1500 and 1600 h. Each RB was then withdrawn from the pile and the tip's temperature determined using an IR. Data were analyzed using repeated measures in a mixed model containing treatment (T = LST and RB), date as a covariate (D), and the interaction to test for heterogeneity of slope. Compost pile was a random effect. Date ($P < 0.001$) and T×D ($P < 0.001$) showed differences, whereas T was not significant ($P = 0.48$; 57.8 and 54.5°C for LST and RB, respectively, SE = 3.04). Date was used as a covariate as temperature in working mortality compost piles will spike soon after pile formation and slowly decline. As an example, LST recorded a temperature of 64.6°C on d 3 of data collection but only 50.4°C on d 30. The T×D test recorded a slope estimate of -0.320 for LST and -0.018 for RB (probability of slope > 0 of $P < 0.001$ and $P = 0.75$ for LST and RB, respectively). These results suggest that RB can be used to monitor mortality compost pile temperature but is not accurate enough to model the normal decline in temperature over time. Temperature of RB may have differed from LST due to location on reinsertion into the pile (cooler or hotter spot than LST tip) and alignment of IR on RB to record accurate RB temperature and not temperature of surrounding material. Using an IR with RB may be an acceptable method for monitoring mortality compost pile temperature and would be a cheaper alternative for producers composting multiple mortalities than to purchase LST for each pile. However, RB is not appropriate for use when precise temperature measurement is needed.

Key Words: goats, mortality compost, temperature

1483 (T242) Milk production, dry matter intake and body condition score evaluated in cross-bred commercial cows supplemented with OmniGen-AF during and following heat stress. A. E. Holland[1], J. D. Chapman[*1], and L. O. Ely[2], *[1]Prince Agri Products, Inc., Quincy, IL, [2]UGA, Athens, GA.*

Dairy cows in the United States are affected by heat stress for a significant part of the year, resulting in reduced dry matter intakes (DMI), milk yields (MY) and profits. In 2012, a 15-wk study (July 9 to October 16) was conducted in Texas to evaluate MY, DMI, and body condition score (BCS) in multiparous cross-bred (H x J) cows fed *OmniGen-AF* (OG) and subjected to heat stress. Two-hundred sixty-six early- to mid-lactation cows were enrolled based on parity, days in milk (DIM) and current MY and assigned to either the basal diet without OG (Controls, $n = 123$h) or basal diet plus OG ($n = 143$h). OG was fed at 56 g/h/d. The average parity and DIM for Controls and OG cows were 3.25, 134 d and 3.25, 130 d, respectively. Diets were fed as a TMR and orts collected daily to calculate DMI. Cows were housed in free-stalls with heat abatement and milked 3x/d. BCS was assessed at weeks 4, 10, and 15. Daily temperature (°C) was measured and weekly highs and lows calculated. Individual milk weights were retrieved from Westfalia Surge Dairy Plan System. Only cows with wk 1 and 15 milk weights and at least 12 total weekly weights were used. Data were analyzed using PROC GLM (SAS) and significance tested to $P < 0.05$. High and low average weekly temperatures (°C) for weeks 1 to 7 and 8 to 15 were 35.9, 21.8 and 25.9, 12.8, respectively. DMI did not differ between Controls or OG cows during wk 1 to 7 (26kg/d) or wk 8 to 15 (29.7kg/d). No differences in BCS were detected between Controls or OG cows at wk 4 (3.01), 10 (2.94) or 15 (2.75). Wk 1 to 7 MY's were not different between Controls (36.3kg/d) and OG cows (37.1kg/d); however, they differed ($P < 0.004$) in wk 8 to 15 (33.2kg/d; 35.5kg/d, respectively). OG cows MY averaged 1.3kg/d more ($P < 0.048$) than Controls from wk 1 to 15. MY's of Controls ($n = 43$h) and OG ($n = 51$h) cows that were 120 DIM or less at the start were not different in wk 1 to 7 (40.4kg/d; 42kg/d), however differed in wk 8 to 15 (36.5kg/d; 39.4kg/d, $P < 0.005$). Controls ($n = 80$h) and OG ($n = 79$h) cows 121 DIM or greater at the start were not different in MY, until wk 15 (28.8kg/d; 31.2kg/d, $P < 0.032$). All cows showed the typical MY and DMI response to heat stress; however, cows fed OmniGen-AF were observed to recover sooner as measured by milk production.

Key Words: heat stress, lactation, OmniGen-AF

1484 (T243) Factors affecting transition success in tie stall herds. D. E. Santschi[*1], M. S. Perreault[1,2], S. Adam[1], R. Lacroix[1], and D. M. Lefebvre[1], [1]*Valacta, Ste-Anne-de-Bellevue, QC, Canada,* [2]*Université Laval, QC, Canada.*

The transition period is the most critical time in the lactation cycle of a cow. It is generally accepted that a successful transition will have a positive impact on performances in the following lactation. Several years ago, Nordlund and collaborators have developped the Transition Cow Index (TCI): a tool to objectively evaluate transition. These authors have previously identified feedbunk space, number of group changes and size and comfort of rest area as the main factors affecting transition success in freestall herds. The aim of the present study was to identify factors that have an impact on transition success specifically in tie stall herds. Tie stall dairy herds (n = 48) from Québec, Canada, were selected based on their average TCI to have high and low TCI herds. Each herd was visited and producers were asked to complete a survey on their management decisions and practices (examples: number of place changes, number of daily feed push ups, boluses). In addition, several observations and measures (examples: stall dimensions, type and amount of bedding, lighting) were taken on each farm. Results suggest that nervousness of cows was the most important factor affecting transition success (calm vs. nervous cows, observed on the day of the visit; $P = 0.04$). Use of straw and woodshavings as bedding at any stage of the transition period significantly increased TCI ($P \leq 0.03$) whereas type of flooring (any type of mat vs. concrete) had no impact ($P \geq 0.15$). Providing a Rumensin bolus to dry cows tended to improve TCI ($P = 0.09$). Number of place changes during the transition period ($P = 0.09$) and number of times feed is pushed back ($P = 0.07$) tended to positively impact TCI. Stall dimension factors significantly correlated with TCI are reported in Table 1484.

Key Words: transition success, TCI, tie stall

Table 1484.

Factor	Corr. Coeff.	*P* value
Stall length far-off cows	0.35	0.02
Stall length precalving cows	0.40	< 0.01
Stall width precalving cows	0.32	0.03
Stall width fresh cows	0.32	0.02

1485 (T244) Effect of spatial orientation and shade on internal environment of a wooden 3-calf hutch. J. D. Allen[*1], and L. W. Hall[2], [1]*Northwest Missouri State, Maryville,* [2]*University of Arizona, Tucson.*

The objective of this study was to determine internal environments of California-style 3-calf hutches according to a combination of spatial orientation and shade. During mid-autumn at the University of Arizona's Campus Agricultural Center, Tucson, 8 California-style (3 cubicles/hutch) were designated to 1 of 2 treatments: exposure to direct sunlight (DS) or placement underneath a drylot shade structure (NDS). Hutches within each group were oriented to 1 of 4 directions: north, south, east, and west. Hutches were equipped with 6 temperature/relative humidity data loggers (two loggers/cubicle) evenly placed at 41 cm above the slatted wood flooring and 41 cm from the sides of the cubicle. For 4 d, each hutch was rotated clockwise once every 24-h period and before daylight hours so that each hutch was exposed to all 4 directions at least once. Ambient condition data were analyzed as a complete randomized block design with hutch as the experimental unit. Overall, DS hutches had a greater average temperature-humidity index (THI) (62.7 vs. 61.5 ± 0.17; $P < 0.01$) compared to NDS hutches. However, DS hutches had greater 24-h range ($P < 0.01$) for THI (56.1–69.2 vs. 57.4–65.7 ± 0.19), ambient temperature (26.3–13.4 vs. 22.5–14.6 ± 0.18°C), and relative humidity (24.8–42.3 vs. 27.5–39.9 ± 0.37%) compared to NDS hutches. A 24-h THI range of 60.5 (north-facing NDS) to 63.6 (east-facing DS) with a temperature range of 17.7 (north-facing DS) to 20.6°C (east-facing DS) was observed. Highest THI ($P < 0.01$) was recorded for all treatments except west-facing NDS during 1200 to 1800 h (THI > 70) compared to other 6-h periods (0000 to 0600, 0600 to 1200, 1800 to 0000 h). South-facing DS hutches recorded the greatest THI range (51.5 to 75.7; $P < 0.01$), while west-facing NDS hutches had the least THI range (57.3 to 64.5; $P < 0.01$). Grid mapping of daytime and nighttime THI for each treatment showed THI uniformity within each hutch was dependent on both orientation and shade. Results indicate shaded wooden three-calf hutches are kept at a cooler and less variable environment compared to unshaded hutches during a mid-autumn, southwestern climate. Also, a 13-point THI difference during a 24-h period can be observed within a hutch exposed to direct sunlight.

Key Words: calf hutch, internal environment, spatial orientation

1486 (T245) Effect of deterred and undeterred bird depredation on nutrient composition of a cattle diet and growth performance in cattle at a Southwestern feedlot facility. J. D. Allen[*1], L. W. Hall[2], S. Garcia[2], and J. Marchello[2], [1]*Northwest Missouri State, Maryville,* [2]*University of Arizona, Tucson.*

A summer study was performed to determine the effect of bird depredation on nutrient composition of a diet fed to and performance parameters of feedlot cattle with open or limited exposure to depredating birds at the University of Arizona West Agriculture Campus (Tucson). This study also investigated feeding preference of individual feedstuffs used at the feedlot. Feeder cattle (n = 50; 170 ± 15 kg) were sorted by gender then randomly assigned to 1 of 8 pens assigned to 1 of 2 treatments: open feed trough exposure to the existing bird

population (OP) or limited feed trough exposure to the bird population utilizing self-closing wire gates (LM). Cattle were fed until backfat ultrasound measurement reached 1cm (476.5 ± 2.8 kg). Diets were sampled at 0, 7, and 24 h post-feeding and analyzed for DM, NDF, ADF, CP, ash, and starch. Cattle performance parameters included G:F ratio, ADG, cost per kg of gain, and final BW. On separate days, DM disappearance was recorded for either individual feedstuffs included in cattle diet or grains varying in processing level placed in troughs not exposed to cattle. Cattle and feed data were analyzed as a complete randomized design with pen as the experimental unit. Both CP and ADF were greater ($P < 0.02$) in OP versus LM troughs at 7 and 24 h, although starch was greater ($P < 0.02$) in LM versus OP troughs after 24 h. Although LM and OP cattle had equivalent ADG, LM cattle had greater G:F ratio ($P < 0.02$), lower cost per kg gain ($P < 0.05$), and tended ($P < 0.10$) to have lower final BW when compared to OP cattle. Dry matter disappearance for diet feedstuffs was greatest ($P < 0.01$) for steam-flaked corn, followed by SBM, mineral mix, alfalfa, and urea, respectively. DM disappearance for grain type was greatest ($P < 0.01$) for whole milo, followed by rolled corn, steam-flaked corn, ground milo, ground barley, ground corn, and whole corn and whole barley, respectively. Birds feeding in the trough included pigeon (*Columbia livia*), mourning dove (*Zenaidura macroura*), and Eurasian dove (*Streptopelia decaocto*). Results indicate that bird populations present at Southwestern cattle feeding operations are capable of altering production parameters in cattle as well as altering nutrient composition in feed through feedstuff preference.

Key Words: bird depredation, cattle, nutrient loss

1487 (T246) Predicting Holstein heifer growth by genomic traits.

D. E. Cook*[1], D. K. Combs[1], R. W. Bender[1], P. M. Krump[1], and K. A. Weigel[2], *[1]Dep. of Dairy Science University of Wisconsin, Madison, [2]University of Wisconsin, Madison.*

Assessment of heifer weights and ADG is a recommended practice for managing dairy heifers, however the genetic variance of mature animal size obfuscates the meaning of a limited number of measured weights and ADG on a commercial dairy. The objective of this study was to use type traits and PTA milk from the heifer's first genomic test to predict the 24-mo body weight. This would allow an adjusted growth curve to be applied to heifers individually and management decisions made on the animal's current body weight status or deviation or both from its genetic potential. A database of heifers ($n = 802$, genotyped $n = 561$) and their body weights ($n = 2373$, ranging from 4 mo of age to 26 mo) was used in this study. An exponential model for heifer growth by age was made for all body weights, to fix the shape of the growth curve. A nonlinear regression was then fitted using the exponential model and the individual animal's measurements to solve for the model coefficient, setting the amplitude of the growth curve by animal. This resultant coefficient was regressed against the animal's PTA milk and type traits, using a criteria of $P > 0.20$ for removal of variables. The resultant regression equation ($R^2 = 0.12$) consisted of terms: PTA milk, final score, stature, body depth, rear leg side and rear view, udder height, udder depth, front and rear teat placement, and teat length. Using the genomic model by animal the mean square error for the growth model was reduced from 4937 to 4451. The present model, based on genomic body traits, did not yield the desired level of body size prediction to be utilized as an on-farm heifer assessment tool.

Key Words: heifer, growth, management

1488 (T247) Blood parameters in transition dairy cattle and their effects on milk production.

C. H. Ramires[1], R. B. Navarro[2], R. M. Silva[3], G. T. Santos[4], R. Locatelli-Dittrich[1], and R. D. Almeida*[1], *[1]Universidade Federal do Paraná, Curitiba–Paraná, Brazil, [2]Capal Cooperativa Agroindustrial, Arapoti- Paraná, Brazil, [3]Kemin do Brasil, Indaiatuba–São Paulo, Brazil, [4]Universidade Estadual de Maringá, Maringá–Paraná, Brazil.*

Circulating metabolites nonesterified fatty acids (NEFA), β-hydroxybutyrate (BHBA) and cholesterol are commonly used as parameters of negative energy balance (NEB) or ketosis in dairy cows, whereas concentrations of aspartate aminotransferase (AST) indicate the occurrence of hepatic lipidosis. The objective of this study was to evaluate the effects of blood parameters on milk production in pre and postpartum Holstein cows. Blood samples were collected from 197 animals in the prepartum (-14 to -1 d) and 285 animals postpartum (+1 to +14 d) from 30 herds of Parana State, Southern Brazil. At each visit, a sample of 10 mL of blood was collected from the coccygeal vessels into sterile tubes without anticoagulant and kept refrigerated until analysis. After collection, blood samples were centrifuged and the serum was analyzed in an automatic biochemical analyzer using commercial kits for NEFA, BHBA, AST and cholesterol parameters. Milk production was assessed using mature-equivalent 305-d (ME305) milk yield estimated at 100 d in milk. While controlling for body condition score (BCS) and parity, the effects of elevated NEFA, BHBA, and cholesterol concentrations on ME305 milk yield were estimated, with herd as a random effect. The mean values for the prepartum were 0.23 ± 0.21 mmol/L NEFA; 0.46 ± 0.27 mmol/L BHBA; 57.48 ± 16.34 U/L AST; and 84.00 ± 19.14 mg/dL cholesterol. In cows and heifers, ME305 milk yield was decreased ($P < 0.05$) by 760 kg when prepartum NEFA concentrations were ≥ 0.33 mEq/L. The mean values in the postpartum group were 0.53 ± 0.40 mmol/L NEFA; 0.64 ± 0.44 mmol/L BHBA; 85.17 ± 31.50 U/L AST; and 84.35 ± 23.45 mg/dL cholesterol. In this postpartum group, NEFA and BHBA were ($r = 0.49$; $P < 0.01$) correlated among themselves and with AST ($r = 0.31$ and $r = 0.27$, respectively; $P < 0.01$). In all animals sampled postpartum, ME305 milk yield

was increased ($P < 0.05$) by 852 kg when BHBA concentrations were $\geq$ 0.97 mmol/L. In primiparous and multiparous sampled postpartum, ME305 milk yield was increased by 492 and 1376 kg on hypercholesterolemic animals (> 120 mg/dL), compared with normocholesterolemic (between 80 and 120 mg/dL) and hypocholesterolemic animals (< 80 mg/dL), respectively. In cows sampled postpartum, ME305 milk yield was decreased ($P < 0.05$) by 793 kg when NEFA concentrations were $\geq$ 0.72 mEq/L. This study suggests that increased concentrations of NEFA and lower concentrations of cholesterol and BHBA had detrimental effects on milk production.

Key Words: β-hydroxybutyrate, cholesterol, nonesterified fatty acids

---

1489 (T248) A comparison of two implant protocols: Synovex-Choice and Synovex-Plus vs. Synovex-S and Revalor-S on steer feedlot performance and carcass characteristics. H. R. Nielson*[1], A. F. Summers[2], and R. N. Funston[1], [1]*University of Nebraska, West Central Research and Extension Center, North Platte,* [2]*University of Nebraska, Lincoln.*

An experiment was conducted to determine the impact of two implant protocols on steer feedlot performance and carcass characteristics. Over a 2-yr period, 109 crossbred (5/8 Red Angus, 3/8 Continental) steers were randomly assigned to 1 of 2 implant protocols; 1) Synovex-Choice [100 mg of trenbolone acetate (TBA) and 14 mg of estradiol benzoate (EB)] implanted at the beginning of the feeding period (CHPL); or 2) Synovex-S (200 mg of progesterone and 20 mg of EB; SS) as initial implant. Steers were fed for approximately 100 d, and the CHPL treatment was re-implanted with Synovex-Plus (200 mg of TBA and 28 mg of EB) while the SS treatment received Revalor-S (120 mg of TBA and 24 mg of estradiol). At 205 d on feed, steers were shipped to a commercial abattoir for slaughter. Carcass characteristics were evaluated 24 h following slaughter; HCW was determined on d of harvest. Average daily gain was similar ($P = 0.39$) for CHPL (1.75 ± 0.08 kg/d) and SS (1.70 ± 0.08 kg/d) steers. There was no difference ($P = 0.37$) in HCW for CHPL compared with SS steers (380 ± 7 vs. 374 ± 7 kg, respectively). Yield grade was also not affected ($P = 0.16$) by treatment, 2.5 and 2.7 ± 0.3 for CHPL and SS, respectively. There was no difference in LM area ($P = 0.98$) between CHPL and SS (90.52 vs. 90.52 ± 2.26 cm^2), and back fat was also similar ($P = 0.13$) between the treatments (1.37 vs. 1.50 ± 0.15 cm, CHPL vs. SS, respectively). Marbling score was similar ($P = 0.19$) between treatments (501 vs. 525 ± 13, CHPL and SS, respectively) resulting in a similar percentage of steers grading USDA Choice [CHPL vs. SS, 93 ± 3% vs. 96 ± 3% ($P = 0.42$)] and upper 2/3 USDA Choice [CHPL vs. SS; 47 ± 7% vs. 54 ± 7% ($P = 0.51$)]. Net revenue was similar ($P = 0.36$) between CHPL ($1083.11 ± 37.83) and SS ($1103.43 ± 37.83) steers. Both implant regimens utilized in the current study resulted in similar feedlot and carcass characteristics.

Key Words: carcass characteristics, feedlot performance, implants

---

1490 (T249) Mitigating heat stress in dairy cattle via conductive cooling. K. M. Perano*, K. G. Gebremedhim, J. G. Usack, T. J. Shelford, C. A. Gooch, and L. T. Angenent, *Cornell University, Ithaca, NY.*

The U.S. dairy industry, a $37 billion-per-year industry (2012), loses more than $1.5 billion in a typical year to the effects of heat stress on lactating dairy cattle. High ambient temperature or humidity leads to cows having trouble disposing of metabolic heat, causing an increase in respiration rates and body temperature along with a decrease in milk production. Our objective was to design, build, and test a conductive cooling system for relieving heat stress in lactating dairy cattle. Our study used eight first-lactation Holstein cows producing 34.4 ± 3.7 kg/d of milk at 166 ± 28 d in milk. Cows were milked twice per d at 0600 and 1800 h. Cows were exposed to heat stress in a climate-controlled room from 0930 until 1730 h daily but moved to well-ventilated pens at night. During the time the heat stress occurred, each of the four experimental cows was conductively cooled by pumping chilled water through a waterbed in her stall, but the four control cows were given no heat stress relief. The cooling system was tested at two different heat stress levels (THI = 81.3 ± 0.7 and THI = 79.7 ± 0.8) as well as two different chilled water temperatures (4.5°C and 10°C) for a total of four treatments. Each treatment lasted for 7 d. Milk production, feed consumption, and rectal temperature were recorded twice daily. Respiration rates and skin temperatures were measured five times per day. Data loggers recorded the cooling water temperature, the ambient temperature and humidity, and the vaginal temperature as well as standing and lying behavior of each cow. Results from the higher heat stress/lower water temperature treatment show that conductive cooling removed ~850 Watts (about 60% of the total metabolic heat from a lactating Holstein cow) whenever the cow was lying down. This significantly reduced the effects of the heat stress, with cooled cows producing 35.5 ± 2.0 kg/d of milk while control cows produced 26.2 ± 4.7 kg/d of milk ($P = 0.024$). Rectal temperatures for cooled cows were 39.2 ± 0.6°C while control cows were 40.3 ± 0.6°C ($P = 0.039$). Respiration rates were 64 ± 10 breaths/min for cooled cows compared to 84 ± 10 for control cows ($P = 0.033$). Such results indicate that conductive cooling shows promise for mitigating heat stress in lactating dairy cattle.

Key Words: conductive cooling, heat stress, milk production

1491 (T250) Changes in behavioral and physiological parameters around estrus in partially synchronized cows. K. A. Dolecheck*, W. J. Silvia, G. Heersche Jr., A. E. Sterrett, B. A. Wadsworth, and J. M. Bewley, *University of Kentucky, Lexington.*

The objective of this study was to compare estrus detection potential of cow behavioral and physiological parameters collected by multiple precision dairy farming technologies. Technologies included the SensOor (Agis Automatisering, Harmelen, Netherlands), DVM bolus (DVM Systems, LLC, Greeley, CO), HR Tag (SCR Engineers Ltd., Netanya, Israel), IceQube (IceRobotics Ltd., Edinburgh, Scotland), and Track a Cow (Animart Inc., Beaver Dam, WI, and ENGS, Rosh Pina, Israel). Ovulation was synchronized for 35 cows in three groups between January and June 2013 at the University of Kentucky Coldstream Dairy using a modified G7G/Ovsynch ending after the last $PGF_{2\alpha}$ injection (Day 0) to allow estrus expression. Visual observation of cows for four 30-min periods at 0330, 1000, 0230, and 2200 h on d 2, 3, 4, and 5 confirmed estrus by recording when cows stood to be mounted. Eighteen of the 35 cows stood to be mounted at least once during the observation period and were used for analysis. The GLM procedure of SAS (SAS Institute, Inc., Cary, NC) was used to compare differences between the 24-h period surrounding the standing event (estrus) and the week preceding that period (non-estrus) for all technology parameters. Significant differences ($P < 0.05$) between estrus and non-estrus were observed for the following parameters (reported as estrus vs. non-estrus ± SE): SensOor minutes ruminating/h (16.02 vs. 22.68 ± 0.84), SensOor minutes feeding/h (14.48 vs. 8.86 ± 0.94), SensOor minutes of high activity/h (13.66 vs. 4.18 ± 0.79), HR Tag minutes ruminating/2 h (22.30 vs. 28.67 ± 1.40), HR Tag activity units/2 h (49.10 vs. 26.74 ± 2.19), IceQube lying bouts/h (0.47 vs. 0.70 ± 0.06), IceQube total motion units/h (912.38 vs. 316.82 ± 59.82), IceQube steps/h (224.41 vs. 84.53 ± 14.09), IceQube minutes lying/h (16.35 vs. 24.12 ± 1.19), and Track a Cow activity units/h (197.07 vs. 78.19 ± 26.29). No significant differences between estrus and non-estrus were observed for SensOor mean temperature/h, DVM bolus twice-daily temperature, and Track a Cow lying percent/h. This data demonstrates that multiple measureable parameters may be useful for detecting estrus events.

Key Words: precision dairy farming technologies, estrus detection

1492 (T251) Effect of maternal heat stress during the dry period on development of immune system of offspring. B. M. Ahmed[*1], A. P. A. Monteiro[1], S. Tao[1], K. E. Merriman[2], J. P. Driver[2], B. L. Artiaga[1], J. Hayen[1], I. M. Thompson[1], C. D. Nelson[2], and G. E. Dahl[1], *[1]University of Florida, Gainesville, [2]Dep. of Animal Sciences, University of Florida, Gainesville.*

Maternal heat stress during the dry period affects calf immune response during postnatal life, but it is still unknown how in utero heat stress affects calf's immune system development. The objective was to evaluate the effects of in utero heat stress on distribution of different immune cell types in blood and primary and secondary lymphoid tissues of the calf. Cows were dried off 60 d before expected calving and randomly assigned to one of two treatments: heat stress (HT) or cooling (CL). During the dry period, all cows were housed in a freestall barn with fans over the feed line and stalls, but only the feeding area for CL cows was equipped with soakers. Heat stress was moderate compared with other studies, as HT cows had only 0.1°C increase in rectal temperature and 8 breath/min increase in respiration rate compared with CL cows. Immediately after birth, singleton calves (HT: $n = 200$; CL: $n = 188$) were weighted and then fed 3.8 L of colostrum (score: bull < 80; heifer > 80) within 1 h after birth. Blood samples were collected from a subset of heifers (HT: $n = 12$; CL: $n = 10$) at birth before colostrum feeding, d 3, 28, and 56 of age to evaluate the proportion of blood T and B lymphocytes, granulocytes, monocytes, and γδ-T cells by flow cytometry. Additionally, a subset of bull calves (5/treatment/day) were randomly selected and slaughtered at birth (without colostrum feeding), 1 and 2 d after birth. Thymus and spleen were weighed and then a sample was excised, homogenized and assayed using flow cytometry to determine the proportion of different immune cell types. No difference was observed between treatments for calf birth weight (CL: 41.0; HT: 40.6 kg; $P = 0.32$). However, the thymus of CL bull was proportionally heavier (0.18 vs. 0.14% of body weight, respectively; $P < 0.05$) compared with HT calves. Preliminary analyses indicate that treatments had no impact on the proportion of different immune cells of calf blood during the preweaning period. Thus, we conclude that the slight difference in heat strain on HT and CL cow during the dry period has no significant impact on general fetal growth during the dry period and blood immune cell profile during the preweaning period in current study; however, it seems that late gestation maternal heat stress influences fetal primary lymphoid tissue development.

Key Words: heat stress, dry period, dairy calf

1493 (T252) Impact of dry period heat stress on milk yield, reproductive performance and health of dairy cows. I. M. Thompson*, A. P. A. Monteiro, G. E. Dahl, S. Tao, and B. M. Ahmed, *University of Florida, Gainesville.*

Two studies were performed to determine the effects of heat stress during the dry period on subsequent lactation yield, occurrence of health disorders, and reproductive performance. In experiment 1, cows were dried off 60 d before calving and assigned to cooling (CL, n = 250) or heat stress (HT, n = 250). CL cows were housed with sprinklers, fans and shade, whereas the HT group had fans and shade. All cows were cooled postpartum. Rectal temperature (RT) and respiration rate (RR) were recorded during the dry period. BCS was recorded weekly during the dry period and at d 7 and 33 postpartum. Milk yield was recorded monthly. Occurrence of postpartum disorders was evaluated during the first 60 DIM. Reproductive performance included metritis check (MC), days to first breeding (DTAI) and pregnancy rates. In experiment 2, records of 147 multiparous cows over 5 yr that were under cooling (n = 73) or heat stress (n = 74) during the dry period were analyzed. In those studies, HT cows did not have fans or soakers. Traits analyzed were 305 d milk production, number of breedings, and occurrence of postpartum health disorders. In experiment 1, relative to HT, CL cows had lower RT (39.0 vs. 39.1°C; P = 0.03) and RR (51 vs. 59 breath/min; P < 0.01) when dry. BCS during the dry period and postpartum, DTAI and MC33 did not differ between treatments. CL cows tended to have a greater incidence of metritis at d 7, but no other differences in postpartum health disorders were observed. Milk yield for the first 2 mo of lactation did not differ. In experiment 2, HT cows had higher RT (39.0 vs. 39.4°C; P < 0.001) and RR (48 vs. 76 breath/min; P = 0.02) than CL cows. Additionally, CL cows produced 5.3 kg/d more milk (P = 0.01) than HT cows. BW and BCS after calving did not differ between treatments, but CL cows gained more BW and increased BCS during the dry period versus HT cows. Reproductive performance did not differ between treatments. CL cows had a higher incidence of ketosis, and tended to have a higher incidence of metritis and retained placenta versus HT cows. Cooling dry cows during the dry period improves subsequent lactation performance, but the severity of heat stress is a significant influence on the response.

Key Words: heat stress, dry period, lactation

1494 (T253) Extending the interval from Presynch to initiation of Ovsynch in a Presynch-Ovsynch protocol did not reduce fertility of lactating dairy cows not detected in estrus that received timed artificial insemination. J. O. Giordano[*1], M. J. Thomas[2], G. K. Catucuamba[2], and M. D. Curler[2], [1]*Dep. of Animal Science, Cornell University, Ithaca, NY,* [2]*Dairy Health and Management Services, LLC, Lowville, NY.*

Our objective was to determine if extending the interval from Presynch to initiation of Ovsynch by 2 d (from 12 to 14) in a Presynch-Ovsynch protocol would reduce pregnancies per AI (P/AI) for cows not detected in estrus that receive timed AI (TAI). Lactating dairy cows (n = 1817) from four commercial farms in New York (Farm A = 218, B = 1031, C = 258, and D = 310) were enrolled in the Presynch-Ovsynch protocol to receive TAI at 73 ± 3 DIM. Cows were blocked by parity and randomly assigned to two groups: PS12 (n = 909; PGF-14d-PGF-12d-Ovsynch-56) or PS14 (n = 908; PGF-14d-PGF-14d-Ovsynch-56). Timed AI was performed approximately 16 h after GnRH. Cows detected in estrus at any time from the second PGF injection of Presynch until the day before TAI were inseminated. Pregnancy was assessed at 39 ± 3 d after AI using transrectal ultrasound. The percentage of cows receiving TAI was greater (P < 0.001) for PS14 than PS12 (55.2 vs. 48.5% respectively), was greater (P < 0.001) for farm D (70.7%) than A (60.1%) and C (57.8%) whereas farm B (43.0%) had the lowest percentage of cows receiving TAI. More (P < 0.001) multiparous (58.4%; 661/1131) than primiparous (41.0%; 281/686) cows received TAI. There was no treatment by farm interaction (P = 0.74) or treatment by parity interaction (P = 0.96) for the percentage of cows receiving TAI. Pregnancies per AI for cows receiving AI after detection of estrus was similar (P = 0.41) for PS12 and PS14 (34.6 vs. 37.4% respectively), was not affected (P = 0.44) by farm, and was similar (P = 0.36) for primiparous and multiparous cows (37.5 vs. 34.5% respectively). Pregnancies per AI for cows receiving TAI after completing the Presynch-Ovsynch protocol were similar (P = 0.98) for PS12 and PS14 [35.4 (156/441) vs. 35.5% (178/501), respectively], tended to differ by farm (P = 0.10), and were similar (P = 0.50) for primiparous and multiparous cows (37.1 vs. 34.8% respectively). Also, there was no treatment by farm (P = 0.91) or treatment by parity interaction (P = 0.34) for P/AI after TAI. Thus, extending the interval from the second PGF injection of Presynch to the initiation of the Ovsynch protocol by 2 d (from 12 to 14 d) did not reduce fertility of lactating dairy cows that were not detected in estrus and completed Presynch-Ovsynch to receive TAI.

Key Words: Presynch-Ovsynch, timed AI, dairy cow

1495 (T254) Mortality and herd turnover rates in large dairy herds in the upper Midwest United States. T. Evink*, and M. I. Endres, *University of Minnesota, St. Paul.*

The objectives of this study were to describe mortality and herd turnover rates in large Upper Midwest dairy herds, and evaluate the association between breed and mortality rates. The study included 15 dairy farms in Minnesota, Wisconsin, Iowa, and South Dakota. All farms had over 2500 lactating cows housed in a freestall system. Twelve of the farms had Holstein cows, two farms had Jersey cows, and one farm had Jersey and Holstein crosses. Herd size (mean ± SD) was 4972 ± 2652 cows with a range of 2600 to 13,250 cows. On farm records were obtained for 2 yr on each farm from July 2011 to July 2013. Sold and died events were examined from the on farm record keeping system to determine mortality and herd turnover rates. Herd turnover rate was calculated as the number of animals that were sold or died during a 1-yr period, divided by the average herd size during that 1-yr period. Mortality rate was calculated as the number of animals that died during a 1-yr period, divided by the average herd size during that period. Overall mortality rate was 7.4 ± 2.1%. Deaths on farm were categorized as injury, mastitis, lameness, sickness, down cow, transition diseases, dystocia, euthanasia, miscellaneous, or unknown reasons. Main causes of death were sickness (33.5 ± 17.3), unknown reasons (15.3 ± 24.6), and injury (11.1 ± 10.6). Overall herd turnover rate was 41.6 ± 5.9%. Reasons for turnover were categorized as low production, lameness or injury, mastitis, reproduction, transition problems, abortion, udder conformation, sickness, miscellaneous, or unknown reasons. Main reasons for turnover were low production (30.0 ± 22.0), mastitis (16.4 ± 11.9), and sickness (12.7 ± 5.2). Turnover rate during the first 60 DIM was 8.3 ± 2.3%. The PROC MIXED in SAS was used to evaluate the association between mortality rate and breed (Jersey vs. Holstein). Breed was associated with yearly mortality rate (P = 0.038); mortality rates (LSMeans ± SE) were 5.3 ± 0.01 and 7.6 ± 0.003 for Jersey and Holstein herds, respectively. Mortality rate in the first 60 DIM was 3.1 ± 0.003 for Holstein and 2.2 ± 0.01 for Jersey herds and there was no association with breed. Based on these results, Jersey cows appear to have lower overall mortality rates but similar early lactation mortality rates compared to Holstein cows in large freestall herds.

Key Words: mortality rate, turnover rate, large dairy herd

1496 (T255) Biased milk production programmed by fetal sex affects sexed semen economics. A. De Vries*[1], K. Hinde[2], A. J. Carpenter[3], J. Clay[4], and B. Bradford[3], [1]*University of Florida, Gainesville,* [2]*Harvard University, Cambridge, MA,* [3]*Kansas State University, Manhattan,* [4]*Dairy Records Management Systems, Raleigh, NC.*

Recent research has shown that Holstein dairy cows produce more milk per lactation after giving birth to female calves and when gestating female calves compared to male calves. The objective of this study was to evaluate how the economics of the use of sexed semen are affected by these differences in milk production. A herd budget simulation program was used that included separate daily cash flow projections for heifers and at least 4 parities of cows. Cash flows were based on lactation curves, feed intakes, reproductive parameters, culling and prices for milk, feed, calves, cull cows, semen, among other inputs. Based on the recent research, a first parity cow produced 185 kg per lactation more milk when she had given birth to a female calf and was gestating a female calf compared to giving birth to and gestating a male calf. A second parity cow produced 269 kg per lactation more milk when she had given birth to female calves in the current and first parity. Third and greater parity cows produced 100 kg more milk when giving birth to a female compared to a male. Other combinations of males and females resulted in smaller effects. Compared to conventional semen, sexed semen reduced the probability of conception by 20% and was $15 more expensive. Female calves were $100 more valuable than male calves. Cow pregnancy rates were 21% without sexed semen. Five sexed semen scenarios were evaluated, ranging from 1x sexed semen in heifers to 3x in heifers and 2x in first parity cows. Sexed semen break-even prices ranged from $3 to-$2 without the effects of fetal sex on milk production, compared to no use of sexed semen. Including the effects of fetal sex on milk production, sexed semen break-even prices ranged from $15 to $4. Break-even female calf prices, compared to male calf prices, were up to $29 lower when including the effects of fetal sex on milk production than when ignoring these effects. In conclusion, the effects of fetal sex on milk production make the use of sexed semen more economically feasible and should be included in economic calculations.

Key Words: fetal sex, milk production, sexed semen, economics

1497 (T256) Study the temperature-humidity index and its effect on performance of dairy cows in Isfahan. G. Ghorbani*, and A. Ahangaran, *Isfahan University of Technology, Iran.*

A temperature-humidity index (THI) is a single value representing the combined effects of air temperature and humidity associated with the level of heat stress. The objective of

this study was to evaluate the effects of THI on milk yield and milk composition of dairy cows in climatic conditions of seven Isfahan dairy farms. The experiment performed during in July 2012 to October 2013. In this study, eight THI with different weightings of dry bulb temperature and humidity were compared. Ambient temperature and relative humidity were measured every 15 min with data loggers located throughout the farm. According to THI values, from mid-October to early May the heat stress was lower than the threshold, with lowest values in January. Then THI was higher than threshold until mid-October, which was the highest level in July. Indices with higher weightings of humidity are more appropriate for humid climates, and indices with the most emphasis on ambient temperature are more suitable for semiarid climates. Since that Isfahan is located in the dry climate, THI 5 is the best indicator of its eight temperature–humidity indicators. The threshold for heat stress was 65 by THI 5. When THI increased one unit upper than treshold, average milk production decreased 0.5 Kg. Disintegration of estimated THI thresholds of heat stress into corresponding temperature and relative humidity revealed that heat stress occurred in Isfahan at temperatures $\geq$ 21°C and relative humidity of 25%. Results clearly showed a negative relationship between milk production and THI. Indeed, as THI increases from 49.1 in the winter season to 70.8 in the summer season, heat stress reduced total milk production by 38.5 to 36.1 kg, respectively. This decrease can be largely explained by the effect of summer heat stress, particularly in July, August and September when THI values are well above the critical threshold of 65. The reason for the drop in milk yield during the early fall could be explained by the carry over effect of the unfavorable conditions during the summer particularly in the absence of environmental control systems.

Key Words: temperature-humidity index, heat stress, milk loss

---

1498 (T257) The influence of body weight on the efficiency of dairy cows. P. L. Kunz*, and A. Reinhard, *Bern University of Applied Sciences, Zollikofen, Switzerland.*

Questions about the efficiency of dairy cows are a consequence of the increasing pressure on milk prices. Efficiency is defined as the relationship between energy output (milk energy) and energy input (feed energy). For methodological reasons, it is often only the energy output (milk) which is assessed, ignoring the energy input (feed energy). As a result, research into the efficiency of dairy cows has so far shown uneven results. The aim of this study was to calculate efficiency by measuring the effective daily energy intake and energy expenditure in milk, and to investigate whether the body weight of cows had an influence on their efficiency. Efficiency was defined as: efficiency = (milk energy (MJ)/net energy intake (MJ NEL). Data were collected from the Holstein Frisian and Brown Swiss dairy cows at the research centre of the Swiss Federal Institute of Technology (Zurich). Throughout lactation and the subsequent dry period, the cows were weighed daily. The quantity of milk produced was recorded twice daily and the milk ingredients measured monthly. Feed samples of all ration components were taken every month and analysed. Using scales installed under each feed trough, the feed intake of individual cows was measured continuously during the whole lactation. In this way, the daily energy intake and the daily energy output in milk could be quantified. Data from 450 lactations of 158 cows were collected. After eliminating incomplete datasets, 105 lactations of 65 cows (40 Holstein Frisian and 25 Brown Swiss cows) were submitted to statistical analysis. The results show that the body weight of cows with two or more lactations positively correlated with both daily feed intake ($P = 0.018$) and milk yield ($P = 0.022$). This means that an additional 100 kg body weight required 2.0 kg DM/day more feed intake and yielded 630 kg more milk per lactation. However, there was no significant correlation between body weight and efficiency ($P = 0.39$), not even after dividing the samples by breed and lactation numbers. In this sample, heavy cows were equally efficient as light cows, compensating for their increased maintenance requirement by higher feed intake and higher milk yield. The differences in efficiency between individual cows must therefore be explained by other factors.

Key Words: dairy cow efficiency

1499 (T258) Effects of supplementation with propylene glycol in heat-stressed dairy goats. S. Hamzaoui[1], A. Salama[*1,2], G. Caja[1], E. Albanell[1], and X. Such[1], *[1]Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Spain, [2]Animal Production Research Institute, Dokki, Giza, Egypt.*

We hypothesized that supplementation with propylene glycol would increase blood glucose and spare amino acids for milk protein synthesis rather than glucose production. To test this hypothesis, we used eight multiparous Murciano-Granadina dairy goats (40.8 ± 1.1 kg BW; 84 ± 1 DIM) individually kept in metabolic cages. The design was a replicated 4 × 4 Latin square of 4 periods, 21 d each (14 d adaptation, 5 d for measurements). Goats were allocated to one of 4 treatments in a 2 × 2 factorial arrangement. Factors were no propylene glycol (C) or 5% of Propylene glycol (PG), and thermal neutral (TN; 15 to 20°C) or heat stress (HS; 12 h/d at 37°C and 12 h/d at 30°C) conditions. This resulted in 4 treatment combinations: TN-C, TN-PG, HS-C, and HS-PG. Feed intake, milk yield, milk composition, and blood parameters were measured. No significant interaction was detected between ambient temperature and PG effects. Compared to TN, HS goats had lower feed intake, FCM, and milk contents of fat, protein and lactose. The PG increased blood glucose and insulin, but decreased DMI, blood NEFA and β-hydroxybutyrate, resulting in lower milk fat with no change in milk protein content. In

conclusion, supplementation of heat-stressed dairy goats with propylene glycol did not affect milk yield or milk protein content, and caused milk fat depression syndrome.

Key Words: heat stress, propylene glycol, dairy goats

Table 1499.

Item	Treatment				SEM	*P* <	
	TN-C	TN-PG	HS-C	HS-PG		Temp[1]	PG
DMI, Kg/d	2.34	2.18	1.59	1.38	0.09	0.001	0.060
Milk yield, L/d	1.86	1.80	1.79	1.66	0.18	0.210	0.258
3.5% FCM[2], L/d	2.12	1.78	1.85	1.48	0.16	0.001	0.001
Milk composition, %							
Fat	4.43	3.46	3.78	2.89	0.21	0.009	0.001
Protein	3.55	3.54	3.14	3.15	0.21	0.074	0.999
Lactose	4.47	4.46	4.31	4.29	0.06	0.064	0.886
Blood measurements							
Urea, mg/dL	25.7	23.9	18.4	18.1	1.54	0.007	0.628
Glucose, mg/dL	56.1	61.7	56.1	57.6	1.28	0.120	0.012
Insulin, µg/L	1.14	1.54	1.03	1.43	0.23	0.637	0.091
Lactate, mmol/L	0.51	0.52	0.46	0.51	0.04	0.488	0.446
NEFA, mmol/L	0.10	0.06	0.07	0.03	0.02	0.116	0.021
β-hydroxybutyrate, mmol/L	0.65	0.48	0.77	0.48	0.07	0.369	0.002

[1] Effect of ambient temperature
[2] 3.5% fat-corrected milk = L of milk yield × [0.432 + 0.162 × (fat %)].

1500 (T259) The effects of technology use in feedlot production systems on the heat stress and blood metabolites of finishing steers. B. C. Bernhard*[1], C. L. Maxwell[1], C. F. O'Neill[1], B. K. Wilson[1], C. G. Hixon[1], C. Haviland[1], A. Grimes[1], M. S. Calvo-Lorenzo[1], C. J. Richards[1], D. L. Step[1], B. P. Holland[2], and C. R. Krehbiel[1], *[1]Oklahoma State University, Stillwater, [2]Merck, Volga, SD.*

Crossbred, black-hided steers (n = 336; initial BW = 379 ± 8 kg) were utilized in a RCBD (8 pens/treatment; 14 steers/pen) to determine the effects of technology use in feedlot production systems during the summer on heat stress. Treatments consisted of an all-natural treatment (receiving no growth promoting technologies; NAT), a conventional treatment (implanted with 40 mg of estradiol and 200 mg of trenbolone acetate on d 0, and fed 33 and 9 mg/kg of monensin and tylosin daily, respectively; CONV), and a CONV treatment plus the addition of a β-adrenergic agonist (zilpaterol hydrochloride at 6.76 g/ton for the last 20 DOF with a 3–4 d withdrawal; CON-V-Z). Blood was collected every 10 d during the β-agonist period (d 112 to 132) on seven steers/pen to determine blood gases, pH, and metabolites. The same subset of steers was evaluated for respiration rates and panting scores during the final 23 DOF, and rumen temperatures were continuously measured. All blood metabolites measured were within clinically normal concentrations throughout the experiment. Blood pH was greater for the CONV-Z cattle compared to the NAT cattle (7.41 vs. 7.37; $P < 0.01$) and CONV cattle intermediary (7.39) at d 122. The CONV-Z cattle had reduced lactate concentrations compared to NAT and CONV cattle at d 122 (13.5 vs. 28.9 and 27.3 mg/dL, respectively) and 132 (12.5 vs. 25.1 and 27.2 mg/dL, respectively; $P < 0.01$). Conventional cattle exhibited greater glucose concentrations than NAT and CONV-Z (88.9 vs. 83.9 and 82.5 mg/dL, respectively; $P < 0.01$). The CONV-Z cattle exhibited greater potassium concentrations than NAT and CONV cattle at d 122 (4.40 vs. 4.16 and 4.23 mmol/L, respectively; $P < 0.01$). The CONV-Z cattle showed increased severity in the morning panting score compared to CONV and NAT cattle (1.23 vs. 1.00 and 1.08, respectively; $P < 0.03$), and the afternoon panting score compared to CONV cattle (1.84 vs. 1.67; $P < 0.01$), with NAT cattle intermediary (1.76). Respiration rates were lowest for CONV cattle, intermediate for NAT cattle, and highest for CONV-Z cattle in the morning (99.5 vs. 105.0 vs. 112.8 breaths/min, respectively) and afternoon (120.1 vs. 125.8 vs. 133.8 breaths/min, respectively; $P < 0.01$). The NAT cattle had lower mean rumen temperatures compared to CONV cattle in the morning (39.56 vs. 39.71°C; $P < 0.01$) and afternoon (40.70 vs. 40.95°C; $P < 0.01$), with CONV-Z cattle intermediary (39.62 and 40.88°C). Based on these results, zilpaterol increased respiration score and rate, as noted on the product label.

Key Words: β-adrenergic agonist, heat stress, respiration rate

1501 (T260) The effects of technology use in feedlot production systems on feedlot performance, carcass characteristics, and feeding behaviors of crossbred beef steers. C. L. Maxwell[1], B. C. Bernhard*[1], C. F. O'Neill[1], B. K. Wilson[1], C. Hixon[1], C. Haviland[1], A. Grimes[1], M. S. Calvo-Lorenzo[1], D. L. VanOverbeke[1], G. G. Mafi[1], C. J. Richards[1], D. L. Step[1], B. P. Holland[2], and C. R. Krehbiel[1], *[1]Oklahoma State University, Stillwater, [2]Merck Animal Health, DeSoto, KS.*

The objectives of this study were to examine the effects of a technology enhanced system compared to an all-natural production program on feedlot performance, feeding behaviors and carcass characteristics. Crossbred beef steers (n = 54; initial BW = 391 ± 2.6 kg) were randomized to one of two treatments in a RCBD (13 to 14 steers/pen; 27 steers/treatment). Treatments consisted of an all-natural treatment (NAT), and a conventional treatment (CONV-Z). The NAT cattle received no growth promoting technologies. The CONV-Z cattle were implanted with 40 mg of estradiol and 200 mg of trenbolone acetate on d 0, and were fed 33 and 9 mg/kg of monensin and tylosin daily, respectively as well as zilpaterol hydrochloride at 6.76 mg/kg (90% DM basis) for the last 20 DOF. Gain was improved by 45.1% (1.77 vs. 1.22 kg/d; $P < 0.01$) and feed efficiency by 45.5% (0.163 vs. 0.112; $P < 0.01$) for CONV-Z steers compared to NAT steers. Daily water intake was numerically greater for NAT steers compared to CONV-Z steers consistently throughout the study (56.26 vs. 53.59 L/d; $P = 0.43$).

Thus, total water and feed efficiency was improved by 50% for CONV-Z steers compared to NAT steers (0.027 vs. 0.018; $P < 0.01$). NAT steers consumed more (8.22 vs. 7.59 meals/d; $P = 0.03$), smaller feed meals (1.34 vs. 1.46 kg/meal; $P = 0.02$), resulting in more time spent at the feed bunk (85.36 vs. 73.19 min/d; $P < 0.01$) throughout the day compared to CONV-Z steers. Water meal length was greater for NAT steers compared to CONV-Z steers (3.23 vs. 2.58 min/meal; $P < 0.01$), resulting in more time spent at the water trough throughout the day (23.71 vs. 17.80 min/d; $P < 0.01$). Dressing percentage was increased by 2.17% units (65.31 vs. 63.14; $P < 0.01$) for CONV-Z steers compared to NAT steers, resulting in a 48 kg heavier carcass (388 vs. 340, kg; $P < 0.01$). *Longissimus* muscle area was increased by 11.09 cm^2 (87.25 vs. 76.15, cm^2; $P < 0.01$) for CONV-Z steers compared to NAT steers, and marbling score was greater for NAT steers compared to CONV-Z steers (504 vs. 410; $P < 0.01$). The results of this experiment show that CONV-Z production improves feedlot performance and resource-use efficiency compared to NAT with differences in feed and water intake behavior.

Key Words: beef cattle, conventional, natural

1502 (T261) Survey of fatty acid profile of milk fat in Italian Water buffalo. M. G. Manca[1], G. Cosenza[2], E. Apicella[2], A. Pauciullo[3], A. Coletta[4], A. Nudda[*1], N. P. P. Macciotta[5], L. Zicarelli[6], and L. Ramunno[7], *[1]Dipartimento di Agraria, University of Sassari, Italy, [2]Dep. of Agriculture, University of Naples Federico II, Italy, [3]ISPAAM, Laboratory of Animal Cytogenetics and Gene Mapping, National Research Council, Naples, Italy, [4]ANASB, Italian National Association of Buffalo Breeders, Caserta, Italy, [5]Università di Sassari, Italy, [6]Dep. of Veterinary Medicine and Animal Production, University of Naples Federico II, Italy, [7]Dep. of Agriculture, University of Naples, Italy.*

Dairy buffalo farming has a relevant economic importance in Italy, mainly due to the high value of the most important dairy product, the mozzarella. Fat is a major component of buffalo dairy products. Its consumption can provide great opportunities for increasing the intake of fatty acids (FA) with potential health properties, especially as far as CLA isomers and omega-3 FA are concerned. Therefore the purpose of this survey was to investigate the variation in FA profile of milk fat of Mediterranean water buffalo fed a total mixed ratio composed mainly by corn silage and pelleted concentrate. Milk samples from 398 Italian Water buffaloes farmed in 18 herds located in Campania were collected at different months of production. FA composition of milk samples was determined by GC. Data were analyzed using a linear model, that includes age, days in milk (DIM) and month of calving as fixed effects and herd as a random effect. Saturated FA (SFA) represented 71.6% of total FA (ranging from 57.9% to 85.9%) and C16:0 and C18:0 were the most represented (34.8% and 11.1%, respectively). Monounsaturated FA (MUFA) were 25.17% of total milk FA (ranging from 12.6% to 37.4%) and C18:1c9 represent the majority (76% of total MUFA). The concentration of polyunsaturated FA (PUFA) was 3.21% of total FA ranging from 1.39% to 5.11%. with C18:2 n6 predominating (49% of total PUFA) while C18:3 n3 was present in a lower amount 0.32% of total FA. Trans FA (TFA) represented 1.70% of total FA with C18:1 t11 the most abundant (59% of total TFA). CLA isomers amounted to 0.76% of total milk FA and the isomer c9, t11 CLA represent the majority (55% of total CLA). Statistical analysis showed that milk FA were not significantly influenced by the age of animal, except for TFA content ($P < 0.05$) that was higher in younger animals (1.94%). Month of calving significantly influenced FA composition of buffalo milk only for total CLA and TFA ($P < 0.05$), evidencing a seasonality effect of these traits. DIM affected significantly all the group of FA analyzed ($P < 0.01$) denoting a marked lactation curve effects. The FA profile obtained in this study is typical of animals farmed in intensive systems, with a reduced occurrence of unsaturated fatty acids, compared to graze-based systems.

Key Words: buffalo milk, fatty acid profile

1503 (T262) Comparative study between 5% copper sulfate and a β-ionone and limonene solution in a split footbath. A. C. Thompson*, and J. M. Bewley, *University of Kentucky, Lexington.*

Digital dermatitis (DD) is a major cause of lameness in dairy herds (NAHMS, 2002) often controlled with a copper sulfate footbath. Alternative solutions are being explored as copper retards crop growth and yield when waste footbath solution is applied to fields. An alternative to copper sulfate is a β-ionone and limonene solution (RotNot, Neogen Corporation, Lexington, KY). The objective of this study was to compare the frequency and severity of DD using a β-ionone and limonene solution versus copper sulfate. The study was performed on a commercial farm in Kentucky from March 2, 2013,through May 25, 2013, with 91 lactating Holstein cows. Footbath solutions were delivered through the use of a split footbath with a β-ionone and limonene solution, at a concentration of 1:1000 on the right hooves and 5% copper sulfate on the left hooves. The DD lesions were scored every 3 wk using the Döpfer scoring system (Döpfer et al., 1997): M0 indicates no lesion; M1 represents an early growth less than 2 cm in size and generally not painful; M2 indicates a growth greater than 2 cm and painful to the touch; M3 represents a growth in the healing stage covered with a scab; and M4 designates a chronic non painful growth. The FREQUENCY procedure of SAS (SAS Institute Inc., Cary, NC) was used to run a chi-square test. The results indicated a significant change in DD frequency from the beginning (29.1%) to the end (52.7%) of the study across treatments ($P < 0.01$). McNemar's test statistic indicated that no significant difference existed in the proportions of M1 and M2 lesions between the beginning (21.9%) and end of the

study (27.5%) for 5% copper sulfate ($P = 0.42$). McNemar's test indicated a significant increase in M1 and M2 lesions with a β-ionone and limonene solution from the beginning (13.2%) to the end (52.7%) of the study ($P < 0.01$). These results suggest that copper sulfate was more effective at preventing DD lesions than a β-ionone and limonene solution. A β-ionone and limonene solution footbath may not be a viable alternative to 5% copper sulfate footbath for DD lesion prevention.

Key Words: digital dermatitis, copper sulfate, split footbath, hoof care

1504 (T263) Comparison of milk components before and after passing through a novel inline milk filter.

D. T. Nolan*[1], M. J. Bakke[2], and J. M. Bewley[1], *[1]University of Kentucky, Lexington, [2]Custom Dairy Performance, Clovis, CA.*

The UV Milk Filter (GERA Ltd., Voronezh, Russia) is a new inline filter designed to help remove foreign matter and abnormalities in milk. UV Milk Filters are different from standard single-ply polyester fabric because they are spindle woven, making them thicker than the industry standard. The objective of this study was to determine if passing milk through the UV Milk Filter changed milk fat, protein, lactose, solids, or SCC. Samples were collected at the University of Kentucky Coldstream Dairy between Nov. 30 and Dec. 10, 2013. Before each milking, a new UV Milk Filter was placed in the filter holder within the pipeline. When milking was completed, three 90-mL samples were collected from two different points: 1) at the receiver jar, before the milk had gone through the filter, and 2) at the point the milk enters the bulk tank, after the milk from the receiver jar had passed through the filter. Therefore, a total of six samples were collected at each milking for 20 milkings ($n = 120$). Mean fat, protein, lactose, solids, and SCC were calculated for each milking ($n = 20$). The GLM procedure of SAS (Cary, NC) was used to determine the effects of the UV Milk Filter on milk component averages taken before and after milk had passed through the filter. Results are depicted in Table 1504. The results show that the UV Milk Filter can successfully filter milk without changing its composition.

Key Words: UV milk filter, milk composition

Table 1504. Milk component averages and corresponding *P*-values for the differences in milk before and after it had passed through the UV Milk Filter

	Treatment		
Component	Before Filter	After Filter	*P*-value
Fat	4.48%	4.43%	0.84
Protein	3.09%	3.12%	0.64
Lactose	4.90%	4.91%	0.91
Solids	8.93%	8.96%	0.53
SCS	3.30	3.43	0.75

PRODUCTION, MANAGEMENT, AND THE ENVIRONMENT: **REDUCING THE ENVIRONMENTAL FOOTPRINT THROUGH NUTRITION AND MANAGEMENT**

1505 (W216) Methane and carbon dioxide emissions from manure of dairy cows fed red clover- or corn silage-based diets supplemented with linseed oil.
F. Hassanat*, D. I. Massé, and C. Benchaar, *Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada.*

The objective of this study was to examine the effects of forage source (red clover: RC vs. corn silage: CS) and linseed oil (LO) supplementation of dairy cow diets on CH_4 and CO_2 emissions from manure storage. The diets contained 57% of RC or CS, on dry matter (DM) basis while LO was supplemented at 4% of dietary DM. For this purpose, twelve lactating cows were used in a block design with a 2 × 2 factorial arrangement of treatments. Manure (feces and urine) was collected from each cow on 2 consecutive days, mixed (1:1) with an inoculum from a bioreactor, and stored (at 20°C) under anaerobic conditions in glass bottles (6 replicates/cow) for 17 wk. Quantity of gas produced was measured daily and sampled to determine gas composition. The PROC MIXED of SAS was used to determine the effects of forage source, LO supplementation and their interaction, and statistical significance was declared at $P \leq 0.05$. Interactions between forage source and LO supplementation were not significant ($P \geq 0.16$) for the measured variables. Compared to manure from cows fed RC-based diets, manure of cows fed CS-based diets emitted more ($P < 0.01$) CH_4 (182 vs. 118 L/kg of organic matter, respectively) and CO_2 (134 vs. 91 L/kg of organic matter, respectively). Emissions of CH_4 and CO_2 from manure also increased ($P \leq 0.05$) by 15% and 11% for CH_4 and CO_2, respectively, when cows were fed LO-supplemented diets compared to those fed non-supplemented diets. Organic matter losses were higher ($P < 0.01$) from manure of cows fed CS-based diets compared to manure of cows fed RC-based diets (30.6 vs. 22.5%, respectively). Organic matter losses of manure increased (+ 12%) with the addition of LO to the diets. Thus, it can be concluded that CH_4 and CO_2 emissions and organic matter losses from manure storage are higher if cow are fed CS-based diets compared to RC-based diets, and increase if LO is supplemented to the diet at 4% of dietary DM.

Key Words: manure, CH_4 emissions, forage source, linseed oil

1506 (W217) Life cycle assessment of heavy pig production in a sample of Italian farms.
G. Pirlo[*1], S. Carè[2], G. Della Casa[2], R. Marchetti[2], G. Ponzoni[2], V. Faeti[2], V. Fantin[3], P. Msoni[3], P. Buttol[3], and F. Falconi[4], *[1]Consiglio per la Ricerca e Sperimentazione in Agricoltura, Cremona, Italy, [2]Consiglio per la Ricerca e Sperimentazione in Agricoltura, San Cesario S/P, Italy, [3]ENEA, Bologna, Italy, [4]LCA-Lab, Bologna, Italy.*

The purpose of this study was to estimate the environmental impact of breeding and fattening of heavy pig used for Italian cured ham production. For this purpose, a life cycle assessment (LCA) was applied to two samples of four breeding farms and of eight fattening farms. The functional unit was 1 kg of body weight of fattened pig. The system was subdivided into breeding and fattening phases. The following impact categories were analyzed: global warming (GW), abiotic resource depletion (AD), photochemical ozone formation (*P*O), acidification (AC), and eutrophication (EU). Reference units were kg of CO_2eq for GW, kg of Sbeq for AD, kg of C_2H_4eq for PO, kg of SO_2eq for AC, and kg of PO_4^{3-}eq for EU. System boundaries included the following farm activities: 1) on-farm energy consumption (EC); 2) manure management (MM); 3) manure application (MA); 4) on-farm feed production (ONFP); 5) off-farm feed production (OFFP); 6) enteric fermentation (ENF); and 7) transports (TR). Average final body weight was 167 ± 5.2. LCA was performed with the support of SimaPro 7.3.3 software. The average environmental impacts associated with 1 kg of fattened pig body weight were: GW 3.43 kgCO_2eq, AD 3.13 E-3 kg Sbeq, PO 1.78 E-3 kg C_2H_4eq, AC 5.37 E-2 kg SO_2eq, EU 3.20 E-2 kg PO_4^{3-}eq. Percentage contribution of breeding and fattening phases to GW, AC, PO, AC, and EU were: 30 and 70; 23 and 77; 31 and 69; 37and 63; 30 and 70, respectively. Normalization analysis showed that the major contributions to the environmental impact of 1 kg of fattened pig body weight come from GW, AC and EU, whereas AD and PO are negligible.

Key Words: heavy pig, life cycle assessment, sustainability

1507 (W218) Control of water consumption in swine barns: One step-closer to real time management.
C. Pineiro*, P. Castro, J. Morales, and G. Montalvo, *PigCHAMP Pro Europa, Segovia, Spain.*

Providing enough quality water is essential for good livestock husbandry. Given that drinking water needs are farm- and management-specific, water-metering equipment to obtain accurate measurements of water use should be applied in each location. The aim of this study was to use new technologies to monitor and predict daily water consumption of fattening pigs. To monitor water consumption, a real-time sensor monitoring system was installed and set in the fattening unit of

one Spanish commercial swine farm. The fattening unit consisted of two buildings, both including about 1000 pigs. Each building was filled with one-only batch of pigs, 60 d of life at the entrance. Pigs were allotted in pens of 10 pigs, with a stock density of 0.70 m^2/pig, natural ventilation, partly slatted concrete flooring and one hopper and one cup drinker per pen. Feed and water were available ad libitum. The metering system consisted in one flow and one temperature sensors, connected to a processing unit which polled the data from these devices and uploaded it to the database. Four batches of pigs were followed up in each building, registering water intake, room temperature and daily control of mortality and health. Water consumption was daily calculated per pig from 60 to 150 d of life. Simple linear regression was conducted to predict water intake in L per animal and day from age in days using the REG procedure of SAS. As expected, water consumption was highly correlated to age (r square = 0.72). In the experimental farm where this measurement was conducted, the most statistically valid equation to predict water consumption was y = 0.0324x– 0.2081, where y is individual daily water intake (L) and x is age in days. Therefore, an average water consumption range of 1.73 to 4.65 (at 60 to 150 d of age) L per animal and day was obtained. Values found in bibliography differ significantly among different authors and are higher than the mean values obtained in the present study, being the average difference 22.4% with the lower interval reviewed in the bibliography and 48.9% with the upper one. This system allows monitoring water consumption in a particular facility and then detecting in an early stage any significant deviation of water intake from the expected range. In addition, knowing water consumption in detail also allows ensuring proper dosing rate of medication provided through the watering system.

Key Words: water consumption, monitoring, pigs

1508 (W219) Increasing milk yield affects sustainability of dairy cattle production in terms of cultural energy use efficiency. H. Koknaroglu*, H. Saglam, and O. Koskan, *Suleyman Demirel University, Isparta, Turkey*.

Purpose of this study was to conduct cultural energy analyses of dairy cows having different levels of milk yield. Cultural energy (CE) is the energy other than solar energy needed to produce food and fiber and energy output/input ratios is one of the most useful methods to examine the potential long-term sustainability of various agricultural practices and this analysis is performed to quantify the energy return from products produced relative to the CE invested to produce the product. Study was conducted at a commercial dairy farm, which specialized only in dairying and had 175 heads lactating cow during a production year which covered Dec. 15, 2010, through Dec. 15, 2011. At the farm lactating cows were grouped into four levels according to their milk yield and were fed accordingly. Groups were classified as low (LO), low-intermediate (LI), intermediate (IM) and high (HI). At the first visit to the farm a file that recorded milk production of each cow and number of lactating cows per group was formed and these records were recorded for every day. Feed intake of cows was also recorded every day. Cultural energy used for feed and other production inputs was derived from their corresponding feed consumption and resource expenditure and their corresponding values from literature. Energy value of the milk comprised the output. Total cultural energy expenditure increased as milk yield increased ($P < 0.05$). Cultural energy expended for feed constituted more than half of the total cultural energy expenditure and increased as milk yield increased ($P < 0.05$). Cultural energy expended per kg milk and per Mcal protein energy decreased as milk yield increased and was lowest for HI group ($P < 0.05$). Energy use efficiency defined as the Mcal input/Mcal output was better for HI and worse for LO and as milk yield increased energy use efficiency became better ($P < 0.05$). Results show that higher yielding lactating cows convert cultural energy into food energy better than lower yielding cows. Thus optimum milk yield not interfering cows' health should be sought for sustainable dairy production.

Key Words: dairy cattle, milk yield, sustainability, cultural energy

---

1509 (W220) Effect of astaxanthin production by the yeast *Phaffia rhodozyma* on growth performance, blood profiles, meat quality, and slurry noxious gas emission in broilers. S. Kim, S. D. Upadhaya, and I. H. Kim*, *Dep. of Animal Science, Dankook University, Cheonan, South Korea*.

A ban on specific antibiotic growth promoters in animal diets was introduced in the world from 1980s, on the basis of the Precautionary Principle. A prospective alternative to antibiotics that is currently being evaluated is yeast and its derivative products. *Phaffia rhodozyma* is discovered from the yeast that is strikingly different from the other pigmented yeasts in producing the carotenoid pigment astaxanthin. Astaxanthin exhibits a wide variety of biological activities, including antioxidative, anti-*Helicobacter pylori*, anticancer and anti-inflammatory effects in animals. A total of 432 1-d-old male broilers (Arbor Acres) were used in a 29-d experiment and each dietary treatment consisted of nine replicate cages, with 16 broilers per replicate. Birds were randomly allotted to 1 of 3 corn-soybean meal based diets supplemented with 0 mg (CON, basal diet), 1000mg (TRT 1, CON + astaxanthin production 0.1%) or 2000mg (TRT 2, CON + astaxanthin production 0.2%) per kg feed, giving an intake of approximately 0 mg, 2.3 mg, and 4.6 mg astaxanthin/kg feed, respectively. All broilers were fed maize-soybean meal-based diets that were formulated to meet or exceed the National Research Council (1994), nutrient recommendations. The broilers were weighed and feed intake were recorded on d 14 and 29 for calculating BW gain (BWG), feed intake (FI), and feed conversion ratio

(FCR). At d 29, 2 birds were randomly selected from each replication (18 broilers per treatment) and slaughtered by cervical dislocation for meat quality. All data were subjected to GLM procedures of SAS (1996) as a randomized complete block design, with pen as the experimental unit. Differences among treatments were separated by Duncan's multiple range tests; $P < 0.05$ was considered statistically significant. The inclusion of astaxanthin linearly improved ($P < 0.05$) body weight gain in the phase 2 (969, 989, 1024 g; 15~29 d) and during the overall experimental period (1377, 1401, 1439 g; 1~29 d).No significant linear effects were observed in the red blood cells, white blood cells, and lymphocytes in response to TRT1 and TRT2 ($P > 0.05$). The ammonia emission from slurry obtained from broilers in the CON group was significantly higher than that of slurry obtained from broilers in the TRT1 and TRT2 (17.98 vs. 14.42, 14.32 ppm; $P < 0.05$). Taken together, these results indicated that supplementation with astaxanthin could improve body weight gain and reduced slurry ammonia emission in broilers.

Key Words: blood profiles, broiler, noxious gas emission, *Phaffia rhodozyma*

1510 (W221) Assessing variability in whole-farm environmental impact estimates using a partially-stochastic beef production model. K. A. Johnson, and R. R. White*, *Washington State University, Pullman.*

Environmental impact (EI) studies often aim to identify resource use and greenhouse gas (GHG) emissions from an average production system without accounting for biological variability. These models are frequently used as means to compare EI between systems but they do not account for the variability expected in EI calculations. Our objectives were to develop a partially-stochastic model of beef EI and to use that model to examine implications of increased efficiency through improved calving rate. A whole-system model of beef production EI was adapted to account for the variability in land use, water use and GHG estimates. Variability in animal production parameters was not assessed. Three scenarios were tested: LOW (80% conception), CON (89% conception) or HIGH (100% conception). Projected changes in calving rate were compared with and without accounting for EI ranges. Reported state average crop yield and irrigation values were collected over a 20-yr period and used to represent variability in yield and irrigation estimates. Equations for CH_4 and N_2O were varied by their reported confidence bounds. Land use was expressed in m^2/kg hot carcass weight beef (HCWb), water use was in L/kg HCWb and GHG were calculated as CO_2–equivalents (CO_2e)/kg HCWb. The LOW scenario (Table 1510) had the greatest EI while the HIGH scenario had the lowest. This is in agreement with current literature relating efficiency to EI. When the variability around each environmental estimate was accounted for (Table 1510), the ranges described by the model overlapped considerably for all levels of operation efficiency. As a percentage of the mean, crop yield variability resulted in land use estimates with an error bound of about 200% while GHG and water use varied by about 100%. Variability associated with EI estimates was typically greater than the projected differences between treatments simulated. The variability may be consistent with true biological variability thus before accurate assessments of on-farm management to improve EI can be conducted, better methods to understand and account for the causes of this variability must be developed.

Key Words: environmental impact, variability, beef production

Table 1510. Means and ranges of EI metrics across efficiency scenarios

Scenario	Land Use (m^2/kg HCWb)	Water Use (L/kg HCWb)	GHG (CO_2e/kg HCWb)
LOW	82 (50.1– 246.9)	258.1 (226.9– 328.1)	21.5 (10.4– 34.3)
CON	75 (45.9– 224.5)	265.8 (217.7– 315.0)	19.9 (9.8– 31.7)
HIGH	68 (42.0– 203.3)	258.1 (211.1– 306.0)	18.5 (9.1– 29.3)

1511 (W222) Environmental assessment of a representative grass-finished beef operation in southern Pennsylvania. J. A. Dillon*[1] and C. A. Rotz[2], [1]*Dep. of Animal Science, Pennsylvania State University, University Park,* [2]*USDA-ARS Pasture Systems and Watershed Management Research Unit, University Park.*

The objective of this study was to quantify environmental impacts of a representative grass-finished beef operation in southeastern Pennsylvania. A farm-gate life cycle assessment was conducted using the Integrated Farm System Model to estimate greenhouse gas emissions, reactive nitrogen loss, and water and energy use. Parameters describing the operation were obtained from published survey results of pasture finishing beef producers in the northeastern United States. Cattle were rotationally grazed on 101 ha of perennial cool season grass-legume mixed pasture. Supplementation included silage and dry hay produced on the farm. Alfalfa silage was purchased for winter feeding and the final finishing phase. Net forage production was 652 t DM. The Angus herd consisted of 80 cows, 12 replacement heifers, 60 stockers, and 59 finishing cattle on a spring calving cycle. Calf weaning weight and average mature cow weight were 182 kg and 454 kg, respectively. Cattle were finished at 21 mo of age on high quality pasture and silage, with an ADG of 0.9 kg/d and shrunk body weight (SBW = 96% of live weight) of 477 kg. Simulation results over 25-years of historical weather for Lancaster, PA were sensitive to pasture management. When pastures were limed, average annual carbon footprint was 14.4 ± 0.5 kg CO_2e/kg SBW sold, requiring 27.3 ± 1.9 MJ of energy/kg SBW sold. When lime was not applied to pastures, the average annual carbon footprint was 12.6 ± 0.4 kg CO_2e/kg SBW, requiring 12.6 ± 0.7 MJ of energy/kg SBW. Total water use

(water footprint) for both scenarios was 13,900 ± 1350 L H_2O/kg SBW, and the water footprint excluding rainfall was 41 ± 2 L H_2O/kg SBW. The reactive nitrogen footprint was 91.0 ± 29.5 g reactive N loss/kg SBW. Generating data related to the environmental impacts of grass finished beef production provides a baseline for management decisions intended to improve the sustainability of production systems.

Key Words: grassfed beef, environment, carbon footprint

1512 (W223) A modeling assessment of cow management decisions, sustainability and durability of beef production systems.

R. R. White* and K. A. Johnson, *Washington State University, Pullman.*

Sophisticated calculations of system durability should be incorporated into sustainability assessments. The objective of this study was to assess how cow herd management affected the environmental impact (EI), economic viability and stability of a simulated beef herd. A modeling approach was used incorporating dynamic simulation of cattle genetic improvement with cradle-to-farmgate EI and income over feed costs (IOFC). Two 15-yr systems were simulated, one looking at culling rates of 1, 5, 10, 15, or 20% (CULL) and one assessing culling rate differences with a trauma (random removal of 30% of the breeding herd) occurring in the fifth year (CULL+T). Yearly changes in genetic merit were simulated using Markov Chain Monte Carlo sampling, expected progeny differences and the Key equation. Changes in conception/birth rate, mature weight, offspring daily gain, birth weight, weaning weight and yearling weight were tracked. Land use, water use and greenhouse gas emissions (GHG) and IOFC per kg hot carcass weight beef (HCWb) produced were calculated annually and yearly change was compared across culling levels. Trauma effects were calculated by interpolating across the points where the trauma occurred and calculating the cumulative difference between the CULL+T and interpolated lines. In the CULL scenario, the 15% cull rate resulted in the largest average annual improvement in EI and IOFC. Average yearly reductions in land, water and GHG were 2.4 ± 5.7 m^2/kg HCWb, 29 ± 77 L/kg HCWb and 0.26 ± 0.53 kg CO_2–equivalents (CO_2e)/kg HCWb. Annual change in IOFC was $0.03 ± $0.09/kg HCWb. In the CULL+T scenario, a 2-yr system depression occurred, and IOFC and EI were compromised. Culling at 10% was the least stable option; beef produced during the 2-yr trauma period had greater land use, water use and GHG (4.0 m^2/kg HCWb, 420 L/kg HCWb and 3.74 kg CO_2e/kg HCWb) compared with the no trauma line. Culling at 5% was the most stable treatment; environmental changes were only 3.4 m^2/kg HCWb, 374 L/kg HCWb and 3.26 kg CO_2e/kg HCWb. Culling at 1% was the most economically stable treatment; IOFC decreased $0.27/kg HCWb, substantially lower than losses seen with 10 or 15% culling (-$0.32/kg HCWb). Management that best optimized EI and IOFC did not always result in the most durable system. This model presents one framework for assessing durability that is applicable to multiple cow management decisions.

Key Words: cow-calf, sustainability, durability

1513 (W224) Nitrogen excretion from beef cattle for 6 cover crop mixes as estimated by a nutritional model.

E. E. Grings*, A. Sackey, M. J. Hansen, V. Owens, D. Beck, and P. Sexton, *South Dakota State University, Brookings.*

The objective of this study was to predict fecal and urinary N excretion for different maturities of beef cattle using model simulations based on compositional analysis of cover crop mixes. Two replicates of six forage mixes containing differing legumes with and without rape were grown under dryland conditions at Dakota Lakes Research Farm near Pierre, SD, in 2010 and 2011. Samples were analyzed for DM, CP, soluble CP, ADF, NDF, acid detergent insoluble CP, neutral detergent insoluble CP, lignin, starch, simple sugars and crude fat. Data was entered into the Large Ruminant Nutrition System model (LRNS) for estimation of N excretion. Two animal scenarios were analyzed: a non-lactating, pregnant beef cow and replacement beef heifer. Dry matter intake was set to 2.33% of BW for all simulations. The experiment was a split-plot arrangement of a randomized complete block with animal type and cover crop mixture as the whole plot and harvest date as the sub-plot. Forage mix and harvest date were treated as fixed factors and replications were considered random. Student's *t* test was used to separate mean effects when an *F* test was significant ($P = 0.05$). Crude protein concentrations of forage mixes were always at least 14% but CP content was affected by month within year ($P < 0.01$). Predictions of N utilization, except kg/d of fecal N excreted, were affected by forage mix. Fecal N excretion ranged from 33.6 to 43.7% and urinary excretion from 52.5 to 58.8% of N intake. Predicted N intake varied by month within year due to varied CP concentration of the mixes. Differences in N intake resulted in difference in the amount of predicted N excreted (kg/d) for cows, but not heifers. The predicted percentage of N intake excreted in feces did not differ by animal maturity. There was an animal maturity by month within year interaction for urinary excretion both when expressed as total kg/d excreted and percentage of N intake. Urinary N excretion varied from a low of 43.8% of intake for heifers to a high of 66.4% for cows. These types of estimates may be useful to make assessments about N flows in crop-livestock systems.

Key Words: forage, nitrogen, beef cattle

1514 (W225) Effect of crude glycerin associated with energy sources on enteric methane emission from finishing Nellore bulls on pasture in the dry season. A. José Neto*[1], L. G. Rossi[2], A. F. Ribeiro[1], B. R. Vieira[1], E. E. Dalanttonia[5], J. Duarte Messana[2], E. Garbin Sgobi[2], and T. T. Berchielli[1], *[1]Universidade Estadual Paulista "Julio de Mesquita Filho", Jaboticabal, Brazil, [2]Universidade Estadual Paulista, Jaboticabal, Brazil.*

The objective of this study was to evaluate the enteric methane emission, average daily gain (ADG) and daily carcass gain (GC) of finishing Nellore young bulls maintained on tropical pasture during the dry season and supplemented with 28% crude glycerin (CG) in the supplement (DM basis) and replacing corn or soybean hulls, with or without a source of oil. Thirty six Nellore young bulls with 510.02 ± 40.66 kg average initial BW were distributed in a completely randomized design (three animals per paddock and three paddocks per treatment) with four experimental treatments and nine replicates in a 2 × 2 factorial arrangement (high or low starch, with or without a source of oil). Paddock was the experimental unit, and the model effects included each treatment. The animals were raised (finishing phase) *Brachiaria brizantha* cv. Xaraés in the dry season (June to October 2013) with the treatments supplemented at the rate of 1000 g/100 kg BW. The supplements were: T1, CG with high starch (corn), T2, CG with low starch (soybean hulls), T3, CG with high starch and a source of oil (corn and soybeans) and T4, CG with low starch and a source of oil (soybean hulls in soybean grain). The sulfur hexafluoride SF_6 tracer method was used to measure eructated CH_4. Average daily gain (ADG) was obtained by weighing animals at the beginning and end of methane measurement period (28 d). The animals were slaughtered at d 133 of the trial with determined carcass weight. Data were analyzed using the PROC GLM procedure of SAS with significance level at $P < 0.05$ including daily carcass gain (GC, kg d^{-1}) and average daily gain (ADG, kg d^{-1}) of the animals. Methane emission was expressed per year (kg CH_4 yr^{-1}), per day (g CH_4 d^{-1}), per kilogram of carcass produced (kg CH_4 kg CAR^{-1}) and per kilogram of average daily gain (kg CH_4 kg ADG^{-1}). Differences were not detected ($P > 0.05$) between treatments with average values of 0.65 kg d^{-1}, 0.68 kg d^{-1}, 47.22 kg yr^{-1}, 129.37 g d^{-1}, 0.20 kg CH_4 kg CAR^{-1} and 0.25 kg CH_4 kg ADG^{-1}, respectively. The average daily weight and enteric methane emission of Nellore bulls on pasture was not affected by supplementation of crude glycerin.

Key Words: beef cattle, glycerol, greenhouse gas

1515 (W226) Enteric methane emission from beef cattle fed diets containing crude glycerin associated with energy sources. L. G. Rossi[1], A. José Neto*[2], B. R. Vieira[2], E. E. Dalanttonia[2], A. S. Gómez I[2], and T. T. Berchielli[2], *[1]Universidade Estadual Paulista, Jaboticabal, Brazil, [2]Universidade Estadual Paulista "Julio de Mesquita Filho", Jaboticabal, Brazil.*

The objective of this study was to evaluate the enteric methane emission of Nellore young bulls finished in feedlot fed diets containing 10% crude glycerin (CG; DM basis) replacing corn or soybean hulls, with or without a source of oil. Twenty eight Nellore young bulls with 395 ± 32 kg of average initial body weight and 20 ± 2 mo were distributed in a completely randomized design with four experimental treatments and seven replications in a 2 × 2 factorial arrangement (high or low starch, with or without a source of oil). The treatments were: T1, CG with high starch (corn), T2, CG with low starch (soybean hulls), T3, CG with high starch and a source of oil (corn and soybeans), and T4, CG with low starch and a source of oil (soybean hulls in soybean grain). All treatments contained 60% corn silage and 40% concentrate. The sulfur hexafluoride SF_6 tracer method was used to measure eructated CH_4. Data were analyzed using the PROC GLM procedure of SAS with significance level at $P < 0.05$. Methane emission was expressed per day (g CH_4 d^{-1}), per kilogram of carcass produced (g CH_4 kg CAR^{-1}) and per kilogram of average daily gain (g CH_4 kg ADG^{-1}). Differences were not detected between treatments for all variables ($P > 0.05$). However, when compared the effects between factors, differences were detected, with average values of 118.74 and 164.40 g CH_4 d^{-1} ($P < 0.001$), 101.93 and 140.78 g CH_4 kg ADG^{-1} ($P < 0.01$), 141.14 and 180.46 g CH_4 kg CAR^{-1} ($P < 0.02$) to the factors with or without a source of oil, respectively. The starch in the diet did not affect enteric methane emission for all variables ($P > 0.05$). However, may be affected when an oil source with crude glycerin is added in diet Nellore young bulls finished in feedlot.

Key Words: environment, glycerol, ruminant

1516 (W227) Using fecal phosphorus, calcium and ash excretion to predict total and inorganic phosphorus intake of beef cattle consuming a forage-based ration. D. D. Harmon*, J. K. Smith, and M. A. McCann, *Virginia Polytechnic Institute and State University, Blacksburg.*

To mitigate the environmental and economic impact of phosphorus (P) supplementation in excess of beef cattle requirements, producers are currently being encouraged to re-evaluate P supplementation strategies. One of the major limiting factors in doing so is that P intake of grazing cattle is generally unknown. The objective of this evaluation was to determine the ability of fecal total P (P_t) and fecal inorganic P (P_i), calcium (Ca) and ash fractions to explain variation in P_t and P_i

intake. Results of dietary and fecal P_t, P_i, Ca and ash analyses were obtained from two previous experiments that quantified P excretion of beef cattle supplemented with P from different dietary sources. Steers included in each of the two experiments were fed a basal ration of low P chopped grass hay (0.10 and 0.13%) and supplemented with increasing levels of dicalcium phosphate (0, 33, 65, 95 g/d) or increasing levels of corn gluten feed (0, 0.5, 1.0, 1.5 kg/d) to provide increasing levels of dietary P that were below, met or exceeded NRC recommended P requirements. Steers in the dicalcium phosphate trial were 304 ± 22 kg BW and steers in the corn gluten trial were 427 ± 79 kg BW. Daily feed intake measurements and total fecal collections were used to quantify P_t, P_i, Ca and ash content (expressed as a percentage of DM) of feed offerings, orts and feces. Values were then used to determine respective nutrient intake and excretion. All statistical analyses were conducted using JMP Pro. Interpretation of the results of an initial factor screening indicated that fecal percentage of P_t, P_i, Ca and ash explained a significant ($P < 0.05$) portion of the variation in P_t and P_i intake. Full four-way factorial regression models were generated to predict P_t ($R^2 = 0.79$; $P < 0.0001$) and P_i ($R^2 = 0.83$; $P < 0.0001$) intake expressed in g per d using the Fit Model procedure. Refinement of the full factorial model using the reverse stepwise personality supports the use of the full factorial design, as removal of higher-order interactions resulted in a reduction of the R^2 value. These results indicate the ability of fecal P_t, P_i, Ca and ash percentages and their interactions to explain the majority of the variation in P_t and P_i intake. These and additional measurements could be utilized to develop a fractional P intake prediction model for beef cattle.

Key Words: beef, phosphorus, prediction

1517 (W228) Influence of low doses tannins extract addition on the presence of *Escherichia coli* in feces of beef cattle. T. D. J. Heras*[1], I. Enriquez[1], B. J. Cervantes[2], S. M. Gaxiola[1], J. A. Romo[1], and R. Barajas[1], *[1]FMVZ-Universidad Autónoma de Sinaloa, Culiacan, México, [2]Ganadera los Migueles, S.A. de C.V., Culiacan, México.*

Feces of twenty bulls 430 ± 4.5 kg (75% Brahman breed with remainder of Brown Swiss or Charolais) fed finishing diets were used to determine the influence of Influence of low doses tannin extract addition on the presence of *Escherichia coli* in feces of beef cattle. From each of four commercial feedlot pens containing 70 bulls, five bulls were randomly selected and moved to squeeze and fecal samples were taken. Feces of five bulls from a common pen were pooled and constitute the experimental unit. Pooled fecal sample were divides in four portions of proximately 60 g (wet basis), one portion was used for DM determination, and remainder three fecal samples by pen were randomly assigned for addition or not tannins extract (TE) as follows: 1) Feces without extra addition (Control); 2) Control plus 0.1008 g of condensed tannins extract (CTE); and 3) Control plus 0.1008 g of hydrolyzable tannins extract (HTE). TE was fed as SilvaTeam (Argentina). Feces was thoroughly mixed and placed on piece of Kraft paper underground 0.70 m outside of pen and covered with a 0.4 × 0.4 × 0.25 cm metal mesh cage, and exposed to feedlot environment during 0, 24, 48 or 72 h. Aliquots from each TE schedule, exposed time and pen were taken, and by triplicate placed in a *E. coli* selective medium and incubated during 24 h at 45°C, after incubation Colonies Former Units (CFU) were counted and transformed to $\log_{10}$CFU. Results were analyzed by ANOVA for a completely randomized design with a 3 × 4 factorial arrangement. Feces DM were 27.27%, and then TE dose was 0.6% of fecal DM. At 0 h, *E. coli* presence was 4.19, 4.08, and 4.28 $\log_{10}$CFU for Control, CTE and CTH, respectively. At 48 h CTE tended ($P = 0.07$) to decrease *E. coli* presence compared with 0 h (4.08 vs. 1.13 $\log_{10}$CFU). At 72 h CTE tended to diminished ($P = 0.07$) *E. coli* in bovine feces with means values of 4.07, 3.22 and 1.76 $\log_{10}$CFU for Control, CTE and HTE, respectively. It is concluded; that the addition of condensed tannin extract at very low concentration could contributes to reduce the *Escherichia coli* population in the feces of feedlot cattle.

Key Words: *Escherichia coli*, bovines, tannins extract

1518 (W229) Phosphorus excretion in beef steers as impacted by increasing levels of dicalcium phosphate supplementation. E. A. Riley, D. D. Harmon*, J. K. Smith, A. L. Zezeski, S. P. Greiner, K. F. Knowlton, and M. A. McCann, *Virginia Polytechnic Institute and State University, Blacksburg.*

Feeding phosphorus (P) to grazing cattle in excess of requirements can lead to increased P in surface water. The objective of this study was to determine the impact of increasing levels of dicalcium phosphate as a supplemental inorganic source of P. Eight Hereford steers, 304 ± 22 kg of BW, were randomly assigned to one of four dietary P treatments in a 4 × 4 replicated Latin square. Steers were fed a ration containing 80 ± 1% chopped grass hay (0.10%P) and 0, 33, 65 or 95 g/d of dicalcium phosphate. All steers were supplemented with 0.79 kg/d beet pulp, 0.23 kg/d rumen-protected fat supplement and 20 g/d trace mineral salt. Diets were formulated to approximate 50, 100, 150, and 200% of dietary P requirement for a growing beef steer. Steers were housed in individual pens and fitted with total fecal collection bags. Each period consisted of a 9-d adjustment period followed by a 5-d collection period. Following the final collection of each period, a 10-mL blood sample was collected via jugular venipuncture and analyzed to determine plasma inorganic P (P_i) concentration. Samples were analyzed for P_i and total P (P_t) using the molybdovanadate yellow and blue methods, respectively. Data were analyzed using the PROC GLIMMIX procedure of SAS with a model that included diet and period. Linear,

quadratic and cubic treatment effects were evaluated using preplanned contrasts. Dietary P increased linearly ($P < 0.05$) across diets at levels of 3.88, 10.45, 16.47 and 22.28 g/d, respectively. Total P excretion increased linearly with increasing dietary P content (7.73, 11.41, 15.50, and 21.51 g/d; $P < 0.05$) as did P_i excretion (3.19, 6.51, 10.50, 14.67 g/d, $P < 0.05$) and thus P_t excretion was highly correlated ($P < 0.05$; $r = 0.94$) with P_i excretion. Apparent P digestibility increased quadratically with increasing dietary P (−110.67, −9.32, 5.83, and 3.75%, $P < 0.05$), with negative digestibility's suggesting dietary P levels below requirement. P solubility ([P_i/P_t] x 100) increased quadratically with increasing dietary P (39.71, 56.64, 66.60, and 67.85%, $P < 0.05$), indicating that the percentage of water soluble P increases when feeding P levels above requirements. Similar to fecal P trends, blood plasma P_i increased linearly with increasing levels of dietary P (6.40, 8.35, 8.72, and 9.19 mg/dL, $P < 0.05$). Beef cattle operations can reduce environmental impacts by closely matching P supplementation to P requirements.

Key Words: beef, phosphorus, excretion

1519 (W230) Estimation of heat production and energy conversion efficiency using real time measurements of methane and carbon dioxide fluxes in mid-lactation holstein cows. A. B. D. Pereira*[1], A. F. Brito[1], and S. A. Utsumi[2], *[1]University of New Hampshire, Durham, [2]Dep. of Animal Science, Michigan State University, Hickory Corners.*

Real time measurements of CH_4 (Q_{CH4}) and CO_2 (Q_{CO2}) fluxes were used in a pilot study to estimate heat production[1] (HP) and energy conversion efficiency in lactating dairy cows. Oxygen utilization (Q_{O2}) was estimated according to the respiration quotient[2]. Eleven multiparous and four primiparous lactating Holstein cows averaging 176 ± 34 DIM, 42.9 ± 6.8 kg of milk yield and 681 ± 48 kg of BW were blocked by DIM, parity, and DMI (as % of BW) and, within each block, randomly assigned to 1 of 2 treatments: restricted intake (RI) (90% DMI) or ad libitum intake (AI) according to a crossover design. Each experimental period lasted 22 d with 14 d for treatments adaptation and 8 d for data and sample collection. Diets contained (DM basis): 40% corn silage, 12% grass-legume haylage, and 48% concentrate. Spot gas measurements were taken in 5-min sampling periods from all cows using a portable automated head chamber system [GreenFeed (GF); C-Lock Inc., Rapid City, SD] with intervals of 12 h between the two daily samplings. Sampling points were advanced 2 h from a day to the next to yield 14 gas samplings/cow over 7 d to account for diurnal variation in Q_{CH4} and Q_{CO2}. Data were analyzed using the Fit Model procedure in JMP, and least square means are reported. Cows on RI converted more feed gross energy[3] into milk energy[4] (28.3 vs. 27.0%, SEM = 0.63; $P = 0.04$) and more DMI into metabolizable energy[5] than AI cows (11.8 vs. 11.3 MJ/kg of DMI; SEM = 0.22 $P = 0.02$). Conversely, RI cows yielded more HP/kg of DMI (6.65 vs. 6.36 MJ/kg; SEM = 0.18; $P = 0.04$). Our results suggest that the proposed methodology has potential to identify more efficient dairy cows according to real time measurements of Q_{CH4} and Q_{CO2} using the GF.

Equations used for estimations:

[1]Estimated
$$HP_{MJ/cow/d} = [(3.86 \times Q_{O2}) + (1.2 \times Q_{CO2}) - (0.518 \times Q_{CH4})] \times 4.184/1000 \text{ (Brouwer, 1965)}$$

[2]$Q_{O2}/Q_{CO2} = 0.95$ (Madsen et al., 2010)

[3]Gross energy
$$\text{intake}_{MJ/cow/d} = [\text{dietary } CP_{\%} \times DMI_{kg} \times 17 \times 0.6] \times 4.184 \text{ (IPCC, 2006)}$$

[4]Milk
$$\text{energy}_{MJ/cow/d} = [(0.384 \times fat_{\%}) + (0.223 \times protein_{\%}) + (0.199 \times lactose_{\%}) - 0.108] \times \text{milk yield}_{kg/cow/d} \text{ (AFRC, 1993)}$$

[5]Metabolizable
$$\text{energy}_{MJ/cow/d} = HP + \text{Milk energy} \pm (19.99 \times \text{kg of mobilized weight}) \text{ (AFRC, 1990)}$$

Key Words: energy conversion efficiency, heat production, GreenFeed

---

1520 (W231) Effect of dietary nitrate and organic copper supplementation on dairy enteric methane and nitrous oxide emissions. S. J. Werth*[1], Q. Wang[1], C. J. Neumeier[1], G. Getachew[1], D. H. Putnam[1], A. R. Castillo[2], and F. M. Mitloehner[1], *[1]University of California–Davis, Davis, [2]University of California Cooperative Extension, Merced.*

Previous research on nitrate (NO_3^-) supplementation in dairy cattle diets demonstrated that NO_3^- is effective in decreasing methane (CH_4) production; however, it also induced nitrous oxide (N_2O) production under the rumen simulated conditions. One possible strategy to mitigate concomitant N_2O emission is by enhancing the activity of nitrous oxide reductase (N_2OR) to increase the reduction of N_2O to nitrogen gas (N_2). Nitrous oxide reductase is a metalloenzyme with one enzyme that contains 12 copper (Cu) atoms to be fully active. Copper availability under rumen condition is typically low, which could impede N_2OR activity and therefore the reduction of N_2O to N_2. Organic (OG), compared to inorganic (IN) Cu, might have a higher availability to microbes under rumen conditions. Organic Cu forms strong chelation complexes with small organic compounds, which renders the Cu complex high stability under the rumen environment (Stevenson, 1994), this may result in higher availability of OG Cu. The present study investigated the effect of OG vs. IN Cu on

decreasing NO_3^- induced N_2O production in the simulated rumen using in vitro gas production systems. Gas and liquid samples were obtained from the system every two-hours and were analyzed for carbon dioxide, CH_4, N_2O, NO_3^-, nitrite, and ammonium (NH_4^+) concentrations. Nitrate was totally consumed after 8h. Nitrate decreased ($P < 0.01$) ruminal CH_4 by 30.1% but increased ($P < 0.001$) N_2O production from 0 to 7.1 uL/g DM. Organic Cu was effective in decreasing ($P < 0.05$) NO_3^- induced N_2O production by 24.7% during enteric fermentation. Ammonium concentration in the rumen fluid was lower ($P < 0.01$) with the supplementation of NO_3^- compared to urea especially during the early incubation period. In summary, NO_3^- and OG Cu feeding decreased ruminal CH_4 and N_2O production concomitantly although total greenhouse gas gasses were not affected by OG Cu supplement.

Key Words: cattle, greenhouse gas, nitrous oxide reductase

1521 (W232) Influence of tannins extract addition on in vitro gas production of feces from beef cattle. R. Barajas*, E. X. Murillo, N. Castro, and E. A. Velazquez, *FMVZ-Universidad Autónoma de Sinaloa, Culiacan, México.*

Feces of 15 bulls 392 ± 5.1 kg (75% Brahman breed with remainder of Brown Swiss or Charolais) fed finishing diets were used an experiment to determine the influence of tannins extract addition on in vitro gas production of feces from beef cattle. From each of three commercial feedlot pens containing 72 bulls, five bulls were randomly selected and moved to squeeze and fecal samples were taken. Feces of five bulls from a common pen were pooled and constitute the experimental unit. Pooled fecal sample were divides in three portions of proximately 200 g (wet basis), one portion was used for DM determination, and two remainder fecal samples by pen were randomly assigned to one of two treatments: 1) Feces without extra addition (Control); 2) Control plus addition of 2 g of a tannins extract/100 g of wet feces (TE). Tannins extract were proportioned as SilvaFeed Bypro (SilvaTeam, Argentina), a premix integrated mainly for condensed tannin from quebracho tree blended with a minor proportion of hydrolyzable tannins from chestnut. Aliquots of 50 g (wet basis) were placed in 600 mL flask (three by treatment), closed and connected with a plastic pipe to a 250 mL glass graduate probet inverted in a water bath. Flask were incubated at 37°C during 24, and gas production was accounted as the amount of water displaced by gas inside of each probet, and was expressed as mL of gas by g of feces DM basis. This procedure was repeated during four consecutive days. Results were analyzed by ANOVA for a complete randomized block design where day run constitutes the block. Fecal dry mater content was 26.9% and dose of tannin extract was equivalent to 7.45% DM basis. The addition tannins extract diminished ($P < 0.001$) in 45% the in vitro gas production respect to Control treatment (8.92 vs. 16.24 mL/g of feces DM). It is concluded, that tannin extract addition could contributes to decreases gas production of feces from finishing beef cattle.

Key Words: feces, gas production, tannins

1522 (W233) Quantification of cephapirin in dairy cow feces and urine using solid phase extraction (SPE) coupled with ultra performance liquid chromatography-tandem mass spectrometry (UPLC/MS/MS). P. P. Ray*[1], K. F. Knowlton[2], C. Shang[3], and K. Xia[3], *[1]Dep. of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, [2]Virginia Tech, Blacksburg, [3]Dep. of Crop and Soil Environmental Sciences, Virginia Polytechnic Institute and State University, Blacksburg.*

Antibiotic use in animal agriculture has been under scrutiny for two decades because of the persistency of excreted antibiotics in the environment and their potential contribution to bacterial antibiotic resistance. Cephapirin, a cephalosporin antibiotic, is commonly used for dry cow therapy and other therapeutic treatments in dairy cows. Fecal and urinary excretion of cephapirin could introduce this compound into the environment with land application of manure or runoff from the feedlot or barnyard. To date, however, the environmental loading of cephapirin by the livestock industry remains un-assessed, largely due to a lack of appropriate analytical methods. Therefore, an analytical method was developed and validated to qualify and quantify cephapirin in dairy cow feces and urine. The method includes extraction with phosphate buffer (0.05 M) and methanol at 50:50 (v/v) followed by solid-phase extraction (SPE) clean-up via elution through hydrophilic-lipophilic-balanced cartridges and filtering through 0.2-µm filters. Cephapirin in clarified sample extracts was qualified and quantified using ultra performance liquid chromatography-tandem mass spectrometry (UPLC/MS/MS). The limit of quantification (LOQ) of the developed method was 4.02 ng/g and 0.96 ng/mL for feces and urine, respectively. Recovery of cephapirin from spiked blank feces and urine was 64 to 73% and 81 to 84%, respectively. Intra- and inter-day variation [residual standard deviation (RSD), %] were used to estimate repeatability and reproducibility of the method, and ranged from 7.9 to 8.2% for feces and 3.07 to 9.59% for urine. This method was applied to feces and urine collected from dairy cows within 8 h of cephapirin administration. Trace amounts (ng/g) of the compound were detected in feces and very high concentrations (133 to 480 ng/mL) in urine. The described method is sensitive, accurate, and robust and will advance understanding of the fate and environmental impact of antibiotics used on farms.

Key Words: cephapirin, dairy cow feces and urine, ultra performance liquid chromatography-tandem mass spectrometry

1523 (W234) Method development and application: Solid phase extraction (SPE) clean-up and ultra performance liquid chromatography-tandem mass spectrometry (UPLC/MS/MS) quantification of pirlimycin in dairy cow feces and urine. P. P. Ray*[1], K. F. Knowlton[2], C. Shang[3], and K. Xia[3], *[1]Dep. of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, [2]Virginia Tech, Blacksburg, [3]Dep. of Crop and Soil Environmental Sciences, Virginia Polytechnic Institute and State University, Blacksburg.*

In the last two decades antibiotic excretion by livestock has received significant attention because of the contribution of excreted antibiotics to bacterial antibiotic resistance. Reliable and accurate quantification of antibiotics in feces and urine is critical to assess environmental loading of antibiotics by the livestock industry in the effort to maintain or improving the sustainability of animal agriculture. Pirlimycin, a lincosamide antibiotic, is one of the most commonly used antibiotics for the treatment of mastitis in dairy cows. There is no published data on pirlimycin loading to the environment via fecal and urinary excretion, probably due to inadequate methodology to quantify pirlimycin in fecal and urine matrices. Therefore, the objective of this study was to develop and validate an analytical method to qualify and quantify pirlimycin in dairy cow feces and urine. Samples were extracted with methanol+0.05 M phosphate buffer (70:30, v/v). Sample extracts were cleaned using solid phase extraction (SPE) via elution through hydrophilic-lipophilic-balanced (HLB) cartridges and filtering through 0.2-μm filters. Clarified extracts were analyzed for pirlimycin using ultra performance liquid chromatography-tandem mass spectrometry (UPLC/MS/MS). This method was sensitive with a limit of quantification (LOQ) of 1.47 ng/g wet feces and 0.90 ng/mL urine. The developed method recovered 80 to 108% of pirlimycin spiked in feces and recovery was 89 to 98% in urine. Repeatability and reproducibility of the method was estimated by intra- and inter-day variations [residual standard deviation (RSD) %], and ranged from 2.3 to 13% and 2.3 to 14% for feces and urine, respectively. With the application of this method to samples collected in the 10 h following intramammary dosing, pirlimycin was detected at 61.2 to 71.8 ng/g and 153 to 254 ng/mL in feces and urine, respectively. This sensitive, accurate, and robust method can be used to quantify trace amounts of antibiotics in dairy cow feces and urine, and may help in the assessment of fate and environmental impact of antibiotics used on farms.

Key Words: pirlimycin, dairy cow feces and urine, ultra performance liquid chromatography-tandem mass spectrometry

1524 (W235) A larger proportion of grass feed components in the ration was associated with higher methane production rates of dairy cows. C. C. Metges*[1], M. Derno[1], J. Ziessler[1], N. Krattenmacher[2], G. Thaller[3], and B. Kuhla[1], *[1]Leibniz Institute for Farm Animal Biology (FBN), Dummerstorf, Germany, [2]Institute of Animal Breeding and Husbandry, Kiel University, Germany, [3]Christian-Albrechts-Universität, Kiel, Germany.*

Ruminants can utilize feedstuffs which are not in competition with human food. In 10 German Holstein cows, 4 in first (L1; BW 562 kg) and 6 in second (L2; BW 615 kg) lactation, 2 TMR rations fed ad lib were compared in regard to methane production. Ration 1 (R1) contained a mixture of grass silage, grass hay + straw (total of 22% DM), and corn silage (32% DM), and was fed to all cows from 20 to 103 DIM. Subsequently, from 104 to 140 DIM, cows received ration 2 (R2), comprising 41% DM of the grass silage, grass hay + straw mixture, and 18% DM of corn silage. Starch, fat and energy contents of R1 and R2 were 18, 4.5% DM, and 7.2 MJ NEL/kg, and 10, 2.7% DM, and 6.7 MJ NEL/kg, respectively. Water was offered ad lib. Appropriately acclimatized cows were measured in respiration chambers (see citation below) on 99 and 135 DIM for 36 h. The respective rations and water were provided ad lib. DMI, ECM yield, and methane production per d were determined. Data was analysed by PROC MIXED of SAS. DMI did not differ among rations and lactation number ($P > 0.1$). However, ECM was lower with R2 (L1: 23.3. vs. L2: 29.2 kg/d) than with R1 (L1: 30.9 vs. L2: 36.3 kg/d) as well as in L1 than in L2 cows ($P < 0.05$). Methane production was affected by ration but not by BW or lactation number with higher values in cows fed TMR with higher contents of grass components and lower proportions of corn silage (R2 vs. R1: 513 vs.455 L/d; 18 vs. 12 L/(kg ECM * d); 39 vs. 34 L/(kg DM * d); $P < 0.05$). In conclusion, using larger amounts of feedstuffs less in competition with human food, i.e., grass and straw, contributes relatively more to greenhouse gas emissions. The lower ECM yield with R2 was partly due to progressing stage of lactation. Citation: Derno et al. J. Dairy Sci. 92:2804–2808, 2009.

Key Words: dairy cow, starch content, methane emission

1525 (W236) Effect of eco-saline system on some hematological and biochemical parameters in damascus goats raised under semiarid conditions. E. B. Abdalla*, *Faculty of Agriculture, Ain Shams University, Cairo, Egypt.*

The effect of eco-saline system, composed of saline water and salt-tolerant plants, on hematological and biochemical responses of Damascus goats was investigated from August 2009 to June 2010. Forty-eight adult female Damascus goats were

equally assigned randomly into four groups. The first group (G1) fed berseem (*Trifolium alexandrnum*) hay (BH) and drank fresh water (247 ppm total dissolved solids), the second group (G2) fed BH hay and drank saline water (5980 ppm total dissolved solids), the third group (G3) fed salt-tolerant alfalfa (*Medicago sativa*) and drank fresh water and the fourth group (G4) fed alfalfa and drank saline water. Body weight changes, hematological and biochemical parameters were measured. Does of G1, G2, G3 and G4 gained 6.64, 8.2, 4.11 and 5.14 kg, respectively during gestation period. Feeding salt-tolerant plants and drinking saline water was negatively affected ($P < 0.05$) hemoglobin (Hb), mean corpuscular hemoglobin (MCH) and mean corpuscular hemoglobin concentration (MCHC) during different stages of pregnancy. However, packed cell volume (*P*CV %) and erythrocytes cell counts (RBCs) were not affected. Animals on saline water had significantly lower white blood cell counts than goats given fresh water. Values of WBCs increased with advancing pregnancy. Total protein (TP), albumin (A), globulin (G) and albumin/globulin ratio (A/G %) as well as alanine transferase (ALT) concentration of different groups were within the normal ranges reported for goats during different eco-saline systems. However, aspartate transferase was higher in salt tolerant groups. Except for phosphorus, serum minerals were higher in alfalfa groups. Concentrations of aldosterone of does fed salt-tolerant alfalfa were higher significantly than does fed berseem hay. It could be concluded that utilization of salt-tolerant plants as animal feeds in salt affected lands could be an appropriate option for alleviating the desertification problems and providing alternative feed resources, particularly in summer and autumn seasons when the other conventional forage resources are in short supply. Also, these results suggest that saline water can be used as a source of drinking water without any adverse effects on hematological and performance of Damascus goats.

Key Words: salt-tolerant plants, saline water, Damascus goats

1526 (W237) Fibrolytic bacteria isolated from the rumen of North American moose (*Alces alces*).

S. L. Ishaq* and A. D. G. Wright, *University of Vermont, Burlington.*

Fibrolytic bacteria were isolated from the rumen of North American moose (*Alces alces*), which eat a high-fiber diet of browse. It was hypothesized that fibrolytic bacteria isolated from the moose rumen could be candidates to improve fiber degradation and animal production. In vivo, an increase in cellulose degradation can increase weight gain, milk, and wool production. In industrial systems, digestion by microorganisms or enzymes can increase forage digestibility for livestock, improve ensiling, or provide glucose from biomass for bioethanol-production. Thirty-eight isolates were cultured from rumen digesta samples collected in October 2010 in Vermont. Using Sanger sequencing of the 16S rRNA gene, culturing techniques, and optical density, isolates were identified and screened for biochemical properties important to plant carbohydrate degradation. Isolates had the following percent identity to known sequences in NCBI: *Bacillus licheniformis*, 98- 100% ($n = 22$); *Enterococcus fecalis*, 95– 99% ($n = 6$); *Staphylococcus saprophyticus*, 99- 100% ($n = 4$), *B. chandrigarhensis*, 98% ($n = 1$); *B. firmus*, 98% ($n = 1$); *B. flexus*, 100% ($n = 1$); *B. niabensis*, 95% ($n = 1$); *Enterobacter ludwigii*, 99% ($n = 1$), and *Paenibacillus woosongensis*, 98% ($n = 1$). Using a 97% identity cutoff for near full-length 16S rRNA gene sequences, there are 22 novel strains of *B. licheniformis*; one novel strain each of *B. chandrigarhensis*, *B. firmus*, and *B. flexus*; one novel species of *Bacillus*; three novel strains of *Enterococcus fecalis*, two novel *Enterococcus sp*., one novel strain of *Enterobacter ludwigii*; one novel strain of *P. woosongensis;* and four novel strains of *S. saprophyticu.* Isolates were able to digest cellulose ($n = 38$), cellobiose ($n = 34$), xylan ($n = 31$), starch ($n = 25$), carboxymethylcellulose ($n = 24$), and lignin ($n = 20$) under minimal nutritional conditions. Fifteen isolates were able to digest all six carbohydrates tested. Isolates were able to tolerate up to 10% ($n = 17$) salinity, between pH 4.0 ($n = 34$) and pH 10.0 ($n = 33$), and between 20°C ($n = 35$) and 55°C ($n = 36$). Isolates were tolerant to sodium azide ($n = 37$), could reduce potassium tellurite ($n = 3$), metabolize mannitol ($n = 31$), produce indole from tryptophan ($n = 7$), and all isolates could use citrate or proprionate as a sole carbon source, as well as ammonium ions for nitrogen. New, highly efficient species or strains of fibrolytic bacteria could be utilized to improve fiber degradation in ruminants or in industrial applications. The isolates tested showed a wide range of carbohydrate digestion and were able to tolerate adverse growth conditions, making them good candidates for improved fiber digestion in vivo and suitable for high temperature industrial fiber digestion.

Key Words: fibrolytic, bacteria

RUMINANT NUTRITION I

1527 (M241) Metagenomic analysis of the rumen microbiome of dairy cows during the transition period. D. W. Pitta*[1], S. Kumar[1], N. Indugu[1], R. Sinha[2], B. Veiccharelli[1], B. Bhukya[1], and J. Ferguson[1], [1]*University of Pennsylvania, Kennett Square,* [2]*University of Pennsylvania, Philadelphia.*

In the current study we characterized the rumen microbiome of dairy cows belonging to different lactations which were grouped as first lactation (L1; $n = 5$), second lactation (L2; $n = 2$) and third lactation (L3; $n = 2$). The rumen samples were collected using stomach tube method at four time points i.e., 3 wk before the anticipated freshening date (S1), soon after the animal freshened (S2), 4 wk (S3) and 8 wk (S4) into lactation. We pooled the genomic DNA by lactation number (3 lactation groups × 4 sampling times) to yield 12 samples. All animals received the same dry cow ration (CP-14.65%; NDF-43.66%; Starch-21.9%) before calving and the same lactating cow rations (CP-17.21%; NDF-33.14%; Starch-27.19%) post calving. The pooled genomic DNA was subjected to shotgun sequencing on Ion-torrent platform, aligned for contigs using Nextgene and uploaded to MG-Rast server for further analysis. On average 17,000 contigs per sample were obtained and subsequently used for phylogenetic and functional assignments in MG-Rast. Based on the phylogenetic data, both study group and study day tended to have an effect on the community compositions ($P < 0.12$; Permanova test) while study groups differed in their functional profiles ($P < 0.05$; Permanova test). The most abundant bacterial phyla observed were *Bacteroidetes* (60%), *Firmicutes* (20%) and *Proteobacteria* (*7%)* across all communities. As the cows transitioned into lactation, the abundance of *Bacteroidetes* decreased while that of *Firmicutes* increased. The phylum *Proteobacteria* increased in abundance with the onset of lactation and also with increased parity. The abundance of archaeal communities were found to be higher in the dry period but reduced at the onset of lactation. Both carbohydrate and protein metabolism were the most predominant functional activities with a progressive increase ($P < 0.1$) in protein utilization from L1 to L3 dairy cows. Differences also occurred in the carbohydrate and protein metabolism before and after the onset of lactation ($P < 0.05$). This study is the first report to demonstrate distinct shifts in both phylogenetic and the associated metabolic activity in both primiparous and multiparous dairy cows in their transition period.

Key Words: dairy cows, transition period, rumen microbiome, Ion-torrent, metabolic potential

1528 (M242) Peripartal supplementation of Smartamine M has positive effects on blood neutrophil activation in dairy cows. J. S. Osorio[1], P. Ji[2], J. K. Drackley[3], D. N. Luchini[4], and J. J. Loor*[5], [1]*University of Illinois, Champaign,* [2]*William H. Miner Agricultural Research Institute, Chazy, NY,* [3]*University of Illinois, Urbana,* [4]*Adisseo S.A.S., Alpharetta, GA,* [5]*University of Illinois, Urbana-Champaign, Urbana.*

An effective immune response relies on efficient activation of polymorphonuclear neutrophils (*P*MN). We evaluated mRNA expression of genes associated with metabolism of Met, glutathione, and glucose as well as inflammation, cellular receptors, and oxidative stress in PMN during the peripartal period. Twenty-eight multiparous Holstein cows in a randomized complete block design were fed a controlled-energy diet (CE, $n = 9$; 1.24 Mcal/kg DM; high-straw) during the dry period (approximately 50 d), switched to a moderate-energy (ME, $n = 9$; 1.54 Mcal/kg DM) during the last 21 d before calving, or ME plus Smartamine M (SM, $n = 10$; Adisseo France S.A.S.). After calving all cows received the same lactation diet (1.75 Mcal/kg DM). The SM (0.07% of DM) was top-dressed over the ME diet from -21 through 30 DIM. Daily dry matter intake (DMI) and milk yield were recorded. Whole blood leukocyte phagocytosis (Phagotest) was assessed and RNA from PMN was extracted from samples collected at -10, 3, and 21 DIM. Data were analyzed using the PROC MIXED of SAS. Although prepartal DMI was not affected ($P = 0.21$) by diet, postpartal DMI was lower ($P < 0.005$) in ME than CE and SM. Milk yield was also lower ($P < 0.05$) in ME than CE and SM. There was a greater ($P < 0.001$) phagocytosis in CE cows than ME and SM. Although phagocytosis decreased ($P = 0.02$) from -10 to 21 DIM regardless of treatment, there was a trend ($P = 0.10$) for an increase in phagocytosis in SM. The selectin L (*SELL*) mRNA expression was greater in SM cows at 21 DIM than CE ($P < 0.001$) and to a lesser extent ($P = 0.11$) than ME. In fact, *SELL* increased ($P < 0.001$) in SM cows from -10 to 21 DIM, while it decreased ($P = 0.006$) in CE and was unchanged ($P = 0.87$) in ME. The diet×time effect ($P = 0.005$) for superoxide dismutase 2 (*SOD2*) expression was associated with greater ($P < 0.06$) expression at 21 DIM in SM than CE and ME cows. This was reflected in a linear decrease of *SOD2* expression in CE ($P < 0.001$) and ME ($P = 0.001$), while it remained unchanged in SM ($P = 0.65$). The lower performance in cows fed ME might be related to impaired neutrophil activation, which appears to have been corrected by SM supplementation.

Key Words: immune function, transition cows, methionine

1529 (M243) Effect of a limited supply of phenylalanine, threonine, and tryptophan on mammary metabolism of dairy cows. I. H. Iroshan[1], H. Lapierre[*2], and L. Doepel[1], [1]*University of Calgary, AB, Canada,* [2]*Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada.*

Mammary metabolism is altered by deletion of essential AA (EAA) from an abomasal infusion of a total AA mixture. The objective of this study was to examine the effect of a limited supply of Phe, Thr and Trp on mammary uptake of AA and energy substrates. Five Holstein cows (63 ± 1.6 d in milk) in second lactation were used in a 5 × 5 Latin square with 10-d periods. The diet supplied 100% of net energy and 70% of metabolizable protein requirements based on NRC recommendations. Treatments were abomasal infusions of water (CTL), all AA with casein profile (TAA), TAA without Phe (No-Phe), TAA without Thr (No-Thr), and TAA without Trp (No-Trp). Mammary AA and energy substrate uptake was determined from arterio-venous differences (AV-diff) of 6 blood samples collected every 2 h on d 10, with mammary plasma flow (MPF) estimated using the Fick principle (*P*he+Tyr). Treatment differences were determined using contrasts, comparing each treatment to TAA. Arterial concentrations of Phe, Thr, and Trp decreased ($P < 0.01$) with their respective deletions. The mammary gland responded to a deficiency of Phe and Thr by reducing milk protein secretion through different mechanisms. With No-Phe, Phe uptake decreased mainly through a reduction ($P < 0.01$) of AV-diff as MPF only numerically increased. When Thr was deficient, MPF increased by 32%, and despite a large decreased ($P < 0.01$) AV-diff, Thr uptake only numerically (13%) decreased. Mammary uptakes of acetate, β-hydroxybutyrate, glucose and lactate were not affected by treatments. A limited supply of Trp had minimal impacts on mammary metabolism.

Key Words: amino acids, mammary metabolism, dairy

1530 (M244) Effects of supplementing rumen-protected met and lys on diets containing soybean meal or canola meal in lactating dairy cows. G. A. Broderick[*1], and A. Faciola[3], [1]*U.S. Dairy Forage Research Center, Madison, WI,* [2]*University of Wisconsin–Madison, Madison,* [3]*University of Nevada, Reno.*

Previously, replacing solvent soybean meal (SBM) with equal CP from canola meal (CM) was found to increase milk yield in lactating dairy cows by about 1 kg/d. We tested whether supplementing rumen-protected Met and Lys (RPML) would improve milk and protein yield in cows fed either CM or SBM. Sixteen lactating Holstein cows were blocked by DIM and parity into 4 squares of 4 cows each in a replicated 4 × 4 Latin square. There was a 2 × 2 arrangement of treatments: equal CP supplemented as either SBM or CM, with or without added RPML to provide 10 g absorbed Met/d (Mepron) plus 22 g absorbed Lys/d (AminoShureL). Cows within squares were randomly assigned to treatment sequences and fed experimental diets for 3-wk periods before switching diets. All diets contained (DM basis) 41% alfalfa silage, 25% corn silage, 2.3% mineral-vitamin premix, 1.4% ground shelled corn and 17% CP. Soybean meal diets contained 22% high moisture corn, 8.7% SBM and 28% NDF; CM diets contained 19% high moisture corn, 11.7% CM and 30% NDF. Data from the last week of each period were analyzed using the PROC MIXEDs of SAS; LS-means are reported in the table. Replacing SBM with CM increased DMI ($P = 0.04$) and tended to increase yields of energy-corrected milk and fat ($P \leq 0.09$), but there were no other affects on production ($P \geq 0.15$). Supplementing with RPML did not influence intake or yield ($P \geq 0.15$) and no significant of protein x RPML interactions were detected ($P \geq 0.15$). These results tended to support previous findings of improved milk yield on CM versus SBM. However, under the conditions of this trial, there were no effects of supplementing with rumen-protected Met plus Lys on either protein source.

Table 1529.

	Treatment						P-value contrast		
	CTL	No-Phe	No-Thr	No-Trp	TAA	SEM	CTL vs. TAA	No-Phe vs. TAA	No-Thr vs. TAA
Milk true protein yield, g/d	715	701	738	840	844	51.0	0.03	0.02	0.05
MPF, L/h	497	601	775	603	524	52.6	0.68	0.24	0.01
Mammary uptake, mmol/h									
Phe	10.1	9.0	10.9	11.9	11.8	0.85	0.04	0.01	0.22
Thr	12.1	12.6	12.6	13.6	14.2	1.06	0.10	0.20	0.18
Trp	2.9	3.0	3.1	2.9	3.1	0.39	0.64	0.81	0.92
Group 1 AA-N	48.5	49.0	51.9	55.9	56.8	3.77	0.04	0.06	0.17
Group 2 AA-N	101.7	126.8	141.8	140.9	130.1	8.85	0.02	0.76	0.26
Mammary uptake:milk output									
Group 1 AA-N	1.05	1.08	1.09	1.03	1.04	0.03	0.85	0.35	0.30
Group 2 AA-N	1.13	1.44	1.55	1.33	1.22	0.08	0.41	0.04	0.01
Non-EAA-N	0.78	0.67	0.62	0.65	0.69	0.05	0.14	0.69	0.21

Key Words: soybean meal, canola meal, rumen-protected AA

Table 1530.

Protein RPML	SSBM -	SSBM +	CM -	CM +	Contrasts		
					Protein	RPML	P x R
Trait							
DMI, kg/d	27.1	27.2	27.8	27.5	0.04	0.66	0.36
Milk, kg/d	38.4	38.1	39.1	38.5	0.18	0.27	0.71
Milk/DMI	1.42	1.40	1.41	1.40	0.79	0.38	0.81
ECM, kg/d	39.3	38.7	40.3	39.6	0.09	0.23	0.88
ECM/DMI	1.45	1.42	1.45	1.44	0.54	0.26	0.59
Fat, kg/d	1.62	1.57	1.67	1.63	0.06	0.14	0.90
Prot, kg/d	1.27	1.27	1.30	1.29	0.14	0.65	0.51
MUN, mg/dl	15.2	15.0	15.0	15.0	0.72	0.60	0.73

1531 (M245) Determination of the comparative bioavailability of lysine in two rumen-protected lysine products using the in vivo plasma lysine response method. H. A. Tucker*[1], M. Miura[2], I. Shinzato[3], C. S. Ballard[1], and H. M. Dann[1], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Ajinomoto Co., Inc., Kawasaki, Japan, [3]Ajinomoto Heartland Inc., Chicago, IL.*

The objective of this study was to use the commercially available rumen-protected lysine (RPL) AjiPro-L (AJI; Ajinomoto Heartland, Inc.) to estimate relative bioavailability of a second generation RPL product (A2G; Ajinomoto Heartland, Inc.). Ten multiparous lactating Holstein cows (109 ± 8 d in milk (DIM)) housed in a tie-stall facility were used in a replicated 5 × 5 Latin square design with 7-d periods. Cows, blocked by DIM and milk production, were assigned to treatment sequence. A common basal diet formulated to meet lysine (Lys) requirement, prepared once daily, was fed proportionately at three time points (33.4% at 0500 h, 33.3% at 1300 h, and 33.3% at 2100 h). Treatments included 0 g/d Lys, 75 g/d AJI, 75 g/d A2G, 150 g/d AJI, or 150 g/d A2G and were administered 3x/d 1 h before each feeding time on d 2 through 7 of each period in amounts proportional to feed offered to simulate inclusion in the diet. Blood samples were obtained from each cow on d 6 and 7 of each period from the tail vein at 2-h intervals starting at 0600 h resulting in four samples/cow/d. Resultant plasma was pooled by day and analyzed for amino acid (AA) concentrations. Data were reduced to a period mean and analyzed using the PROC MIXED (SAS, v. 9.2). The REG procedure was used to generate linear regression models for each RPL product using Lys (μmol) and Lys (% total AA (μmol basis)) to determine the slope of plasma Lys in response to treatment. Using the calculated slope for each product, relative estimated bioavailability of A2G was determined using the slope-ratio assay technique. Dry matter intake and milk yield did not differ ($P > 0.10$) among treatments. Plasma Lys was greater ($P < 0.05$) for 150 g/d AJI (93.8 ± 2.9 μmol) and 150 g/d A2G (95.0 ± 2.8 μmol) when compared to 0 g/d Lys (83.6 ± 2.9 μmol). The slope for A2G treatment was numerically greater (0.007; $r^2 = 0.91$) when compared to the slope for AJI treatment (0.005; $r^2 = 0.99$) when expressing the concentration of plasma Lys relative to that of total AA. This resulted in the calculated bioavailability of A2G being 132.1% of the bioavailability of AJI. Both first and second generation AjiPro-L products increased plasma LYS in lactating dairy cows with some comparative advantage for the second generation product.

Key Words: bioavailability, rumen-protected lysine, dairy cow

1532 (M246) Impacts of feeding ruminally protected phenylalanine and/or methionine to early lactation cows fed diets containing high levels of canola meal. N. Swanepoel*[1,2], P. H. Robinson[1], and L. J. Erasmus[2], *[1]University of California–Davis, Davis, [2]University of Pretoria, Pretoria, South Africa*.

The objective of this study was to determine if either Met or Phe was limiting performance of dairy cows fed a ration containing 200 g/kg of diet DM as canola meal (CM). The design used four pens of 320 early lactation (DIM < 125) cows/pen in a 4x4 Latin square with 28 d periods. Treatments were designed to deliver 8.0 and 7.5 g/cow/d of intestinally absorbable Met and Phe, respectively with treatment pens fed ruminally protected (RP) Phe (RPP) and RP Met (RPM), separately or in combination, mixed into the same control TMR based on alfalfa hay, winter wheat and corn silage, almond hulls, corn grain, fuzzy and cracked pima cottonseed and mineral premix. There were no difference in the chemical profiles of the TMR fed to the four treatments with CP, NDF, Fat and Starch amounting to 170, 310, 53, and 193 g/kg DM in the base TMR. There were no changes in plasma AA levels except plasma Met, which increased with both Met treatments, and plasma Trp that decreased with both Phe treatments. DM intake was not affected (avg: 27.6 ± 0.40 kg/d) by feeding either RP AA or the combination. Compared to control, supplemental Met increased milk protein (30.71 vs. 30.18 g/kg; $P < 0.01$) and fat (34.74 vs. 34.16 g/kg; $P = 0.01$) content, while decreasing milk lactose (47.47 vs. 47.80 g/kg; $P < 0.01$) content, thereby shifting milk energy amongst milk components without affecting milk energy output. Even though Phe alone had no effect at all on animal performance, adding it in combination with Met diverted energy away from milk components towards body condition score (BCS) gain, which increased (0.08 vs. 0.04 BCS unit change/28d; $P < 0.01$). Even though the supplemented Phe did not increase plasma Phe levels, or animal performance, it was clearly delivered and biologically active based on the finding that it changed the way that Met was utilized. While results suggest that neither Met nor Phe was a limiting AA in this study, results do suggest that both were bioactive. It may be time to reconsider the limiting AA

concept in lactating dairy cows in favor of accepting that AA may be bioactive to the extent of changing animal performance, even when they are not limiting.

Key Words: urine spot samples, amino acids, allantoin

1533 (M247) Ruminal degradation and intestinal digestibility of crude protein and amino acids and correction for microbial contamination in rumen-undegradable protein.

H. A. Paz Manzano[*1], E. Castillo-Lopez[2], T. J. Klopfenstein[1], and P. J. Kononoff[3], *[1]University of Nebraska-Lincoln, Lincoln, [2]University of Saskatchewan, Saskatoon, Canada, [3]University of Nebraska, Lincoln.*

Two Holstein cows fitted with ruminal and proximal duodenal cannulas were used to determine crude protein (CP) and AA ruminal degradation using an in situ incubation of 16 h and intestinal digestibility using the mobile bag technique (pore size 50 μm). Bacterial contamination of the rumen-undegradable protein (RUP) was corrected using purines or DNA as bacterial markers. The feedstuffs evaluated were: three sources of blood meal (BM1, BM2, and BM3), canola meal (CM), low-fat distillers dried grains with solubles (LFDG), soybean meal (SBM), and expeller soybean meal (ESBM). Data were analyzed as a randomized complete block. Ruminal degradation of CP varied ($P < 0.001$) across feedstuffs, 85.3, 29.8, 40.7, 75.7, 76.9, 68.8, and 37.0 ± 3.93% for BM1, BM2, BM3, CM, LFDG, SBM, and ESBM, respectively. Ruminal degradation of both total essential AA and nonessential AA followed a similar pattern to that of CP. Based on the ratios of AA concentration in the RUP to AA concentration in the original feed, ruminal incubation decreased (ratio < 1; $P < 0.001$) the concentrations of His, Lys, and Trp and increased (ratio > 1; $P > 0.001$) the concentrations of Ile and Met across feedstuffs. Estimations of BCP contamination using purines were 0.75 ± 0.86, 0.65 ± 0.88, 0.55 ± 0.91, 2.50 ± 0.88, 6.45 ± 0.91, 2.61 ± 0.88, 10.8 ± 0.91% CP and using DNA were 0.68 ± 0.86, 0.18 ± 0.88, 0.63 ± 0.91, 4.52 ± 0.88, 2.58 ± 0.91, 1.36 ± 0.88, and 2.49 ± 0.91% CP for BM1, BM2, BM3, CM, LFDG, SBM, and ESBM, respectively. Intestinal digestibility of RUP could not be estimated for BM1, BM3, and SBM due to insufficient recovery of residue. For the remaining feedstuffs, intestinal digestibility of RUP was highest ($P < 0.001$) for ESBM, followed by BM2 and LFDG, and lowest for CM, 98.8, 87.9, 89.7, 72.4 ± 1.40%, respectively. Intestinal absorbable dietary protein was higher ($P < 0.001$) for BM2 compared to CM and LFDG, 61.7, 17.9, and 20.7 ± 2.73% CP, respectively. Ruminal degradation and intestinal digestibility of AA determine the supply of intestinal absorbable AA across feedstuffs. These factors are not constant across AA within feedstuffs and nutrition models need to account for them to increase the accuracy to predict the AA supply to the animal.

Key Words: rumen degradation, intestinal digestibility, amino acids, bacterial CP contamination

1534 (M248) Validation of the bioavailability of the second generation AjiPro-L using the in vivo plasma lysine response method.

N. L. Whitehouse[*1], A. F. Brito[1], A. Crowther[1], A. B. D. Pereira[1], C. G. Schwab[2], I. Shinzato[3], and M. Miura[4], *[1]University of New Hampshire, Durham, [2]Schwab Consulting, LLC, Boscobel, WI, [3]Ajinomoto Heartland Inc., Chicago, IL, [4]Ajinomoto Co., Inc., Kawasaki, Japan.*

Six lactating multiparous Holstein (DIM = 64 to 314) equipped with ruminal cannulas were used in a 6 × 6 Latin square study with 7-d periods. The treatments were: 1) 0 g/d Lys, 2) 60 g/d of infused Lys, 3) 30 g/d of fed Lys from AjiPro-L, 4) 60 g/d fed Lys from AjiPro-L, 5) 30 g/d fed Lys from AjiPro-L 2G, and 6) 60 g/d fed Lys from AjiPro-L 2G. The infusion treatments consisted of Lys-HCl and were infused continuously into the abomasum via the ruminal cannulas. To ensure complete consumption, the AjiPro-L and AjiPro-L 2G were mixed with 1 kg of TMR and placed in tubs in front of the cows 30 min before each of the 3 daily feedings. Blood samples were obtained from each cow on the last 3 d of each period every 2 h, four times daily, from the tail vein, centrifuged, deproteinized, and composited into one daily sample/cow. Deproteinized plasma was analyzed for AA. Data for plasma AA concentrations (μmol basis) were analyzed using the PROC MIXED and PROC REG procedures of SAS. The bioavailability of AjiPro-L, calculated by comparing the slopes of the infused and fed AjiPro-L (Lys as % of total AA), was lower than previous evaluations using the same methodology. The infusion slope observed herein, obtained from two doses (0 and 60 g/d), was larger than those obtained previously, which were obtained using three doses (0, 30, and 60 g/d); this may explain the discrepancies among studies. To increase precision, it is recommended that at least 1 additional dose of infused Lys between 0 and 60 g/d should be used. It is important to note that the slope for the AjiPro-L 2G (i.e., 0.01011; $P < 0.01$) was greater than the slope for the AjiPro-L (i.e., 0.00682; $P < 0.01$) resulting in a 48% improvement in bioavailability of Lys from the AjiPro-L 2G based on the ratio of the 2 slopes. It can be concluded that the bioavailability of Lys from AjiPro-L 2G was better than that from AjiPro-L. Further research is needed to test these 2 RP-Lys products.

Key Words: AjiPro-L, bioavailability, lysine

1535 (M249) Comparison of duodenal nitrogen and amino acid flows in dairy cows fed a corn straw or mixed forage diet. C. Qin[1,2], P. Sun[1], D. P. Bu[*1], J. Q. Wang[1], P. Zhang[2], and P. An[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Hunan Provincial Key Laboratory for Genetic Improvement of Domestic Animal, College of Animal Science and Technology, Hunan Agricultural University, Changsha, China*.

Knowledge to duodenal nitrogen and amino acid flows may provide guidance to nutritionists with dairy rations. This study was conducted to evaluate the effects of dietary factors that alter ruminal fermentability on duodenal flows of nitrogen and amino acids (AAs). Twenty-four primiparous, lactating, ruminally and duodenally fistulated Holstein cows were used in this study. Cows were randomly assigned to high forage diet (HF, forage:concentrate = 60:40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diet (LF, forage:concentrate = 40:60) with corn straw as the forage source. This study lasted for 11 wk with 2-wk of preliminary period and 9-wk of trial period. Co-EDTA, Cr_2O_3 and $YbCl_3 \cdot 6H_2O$ were used as indicators in the last 3 wk. Samples were collected in the last three trial days and all samples were kept at -20°C for further analysis. Data were analyzed using the PROC MIXED (SAS 9.1) and expressed as gram per day (g/d). The HF diet had positive effect on flows of duodenal total nitrogen (369.75 and 539.39), Arg (90.53 and 136.20), His (37.65 and 55.97), Ile (100.24 and 150.44), Leu (157.25 and 234.10), Lys (132.31 and 202.80), Met (26.63 and 40.31), Phe (92.81 and 145.96), Thr (79.00 and 123.04), Val (110.39 and 168.14), Asp (183.23 and 277.74), Ser (59.45 and 91.31), Glu (253.40 and 372.30), Ala (118.30 and 178.80), Cys (16.83 and 23.67), Tyr (55.99 and 84.45), Pro (82.58 and 120.45), essential AA (826.82 and 1256.97), non-essential AA (903.03 and 1339.11) and total AA (1729.85 and 2596.08) ($P < 0.05$). Duodenal Gly flow tended to be higher in cows fed with HF diet (133.26 and 190.40, $P = 0.07$). Flows of duodenal bacterial nitrogen (215.93 and 263.27), endogenous nitrogen (37.82 and 37.95) and non-degradable nitrogen (136.35 and 183.61) were not affected by dietary treatments ($P > 0.05$). In conclusion, dietary systems played a role in duodenal nitrogen nutrition flows, and duodenal total nitrogen and amino acid flows were depressed when cows fed a low forage diet.

Key Words: forage pattern, dairy cow, duodenal nutrition flow, nitrogen nutrition

1536 (M250) Comparison of mammary amino acid utilization in dairy cows fed a corn straw or mixed forage diet. C. Qin[1,2], P. Sun[2], D. P. Bu[2], J. Q. Wang[*1,2], P. Zhang[3], and P. An[2], *[1]Heilongjiang Bayi Agricultural University, Daqing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [3]Hunan Provincial Key Laboratory for Genetic Improvement of Domestic Animal, College of Animal Science and Technology, Hunan Agricultural University, Changsha, China.*

It is reported that changes in mammary amino acid (AA) utilization associate with dietary systems. In this study, we investigated AA transformation efficiency (AATF) from mammary gland to milk production in dairy cows fed different diets. Twenty-four first lactating Holstein cows were used in this study. Cows were randomly assigned to high forage diet (HF, forage:concentrate = 60:40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diet (LF, forage:concentrate = 40:60) with corn straw as the forage source. This study lasted for 11 wk with 2 wk of preliminary period and 9-wk of trial period. Milk samples, blood in perineal artery and jugular vein were collected on the last morning of the trial, respectively. All samples were kept at -20°C for further analysis. To estimate AATF data were fitted to the model AATF = A/(B*C), where: A (g/d) was milk AA yield; B (g/L) was the concentration difference of plasma AA in perineal artery and jugular vein; C (L/d) was blood flow volume in mammary gland. Data were analyzed by PROC MIXED (SAS 9.1). The results showed that transformation efficiency of Phe increased in cows fed HF diet (0.72 vs. 0.88, $P < 0.01$). We observed that transformation efficiency of Thr (0.77 vs. 0.61), Asp (16.84 vs. 7.62) and Ser (2.01 vs. 1.26) was lower in HF group ($P < 0.05$), and HF diet tended to have a negative effect on non-essential AA transformation efficiency (1.95 vs. 1.45, $P = 0.08$). However, transformation efficiency of Arg (0.35 vs. 0.34), His (1.04 vs. 1.07), Ile (0.57 vs. 0.61), Leu (0.68 vs. 0.72), Lys (0.80 vs. 0.73), Met (0.74 vs. 0.60), Val (0.64 vs. 0.67), Glu (1.81 vs. 2.06), Gly (1.06 vs. 0.99), Ala (0.71 vs. 0.70), Cys (1.09 vs. 2.64), Tyr (0.80 vs. 0.84), Pro (3.75 vs. 3.32), essential AA (0.65 vs. 0.65) and total AA (1.01 vs. 0.97) were not affected by dietary treatment ($P > 0.05$). These results indicated that feeding a high forage diet to cows depressed mammary utilization of some amino acids but improved phenylalanine conversion efficiency.

Key Words: diet system, mammary gland, amino acid utilization

1537 (M251) Plasma L-methionine and supplemental L-methionine precursor responses to rumen administration of a rumen protected DL-methionine source or different levels of 2-hydroxy-4-methylthio-butanoic acid. *G*. I. Zanton*, S. E. Bettis, and M. Vazquez-Anon, *Novus International, Inc., St. Charles, MO.*

The L-enantiomer of methionine (Met) is the form that can be used for biological functions. Supplemental precursors of L-Met such as D-Met or 2-hydroxy-4-methylthio-butanoic acid (HMTBa) must be converted to L-Met to be incorporated into protein. The objective of this study was to evaluate the plasma response of L-Met and supplemental L-Met precursors to a rumen pulse dose of protected DL-Met (Smartamine M, Adisseo, France; RPM) or different levels of HMTBa. Six rumen cannulated Holstein steers (initial BW = 250 ± 6 kg SD) were fed a common basal diet and pulse dosed with different treatments according to a partially replicated Latin square design. Treatments administered to the rumen were 80 (H80), 120 (H120), or 160 (H160) mg HMTBa/kg BW (Provided as MFP feed supplement, Novus International, St. Charles, MO) or RPM at 80 mg DL-Met/kg BW (RPM80); where, based on previous research, H160 and RPM80 were hypothesized to provide similar levels of absorbed Met activity (64 mg/kg BW). Ruminal pulse dose coincided with morning feeding and occurred at t = 0 with 11 plasma samples taken from the coccygeal vein over the ensuing 48 h and analyzed for HMTBa, D-Met, and L-Met. Statistical contrasts were linear and quadratic effects of level of HMTBa and H160 vs. RPM80 with significance declared at $P < 0.05$. Baseline L-Met was not different between treatments averaging 2.75 mg/L; L-Met precursors were not detected in baseline samples. Plasma profiles of L-Met and supplemental L-Met precursors differed between levels and sources ($P < 0.01$). The change in L-Met from baseline area under the response curve through 48 h (AUC) was linearly increased ($P < 0.02$) as HMTBa increased; L-Met AUC for H160 did not differ from RPM80 (128 vs. 147 ± 17 mg·h/L, respectively; $P > 0.40$). Likewise, supplemental L-Met precursor AUC linearly increased as HMTBa level increased; HMTBa AUC for H160 did not differ from RPM80 D-Met AUC (140 vs. 117 ± 11 mg·h/L, respectively; $P > 0.14$). When not separated on a chiral column, D- and L-Met are combined during plasma Met analysis; when analyzed values for D-Met or HMTBa were added to analyzed values for L-Met, there was no difference between AUC for H160 and RPM80 (268 mg·h HMTBa + L-Met/L vs. 264 mg·h D- + L-Met/L ± 24, respectively; $P > 0.90$). It is concluded that supplying a pulse dose of 64 mg methionine activity/kg BW as RPM or HMTBa resulted in plasma L-Met concentrations that were not different.

Key Words: methionine, dairy, bioavailability

1538 (M252) Effects of the ideal profiles of lysine, methionine, threonine, phenylalanine, histidine, and valine on milk protein synthesis gene network expression in bovine mammary epithelial cells. S. Li[1,2], W. Zhao[2,3], A. Hosseini[4], J. X. Liu[1], and J. J. Loor[*2], *[1]Zhejiang University, Hangzhou, China, [2]University of Illinois, Urbana, [3]Northwest A & F University, Yangling, China, [4]University of Bonn, Germany.*

Amino acids (AA) are essential precursors for milk protein synthesis in mammals. In recent years it has become evident that the AA-mediated protein synthesis response within mammary cells is partly regulated through the mTOR pathway. Thus, AA not only are building blocks of proteins but also are one of the key molecules that serve as upstream components of the signaling pathways that regulate protein synthesis. Although the effects of AA on signaling through mTOR in mammary cells have been explored, little is known about the transcriptional response, particularly regarding the 6 essential AA [lysine (Lys), methionine (Met), threonine (Thr), phenylalanine (Phe), histidine (His), and valine (Val)] for which ideal recommendations have been proposed. The specific objective of this study was to investigate how changing the ratio of Lys to Thr, Lys to His, and Lys to Val affected the expression of genes associated with pathways of insulin, mTOR, and Jak2-Stat5 signaling and also glucose and AA transport in MacT cells. Target genes plus three internal controls were measured using qPCR. Triplicate cultures with the optimal AA ratio (OPAA; Lys:Met 2.9:1; Thr:Phe, 1.05:1; Lys:Thr, 1.8:1; Lys:His, 2.38:1; Lys:Val, 1.23:1) plus the mTOR inhibitor rapamycin (OPAARMC, control) or OPAA, 2.1:1 Lys:Thr (LT2.1), 1.3:1 Lys:Thr (LT1.3), 3.05:1 Lys:His (LH3.0), and 1.62:1 Lys:Val (LV1.6) were incubated for 12 h. Compared with OPAARMC the OPAA treatment upregulated SLC1A5, SLC7A5, and RPS6KB1, and downregulated expression of IRS1, AKT3, TSC2, and EEF1A1. Greater expression of SLC1A5, SLC7A5, SLC2A1, SLC2A8, STAT5B, and RPS6KB1 and lower expression of TSC2 and EEF1A1 were observed in response to LT2.1, LT1.3 and LH3.0 compared with OPAARMC. Treatment with LV1.6 as compared with LT2.1, LT1.3 and LH3.0 had similar effects on expression of SLC1A5, SLC7A5, SLC2A1, SLC2A8, STAT5B, and RPS6KB1. In addition, treatment with LV1.6, LH3.0, and LT2.1 compared with OPAA and control led to greatest upregulation of mTOR. However, only LV1.6 up-regulated TSC1 and TSC2 and downregulated EIF4EBP1 relative to OPAA and control. Overall, our study revealed unique effects of essential AA ratios, and particularly Lys:Val, on the molecular phenotype associated with milk protein synthesis regulation in mammary cells.

Key Words: mTOR, nutrigenomics, milk protein synthesis

1539 (M253) Changes in plasma methionine concentrations after administration of two different doses of rumen protected methionine.

P. D. Carvalho[*1], N. E. Lobos[2], M. Z. Toledo[2], E. Trevisol[2], V. G. Santos[2], R. V. Barletta[2], G. M. Baez[2], A. Garcia-Guerra[2], J. N. Guenther[2], A. H. Sousa[2], D. Luchini[3], P. M. Fricke[2], R. D. Shaver[1], and M. C. Wiltbank[1], *[1]University of Wisconsin, Madison, [2]Dep. of Dairy Science, University of Wisconsin–Madison, Madison, [3]Adisseo, Alpharetta, GA.*

Feeding rumen-protected limiting amino-acids, such as methionine (MET), to dairy cows may allow feeding of diets with lower amounts of crude protein while increasing milk protein and feed efficiency. Information on the changes of circulating MET concentrations after feeding may provide valuable information on both its usage and its metabolism, which could then be used by field nutritionists. The objective of the present experiment was to determine changes in plasma MET concentrations after administration of a single bolus of rumen-protected methionine (RPM). Non-lactating, non-pregnant dairy cows (n = 16) weighing 694 ± 16 kg were randomly assigned to three treatments: 1) untreated control (n = 4); 2) bolus containing 10 g of RPM (Smartamine; 6 g of metabolizable MET; n = 6); and 3) bolus containing 20 g of RPM (Smartamine; 12 g of metabolizable MET; n = 6). Blood samples were collected at 12h before treatment, immediately before treatment, and at 6, 12, 18, 24, 36, and 48h after treatment. Plasma was assayed for free amino acid by gas chromatography using a commercial kit (EZ:faast-GC-FID Physiological, Phenomenex). Data were analyzed by repeated measures using the PROC MIXED of SAS. Plasma MET concentrations tended to differ among treatments (P = 0.08) and were greater for cows receiving the 20 g bolus, intermediate for cows receiving the 10 g bolus, and least for control cows (peak average 57.5 ± 0.8μM, 26.9 ± 0.2μM, and 20.3 ± 0.2μM, respectively). Before treatment, all cows had low MET concentrations (21.4 ± 0.5μM), and MET concentrations remained low throughout the experimental period in controls. At 12 and 18h, MET concentrations increased (P = 0.09) by 30% in cows receiving the 10 g bolus (26.5 ± 0.2μM) compared to control cows (20.3 ± 0.1μM); however, cows receiving the 20 g bolus increased more than 100% (50.4 ± 4.1μM) and were greater than either controls (P < 0.01) or cows treated with the 10 g bolus (P < 0.01). By 24 h after treatment, MET concentrations differed among treatments (P < 0.001) and were least for controls (22.7 ± 0.1μM), intermediate for cows receiving the 10 g bolus (23.7 ± 0.1μM), and greater for cows receiving the 20 g bolus (29.6 ± 0.1μM). Methionine concentrations did not differ among treatments (P = 0.85) at 36 and 48 h. Lysine concentrations did not differ among treatments (P = 0.52) and were 143.3 ± 5.2μM, 133.3 ± 5.4μM, and 139.6 ± 6.8μM for controls, cows receiving 10 g of RPM, and cows receiving 20 g of RPM, respectively. In conclusion, plasma MET concentrations were affected by treatment dose and time after treatment. Time after treatment should be considered when evaluating effectiveness of MET supplementation. *Supported by Hatch project WIS01240 and Adisseo USA, Inc.*

Key Words: methionine, dairy cow, amino acids

1540 (M254) A three-step in vitro procedure for evaluating rumen-protected lysine products.

Y. Miyazawa[1], M. Miura[*2], T. Fujieda[2], I. Shinzato[3], S. W. Fessenden[4], and M. D. Stern[4], *[1]Ajinomoto Co., Inc., Kawasaki, Japan, [2]Ajinomoto Co., Inc., Tokyo, Japan, [3]Ajinomoto Heartland, Inc., Chicago, IL, [4]University of Minnesota, St. Paul.*

The three-step in vitro procedure is used for estimating intestinal digestibility of the RUP fraction of feedstuffs. However, rumen protected amino acid products have been evaluated in various ways for estimates of bioavailability. The objective of this study was to propose a three-step in vitro procedure for rumen-protected Lysine products (RPL), which is composed of buffer solutions with enzymes and can be developed as a standardized method to evaluate RPLs. Three grams of six different RPLs were weighed into nylon bag (5 × 7 cm, pore size 53 ± 10 μm). Bags were incubated using a dissolution apparatus for drug evaluation with rotating paddles at 100 rpm at 39°C. Three individual vessels were allocated to each RPL as ruminal, abomasal and duodenal phases, respectively. Modified McDougal's buffer containing lipase (900 mL) was used to simulate ruminal conditions (pH 6.8). A hydrochloride buffer containing pepsin (900mL, pH 2.0) and a phosphate buffer containing pancreatin and gall powder (900 mL, pH ≈ 7.9) were used to simulate abomasal and intestinal conditions, respectively. After a 20-h incubation in ruminal vessels, aliquot samples of solution were taken, and bags containing each RPL were transferred from ruminal to abomasal vessels. These procedures were repeated after a 2-h incubation followed by incubation in duodenal vessels for 8 h; aliquot buffer samples were taken again. Each buffer sample was analyzed for Lys, and amount of lysine escaping dissolution was calculated by subtracting buffer lysine from original feed lysine provided to the assay. Residual Lys under ruminal conditions was compared with extent of in situ ruminal protection. Statistical differences (P < 0.05) were tested by a one-way ANOVA. In vitro ruminal protection measured by this procedure correlated (P < 0.05) with in situ ruminal protection with a correlation coefficient of > 0.9. The RPLs showed various characteristics; high/medium/low ruminal protection and high/low post-ruminal Lys release. However, when pH of the ruminal buffer was reduced, one of the RPLs showed an increase (P < 0.05) in ruminal protection using in vitro procedures (46.2 ± 9.3% at pH 6.8, 90.0 ± 4.0% at pH 6.2, n = 3). Results from this study indicate that a buffer-based three-step in vitro procedure can be a useful tool to evaluate RPLs, but further research is needed to optimize pH of ruminal conditions.

Key Words: rumen-protected lysine, in vitro procedure, rumen pH

1541 (M255) Histidine requirement of dairy cows determined by the indicator amino acid oxidation (AAO) technique. D. R. Ouellet[*1], G. E. Lobley[2], and H. Lapierre[1], *[1]Agriculture and Agri-Food Canada, Sherbrooke, QC, [2]Rowett Institute of Nutrition and Health, University of Aberdeen, UK.*

The indicator AAO technique has been used successfully to quantify AA requirements in pigs and poultry. This technique was used to evaluate His requirement in dairy cows. Six lactating dairy cows were used in a 6 × 6 Latin square design, with 7-d periods. Cows were fed a TMR balanced to provide 110% and 75% of energy and metabolizable protein (MP; 1653 g/d) requirement, respectively. All AA (813 g/d; casein profile), excluding His, were infused into the abomasum to supply 105% of MP requirement. Treatments were abomasal infusion of His at 0, 7.6, 15.2, 22.8, 30.4 and 38.0 g/d, representing 1.50, 1.83, 2.15, 2.46, 2.78, and 3.09% of MP. On d6, [1-^{13}C]leucine was infused intravenously for 5 h (4.0 mmol/h; prime dose 4.0 mmol). Six blood samples were collected every 20 min during the last 2 h of infusion and the isotopic enrichment of plasma keto-isocaproic acid and CO_2 used to estimate whole body (WB) Leu irreversible loss rate (ILR) and oxidation. On d 7, $NaH^{13}CO_2$ was infused (2 mmol/h; prime dose 2.8 mmol) intravenously, with a similar schedule as d 6, to estimate the WB ILR of CO_2. Leucine and CO2WB ILR were not affected by treatments and averaged 126.8 ± 2.15 mmol/h and 23.4 ± 0.98 mol/h, respectively. Yields of milk and milk protein, and Leu oxidation (indicator AAO) all indicated that a His supply of 1.83%MP was sufficient to meet requirement. However, the consistent decrease in plasma concentrations of carnosine (β-alanyl-His dipeptide) below 2.46%MP suggests provision of His from endogenous pools; this could temporarily mask a dietary deficiency. The indicator AAO method is sensitive and provides similar estimates of requirement to those based on milk protein yield. Nonetheless, to accurately estimate His requirements needs consideration of changes in endogenous pools of His.

Key Words: dairy cow, amino acid oxidation, histidine

1542 (M256) Estimation of histidine requirement in lactating dairy cows. H. Lapierre[*1], D. R. Ouellet[2], and G. E. Lobley[3], *[1]Agriculture and Agri-Food Canada, Sherbrooke, QC, [2]Agriculture and Agri-Food Canada, Sherbrooke, QC, [3]Rowett Institute of Nutrition and Health, University of Aberdeen, UK.*

Although in lactating dairy cows, His and Met show similar hepatic and mammary behaviour, with similar concentration in milk, requirement for His has been variously estimated as 2.4% (Doepel et al., 2004, JDS 87:1279), 2.7% (CPM-Dairy) and 3.2% (Rulquin et al., 2001, INRA ProdAnim 14:265) of metabolizable protein (MP) supply. Such variability may be

Table 1541.

	His supply (% of MP)							*P* value	
	1.50	1.83	2.15	2.46	2.78	3.09	SEM	Linear	Quad.
DMI, kg/d	19.5	20.2	20.1	20.3	20.3	20.3	0.18	0.01	0.06
Yields									
Milk, kg/d	38.6	42.1	42.0	42.5	42.8	42.4	0.66	0.002	0.02
True protein, g/d	973	1141	1152	1168	1163	1139	20.7	< 0.001	< 0.001
Leu oxidation, mmol/h	34.2	24.9	25.2	21.9	24.5	23.3	1.88	0.01	0.02
Plasma concentrations									
His, µM	18.0	24.7	46.4	63.3	61.2	68.4	3.42	< 0.001	< 0.01
Carnosine, µM	6.4	6.9	8.4	9.2	9.3	9.8	0.56	< 0.001	0.29
Anserine, µM	4.8	6.5	5.5	6.6	5.5	5.5	0.71	0.77	0.18

Table 1542.

	His supply (% of MP)					P Value	
	1.60	1.95	2.30	2.65	SEM	Linear	Quadratic
DMI, kg/d	20.1	20.1	20.7	20.7	0.26	0.08	0.92
Yields							
Milk, kg/d	32.3	34.0	36.3	36.8	0.53	< 0.001	0.32
True protein, g/d	875	1035	1057	1116	25.7	< 0.001	0.08
Plasma concentrations							
His, µM	14.5	33.4	51.9	60.1	3.18	0.001	0.12
Hemoglobin, g/100 mL	9.2	9.5	9.7	9.4	0.21	0.41	0.17
Muscle concentrations							
Carnosine, µM	8373	8478	9188	6841	647.9	0.21	0.09
Anserine, µM	1349	1306	1422	993	101.4	0.07	0.09

explained by depletion or replenishment of endogenous pools of His, including intramuscular carnosine and anserine and blood hemoglobin. To test this hypothesis, five multiparous Holstein cows (674 ± 36 kg BW, 92 ± 18 DIM) were used in a 4 × 4 Latin square plus one cow, with 14-d periods. Cows were fed a diet balanced to supply 103% of NEL requirement but only 72% of MP requirement (1610 g/d) providing 34 g/d of digestible His (NRC, 2001). Treatments were abomasal infusion of His at 0, 7.6, 15.2 or 22.8 g/d in addition to a mixture of AA (595 g/d, casein profile). His represented 1.60, 1.95, 2.30 and 2.65% of MP supply, respectively. At the end of each period, six arterial blood samples plus muscle biopsies from the semimembranous muscle were collected. Milk yield plateau was reached at a higher His supply (2.30%MP) than milk protein yield (1.95%MP). Between these supplies, however, milk protein yield could be sustained from depletion of endogenous pools. Observed reductions in muscle carnosine and anserine plus plasma hemoglobin could supply 3.2 g of His/d. Compared with other essential AA, the unique peculiarity that His has additional endogenous labile pools means that depletion and/or replenishment of these pools over short periods may bias estimate of true requirement.

Key Words: histidine, carnosine, dairy cow

1543 (M257) Effects of different protein sources on milk performance and amino acid profile in early lactating dairy cows. X. Q. Zhou[*1,2], D. P. Bu[1], Y. D. Zhang[1], M. Zhao[1], P. Sun[1], and J. Q. Wang[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Northeast Agricultural University, Harbin, China.*

Protein content of feed plays an important role in dairy amino acid profile of bovine milk protein. This study was aimed to investigate different protein sources on milk production performance and milk amino acid profile. Thirty-two Chinese Hostein dairy cows were blocked based on DIM (60 ± 25 d) and milk yield (31.0 ± 3.17kg/d) and randomly divided into group soybean (diet protein, soybean meal 11.29%, extruded soybean 2.06%, whole cottonseed 10.44%, rapeseed meal 4.19%, beet pulpand 4.16% and cottonseed meal 2.13%) and group non-soybean (whole cottonseed 10.44%, rapeseed meal 9.63%, cottonseed meal 6.71% and beet pulp 7.49%). Two diets contained similar forage with the same concentrate-to-forage ratio of 65:35 (DM basis).Experiment lasted for 12 wk with first 2 wk as adaption period. Milk samples were collected weekly and analyzed for milk composition and amino acid profile. Data were analyzed as repeated measurements using PROC MIXED of SAS. Milk yield, milk protein content, milk fat content, milk protein yield and milk fat yield showed no difference between two groups. Compared with group soybean, Cows in group no-soybean increased DMI (20.31vs 17.43kg/d, $P < 0.01$) and milk Pro content (8.48 vs. 8.37 g/100 g AA, $P = 0.04$) but decreased milk Phe content (5.54 vs. 5.60 g/100 g AA, $P = 0.02$) and BCAA (23.49 vs. 23.68 g/100 g AA, $P = 0.08$), especially Leu content (11.69 vs. 11.88 g/100 g AA, $P < 0.01$) in milk protein. There were no difference on content of EAA, NEAA between 2 groups. Results suggest that soybean meal can be partly replaced by miscellaneous meal (rapeseed meal, cottonseed meal and beet pulp) in diets for lactating dairy cows.

Key Words: protein source, milk amino acid profile, dairy cow

---

1544 (M258) Lipogenic gene network expression in bovine mammary epithelial cells in response to the "ideal" profile of Lys, Met, Thr, Phe, His, and Val. S. Li[1,2], W. Zhao[1,3], A. Hosseini[4], J. X. Liu[2], and J. J. Loor[*1], *[1]University of Illinois, Urbana, [2]Zhejiang University, Hangzhou, China, [3]Northwest A & F University, Yangling, China, [4]University of Bonn, Germany.*

Amino acids (AA) not only are building blocks of proteins but also are key factors regulating protein synthesis. In regards to milk protein synthesis, the 6 essential AA (EAA) for which ideal recommendations have been proposed are Lys, Met, Thr, Phe, His, and Val. We hypothesized that the essential AA profile could affect the mRNA expression of genes regulating lipogenic gene networks in bovine MAC-T cells. The specific objective of this study was to study how changing the ratio of Lys to Thr, Lys to His, and Lys to Val affects the expression of lipogenic target genes. Triplicate cultures with the optimal AA ratio (OPAA; Lys:Met 2.9:1; Thr:Phe, 1.05:1; Lys:Thr, 1.8:1; Lys:His, 2.38:1; Lys:Val, 1.23:1) plus rapamycin (OPAARMC, control), OPAA, 2.1:1 Lys:Thr (LT2.1), 1.3:1 Lys:Thr (LT1.3), 3.05:1 Lys:His (LH3.0), and 1.62:1 Lys:Val (LV1.6) were incubated for 12 h. The expression of lipogenic gene networks was evaluated via quantitative PCR of 15 genes plus three internal control genes measured using qPCR. Data were log-transformed and statistically analyzed using the GLM of SAS with treatment as a fixed effect and replicate as random effect. The multiple comparisons were corrected using Tukey's and significance set a $P < 0.05$. Responses to LT2.1, LT1.3, LH3.0, and LV1.6 relative to the OPAARMC included greater expression of ACSS2, FABP3, ACACA, FASN, SCD, LPIN1, INSIG1, SREBF1, PPARD, and NR1H3. Furthermore, LV1.6 increased expression of ACSL1, DGAT1, and RXRA and reduced PPARG expression. Although no effect of OPAA on expression of PPARG was observed, OPAA increased expression of ACSS2, FABP3, ACACA, FASN, SCD, LPIN1, INSIG1, and SREBF1 compared with OPAARMC. Gene network analysis using Ingenuity Pathway Analysis revealed a potentially important role of EAA ratios in the coordination of milk fat synthesis via PPARG and SREBF1. The upregulation of lipogenic gene

networks observed underscore a role of EAA in the regulation of milk fat synthesis during lactation.

Key Words: nutrigenomics, milk fat synthesis, mTOR

1545 (M259) Rumen-protected methionine and choline supplementation during the transition period enhance the proinflammatory cytokine response of whole blood. M. Vailati Riboni[*1,2], Z. Zhou[2], D. N. Luchini[3], A. Minuti[1], E. Trevisi[1], and J. J. Loor[2], *[1]Università Cattolica del Sacro Cuore, Piacenza, Italy, [2]University of Illinois, Urbana, [3]Adisseo S.A.S., Alpharetta, GA.*

The immune system of dairy cows declines in responsiveness during the transition period. In spite of this, there are several factors that can stimulate immune cells and induce the production of proinflammatory cytokines (PIC). The objective of this study was to investigate the effect of supplementing rumen-protected methionine or choline on the production of the proinflammatory cytokine IL1-β by whole blood challenged with *E. Coli* lipopolysacharide (LPS). Twenty-four multiparous Holstein cows were dried off at −50 d from parturition (DFP) and allocated to 1 of 3 treatment groups (n = 8/group) starting on -24 DFP; control (CON; fed a basal diet with a 3.4:1 Lys:Met), methionine (MET; basal diet plus Smartamine M with a 2.9:1 Lys:Met), and choline (CHO; basal diet plus ReaShure, 60 g/d). Blood samples for LPS challenge were collected on -15, −7, 2, 7, and 20 DFP into evacuated tubes containing lithium-heparin and kept at 38°C. An ex vivo whole blood (1 mL) stimulation assay was performed within 30 min using LPS at three different doses, 0 (negative control, CTR), 0.01, and 5 μg/mL blood. Samples were incubated for 3.5 h. At the end of incubation the plasma was collected after centrifugation and used to analyze IL-1β concentration via ELISA. The data were analyzed as a factorial design with repeated measures using PROC MIXED in SAS. There was an overall diet effect ($P < 0.05$) associated with greater IL1-β in cows fed MET and CHO (1812 pg/mL) compared with CON (1043 pg/mL). Similarly, there was an overal LPS effect ($P < 0.05$) with control incubations averaging 52 pg IL1-β/mL compared with 1621 and 3013 pg IL1-β/mL in response to 0.01 and 5 μg LPS. The three-way interaction ($P < 0.05$) revealed that the high LPS dose induced a marked response in IL1-β in both MET or CHO regardless of DFP. In contrast, whereas the high dose of LPS induced a similar response (1500–2,000 pg IL1-β) in CON on -15, −7, 7, and 20 DFP, the response on 2 DFP was markedly greater to the point that IL1-β concentration was similar for CON, MET, and CHO. Overall, results confirmed the responsiveness of blood cells to an inflammatory challenge even in a period of immune suppression. More importantly, data revealed that supplemental methionine or choline during the transition period enhances the PIC response, hence, potentially enhancing the responsivennes to invading pathogens.

Key Words: inflammation, transition period, nutrition

1546 (M260) Amino acid analysis in dairy cow plasma by chloroformate derivatization and gas chromatography. N. E. Lobos[*1], G. A. Broderick[2], P. D. Carvalho[3], D. N. Luchini[4], R. D. Shaver[3], A. H. Souza[5], and M. C. Wiltbank[3], *[1]Dep. of Dairy Science, University of Wisconsin–Madison, Madison, [2]Broderick Nutrition & Research, LLC, Madison, WI, [3]University of Wisconsin, Madison, [4]Adisseo S.A.S., Alpharetta, GA, [5]University of California, Cooperative Extension, Tulare.*

The objective of the experiment was to evaluate gas chromatography (GC) after chloroformate derivatization of AA to quantify dietary effects on plasma AA concentrations in dairy cows. Plasma was obtained from 72 cows participating in a previous trial [Souza et al., J. Dairy Sci. 95(Suppl. 2):353, 2012, abstract] where positive performance effects to Met supplementation were reported. Starting at calving, cows were fed isoenergetic diets formulated to deliver equal metabolizable protein (2875 g MP/d). The control diet (CTR) provided 1.89% Met (% of MP), while the treatment diet (MET) was supplemented with sufficient Smartamine M to increase Met to 2.43% of MP. Results indicated increased milk concentrations of protein (2.92 vs. 2.75%, $P < 0.01$) and SNF (8.73 vs. 8.54%, $P < 0.01$) in cows fed MET. Plasma was harvested from blood samples collected at 50 DIM, and kept frozen at -18°C until analysis. Samples were separated by treatment group (supplemented = 37, control = 35) and combined randomly within parity, into seven plasma composites of four to six cows on each diet. Composites were prepared for GC analysis by using a commercial kit (EZ:faast GC-FID Physiological, Phenomenex). This method involves amino acid collection using solid phase extraction (SPE), derivatization with chloroformate, GC separation in a mid-polar capillary column and flame ionization detection. Quantification was based on area under the curve, using the internal standard ratio method (norvaline). Consistent with performance data, analysis of variance indicated higher plasma free Met levels in MET cows vs. CTR cows (22.9 vs. 16.8 μM, $P < 0.001$). Although the kit manual indicated deproteinization was not required, untreated plasma was difficult to work with because variable plasma concentrations of proteins and phospholipids clogged the SPE resin. Mixing plasma at a 1:1 volume ratio with 5% trichloroacetic acid, followed by centrifugation (12,000 × g), allowed satisfactory SPE of all composites. Ion exchange chromatography coupled with ninhydrin quantification is currently the gold standard for AA analysis. The drawbacks of that methodology are high cost and long runtimes. The modifications to the GC-chloroformate method here presented allow rapid (15 minute) determination of differences in free amino acids in cow plasma at a reasonable cost.

Key Words: rumen-protected, methionine, chromatography

Table 1547.

Variable	Treatments					Contrasts[1]			
	16% CP	14.9% CP+EAA	14.9% CP	13.5% CP +EAA	13.5% CP	1	2	3	4
Urinary N, %	0.15	0.12	0.12	0.11	0.15	< 0.001	< 0.001	> 0.10	> 0.10
Urinary N excretion, g/d	111	113	99	86	100	> 0.10	> 0.10	0.089	0.076
Urine N/N intake, %	18.6	20.7	18.0	16.7	20.1	> 0.10	> 0.10	0.072	0.024
Urea N/total urinary N, %	91	80	77	74	73	0.005	< 0.001	> 0.10	> 0.10
Fecal N, %	2.92	2.88	2.84	2.73	2.86	> 0.10	> 0.10	> 0.10	> 0.10
Fecal N excretion, g/d	199	191	196	172	187	> 0.10	> 0.10	> 0.10	> 0.10
Feces N/N intake, %	34	35	35	34	36	> 0.10	> 0.10	> 0.10	> 0.10

[1] Contrasts: 1 = 16 vs. 14.9; 2 = 16 vs. 13.5; 3 = 14.9 vs. 14.9+EAA; 4 = 13.5 vs. 13.5+EAA

1547 (M261) Effects of supplementing limiting amino acids in diets with reduced CP on nitrogen excretion. M. A. C. Danes*[1], G. A. Broderick[2], and C. Parys[3], *[1]University of Wisconsin–-Madison, Madison, [2]Broderick Nutrition & Research, LLC, Madison, WI, [3]Evonik Industries AG, Hanau, Germany.*

Lowering dietary CP content while supplementing limiting essential amino acids (EAA) has potential to increase N efficiency and decrease N excretion. Ten Holstein cows were blocked by DIM into two 5x5 Latin squares with 5 treatments: (1) positive control (16% CP); 14.9% CP with (2) or without (3) EAA infusion; or 13.5% CP diet with (4) or without (5) EAA infusion. Diets contained alfalfa silage, corn silage, high moisture corn, canola meal, soybean meal and soybean hulls. The infusion solutions were prepared according to AminoCow to provide all limiting EAA and infused continuously into cows' abomasum. Amounts of Met, Lys, His, Leu and Val were, respectively, 11, 11, 5, 5, and 0 g/d for treatment 2 and 15, 27, 11, 22, and 6 g/d for treatment 4. Data from the last 4 d of each 14-d period were analyzed using Proc Mixed. Dry matter intake was not different among treatments ($P > 0.10$) and was highly variable. Therefore, DMI was included in the model to isolate treatment effects. Significance was declared at $P < 0.10$. Contrasts and LS-means are reported. There was no difference among treatments for fecal N excretion. Increasing CP level increased urinary N content and proportion of urea in total urinary N. The EAA infusion on 14.9% CP increased urinary N excretion relative to the same diet without infusion. However, when infused on the 13.5% CP diet, EAA decreased urinary N excretion relative to the same diet without infusion. This suggested that the 14.9% CP diet provided sufficient EAA for milk protein synthesis, while the 13.5% CP diet was EAA deficient and supplementation improved N utilization.

Key Words: amino acid infusion, nitrogen excretion, protein

1548 (M262) Effects of rumen-protected ã-aminobutyric acid on immune function and antioxidant status in heat-stressed dairy cows. J. Cheng[1,2,3], N. Zheng[1,3,4], X. Sun[1,2,3], D. P. Bu[3], L. Pan[3], and J. Wang*[1,3,4], *[1]Ministry of Agriculture–Laboratory of Quality and Safety Risk Assessment for Dairy Products, Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [4]Ministry of Agriculture– Milk and Dairy Product Inspection Center, Beijing, China.*

This experiment was conducted to investigate the effects of rumen-protected γ-aminobutyric acid (GABA) on immune function and antioxidant status in heat-stressed dairy cows. Sixty Holstein dairy cows (141 ± 15 DIM, 35.9 ± 4.3 kg of milk/d) were randomly assigned to 1 of 4 treatments according to a randomized complete block design. Treatments consisted of 0, 40, 80, or 120 mg GABA/kg DM from rumen-protected GABA. The trial lasted 10 wk. The average temperature-humidity indices at 0700, 1400, and 2200 h were 78.4, 80.2 and 78.7, respectively. Blood samples were collected from all of animals via tail vein before the morning feeding on d 0, 21, 42, and 56. Data were analyzed by MIXED model procedure of SAS. Concentrations of immunoglobulin (Ig) A (0.18 and 0.25 vs. 0.16 mg/mL) and IgG (64.62 and 62.14 vs. 32.08 μg/mL) increased ($P < 0.05$) in cows fed 80 or 120 mg/kg GABA, while IgM level showed no difference ($P > 0.05$) when compared with control cows. Compared with control, concentrations of IL-2 (10.84 and 9.37 vs. 6.37 ng/mL) and IL-4 (76.72 and 85.64 vs. 56.63 pg/mL) were higher ($P < 0.05$) in cows fed 80 or 120 mg/kg GABA, and the IL-6 level was higher (124.24 vs. 77.53 pg/mL; $P < 0.05$) in cows fed 120 mg/kg GABA, tended to be higher (89.42 vs. 77.53 pg/mL; $P < 0.10$) in cows fed 80 mg/kg GABA. The TNF-α level was higher (68.50 and 80.82 vs. 49.18 fmol/mL; $P < 0.05$) in cows fed 80 or 120 mg/kg GABA, and tended to be higher (62.29 vs. 49.18 fmol/mL; $P < 0.10$) in cows fed 40 mg/kg GABA. The proportions of $CD4^+$ (9.26 and 9.88 vs. 7.03%) and $CD8^+$ (6.41 and 6.26 vs. 5.15%) T lymphocyte were higher ($P < 0.05$) in cows fed 80 or 120 mg/kg

GABA compared with control, but ratio of $CD4^+/CD8^+$ was not different ($P > 0.05$) among treatments. Compared with control, the activities of SOD (9.59 and 9.52 vs. 8.54 U/mL) and T-AOC (6.11 and 5.64 vs. 3.20 U/mL) increased ($P < 0.05$) in cows fed 80 or 120 mg/kg GABA, but the activities of GSH-Px and MDA were not affected ($P > 0.05$) by GABA supplementation. These results indicate that rumen-protected GABA supplementation to heat-stressed dairy cows can improve the immune function and enhance antioxidant activity.

Key Words: γ-amino butyric acid, immune function, antioxidant activity

1549 (M263) Effects of supplemental rumen-protected methionine and histidine on performance of lactating dairy cows. W. D. Weich*[1], K. F. Kalscheur[1], K. J. Herrick[2], and K. E. Griswold[3], *[1]South Dakota State University, Brookings, [2]Kemin Industries, Inc., Des Moines, IA, [3]Kemin Animal Nutrition and Health, Des Moines, IA.*

Objectives were to determine the effects of rumen-protected methionine (MET) and histidine (HIS) on lactation performance. Twenty-seven multiparous and sixteen primiparous dairy cows blocked by parity, milk production, DIM and breed were assigned a treatment in a randomized complete-block design. Cows were fed a covariate diet for 10 d followed by 4 wk of experimental diets. Treatments were: 1) control diet (CON; formulated for 50.5 g MP MET), 2) CON + encapsulated MET (EM; 18 g of product, +10.8 g MP MET), 3) CON + spray-freeze MET (SFM; 33 g of product, +10.8 g MP MET), 4) SFM + encapsulated HIS (SFMH; 120 g of product, +10.1 g MP HIS). Diets were formulated using AMTS (Version 3.4.7.1). The control diet was balanced to contain 14.7% CP (91% of MP requirements) and maintained a LYS:MET ratio of 3.46:1. Addition of MET products reduced the LYS:MET ratio to 2.85:1. The control diet was created as a single batch in a vertical mixer and rumen-protected amino acids were added to CON at the Data Ranger to create treatments. Amino acid supplementation did not affect DMI, milk yield, feed efficiency, milk protein content or yield. Milk fat concentration and yield were greater ($P < 0.05$) for CON compared with EM and SFM. Differences in MUN among EM, SFM, and SFMH may be related to rumen digestibility of the products. Addition of rumen-protected MET or HIS for cows fed a 14.7% CP diet did not alter production performance.

Key Words: histidine, metabolizable protein, methionine, rumen-protected amino acid

Table 1549.

Item	Treatment				SEM	Contrast[1]
	CON	EM	SFM	SFMH		
DMI, kg/d	27.99	27.69	26.85	27.28	0.70	–
Milk, kg/d	35.30	35.31	35.10	35.20	0.75	–
ECM, kg/d	38.07	36.69	36.25	35.75	0.89	–
ECMFE	1.38	1.33	1.37	1.34	0.03	–
Fat, %	4.03	3.76	3.64	3.80	0.14	A
Fat, kg/d	1.40	1.30	1.25	1.28	0.06	A
Protein, %	3.27	3.23	3.29	3.29	0.05	–
Protein, kg/d	1.15	1.11	1.14	1.14	0.03	–
MUN, mg/dL	10.00	9.97	10.63	10.94	0.13	b, d

[1] SFM vs. SFMH. Uppercase = $P < 0.05$, lowercase = $0.05 < P < 0.10$.

1550 (M264) Canola meals from different plants over two production years differ in rumen-undegraded protein. G. A. Broderick*[1], S. Colombini[2], A. Faciola[3], and M. A. Karsli[4], *[1]Broderick Nutrition & Research, LLC, Madison, WI, [2]University of Milan, Italy, [3]University of Nevada, Reno, [4]Kirikkale University, Turkey.*

Lactation trials showed improved production and N efficiency when dietary soybean meal was replaced with equal CP from canola meal. Three canola meal samples were collected from each of 12 Canadian production plants over 2 yr (total = 72) and analyzed for chemical composition and ruminal protein degradability. The Michaelis-Menten inhibitor in vitro method was used to quantify protein degradation rates and rumen-undegraded protein (RUP), assuming passage rates of 0.16/h and 0.06/h for soluble and insoluble proteins. Differences among plants were assessed using the SAS Mixed model; LS-means for plants over both years, and for each year, are reported in Table 1550. Although CP concentration and NDIN and RUP proportions were unaffected by year ($P \geq 0.21$), NDF and soluble N were lower ($P \leq 0.01$) in canola meal produced in 2011 than 2012. Proportions of NDIN ranged from 18 to 28% of total N but were unaffected by plant ($P = 0.15$). However, differences were detected among plants in CP and NDF concentrations ($P \leq 0.03$) and proportions of soluble N and RUP in total N ($P < 0.01$). Plant x year interactions ($P \leq 0.04$) also were found for concentrations of CP and NDF and proportions of NDIN and RUP, but not for soluble N ($P = 0.19$). Results indicated that differences in canola meal RUP concentration were consistent over 2 production years and, depending on plant of origin, ranged from 38 to 50% of CP, a difference of 30%.

Key Words: canola meal, inhibitor in vitro, rumen-undegraded protein

Table 1550. Mean composition of canola meals from two production years

Plant	CP, % of DM	NDF, % of DM	NDIN, % TN	Sol-N, % TN	RUP, % TN
1	42.8^{ab}	25.7^{cd}	17.7	37.1^{a}	40.1^{ef}
2	41.2^{e}	27.1^{bcd}	24.8	21.3^{de}	42.9^{de}
3	41.7^{de}	26.7^{bcd}	22.9	22.1^{de}	45.4^{cd}
4	43.2^{a}	25.3^{d}	21.2	25.5^{cd}	43.1^{de}
5	42.0^{cd}	27.7^{abc}	20.2	19.5^{e}	49.7^{a}
6	42.7^{abc}	27.0^{bcd}	22.8	28.0^{bc}	47.8^{abc}
7	40.2^{f}	26.0^{bcd}	18.4	30.2^{bc}	40.4^{ef}
8	42.2^{bcd}	27.5^{abcd}	23.2	27.8^{bc}	41.1^{ef}
9	41.3^{e}	29.3^{a}	27.7	32.5^{ab}	46.3^{bc}
10	43.3^{a}	26.3^{bcd}	19.9	32.7^{ab}	38.2^{f}
11	41.5^{de}	25.8^{bcd}	18.3	28.7^{bc}	42.2^{e}
12	37.8^{g}	27.8^{ab}	23.1	21.2^{de}	49.3^{a}
Prob-Plant	< 0.01	0.03	0.15	< 0.01	< 0.01
2011	41.7	25.8	20.9	25.6	43.5
2012	41.7	27.8	22.5	28.8	44.3
Prob-Year	0.84	< 0.01	0.27	0.01	0.21
Plant*Year	< 0.01	< 0.01	0.04	0.19	< 0.01

$^{a-f}$ Means within columns with different superscripts differ ($P < 0.05$).

1551 (M265) Rumen-undegradable protein of blood meal, canola meal, low-fat distillers dried grain with solubles, soybean meal, and expeller soybean meal determined using in situ and in vitro ammonia release procedures. H. A. Paz Manzano*[1], T. J. Klopfenstein[1], and P. J. Kononoff[2], *[1]University of Nebraska-Lincoln, Lincoln, [2]University of Nebraska, Lincoln.*

Two Holstein cows (days in milk 70 ± 17 and milk yield 27.3 ± 8.00 kg) fitted with ruminal cannulas were used to determine rumen-undegradable protein (RUP) using an in situ incubation of 16. In addition, the in vitro ammonia (NH_3) release procedure was used to estimate RUP. The in vitro NH_3 release procedure involves the incubation of equal amounts of N from each feedstuff in ruminal fluid and the measurement of the NH_3 and total VFAs produced. Concentrations of $NH_3$and total VFA were adjusted for a blank (only inoculum). The feedstuffs evaluated were: 3 sources of blood meal (BM1, BM2, and BM3), canola meal (CM), low-fat distillers dried grains with solubles (LFDG), soybean meal (SBM), and expeller soybean meal (ESBM). Data from the in situ procedure were analyzed as a randomized complete block design and the model included the fixed effect of feedstuff and the random effects of replicate and load within feedstuff and data from the in vitro ammonia release were analyzed as a complete randomized design and the model included the fixed effect of feedstuff and the random effect of load within feedstuff. Based on the in situ procedure, RUP was 70.2, 63.0. 59.3, 31.2, 24.3, 23.1, 14.7 ± 3.93% crude protein (CP) for BM2, ESBM, BM3, SBM, CM, LFDG, and BM1, respectively. Based on the in vitro ammonia release procedure, RUP was 67.6, 67.5, 65.8, 48.8, 32.5, 32.3, 32.1 ± 3.46% CP for BM2, BM3, ESBM, LFDG, BM1, SBM, and CM. Compared to RUP values obtained from the in situ procedure, values of RUP from the in vitro ammonia release procedure were greater ($P = 0.01$) for BM1 and LFDG and similar ($P \geq 0.10$) for the remaining feedstuffs. The in vitro ammonia release procedure is a promising method for measuring RUP that avoids the use of cannulated animals and errors that may emerge with washout of residue from the polyester bags, and allows for uniform settings; however, more research is needed to elucidate the factors that cause variability when using this procedure.

Key Words: rumen-undegrabable protein, in situ, in vitro

1552 (M266) Sources of protein and protected methionine on in situ ruminal degradability of crude protein of feed ingredients. F. D. O. Scarpino van Cleef*[1,2], J. M. Bertocco Ezequiel[1], E. Neves Muniz[3], R. L. Galati[4], and E. H. C. B. Van Cleef[1,5], *[1]UNESP, Jaboticabal, Brazil, [2]CNPq, Brasilia, Brazil, [3]Embrapa Tabuleiros Costeiros, Aracaju, Brazil, [4]Federal University of Mato Grosso, Cuiaba, Brazil, [5]FAPESP, Sao Paulo, Brazil.*

The objective of this study was to evaluate crude protein degradability of feed ingredients in diets containing corn gluten or starea as protein sources, with or without 2 g/d protected methionine. Eight male ruminally-cannulated sheep (12 mo old, 51.3 kg BW) were assigned to a replicated 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments (two sources of protein— corn gluten or starea— and with or without protected methionine). The in situ nylon bag technique was used in this trial. Samples of feed ingredients were ground to 5 mm (corn silage), and 2 mm (extruded corn and soybean hulls), and incubated for 6, 12, 24, 48, 72, and 96 h for corn silage, and 1, 6, 12, 24, and 48 h for extruded corn and soybean hulls. Data were fitted to exponential model to estimate degradation parameters, and effective degradability was calculated with passage rates of 2, 5, and 8%/h. Data were analyzed as a replicated 4 × 4 Latin square with PROC MIXED of SAS. There was no interaction of protein sources and protected methionine, thus only the main effects were studied. Variations from 23 to 91% (corn gluten, and starea, respectively) on protein degradability of protein sources do not affect degradability parameters, potential degradability, and effective degradabilities (2, 5, and 8%/h passage rates) of corn silage and soybean hulls. The average potential degradabilities of crude protein observed were 75.9% (corn silage), and 73.6% (soybean hulls). The average effective degradabilities of crude protein for 3, 5, and 8%/h passage rates were respectively 71.6, 68.8, and 67.7% (corn silage), and 66.1, 58.0, and 53.1% (soybean hulls). The addition of protected methionine improves in 4% the potential crude protein degradability and in 2.8, 2.1, and 1.5% the effective degradabilities of corn silage, for 2, 5, and 8%/h passage rates, respectively. It was concluded that regarding fibrous in-

gredients, the variation of 68% units in crude protein degradability of protein sources is not enough to modify the ruminal utilization of crude protein of these ingredients. Furthermore, the protected methionine inclusion improves crude protein degradation parameters for low protein ingredients.

Key Words: degradability, methionine, protein sources

1553 (M267) Supplementation of lysine and methionine in the starter concentrate or milk replacer of dairy calves.

J. T. Silva*, M. R. De Paula, G. Santos, G. Slanzon, and C. M. M. Bittar, *University of Sao Paulo, Piracicaba, Brazil.*

Concentrate and milk replacer available in Brazil are deficient in lysine and methionine for dairy calves, which may benefit from supplementation. Forty-five newborn Holstein male calves were used in a randomized complete block designed experiment and assigned into one of three treatments: 1) Control: no amino acid (AA) supplementation; 2) Starter concentrate: supplementation of lysine and methionine in the concentrate starter to reach daily intakes of 17 g/d and 5.3 g/d, respectively; and 3) Milk replacer: supplementation of lysine and methionine in the milk replacer to reach daily intakes of 17 g/d and 5.3 g/d, respectively. Calves were housed in individual shelters, with free access to water, and were fed starter concentrate and 6 L/d of milk replacer (20% CP, 16% ether extract, and 12.5% solids), divided into two meals, until the 8 wk of life, when they were weaned. Starter concentrate and milk replacer intakes, as well as fecal scores were monitored daily. Body weight, withers height, heart girth and hip width were weekly measured. Data suggest that amino acid supplementation in the concentrate decreased solid feed intake, reducing total dry matter intake after weaning and consequently calves' final body weight (Table 1553). Amino acid supplementation have no beneficial effects on dairy calves' performance.

Key Words: amino acids, growth, milk-feeding period

Table 1553. Performance of dairy calves receiving starter concentrate or milk replacer supplemented with lysine and methionine

	Control	Starter Concentrate	Milk replacer	SEM	$P <$
Body weight, kg					
Initial	39.5	38.9	41.2	1.69	1.000
At weaning	53.5[a]	47.4 b	48.9[b]	1.68	0.023
Final	61.1[a]	50.6 b	53.4[b]	1.68	0.023
Daily gain, g					
Before weaning	245.2	168.6	173.2	31.46	0.167
After weaning	539.7	214.2	358.8	105.6	0.11
Starter intake, g/d					
At weaning	429.9	155.8	270.1	97.98	0.230
Final	1529.9	1035.9	1278.9	97.98	0.230
Total dry matter intake, g/d					
Before weaning	880.9	805.4	813.0	31.4	0.182
After weaning	1329.9[a]	770.5[b]	1089.6[ab]	146.9	0.04
Feed efficiency, daily gain/total intake	0.26	0.11	0.21	0.05	0.091
Fecal score	1.68	1.92	1.83	0.07	0.077
Height withers gain, cm/week	0.68	0.52	0.59	0.07	0.290
Heart girth gain, cm/week	1.15	0.83	0.89	0.12	0.114
Hip width gain, cm/week	0.30	0.20	0.27	0.06	0.206

[ab] means with different subscripts differ ($P < 0.5$)

1554 (M268) Evaluating the plasma free amino acid dose–response method to determine the content of metabolizable methionine in a rumen-protected methionine supplement.

N. L. Whitehouse*[1], C. G. Schwab[2], M. C. Blais[1], A. F. Brito[1], and B. K. Sloan[3], [1]*University of New Hampshire, Durham,* [2]*Schwab Consulting, LLC, Boscobel, WI,* [3]*Adisseo, Alpharetta, GA.*

The plasma free AA dose–response approach has been proposed as the standardized method for evaluating rumen-protected Lys supplements. The method has the advantage of providing animal-derived estimates of efficacy under conditions of commercial use. However, before using the approach for evaluating rumen-protected Met (RP-Met) supplements, it is necessary to confirm that a positive linear relationship exists between increasing amounts of absorbed Met and plasma Met concentrations. The primary objective of this experiment was to confirm linearity in plasma Met response with up to 24 g/d of supplemental MP-Met by abomasal infusion or feeding a RP-Met product. A secondary objective was to determine if technique precision could be improved by including the other plasma sulfur AA (cystine, cystothionine + allocystothionine, homocystine and taurine) with Met (total sulfur AA) as an indicator of Met absorption. Five rumen-cannulated lactating Holstein cows (90–155 DIM), fed a Met-deficient diet, were assigned to a 5 × 5 Latin square with 7-d experimental periods. Treatments (*P*er 25.0 kg/d of DMI) were 0 g/d Met (neg-

ative control), 12 and 24 g/d abomasally infused Met, and 12 and 24 g/d of assumed MP-Met from a RP-Met supplement. Blood samples were taken from the tail vein every 2 h, 4 times daily, the last 3 d of each period, centrifuged, deproteinized, and composited into 1 daily sample/cow. Data for plasma AA concentrations were analyzed using the PROC MIXED and PROC REG procedures of SAS 9.2. The basal diet was confirmed to be Met-deficient by observed increases in milk protein concentration (+0.10 and 0.12% units for infused and fed Met, respectively; $P < 0.05$) with the first level of both infused and fed Met. All plasma sulfur AA responded in a significant linear fashion to both infused and fed Met ($P < 0.05$). Estimates of the MP-Met content of the RP-Met supplement were the same using either plasma Met or plasma total sulfur AA. The plasma free AA dose–response method is applicable for determining the MP-Met content of RP-Met supplements.

Key Words: rumen-protected, methionine, evaluation

1555 (M269) Amino acids supplementation in the milk replacer for dairy calves.

J. T. Silva*, N. B. Rocha, E. Miqueo, T. Manzoni, G. Santos, S. Baldassin, and C. M. M. Bittar, *University of Sao Paulo, Piracicaba, Brazil.*

This study evaluated the performance and fecal scores of dairy calves receiving milk replacer supplemented with lysine and methionine (EAA) to reach daily intakes of 17 g/d and 5.3 g/d, respectively; and two levels of AminoGut (Ajinomoto Animal Nutrition; 10% Glutamine and 10% Glutamic acid). Forty-five newborn Holstein male calves were utilized in a randomized blocks experimental design, and distributed into three treatments: 1) Control: no amino acid supplementation; 2) AminoGut 0.6%: supplementation of EAA and 0.6% AminoGut; and 3) AminoGut 1%: supplementation of EAA and 1% AminoGut. Calves were individually housed, with free access to water and starter concentrate, and received 6L/d of milk replacer (20CP:16EE; 12.5% solids), until the eighth week of life, when weaned. Calves were followed up to the 10 wk of life. Feed intakes and fecal scores were monitored daily; while body weight and body measurements were weekly measured. Even though AminoGut has been proven to benefit animals affected diarrhea, there were no supplementation effects on fecal scores. Supplementation of 0.6% of glutamate increased starter intake, which may benefit animals going through the transition period. However, the low intake observed for all treatments resulted in modest daily gains and final weight, as it has been seen in other trials during summer tropical conditions. *Supported by Fapesp, São Paulo, Brazil.*

Key Words: glutamate, lysine, methionine

Table 1555. Performance of calves receiving milk replacer supplemented with lysine + methionine, and two levels of AminoGut

	Control	AminoGut 0.6%	AminoGut 1%	SEM	$P <$
Body weight, kg					
Initial	37.0	36.8	38.0	1.3	0.089
At weaning	48.2	48.3	47.2	1.9	0.089
Final	54.8	56.1	54.8	2.5	0.089
Daily gain, g					
Before weaning	246.8	270.6	218.7	48.3	0.756
After weaning	430.7	548.4	560.2	79.2	0.418
Starter intake, g/d					
At weaning	104.6 b	280.7 a	248.9 ab	58.1	0.051
Final	1400.3	1226.9	1299.8	206.5	0.270
Total dry matter intake, g/d					
Before weaning	786.5	843.1	806.0	40.6	0.615
After weaning	926.3	1089.3	1077.8	133.9	0.622
Height withers, cm	0.6	0.8	0.7	0.09	0.478
Heart girth, cm	1.3	1.2	1.1	0.17	0.846
Hip width, cm	0.3	0.3	0.3	0.04	0.825
Fecal score	1.8	1.9	1.9	0.08	0.398

[ab] means with different subscripts differ ($P < 0.5$)

1556 (M270) Effects of maternal nutrition and arginine supplementation on characteristics of wool quality in offspring.

J. L. Peine*, P. P. Borowicz, J. S. Caton, and R. R. Redden, *North Dakota State University, Fargo.*

The objectives of this study were to measure effects of maternal nutrition and rumen-protected arginine supplementation on postnatal offspring wool quality and follicle development. We hypothesized that lambs from ewes receiving diets fed to nutrient requirements would have a greater density of wool follicles and improved wool quality compared to lambs from nutrient restricted ewes. We also hypothesized that lambs from restricted ewes receiving a rumen-protected arginine supplement would present similar wool follicle numbers and quality to those lambs from adequately fed dams. To test these hypotheses, multiparous Rambouillet ewes ($n = 32$; 67.6 ± 6.2 kg) were randomly assigned to one of three treatments at 54 ± 3.9 d of gestation in a completely random design. Dietary treatments included 100% nutrient requirements (control, CON), 60% of CON nutrients (restricted, RES), and RES with the addition of a rumen-protected arginine supplement dosed at 180 mg/kg of body weight once daily (RES-ARG). Ewes were penned individually in a temperature-controlled facility. Immediately post-lambing, lambs were separated from ewes and raised independent of their dam until necropsy at 54 ± 3 d of age. A wool sample was taken for quality analysis, in addition to skin samples (3 cm^2) from the side (between the 10th and 12th rib) and britch regions. Following histological preparation and stereological analysis all data were analyzed using the PROC MIXED of SAS. No differences were observed in follicle numbers between treatments for skin samples taken from

the side of the lambs ($P \geq 0.17$). However, in the britch samples lambs from RES-ARG ewes had more ($P = 0.02$) follicles present than lambs from CON ewes, with lambs from RES being both intermediate and similar in follicle number (106 vs. 86 vs. 93 ± 6.3 follicles per 1 mm^2, respectively). There were no differences among treatments for wool quality measures of mean fiber diameter, fiber diameter SD, or comfort factor ($P \geq 0.32$). These data partially support our hypothesis that maternal rumen-protected arginine supplementation may increase the number of developing follicles in offspring, and therefore potentially increase wool production. However, we reject our hypothesis that arginine supplementation will increase wool quality in those lambs from restricted-nutrient dams.

Key Words: arginine, wool, developmental programming

1557 (M271) Effects of maternal nutrition and rumen-protected arginine supplementation on postnatal lamb performance and organ mass. J. L. Peine*, G. Jia, S. T. O'Rourke, L. P. Reynolds, and J. S. Caton, *North Dakota State University, Fargo.*

Our hypothesis was that rumen-protected arginine supplementation would overcome the negative effects of restricted maternal intake during the last two-thirds of gestation on lamb organ mass and postnatal performance. To investigate the effects that arginine supplementation would have, $n = 32$ multiparous, Rambouillet ewes were allocated to one of three treatments in a completely random design at 54 ± 3.9 d of gestation. Dietary treatments included either 100% of requirements (control, CON), 60% of control (restricted, RES), or RES plus a rumen-protected arginine supplement dosed at 180 mg/kg BW once daily (RES-ARG). Ewes were penned individually in a temperature controlled facility, and remained on these treatments through parturition. Upon parturition, lambs were immediately removed from their dam and reared independently. At 54 ± 3 d of age, lambs were necropsied and organs were dissected. Birth weights in lambs from CON ewes were greater ($P = 0.04$) than lambs from RES ewes, with lambs from RES-ARG ewes being intermediate (5373, 4553, and 4697 ± 256.0 g, respectively). At 54 ± 3 d of age, curved crown rump measurements were longer ($P = 0.003$) in lambs from RES-ARG ewes than from RES, with a tendency for lambs from RES-ARG ewes to also be longer ($P = 0.06$) than CON (99.8 vs. 93.9 vs. 96.3 ± 1.28 cm, respectively). Organ mass measurements showed lambs from RES-ARG ewes had greater ($P = 0.05$) liver mass than RES, with lambs from CON ewes being intermediate (490.0 vs. 481.2 vs. 429.5 ± 21.08 g, respectively). In addition, lambs from CON ewes had greater ($P = 0.01$) mass of adrenal glands than lambs from RES ewes. These data support that rumen-protected arginine supplementation may partially mitigate negative effects on postnatal lamb performance and organ mass due to restricted maternal intake during the last two-thirds of gestation.

Key Words: arginine, developmental programming, offspring

1558 (M272) Ultrasonography for investigating the effect of supplementing whole milk with plant-derived complex carbohydrates on curd clearance through the abomasum of dairy calves. K. Singh*[1], S. R. Leath[1], H. V. Henderson[1], T. J. Watson[1], D. Pacheco[2], and C. D. McMahon[1], *[1]AgResearch Ltd, Ruakura Research Centre, Hamilton, New Zealand, [2]AgResearch Ltd, Grasslands, Palmerston North, New Zealand.*

Growth rates of dairy heifer calves and their performance at first lactation are enhanced by supplementing a whole milk diet with plant-derived complex carbohydrates and specific amino acids. At present it is unclear how such changes in nutrition from birth to weaning can affect a dairy cow's subsequent lactations. The aim of this study was to establish the use of ultrasound to investigate if the transit time of milk is influenced by a supplement of plant-derived complex carbohydrates to whole milk. Initially, the use of ultrasonography for detecting curd after feeding whole milk in the abomasa of pre-ruminant dairy heifer calves ($n = 10$) was determined. This was conducted using a sectorial probe (M-Turbo with C60x/5.2MHz transducer; Sonosite USA), at -10, 5, 30, 60, and 120 min after feeding. A score system was developed for fullness of the abomasum (0 to 3) and size of the curds (A to C). In trial 2, 22 calves were individually fed whole milk (control group) until weaning (approximately 80 kg live weight); 4L whole milk per day (2L am and 2L pm) using an automated calf feeder. The remaining calves (supplemented group; $n = 21$) were fed as per above, but whole milk was supplemented with a probiotic (X-Factor [XF], Bell-Booth Ltd, New Zealand) until 18 d of age and then XF was replaced with a source of plant-derived complex carbohydrates and selected amino acids (Queen of Calves [QoC], Bell-Booth Ltd) at a starting dose of 25 g/L whole milk, increasing at d 20 of age to 37.5 g/L, and to 50 g/L from d 21 of age until weaning. The groups were balanced for age, weight and breed. Ultrasonography of the abomasum was conducted as above. Supplementing whole milk with XF did not affect average retention time compared with calves fed whole milk. However, milk supplemented with QoC delayed the transit time of curd 1.4 ± 0.28 h (32%) longer ($P < 0.001$) at 4 wk of age and 0.7 ± 0.34 h (14%) longer ($P = 0.05$) at 8 wk of age, compared with calves fed whole milk alone. These data indicate that milk supplemented with QoC slows transit time of curd in the abomasum, which may allow a greater absorption of nutrients to support early growth.

Key Words: curd, transit time, dairy heifer

1559 (M273) Relationship between non-protein nitrogen and true protein in supplements during the post-weaning phase of Nellore steers in the dry-wet season transition.
B. C. Carvalho[1], R. M. Fernandes[2], C. M. D. Almeida[1], N. M. Jerônimo[1], G. F. Berti[1], C. G. C. Marcolino[1], M. H. Moretti[3], I. M. de Oliveira[*4], F. D. D. Resende[4], and G. R. Siqueira[4], *[1]Centro Universitário da Fundação Educacional de Barretos–Unifeb, Brazil, [2]UNESP-FCAV, Jaboticabal, Brazil, [3]Universidade Estadual Paulista, Jaboticabal, Brazil, [4]APTA–Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil.*

The objective of this study was to evaluate the effect of different levels and rates of protein degradation on the performance of Nellore, recreated on *Brachiaria brizantha* cv. Marandu during the transition period dry water. Seventy-two bulls were used with 412.45 kg body weight (BW) initial, non-castrated Nellore, daily receiving 3 g/kg BW of supplement, these were divided into 12 paddocks. The treatments were: energy protein supplement (SPE) with 25% CP (control), energy protein supplement with 40% CP, one third of the PB of vegetable and two thirds of chemical origin, Supplement energy protein with 40% CP, with two thirds of the PB of vegetable and one third of chemical origin, energy protein supplement with 40% CP, one half PB of plant origin and half of chemical origin. The animals were weighed every 28 d after 16 h of fasting and liquid to obtain the average daily gain (ADG). The experiment took place from September to December 2013, totaling am 84-d evaluation. The experimental unit used was the picket, which is composed of six testeres animals. The experimental design was a randomized block experimental areas and the blocking factor, there were three paddocks per treatment. Data were analyzed using mixed model using the PROC MIXED of SAS software, version 9.2 (SAS, 2008), the 10% level of significance by *t* test. The increase in NNP (40–2/3NNP) depressed ADG ($P = 0.07$) 0.265 kg/day in compared to other treatments with averaged 0.366 kg, 0.419 kg and 0.399 kg for C-25, 40–1/2 NNP and 40–1/3 NNP, respectively. The final body weight was greater ($P = 0.08$) in animals that received 40–1/2 NNP (416.7 kg) compared to those who received C-25 (408.5 kg) or 40–2/3 NNP (404.4 kg). The 40–1/3 NNP treatment with intermediate weight (413.1 kg) did not differ from treatments 40–1/2 NNP ($P = 0.40$) and C-25 ($P = 0.30$). It is concluded that supplementation with 40% CP and one-half NNP is able to generate heavier animals in the transition dry-waters. *Supported by CNPq and Bellman.*

Key Words: average daily gain, *Brachiaria brizantha,* supplementation

1560 (M274) Sulfur sources in protein supplements and their influence on amino acid profiles.
F. P. Leonel[*1], C. J. Silva[2], L. M. Moreira[1], J. M. Carvalho[1], J. C. Carvalho[3], J. C. Pereira[3], T. C. Nunes[1], and R. A. Vieira[4], *[1]Federal University of São João del Rei (UFSJ), Brazil, [2]National University of Brasília, Brazil, [3]Federal University of Viçosa (UFV), Brazil, [4]Norte Fluminense State University, Campos dos Goytacazes, Brazil.*

The present experiment was performed to evaluate the effect of different sulfur sources in protein supplements for cattle in the amino acids profile with respect to the abomasal digesta. Crossbred steers were fed with *Brachiaria dictyoneura* hay, applying different sulfur sources in the protein supplement: 70S elementary sulfur- byproduct (ES70S); 98S elementary sulfur- flowers of sulfur (ES98S); hydrated calcium sulfate (HCS); anhydrous calcium sulfate (ACS) and ammonium sulfate (AS). The dietary treatments were applied at 11:1 nitrogen:sulfur ratio. Five steers which were fistulated in the rumen and abomasum were used in a 5 × 5 Latin square design. The experiment had five 16-d periods, in which the first 10 d were for adaptation period and the subsequent 6 d were utilized to obtain the experimental data. The concentration of available amino acids in the abomasal digesta (g/kg DM) remained with very similar values ($P > 0.05$) in the evaluated diets. The amino acids evaluated in the abomasal digesta remained with the same quantitative profiles, suggesting that their properties do not depend on the sulfur sources encountered in the respective diets.

Key Words: beef steers, amino acid profiles, sulfur nitrogen ration

Table 1560. Amino acid profile in abomasal digesta in different treatments and their coefficient of variation (CV%)

	E70S	E98S	HCS	ACS	AS	CV(%)
	—— mg/kg of DM ——					
Essential amino acids						
Valine	19.52	18.80	18.64	18.96	19.40	10.65
Methionine	20.40	19.82	19.70	19.94	20.30	11.36
Isoleucine	5.46	5.60	5.68	5.52	5.70	18.03
Leucine	18.16	18.38	18.72	18.58	20.22	17.22
Phenylalanine	32.04	30.68	31.86	31.74	32.46	13.68
Histidine	541.54	541.76	529.08	552.12	590.66	14.16
Valine	7.22	7.02	7.12	7.42	7.56	13.24
Lysine	34.92	33.72	34.04	35.28	36.22	14.83
Arginine	18.52	18.04	18.80	18.78	19.16	10.28
Nonessential amino acids						
Aspartic acid	45.34	44.06	44.30	43.80	44.96	12.08
Serina	100.42	101.24	107.62	149.18	114.10	32.64
Cystine	5.58	5.44	5.00	5.24	5.54	12.66
Glutamic acid	45.82	46.38	45.64	45.30	46.98	15.72
Proline	20.30	19.74	19.74	20.20	20.76	13.34
Glycine	21.06	19.98	20.68	19.64	19.86	15.15
Alanine	26.66	25.06	25.18	24.98	26.02	12.45

1561 (M275) Slow-release urea in diets of crossbred lactating cows. F. P. Leonel[*1], B. T. Santiago[2], S. D. J. Vilella[2], J. M. Carvalho[1], J. C. Carvalho[3], M. M. Assis[1], T. C. Nunes[1], and L. M. Moreira[1], [1]*Federal University of São João del Rei* (*UFSJ), São João del Rei, Brazil,* [2]*Federal University of Vales do Jequitinhonha e Mucuri* (*UFVJM), Diamantina, Brazil,* [3]*Federal University of Viçosa* (*UFV), Brazil.*

This work was performed to evaluate the performance of F1 lactating cows (Holstein x Zebu) in response to different levels of substitution of soybean meal by non-protein nitrogen equivalent protein derived from slow-release urea (SRU). Eight cows were used in a duplicate 4 × 4 Latin square design, according to the following treatments: control (100% soybean meal and 0% SRU), 34SRU (66% soybean meal and 34% SRU), 66SRU (34% soybean meal and 66% SRU) and 100SRU (0% soybean meal and 100% SRU). The forage sorghum silage was used. Intakes of dry matter (DMI), crude protein (CPI), neutral detergent fiber (NDFI) were measured. The apparent digestibility of dry matter (MDad) and neutral detergent fiber (NDFad) were evaluated using chromic oxide as an external marker. Milk production was measured. Data were subjected to analysis of variance using the statistical program SAEG, adopting the 5% level of probability. Treatments did not affect DMI, CPI, and NDFI ($P > 0.05$; Table 1561). The results of apparent digestibility of the dry matter and neutral detergent fiber also do not present differences ($P > 0.05$) between treatments. Milk production and composition demonstrated also similar results ($P > 0.05$), when are compared the treatments evaluated in this work. The replacement of soybean meal by slow-release urea (SRU) does not affect the variables of intake and digestibility of dry matter or milk production of crossbred cows.

Key Words: digestibility, intake, milk production, soybean meal

Table 1561. Intake and digestibility of DM and nutrients and milk production

	Treatments					
Variable	Control	34ULL	66ULL	100ULL	CV (%)	*P*
DMI (kg/dia)	18,20	18,44	18,76	17,99	6898	0555
CPI (kg/day)	2,50	2,65	2,62	2,70	11,207	0678
NDFI (kg/day)	5,92	5,59	6,29	5,63	13,216	1408
DMad (%)	57,78	59,77	57,35	57,74	4213	0235
NDFad (%)	38,89	36,40	34,27	35,29	9860	0101
Milk production (kg/day)	13,39	13,88	13,44	12,05	19,621	0744

[1] DMI = dry matter intake; CPI = crude protein intake; NDFI = neutral detergent fiber intake; DMad = apparent digestibility of dry matter; NDFad = apparent digestibility of neutral detergent fiber; CV = coefficient of variation

1562 (M276) Passage rate and efficiency of microbial protein synthesis in buffaloes fed increasing levels of crude protein. E. Machado, L. M. Zeoula*, E. H. Yoshimura, R. B. Samensari, N. W. Santos, B. C. Agustinho, L. D. M. Pereira, and S. C. Aguiar, *Universidade Estadual de Maringá, Maringá, Brazil.*

Optimization of the ruminal passage rate improves the conditions for growth of rumen microorganisms; however, if the dilution rate is too fast, the microbial growth can be reduced. The objective was to evaluate the effect of increasing levels of crude protein (CP) in the diet of buffaloes on the passage rate and efficiency of microbial protein synthesis (EMPS). Four crossbred growing buffaloes were used, weighing 355 ± 3.5 kg of body weight, cannulated in the rumen and distributed in a 4 × 4 Latin square design. The total mixed ration consisted of corn silage (850 g.kg^{-1}) and concentrate (150 g.kg^{-1}) and was formulated to meet the proposed levels of CP (70, 90, 110, and 130 g.kg^{-1}). To determine the dilution rate, a Co-EDTA solution (32 g of Co-EDTA in 500 mL of distilled water) was added via ruminal cannula before the first feeding. Ruminal fluid was collected at time zero (before the first feeding), and 2, 4, 6, 8, 10, 12, 14, 16, and 24 h post-feeding. To estimate the EMPS, spot urine samples were collected. From the concentration of creatinine in the spot urine sample, the urinary volume was estimated and the production of microbial nitrogen was calculated from the amount of absorbed purines, which was estimated as the excretion of purine derivatives in urine using the following equation: $Y = 0.74X + (0.117 W^{0,75})$. The synthesis of microbial nitrogen in the rumen was calculated as a function of absorbed purines: $Y = X70/0.116 \times 0.83 \times 1000$. Data were interpreted using the SAS statistical software (version 9.0). There was a linear effect ($P < 0.01$) for the levels of CP on microbial production, which averaged 244.8, 342.0, 394.8 and 425.2 g of microbial protein for 70, 90, 110, and 130 g.kg^{-1}PB, respectively. According to the regression equation ($Y = 54.62 + 4.70X$, $R^2 = 0.4555$), we observed an increase of 4.70 units in the microbial production for each percentage unit of dietary CP. However, this effect is not observed on the dilution rate and on the EMPS when expressed per unit of fermented carbohydrate, probably due to the relationship between these two parameters. Therefore, if the increase in the dietary CP did not alter the EMPS, it can be concluded that the rumen microorganisms' requirements were met at the lowest level of dietary protein.

Key Words: transit kinetics, nitrogen, purine derivatives

1563 (M277) Effects of test weight and processing method on in vitro intestinal digestibility of barley grain. Y. Zhao[1], S. Yan[2], Z. He[1], U. Anele[1], M. L. Swift[3], T. A. McAllister[4], and W. Yang[*1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, AB, [2]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China, [3]Alberta Agriculture and Rural Development, Lethbridge, Canada, [4]Agriculture and Agri-Food Canada, Lethbridge, AB.*

An in vitro study was conducted to investigate the effects of test weight and processing method on intestinal digestibility of barley grain following ruminal incubation. The study was designed as a 2 × 2 × 2 factorial arrangement with treatments: test weight (TW; low vs. high), precision processing (*P*P; control vs. PP), and processing index (*P*I; 75 vs. 85%). Ten barley samples with 5 low (574 g/L) and 5 high (632 g/L) TW were either dry-rolled with single roller setting (control) or sieved into small and large kernels, then dry-rolled based on kernel size of each fraction (i.e., PP). Each sample was dry-rolled moderately or coarsely with PI of 75 or 85%, respectively. Intestinal DM digestibility (iDMD; % of ruminal residue input) of barley grains was determined using the modified three-step in vitro procedure. Barley samples were incubated in the rumen for 12 h to produce ruminal residues using three beef heifers (650 ± 25 kg BW) fitted with rumen cannula and fed a diet consisting of 70% barley silage and 30% barley grain. Ruminal residues were incubated in 1 N HCl containing 1 g/L of pepsin for 1 h, and then in phosphate buffer (*P*H 7.8) containing pancreatin at 39°C for 24 h. An interaction between TW and PP ($P < 0.02$) and between PP and PI ($P < 0.01$) was detected but not between TW and PI ($P > 0.05$). The iDMD was greater ($P < 0.01$) with high (25.6%) than with low (23.1%) TW of barley grain for control barley, whereas the iDMD was not different between the low (20.2%) and high TW (20.4%) for PP barley. Compared to control processing, PP reduced ($P < 0.01$) the iDMD (*P*P vs. control; 13.5 vs. 21.2%) for processed barley with PI of 85% but not for barley with PI of 75% (27.3%). Decreasing PI from 85 to 75% increased ($P < 0.01$) iDMD from 17.3 to 27.4%. These results indicate that the intestinal digestibility of barley grain varied with TW, processing method, and extent of processing. It suggests that manipulating these factors may partly shift grain starch digestion from the rumen to the intestine, thereby potentially reduce rumen acidosis and improve feed efficiency in feedlot beef cattle fed high-grain diet.

Key Words: barley grain, precision processing, in vitro intestinal digestibility

1564 (M278) Using a fibrolytic enzyme to barley-based finishing diets containing wheat dried distillers grains with soubles: Ruminal fermentation, digestibility, and growth performance in feedlot steers. Z. He[*1,2], M. He[1], N. D. Walker[3], T. A. McAllister[4], and W. Yang[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food CanadaAB, Canada, [2]Key Laboratory for Agro-Ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, China, [3]AB Vista Feed Ingredients, Marlborough, UK, [4]Agriculture and Agri-Food Canada, Lethbridge, AB.*

Two experiments were conducted to evaluate the effects of adding an exogenous fibrolytic enzyme (FE) on ruminal pH and fermentation, digestibility, and growth performance in feedlot beef cattle fed finishing diet containing wheat dried distillers grains with solubles (DDGS). In Exp. 1, four ruminally cannulated Angus heifers (averaged BW of 807 ± 93.9 kg) were used in a repeated 4 × 4 Latin square design. Treatments were: 1) control (CON; 10% barley silage and 90% barley grain-based concentrate); 2) WDG (CON diet substituting 30% wheat DDGS for barley grain); 3) WDGL (WDG diet supplementing with low FE; 1 mL FE/kg diet DM); and 4) WDGH (WDG diet supplementing with high FE; 2 mL FE/kg diet DM). Heifers were fed at restriction of 90% ad libitum twice daily. Digestibility in the total digestive tract was measured using Yb as external digesta marker. Statistical contrasts were generated to compare CON vs. WDG and the linear and quadratic effects of FE dosages (0, 1, and 2 mL FE/kg diet). Digestibility of DM was less ($P = 0.01$) with WDG (67%) than CON diet (71%). Increasing FE linearly ($P < 0.05$) increased starch digestibility from 88.7, 89.7 to 91.3% without affecting digestibility of other nutrients. Adding FE also reduced ($P = 0.03$) ruminal ammonia-N concentration from 13.6 to 10.1 m*M*. In Exp. 2, one hundred and sixty yearling steers (initial BW of 495 ± 37.9 kg) were fed 1 of 4 diets used in Exp. 1. Dry matter intake (10.9 kg/d), final BW (684 kg), and ADG (1.69 kg) did not differ between steers fed CON and WDG diets. However, steers fed WDG reduced ($P < 0.05$) G:F (150 vs. 160 g/kg DMI) and increased ($P < 0.01$) percentage of abscessed livers (49 vs. 15%) compared to steers fed CON. Increasing FE did not affect DMI, final BW, and ADG but tended ($P < 0.09$) to linearly improve G:F (150 to 157), and decreased ($P = 0.03$) incidence of abscessed livers (49 to 25%). Carcass traits were not affected by treatments. These results indicated that inclusion of wheat DDGS at 30% of the ration DM in finishing diets had adverse impacts on digestibility, feed efficiency and animal health. However, supplementing finishing diet containing wheat DDGS with FE potentially offset the negative effect of including wheat DDGS.

Key Words: feed efficiency, fibrolytic enzyme, finishing feedlot steers

1565 (M279) Effects of forage intake to minimize the risk of subacute ruminal acidosis on performance of feedlot finishing cattle. K. M. Koenig*[1], G. E. Chibisa[1], G. B. Penner[2], and K. A. Beauchemin[1], *[1]Agriculture and Agri-Food Canada, Lethbridge Research Centre, AB, [2]University of Saskatchewan, Saskatoon, Canada.*

Growing beef cattle in North America are typically fed high grain diets with a limited amount of forage to maximize productivity cost-effectively. Distillers grains (DG) are now commonly fed as part of the concentrate lowering the amount of fermentable starch in the diet and the potential risk of ruminal acidosis. The objectives of the study were to determine the effects of varying the concentration of forage in barley-based diets containing DG on feed intake, growth performance, and carcass traits of feedlot finishing cattle. A uniform group of 160 cross-bred beef steers was stratified according to initial BW (349.7 ± 22.3 kg) and randomly allocated to 20 pens (5 pens of 8 steers per treatment). The treatments were barley silage at 0, 4, 8, and 12% of diet DM. The remainder of the diet consisted of 80, 76, 72, and 68% barley grain for the 4 diets, respectively, 15% corn dried DG and solubles, and 5% supplement (with monensin at 28 mg/kg diet DM). The diets were fed as a total mixed ration for ad libitum intake (minimum of 5% orts) once per day. Cattle were weighed on 2 consecutive d at the start and end of the experiment and on 1 d every 3 wk throughout the experiment (124 d). The DMI of each pen was determined from feed offered daily and orts at the end of each 3-wk period. The ADG was determined from linear regression of BW over time. Data for DMI for each pen, and BW, ADG, G:F, and carcass traits for each animal were analyzed as a completely randomized design using a mixed linear model with diet as a fixed effect, pen replicate and diet × pen replicate as random effects (except for the model for DMI), and pen as the experimental unit. There was a trend ($P = 0.10$) towards a linear increase in DMI by steers with increasing percentage of barley silage. However, there was no effect ($P > 0.05$) of the barley silage treatments on final shrunk BW (612.7 ± 4.25 kg), ADG (1.86 ± 0.03 kg/d), and carcass traits. Feed efficiency linearly decreased ($P < 0.05$) with increasing percentage of barley silage. Increasing the proportion of barley silage in a barley grain-based diet with DG may reduce the incidence of subacute ruminal acidosis but feed conversion efficiency is reduced.

Key Words: finishing cattle, forage, growth performance

1566 (M280) Saliva production and short-chain fatty acid absorption in beef cattle fed a low- or high-forage diet. G. E. Chibisa*[1], K. A. Beauchemin[1], and G. B. Penner[2], *[1]Agriculture and Agri-Food Canada, Lethbridge Research Centre, AB, [2]University of Saskatchewan, Saskatoon, Canada*.

Based on past research, there are indications that a potential decrease in acid removal from the rumen via epithelial absorption during a bout of ruminal acidosis could possibly be compensated for by an increase in salivation. However, there is limited information on whether similar changes in the relative contributions of salivary bicarbonate and passive and/or facilitated absorption of short-chain fatty acids (SCFA) to pH regulation occur when dietary forage content is altered. Therefore, the objective of this study was to determine the effects of feeding a low- (LF) or high-forage (HF) diet on ruminal fermentation, salivation and SCFA absorption. Eight ruminally-cannulated cattle were used in a crossover design with 49 d periods. The treatments were barley silage at 30 (LF) or 70% (HF) of dietary dry matter (DM). The LF and HF diets contained 45.3 and 30.9% starch and 26.4 and 38.3% physically effective fiber (DM basis), respectively. On d 35, ruminal fluid was collected to determine SCFA concentration. Ruminal pH was continuously measured from d 29 to 35. Eating or resting salivation, was measured by collecting masticate (d 39 and 40) or saliva samples (d 42 and 43) at the cardia, respectively. On d 42 and 43, the temporarily isolated and washed reticulo-rumen technique was used to measure total, and chloride competitive (an indirect measure of protein-mediated transport), absorption of acetate, propionate and butyrate. Total ruminal SCFA concentration and osmolality were higher ($P < 0.02$) in cattle fed the LF compared to the HF diet. Additionally, feeding LF resulted in a longer ($P = 0.02$) duration (h/d) and a larger ($P = 0.05$) area (PH × h/d) that pH was below 5.5. Although there was no diet effect on total and chloride competitive absorption (mmol/h and %/h) of SCFA, eating salivation (mL/min) was lower ($P = 0.02$), whereas resting salivation (mL/min) tended to be lower ($P = 0.10$) in cattle fed a LF diet. The lower ruminal pH in cattle fed the LF compared to the HF diet could be attributed to the increase in SCFA production and decrease in salivation, which were not compensated for by an increase in SCFA absorption.

Key Words: dietary forage content, saliva production, short-chain fatty acid absorption

Table 1567. Forage and total intake, ruminal parameters, microbial synthesis and nitrogen retention

	Energy Source		%of BW		P value			
	Corn	Citrus Pulp	0.3	0.6	ES	S	ES*S	SEM
Total DMI, %BW	1.77	1.76	1.74	1.78	ns	ns	ns	0.27
Forage DMI, %BW	1.32	1.31	1.44	1.18	ns	*	ns	0.26
Digestible DMI, %BW	1.19	1.18	1.08	1.29	ns	**	ns	0.16
Forage digestibility, %	58.00	58.08	57.88	58.2	ns	ns	ns	0.94
pH	6.46[a]	6.38[b]	6.47[a]	6.37[b]	*	*	*	0.09
NH3,mg/dL	6.12	5.96	6.65[a]	5.43[b]	ns	*	ns	0.85
Microbial synthesis, g/d	537.88	511.18	460.87	588.19	ns	*	ns	67.39
Nitrogen retention, % N % intake	29.74	21.88	16.58	35.04	ns	**	ns	5.18

SEM = Standard error of the mean, * = significant, ns = not significant, ES = energy source, S = supplementation.

1567 (M281) Interactions between levels and source of energy supplementation in beef cattle.

J. R. R. Dórea[*1], L. R. Dell Agostinho Neto[1], V. N. Gouvea[2], D. A. Fleury[1], A. V. Pires[1], and F. A. P. Santos[3], *[1]University of Sao Paulo, Piracicaba, Brazil, [2]University of São Paulo–FMVZ/USP, Pirassununga, Brazil, [3]University of São Paulo, Piracicaba, Brazil.*

The objective of this trial was to evaluate the effect of two levels and two sources of energy on voluntary intake and ruminal parameters of Nellore steers grazing intensively managed tropical pasture during the rainy season. Treatments corresponded to two levels of supplementation (0.3 and 0.6% of BW, as fed) combined with two sources of energy concentrate (fine ground corn and pelleted citrus pulp). Eight 24-mo-old rumen-cannulated steers (356 kg BW ± 9.8) were assigned to two 4 × 4 Latin squares and allocated in 2 ha of *Brachiaria brizantha cv.* Marandu (palisadegrass), managed in a rotational grazing system. Chromium oxide was used as an indigestible marker. Concentration of purine derivatives in the urine was used to estimate microbial synthesis. Total DMI was not affected by treatments. Feeding 0.6% of BW of energy supplement decreased forage intake ($P < 0.05$) and increased ($P < 0.01$) digestible DMI. There was interaction ($P < 0.05$) for ruminal pH between source and level of supplementation, with lower pH for steers fed citrus pulp and for steers supplemented at 0.6% of BW. Energy supplementation at 0.6% BW decreased ruminal N-NH_3 ($P < 0.05$) due to greater microbial synthesis ($P < 0.05$), resulting in greater N retention. No differences between ground corn and citrus pulp were observed as an energy supplement for growth cattle. Feeding 0.6% BW of energy supplement is an effective to increase digestible dry matter intake in grazing cattle.

Key Words: energy source, forage intake, supplementation

1568 (M282) Digestibility and nitrogen efficiency of growing beef cattle fed diets containing different proportions of *Stylosanthes* Campo Grande and corn silages.

W. F. D. Souza[1], O. G. Pereira[*2], K. G. Ribeiro[2], S. A. Santos[1], S. C. Valadares Filho[3], V. P. Silva[2], and M. C. N. Agarussi[4], *[1]Universidade Federal da Bahia, Salvador, Brazil, [2]Universidade Federal Viçosa, Minas Gerais, Brazil, [3]Instituto Nacional de Ciência e Tecnologia–Ciência Animal, Viçosa, Minas Gerais, Brazil, [4]University of Delaware, Newark.*

The objectives of this study were to evaluate total, ruminal and intestinal digestibility of nutrients, ruminal pH, ruminal ammonia concentration and nitrogen efficiency in growing beef cattle fed diets with varying proportions of *Stylosanthes* Campo Grande silage (SSt) replacing corn silage (CS). Treatments consisted of diets with ratios of 0:100, 25:75, 50:50, 75:25 and 100:0% SSt:CS. Diets consisted of 50% silage and 50% concentrate, formulated to be isonitrogenous (12.5% CP, DM basis). Ten crossbred Holstein-Zebu bulls with an average initial weight of 272 ± 86 kg, distributed in two 5 × 5 Latin squares were used. The bulls were non-castrated and rumen and abomasum-fistulated. This trial lasted 90 d divided in five experimental periods. Each period lasted 18 d and was divided into 10 d for adaptation to the diets and 8 d to collect samples. Chromium oxide (Cr_2O_3) was used to determine the fecal excretion and abomasum flow of nutrients. All data were analyzed using the PROC MIXED in SAS (version 9.1). Rumen apparent digestibility of CP and the intestinal apparent digestibility of NFC increased linearly ($P < 0.05$), with the addition of SSt to the diet. Intestinal digestibility of DM showed a quadratic effect ($P < 0.05$). Nitrogen balance, urea excretion in urine and urea nitrogen in the blood plasma showed no effect in response ($P > 0.05$) to the inclusion of SSt in the diet. Ruminal pH values were not affected ($P > 0.05$) by proportion of SSt in the diet ($P > 0.05$), but ruminal pH was affected ($P < 0.05$) by the time of collection, for which a cubic model was fit to the data. There was an interaction effect ($P < 0.05$) between treatment and collection time for rumen ammonia nitrogen concentration. Based on the results obtained in this study, it

can be concluded that *Stylosanthes* Campo Grande silage can be used as a source of roughage in the diet of beef cattle during the growing phase at a proportion of 50% of dry matter in the total diet. *Sponsored by FAPEMIG, CNPq and INCT-CA*.

Key Words: ammonia nitrogen, legume silage, ruminal pH

1569 (M283) Influence of *Macleaya cordata* preparation on feedlot performance and carcass characteristics of finishing bulls. R. Barajas*[1], B. J. Cervantes[2], I. Rogge[3], A. Camacho[1], and L. R. Flores[1], *[1]FMVZ-Universidad Autónoma de Sinaloa, Culiacan, México, [2]Ganadera los Migueles, S.A. de C.V., Culiacan, México, [3]Phytobiotics Futterzusatzstoffe GmbH, Eltville, Germany.*

The *Macleaya cordata* is a plant of the *Papaveraceae* family that contains as active components alkaloids of the Benzo[c] Phenanthridine family sanguinarine and chelerythrine; and alkaloids of the protopin family as is protopine and allocryptopine. Their combined effects include mild antimicrobial activity, anti-inflammatory properties, and inhibition of amino acids degradation; those characteristics suggest that *Macleaya cordata* could modify rumen microbial activity and reflect it on feedlot cattle performance. Despite *Macleaya cordata* is used in Europe as feed additive for farm animals, its effects of on feedlot cattle performance are not well-documented. In this research, 80 bulls weighing 380 ± SE 2.41 kg (approximately 75% *Bos taurus* and 25% *Bos indicus* blood), were used in a 91-d feedlot experiment to evaluate the influence of *Macleaya cordata* preparation on feedlot performance and carcass characteristics of finishing bulls. Blocked by initial weight, in a complete randomized block design with a 2 × 2 factorial arrangement, bulls were assigned to treatments as follows: 1) A 89% concentrate corn-cotton seed meal finishing diet (Control); 2) Control plus daily 4 g of *Macleaya cordata* preparation delivering 20 mg of alkaloids (MC); 3) Control plus 40 mg of sodium monensin/kg of DM (MN); and 4) Control plus MC and MN (MM). Results were analyzed for ANOVA as a complete randomized block design with a factorial 2 × 2 arrangement. MC was offered as Sangrovit-RS (Phytobiotics, Germany) a standardized preparation of *Macleaya cordata*; and monensin was supplied as Rumensin 200 (Elanco Animal Health, IN). Zilpaterol hydrochloride (Zilmax; Merck Animal Health) was supplemented during latest finishing. Treatments had no effect ($P > 0.15$) on final weight, ADG, DMI, and hot carcass weight. The inclusion of *Macleaya cordata* tended to increase ($P = 0.10$) diet net energy for maintenance and gain (2.04 *vs.* 1.98 Mcal ENm/kg; and 1.38 *vs*. 1.33 Mcal ENg/kg). Supplementation with *Macleaya cordata* tended ($P = 0.09$) to improve DMI/hot carcass gain ratio (7.946 vs. 8.452 kg DMI/kg of carcass). The addition of MC tended ($P = 0.08$) to reduce KPH-fat (1.96 *vs.* 2.13%). Remainder carcass characteristics were not affected by treatments ($P > 0.15$). It is concluded that the supplementation of *Macleaya cordata* preparation may contribute to improve diet net energy use, feed carcass conversion, and decreases the amount of fat deposited around of kidney, pelvis and heart in finishing bulls.

Key Words: beef cattle, *Macleaya cordata*, sanguinarine

1570 (M284) Supply levels of multiple supplements for beef heifers on pasture during the dry season: ruminal pH and ammonia nitrogen. R. P. D. Silva*, J. T. Zervoudakis, L. K. Hatamoto-Zervoudakis, L. D. S. Cabral, A. J. Neto, J. Q. Soares, A. C. B. Melo, E. R. Donida, P. I. José, R. C. Soares, E. A. Teixeira, and A. J. Possamai, *Federal University of Mato Grosso, Cuiaba, Brazil.*

This research aimed to evaluate the effect of different levels of multiple supplements for beef heifers that were restricted grazing during the dry season on pH and ruminal ammonia nitrogen. Five Nellore heifers were used, with age and initial weights average of 20 mo and 344.0 kg, respectively. The pastures were divided into five paddocks of 0.25 ha each, consisting of *Brachiaria brizantha* cv. Marandu. The experiment was divided into 5 × 5 Latin square design, composed by five experimental periods of 20 d each and five animals. The strategy adopted was to provide multiple supplements (soybean hulls + ground corn grain + soybean meal + sunflower + urea and mineral mix) at levels of 2, 4, 6, and 8 kg/animal/d. The animals were fed in two fixed hours: 50% of the daily amount at 1000 h and 50% at 1500 h, the mineral mixture was offered ad libitum (control). For determination of pH and ammonia concentration in the rumen fluid samples were collected by gavage on the 19 and 20 d of each period, 2 h before supplementation (10 to 0 h time) and 2 h after supplementation of afternoon (15 to 2h time).The availability of total dry matter was 2.29 ton/ha. The strategies of supplementation promoted a reduction of ruminal pH ($P = 0.0343$) and increased the concentration of ruminal ammonia nitrogen (NH_3–N) ($P = 0.0004$) before providing supplements, and after the supplementation the NH3 expressed a quadratic effect ($P = 0.0023$). The values observed for ruminal pH varied from 6.44 to 6.78 before supplementation in the morning and from 6.43 to 6.79 two h after feeding the animals in the afternoon, not harming the ruminal microbiota. Providing high levels of multiple supplements increases the nutritional support for cattle on systems with low level and quality of pasture during the dry season.

Key Words: *Brachiaria brizantha*, replacement effect, rumen

1571 (M285) Comparison of commercially available lick tubs to daily by-product supplementation of calves grazing corn residue. M. Jones*, M. Jones, J.C. MacDonald, T.J. Klopfenstein, G.E. Erickson, A.K. Watson, *University of Nebraska–Lincoln, Lincoln.*

Corn residue is a forage source low in energy and crude protein to meet the needs of growing calves. Providing supplementation increases average daily gain of calves grazing corn residue. The objective of this trial was to compare the use of a commercially available lick tub to daily by-product supplementation of calves grazing corn residue. One hundred twenty five crossbred steers (240 kg ± 2.64) were backgrounded on irrigated corn residue for a 60-d grazing period at the University of Nebraska–Lincoln Agricultural Research and Development Center near Mead, NE. The trial was replicated over two consecutive years (n = 8). Each year, an irrigated corn residue field was divided into eight paddocks, with four replications receiving dried distillers grains (DGS) and four having continuous access to lick tubs. Calves on the DGS treatment received supplementation in a bunk at 1.36 kg/head per d. Stocking rate was calculated based on grain yield of the field at harvest multiplied by an estimated 3.64 kg forage consumed/bu, 85% grazing efficiency factor and number of hectares available for grazing. Data was analyzed using Proc Glimmix with year run as a random effect. Average daily gain (ADG) of steers receiving dried DGS was 0.62 kg/head per day in comparison to 0.38 kg/head per day for steers on the lick tub treatment ($P < 0.01$). Average supplement intake for cattle on the lick tub treatment was 0.76 kg/day on an OM basis compared to 1.28 kg/day for steers receiving dried DGS ($P < 0.01$). Since forage estimations were not taken, supplement efficiency was used to compare the change in gain to intake by dividing ADG by supplement intake. Supplement efficiency for the lick tubs and dried DGS treatments were 43 and 46% on a DM basis ($P < 0.01$) compared to 50 and 48% on an OM basis, respectively ($P = 0.64$). Lick tubs are a convenient method for providing supplementation to calves and on an OM basis, offer similar supplement efficiency when compared with daily by-product supplementation.

Key Words: corn residue, grazing, stocker cattle, supplementation

1572 (M286) Dry matter intake of supplemented cattle under grazing during the dry season. T. O. J. A. Lins*, R. R. Silva, F. B. Mendes, M. M. Lisboa, M. M. S. Pereira, G. Abreu Filho, S. O. Souza, and L. G. Silva, *Universidade Estadual do Sudoeste da Bahia, Itapetinga, Brazil.*

This study aimed to evaluate the dry matter daily intake of cattle supplemented on pasture during dry season. The experiment was conducted in southwest region of the state of Bahia, Brazil. The study was the growing phase of 36 crossbred steers (*Bos taurus* x *Bos indicus*) with initial body weight of 378 kg ± 7.5kg and median age of 14 mo. The animals were distributed in a completely randomized design, with four treatments and eight replicates and were managed in an experimental area formed by a *Brachiaria brizantha* cv. Marandu in a system of intermittent grazing. The supplement was formulated so that the same amount of crude protein (CP%) coming from the supplement was consumed daily by animals in the different treatments. Thus, the treatments were on basis of body weight of animals (% BW): T2, 0.2%BW with 50% CP, T4,0.4%BW with 25% CP; T6, 0.6%BW with16.67% CP, and T8, 0.8%BW with 12.5% CP. The statistical model used was: $Y_{ijk} = \mu + T_i + e_{ijk}$, where: Y_{ijk}- observed value; μ- overall constant; T_i- effect of treatment i and e_{ijk}– randomized error. There was no difference in the daily intake of total dry matter (tDMI) ($P > 0.05$) between treatments. There was a linear effect ($P < 0.05$) in dry matter intake of forage (fDMI), characterizing a substitutive effect. It is concluded that supplementation of steers in growing phase presents better results when used at low levels, although with a high protein content.

Key Words: weight gain, protein supplementation, continuous stocking, substitutive effect

Table 1572. Dry matter intake of supplemented cattle under grazing during the dry season and their respective regression equations and coefficients of determination (R2)

Varibles	Treatment (%BW) 0.2%	0.4%	0.6%	0.8%	Regression equations	R2
tDMI (kg.day-1)	7.41	7.81	8.18	8.09	–	–
fDMI (kg.day-1)	6.63	6.24	5.79	4.96	Y = 7.27025-2.73324X	0.96

1573 (M287) Interaction between grazing management and energy supplementation on behavior of grazing beef cattle. L. R. Dell Agostinho Neto*[1], M. G. M. F. D. Santos[1], M. R. Lovaglio[2], D. F. A. Costa[2], J. R. R. Dórea[2], and F. A. P. Santos[2], [1]*University of Sao Paulo, Piracicaba, Brazil,* [2]*University of São Paulo, Piracicaba, Brazil.*

The objective of this study was to evaluate the effects of two grazing managements, based on canopy height, and two levels of energy supplementation on ingestive behavior of beef cattle grazing an intensively managed tropical grass. Treatments were two pre-grazing heights (25 cm and 35 cm) both managed with stubble height corresponding to 60% of the pre-grazing height (15 cm and 21 cm, respectively) combined with two levels of energy supplementation (0 and 0.6% BW of fine ground corn). Eight 36-mo-old cannulated Nellore steers (487 kg BW ± 6.96 kg) were assigned to two 4 × 4 Latin squares and allocated in 2 ha of *Brachiaria brizantha* pasture. Animals were monitored every 5 min during 24 h to evaluate the ingestive behavior, according to the activities: grazing, rumination and idle. Bite

Table 1573. Grazing time, rumination, idle and bite rate of beef cattle grazing tropical grass

	Management, cm		Supplementation, % of BW		P value			
Activities	25- 15	35- 21	0	0,6	M	S	M*S	SEM
Grazing[1]	292.19	295.94	330.31	257.81	0.8652	0.0032	0.9323	42.9
Rumination[1]	322.5	349.37	350	321.87	0.2497	0.2290	0.9350	42.2
Idle[1]	735.31	704.69	669.69	770.31	0.4379	0.0168	0.9238	73.52
Bite rate[2]	28.79	29.02	28.05	29.76	0.8968	0.3535	0.3962	2.49

[1] Minutes.
[2] Bite/minute

rate was also evaluated. Grazing time was not affected by the managements ($P > 0.05$), however decreased ($P < 0.05$) with the energy supplementation (72.5 min). Both, management and supplementation did not affect rumination and bite rate ($P > 0.05$). Time spent in idle was increased ($P < 0.05$) by energy supplementation (100.62 min). The managements based on 60% of the pre-grazing height did not affect DMI.

Key Words: supplementation, beef cattle, Marandu palisadegrass, ingestive behavior

1574 (M288) Supply levels of multiple supplements for beef heifers on pasture during the dry season: Intake and digestibility of nutrients. R. P. D. Silva*[1], J. T. Zervoudakis[1], L. K. Hatamoto-Zervoudakis[1], L. D. S. Cabral[1], E. Alexandrino[2], R. L. Galati[3], J. Q. Soares[1], A. C. B. Melo[1], E. R. Donida[1], P. I. José[1], A. J. Possamai[1], K. F. Cervelati[1], L. B. D. Freiria[1], and D. A. D. Faria[1], *[1]Federal University of Mato Grosso, Cuiaba, Brazil, [2]Federal University of Tocantins, Araguaína, Brazil, [3]Federal University of Mato Grosso, Cuiaba, Brazil.*

This research aimed to evaluate the effect of levels of multiple supplements for beef heifers that were restricted grazing during the dry season on intake and digestibility of nutrients. Five Nellore heifers were used, with age and initial weights average of 20 mo and 344.0 kg, respectively. The pastures were divided into five paddocks of 0.25 ha each, consisting of *Brachiaria brizantha* cv. Marandu. The experiment was divided into 5 × 5 Latin square design, composed by five experimental periods of 20 d each and five animals. The strategy adopted was to provide multiple supplements (soybean hulls + ground corn grain + soybean meal + sunflower + urea and mineral mix) at levels of 2, 4, 6, and 8 kg/animal/d. The animals were fed in two fixed hours: 50% of the daily amount at 1000 h and 50% at 1500 h, the mineral mixture was offered ad libitum (control). To estimate feed intake, chromium oxide was used as an external marker and indigestible NDF was used as an internal marker. The feces collections were made in 3 d in different collection times. The availability of total dry was 2.29 ton/ha. The intake dry matter, organic matter, crude protein (CP), non-fiber carbohydrates (NFC) and total digestible nutrients, and total apparent digestibility of dry matter, crude protein, total carbohydrates and NFC increased linearly ($P < 0.0001$) and the dry matter intake of forage decreased ($P < 0.0001$) with supplementation levels, it indicates that there was replacement effect. We conclude that providing supplement for grazing cattle in the dry season enhances the digestion of nutrients from forage.

Key Words: *Brachiaria brizantha*, replacement effect, nutrients intake

1575 (M289) Individual and additive value of conventional and non-conventional technologies in beef heifers housed and fed using a GrowSafe feeding system. A. R. Harding*[1], G. K. Jim[2], C. W. Booker[2], E. J. Behlke[2], S. L. Parr[2], S. J. Hannon[2], T. M. Greer[2], Z. D. Paddock[2], M. L. May[2], L. O. Burciaga-Robles[2], and C. R. Krehbiel[1], *[1]Oklahoma State University, [2]Feedlot Health Management Services, Ltd., Okotoks, AB, Canada.*

This study evaluated the effects of conventional and non-conventional production (NCP) technologies in feedlot cattle. A total of 384 yearling heifers (859 ± 77 lb.) were stratified by BW and randomly allocated to 1 of 8 treatments: NCP1: fibrolytic feed enzyme (Econase RDE; Sage Biosciences Inc., Edmonton, Alberta); NCP2: Oleobiotec Ruminant (Oleo; Laboratoires Phodé, Terssac, France); NCP3: CitriStim (ADM Alliance Nutrition Inc., Quincy, Illinois); NCP4: Oleo and CitriStim. All NCP systems received a non-medicated supplement. Blended production systems (BP) included: BP1: non -medicated supplement, Oleo, melengesterol acetate (MGA; Zoetis Canada, Kirkland, Québec), and Zilpaterol hydrochloride (Zilmax; Merck Animal Health, Intervet Canada Corp., Kirkland, Québec) for the last 20 d; BP2: medicated supplement containing Rumensin and Tylan (Elanco Animal Health, Guelph, Ontario), MGA, Oleo, and Zilmax for the last 20 d. Control groups included a negative control (NEG): non-medicated supplement; and conventional production (CP): medicated supplement containing Rumensin, Tylan, and MGA, and Zilmax for the last 20 d. Individuals were randomized within diet treatment to receive an implant (Revalor-200; Merck Animal Health), parasite control (Dectomax Pour-On Solution; Zoetis Canada), both, or neither. Heifers were fed for 123 d and DMI was recorded using GrowSafe feeding systems (GrowSafe Systems Ltd., Airdrie, Alberta). Data

were analyzed using the GLIMMIX procedure (SAS Institute Inc, Cary, North Carolina). Relative to the NEG group, BP2 and CP treatments had greater live and carcass adjusted ADG and improved live G:F ($P < 0.05$) and the BP1, BP2, and CP treatments had improved carcass adjusted G:F ($P < 0.001$). No differences ($P > 0.05$) were detected in carcass characteristics of NCP and BP groups compared to the NEG and CP groups. Implanted cattle had greater ADG and improved G:F vs. non-implanted cattle ($P < 0.001$) while no differences ($P > 0.05$) in feedlot performance or carcass characteristics were detected for parasiticide treatment. No interactions ($P > 0.05$) were identified between diet, implant status and/or parasiticide. These results indicate that conventional production systems improve beef heifer performance.

Key Words: feedlot, cattle, technology

1576 (M290) Effect of pregnancy and feeding level on voluntary intake, digestion and microbial N production in Nellore cows. M. P. Gionbelli*[1,2], M. S. Duarte[2], S. C. Valadares Filho[1,2], E. Detmann[1,2], B. C. Silva[2], D. F. Sathler[2], T. R. Gionbelli[2], F. A. Villadiego[2], and L. H. Silva[2], *[1]Instituto Nacional de Ciência e Tecnologia–Ciência Animal, Viçosa, Minas Gerais, Brazil, [2]Universidade Federal de Viçosa, Minas Gerais, Brazil.*

The objective of this experiment was to evaluate the effects of pregnancy and feeding level on intake, digestibility and efficiency of microbial N production in Nellore cows. Forty-four multiparous Nellore cows (32 pregnant and 12 non-pregnant) with average initial body weight of 451 ± 10 kg were fed either HIGH (ad libitum) or LOW (restricted feeding 1.2 times maintenance according to the NRC) feeding level. The diet consisted of corn silage (85%), ground corn, soybean meal, urea and mineral mixture. The intake was controlled daily and the DMI was evaluated weekly. In vivo apparent total digestibility was estimated using indigestible NDF as an internal marker and microbial N synthesis was estimated using the technique of purine derivatives in urine. Fecal and urine samples were collected every 28 d. The voluntary feed intake reduced as the pregnancy advances in Nellore cows and can be calculated as DMI (kg/d) = (16– 0.0093 × days of pregnancy)/1000 × SBW, where SBW is shrunk body weight. The average DMI of LOW-fed cows corresponded to 102, 98, and 67% of the amount of energy necessary to attend the maintenance and pregnancy energy requirements suggested by NRC for a cow at 0, 135, and 270 d of pregnancy, respectively. However, LOW-fed cows had 0.26 kg/d of average shrunk body gain indicating that the nutrient energy requirements of Zebu cows are likely lower than those suggested by NRC. The interaction between the feeding level and days of pregnancy was significant ($P < 0.05$) for the digestibility of DM, OM, CP, ether extract (EE), NDF corrected for ash and protein (NDF_{ap}) and GE, and the values of TDN. In all these cases there was a reduction in digestibility with increasing gestation age in HIGH-fed cows, while digestibility of OM, CP, EE, NDF_{ap} and GE increased as function of days of pregnancy in LOW-fed cows. The reduction in the digestibility of neutral detergent fiber occurs faster than in dry matter digestibility. These data suggests that the reduction of the digestibility as pregnancy increases in ad libitum fed cows is caused by an increase in the rate of passage as compensation factor for the ruminal volume reduction. There were no direct effects of pregnancy on microbial N production in Nellore cows. *Funded by INCT-CA, CAPES, CNPq, and FAPEMIG.*

Key Words: beef cattle, *Bos indicus*, dry matter intake, gestation, total digestible nutrients, Zebu

---

1577 (M291) Growth and feed intake of Nellore steers fed whole corn diets containing feed antibiotics. B. J. M. Lemos[1], F. G. F. Castro[2], B. P. C. Mendonça[2], A. L. Braga Netto[2], C. E. Dambros[1], D. B. Fernandes[2], V. R. M. Couto[1], and J. J. R. Fernandes*[1], *[1]Universidade Federal de Goiás, Goiânia, Brazil, [2]AgroCria, Goiânia, Brazil.*

The objective was to investigate the effects of feed antibiotics on growth and feed intake of feedlot steers fed whole corn diets. Ninety-eight Nellore steers (302 ± 47 kg of BW and 24 mo of age) were assigned to a randomized complete block design experiment with four blocks (based on initial BW) and five treatments (Mon30: monensin 30 ppm; Virg25: virginiamycin 25 ppm; Mon20+Virg25: monensin 20 ppm + virginiamycin 25 ppm; Fla40: flavomycin 40 ppm; Mon20+Fla20: monensin 20 ppm + flavomycin 20 ppm). Pen was the experimental unit. The experiment consisted of a 100-d period. All steers were fed ad libitum with TMR (88.2% DM, 12.5% CP, 71.5% TDN) with 85% whole grain corn and 15% pelleted protein concentrate on a DM basis. Animals were weighed after a 16-h fast on d 0 and 100 of the experimental period to determine the ADG and feed efficiency (G:F, g of BW gain/kg of feed). No effect ($P > 0.01$) was observed on growth and feed intake of Nellore steers fed whole corn diets containing feed antibiotics (Table 1577). Feed antibiotics tested had the same results. Feed antibiotics tested were able to maintain satisfactory performance in finishing beef cattle fed high-concentrate diets based on whole corn.

Key Words: beef cattle, performance, whole corn diet

Table 1577. Initial body weight (BWi), final body weight (BWf), dry matter intake (DMI) daily (kg/d) and DMI as % of BW, average daily gain (ADG) and feed efficiency (G:F) of Nellore steers fed whole corn diets containing feed antibiotics

	Feed antibiotics						
Variables	Mon30	Virg25	Mon20+ Virg25	Fla40	Mon20+ Fla20	SEM	*P*-Value
No. of pens (steers)	4 (20)	4 (20)	4 (19)	4 (19)	4 (20)	–	–
BWi (kg)	393	387	392	393	393	3.49	0.755
BWf (kg)	539	534	537	544	539	4.38	0.618
DMI							
kg/d	8.4	9.0	8.8	9.3	9.1	0.39	0.578
% of BW	1.8	1.9	1.9	2.0	2.0	0.08	0.731
ADG (kg/d)	1.465	1.466	1.444	1.504	1.463	0.04	0.902
G:F	0.18	0.17	0.17	0.16	0.16	0.01	0.799

1578 (M292) Effects of volume weight, precision processing and processing index on in vitro ruminal fermentation of dry-rolled barley grain. U. Y. Anele*[1], B. Refat[1], M. L. Swift[2], Z. He[1], T. A. McAllister[1], and W. Yang[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, AB, [2]Alberta Agriculture and Rural Development, Lethbridge, Canada.*

A study using batch culture technique was conducted to evaluate the effects of volume weight (VW, g/L), precision processing (PP; sieving grains into large versus small kernels and rolling based on kernel size), and processing index (PI; VW after rolling/VW before rolling × 100%) on kinetics of gas production, dry matter degradability (DMD), molar proportions and total short chain fatty acids (SCFA) of dry rolled barley grain. The study was arranged in a 2 × 2 × 2 factorial design. Gas production and DMD were measured at 3, 6, 12, and 24 h of incubation using rumen fluid from three fistulated beef heifers fed 70% barley silage and 30% barley grain. We hypothesized that incorporating other factors with PI would help improve prediction of the feeding value of processed barley grain. Barley samples were collected monthly from 10 different feedlots in Southern Alberta for 1 yr. Samples were ranked according to their VW into low (< 600 g/L) and high (> 600 g/L), which were later subjected to PP (processed vs. control) before dry-rolled with extent of processing expressed as PI 75 or 85% ± 3. The dry-rolled samples used in the study were not subjected to further grinding. Precision processing x PI interactions ($P < 0.01$) were observed for asymptotic cumulative gas volume, rate, lag time and absolute initial gas produced during the first hour. In addition, a PP × VW interaction ($P < 0.05$) was noted for cumulative gas volume. There were strong interactions ($P < 0.01$) between PP, VW and PI for the b fraction (insoluble but degradable in the rumen) and effective degradability of the samples. Effective degradability coefficients ranged from 0.18 to 0.26. Greater degradability coefficients were noted for processed samples with lower PI. Only PI had an effect ($P < 0.05$) on the rate of DMD. Interactions ($P < 0.05$) between PP, VW and PI were noted for the isobutyric, butyric, isovaleric, valeric and caproic contents of the samples after 6 h of incubation. Total SCFA values ranged from 30.2 to 40.1 mmol/L. Apart from PP and PI interaction ($P < 0.05$) on C_2:C_3, no other interaction was observed after 24 h of incubation. Regression results showed that VW and PP was better in predicting rate of DMD than PI and this is consistent with our hypothesis.

Key Words: barley, beef cattle, degradability, prediction

1579 (M293) Total tract NDF digestion predicted using rumen in vitro measures is related to commercial dairy in vivo total tract nutrient digestion. J. P. Goeser*[1,2], and C. R. Heuer[1,2], *[1]Dep. of Dairy Science, University of Wisconsin–Madison, Madison, [2]Rock River Laboratory, Inc, Watertown, WI.*

Dairy diet in vivo total tract digestion estimates of OM and NDF have been correlated to animal performance and used in the field to assess opportunities for improvement. Measuring in vivo digestion on commercial farms however is time consuming and relatively costly. Our objective was to determine if total tract NDF digestion estimates predicted from rumen in vitro data (TTNDFD) were related to in vivo apparent total tract organic matter (OM) and carbohydrate digestion coefficients. Commercial dairy total mixed ration (TMR) samples ($n = 50$) submitted for in vivo digestion analysis (% of nutrient, using 120h iNDF as an internal marker) were further digested in duplicate for 24, 30, and 48 h using Combs-Goeser rumen in vitro techniques. Potentially digestible NDF (pdNDF, % of NDF) was estimated using 120-h NDFD measures and NDF K_d was calculated using log-linear transformed 24, 30, and 48 h uNDF residues. TTNDFD was predicted by $K_d/(K_d+K_p)$ and a K_p based on NDF passage. In vivo organic matter and carbohydrate digestion coefficients (OMD, NDFD, pdNDFD and starchD) were also determined. TMR nutrient content and in vivo digestion coefficient descriptive statistics were calculated. TTNDFD estimates were regressed on in vivo OMD, NDFD, pdNDFD, and StarchD using SAS JMP Pro v11.0 and residuals assessed for normality. The TTNDFD was significantly ($P < 0.01$) related to OMD, NDFD, and pdNDFD. The regression equation parameters are outlined in Table 1579. These data suggest further evaluation is warranted but demonstrate a significant relationship between TTNDFD predictions and in vivo total tract digestion measures. On commercial dairies, in vitro TTNDFD measures may help identify dairy nutritive opportunities.

Key Words: total tract, NDF, digestion

Table 1579. TMR nutrient and digestion coefficient descriptive statistics and regression model parameters in relation to TTNDFD. Results followed by * or ** differ from zero ($P < 0.05$ and $P < 0.01$, respectively)

	OM	NDF	pdNDF	Starch
TMR Nutrient Content (% of DM)				
Mean	92.01	31.93	19.30	25.15
StDev	1.03	3.74	3.22	4.04
in vivo TMR Digestion Coefficient (% of Nutrient)				
Mean	58.82	37.80	61.88	94.73
StDev	9.45	11.14	14.62	4.66
Regression Model Parameters in Relation to TTNDFD				
Intercept	38.50**	1.09	24.98**	92.36*
Slope	0.56**	1.01**	1.01**	0.07
R2	0.14	0.30	0.18	0.01
RMSE	8.86	9.39	13.38	4.68

Table 1580.

Items	Control	Vet	Tom	± SE	Pro > F
Milk yield (Kg/day)	7.26^{b}	7.91^{a}	7.59^{ab}	0.095	0.007
4% FCM (kg/day)	10.36	11.56	10.93	0.071	0.061
Fat %	6.86	7.10	6.96	0.044	0.072
Total Protein %	3.88^{b}	4.02^{ab}	4.20^{a}	0.051	0.023
Casein %	2.87^{b}	3.14^{a}	3.30^{a}	0.058	0.001
Whey %	0.827	0.804	0.845	0.014	0.495
NPN %	0.037^{a}	0.035^{a}	0.028^{b}	0.001	0.033
True protein %	3.843^{b}	3.985^{ab}	4.172^{a}	0.065	0.031
Urea N. mg/g	28.14^{a}	20.80^{b}	21.00^{b}	0.965	0.000
Lactose %	4.66	4.73	4.68	0.029	0.871
Ash %	0.802	0.800	0.784	0.010	0.776
Total solids %	16.26	16.56	16.82	0.150	0.336
Solids not fat %	9.44	9.46	9.86	0.138	0.405
Total CLA (g/100g fat)	0.23	0.32	0.25	0.053	0.081

1580 (M294) Influence of fibrolytic enzyme supplements on production performance of lactating buffaloes in early lactation.

T. A. Morsy*, and S. Kholif, *National Research Center, Cairo, Egypt.*

The use of biotechnology such as exogenous fibrolytic enzymes to enhance quality and digestibility of fibrous forage is a novel approach for delivering practical benefits to ruminant production systems. A study was conducted to evaluate the use of commercial exogenous enzymes as feed additives with lactating buffaloes on milk yield and composition. Twenty-one lactating buffaloes in early lactation had body weight on average (570 ± 15 kg) were divided into three groups (seven animals each) using complete random design. Animals were fed individually on basic diet total mixed rations (TMR; 60% forage: 40% concentrate, dry matter basis). Treatments were 1) no additives (control), 2) 40 g Tomoko/head/day (Tom), and 3) 40 g Veta-Zyme Plus/head/day (Vet). Animals were milked twice daily and milk production was recorded at every milking. Milk samples were obtained every two wk from each buffalo at all milkings to determine milk composition. The enzyme additive did not alter dry matter intake, but Milk yield, 4% Fat Corrected Milk, and Fat percent significantly increased with (Vet) treatment than all other treatments. However, total protein percent increased ($P < 0.05$) with (Vet) and (Tom) treatments than control. Regarding the milk fatty acids profile, it was found that the total unsaturated fatty acids and conjugated linolenic acid (CLA) were increased ($P = 0.08$) with (Vet) and (Tom) groups compared with control. Therefore, the addition of an exogenous fibrolytic enzyme additive to the diet of lactating buffaloes affected milk production as well as milk quality.

Key Words: fibrolytic enzyme, lactating buffaloes, milk yield and composition

1581 (M295) Effect of two exogenous fibrolytic enzyme preparations on rumen fermentation and in situ degradability kinetics in dairy cattle.

J. J. Romero*[1], E. G. Macias[2], Z. Ma[1], R. M. Martins[3], C. R. Staples[1], and A. T. Adesogan[1], *[1]Dep. of Animal Sciences, University of Florida, Gainesville, [2]Dep. de Zootecnia, Universidad Nacional Agraria La Molina, Lima, Peru, [3]Dep. de Zootecnia, Universidade Federal de Viçosa, Minas Gerais, Brazil.*

The objective was to compare effects of two *Trichoderma reesei* exogenous fibrolytic enzyme preparations (EFE) on the ruminal degradation and fermentation of a bermudagrass- and corn silage-based TMR. Endoglucanase and xylanase activities of a moderate xylanase (MIX) and xylanase-rich (XYL) EFE were 2087 and 2714 and 10,549 and 26,926 µmol/min per g, respectively. Both EFE improved milk production by lactating dairy cows in previous studies. Three ruminally-cannulated lactating Holstein cows (735 ± 8 kg; 159 ± 47 DIM) were assigned to Control (CON), MIX or XYL treatments in a 3 × 3 Latin square design with 23-d periods. The MIX and XYL EFE were added to the ration of the cows just before feeding at rates of 3.4 and 1 mL/kg of TMR DM, respectively. On d 18 of adaptation, ground (4 mm) samples of the TMR were weighed (5 g of DM) into in situ bags, treated with or without the EFE, and massaged to ensure thorough mixing. Exactly 24 h later, bags were placed in the rumens of the cows for 0, 4, 8, 16, 24, 48, and 72 h. All bags were removed simultaneously, washed, dried, and weighed. An exponential model was fitted to the DM degradation data. On d 23, ruminal fluid was collected from each cow just before feeding and every 2 h afterward for 10 h and analyzed for fermentation products and pH. The model used to analyze the fermentation data included effects of treatment, time, treatment by time interaction, period and the random effect of cow. A similar model without the time effect was used to analyze the in situ degradability data. Applying EFE had no effect ($P > 0.1$) on in situ degrad-

ability lag phase, washout fraction, potentially degradable fraction, undegradable fraction, or fractional degradation rate of DM. Also, EFE application did not affect ($P > 0.1$) ruminal pH or concentrations of ammonia-N, total VFA, acetate (A), propionate (P), butyrate, isobutyrate, isovalerate, valerate or the A:P ratio. Adding these EFE to a bermudagrass and corn silage- based TMR did not affect ruminal fermentation or in situ ruminal degradability under the conditions of this study.

Key Words: dairy cattle, enzyme, rumen kinetics

1582 (M296) Proteomic analysis of compositional differences between exogenous fibrolytic enzyme preparations that were effective or ineffective at improving forage digestibility. J. J. Romero*[1], Z. Ma[1], C. Silva-Sanchez[2], and A. T. Adesogan[1], [1]*Dep. of Animal Sciences, University of Florida, Gainesville,* [2]*Proteomics, ICBR, University of Florida, Gainesville.*

The objective was to use novel proteomic tools to identify differences in proportions of key enzymes and auxiliary proteins involved in hemicellulose and lignocellulose degradation between effective and ineffective exogenous fibrolytic enzyme preparations (EFE). We recently examined effects of applying 12 EFE from three companies on in vitro NDF digestibility (NDFD) of bermudagrass haylage (BH). The most- (2A) and second most- (11C) effective EFE were from *Trichoderma reesei* and they increased the NDFD of BH from 35.6 (Control) to 40.4 and 40.0%, respectively. The least effective EFE (9C) was from *T. reesei* and *Aspergillus* spp. and the NDFD of BH treated with this EFE was 36.2% (SEM = 0.55). The relative ratios of proteins in either 11C to 2A or 9C to 2A were analyzed in triplicate using quantitative proteomics. Specifically, EFE were analyzed with isobaric tags for relative and absolute quantitation coupled with liquid chromatography-mass spectrometry (iTRAQ LC-MS/MS). The identification and analysis of proteins were performed using ProteinPilot software version 4.5. Proteins were identified using the National Center for Biotechnology Information database for *T. reesei* and *Aspergillus* spp. The unused score threshold was set to > 1.3 (equivalent to 95% confidence or better). The Student's *t* test was used to measure the significance of the relative ratio of the proteins. The degrees of freedom were the number of distinct peptides within the protein evaluated minus 1. Quantitation was based on at least three unique peptides for each protein. The 2A EFE had 10 times more endoglucanase III, 17 times more acetylxylan esterase with Cellulose Binding Module 1, 33 times more xylanase III, 25 times more β-xylosidase, 7.69 times more polysaccharide monooxygenase with Cellulose Binding Module 1, and 3 times more swollenin compared to 9C. Relative to 11C, 2A had 14.3 times more xylanase III, 14.3 times more β-xylosidase, 7.7 times more endoglucanase III, and 1.9 times more polysaccharide monooxygenase. Therefore, the efficacy of the EFE at increasing NDFD was reflected by the relative proportions of novel xylanolytic and cellulolytic enzymes and auxiliary proteins that they contained.

Key Words: proteomics, enzyme, digestibility

1583 (M297) Effects of ensiling, exogenous protease addition and inoculation on ruminal in vitro starch digestibility in rehydrated corn. L. F. Ferraretto*, S. M. Fredin, R. D. Shaver, and P. C. Hoffman, *University of Wisconsin, Madison.*

Three experiments were simultaneously performed to evaluate the impact of: 1) rehydration and ensiling of dry ground corn on starch digestibility; 2) exogenous protease addition to rehydrated unensiled and ensiled corn on starch digestibility; and 3) exogenous protease addition or inoculation on fermentation profile and starch digestibility of rehydrated ensiled corn. To achieve these objectives, seven treatments ($n = 3$) were performed: dry ground corn (DRY), DRY + water addition to achieve DM content of 70% (WAT), WAT + exogenous protease addition (WATP), WAT ensiled for 30 d (ENS), WATP ensiled for 30 d (ENSP), ENS + inoculation (ENSI) and ENSP + inoculation (ENSPI). Vacuum-sealed bags were used for ensiled treatments. Exogenous protease (DSM Nutritional Products, Basel, Switzerland/Novozymes, Bagsvaerd, Denmark) was added at a rate of 1825 mg of protease per kg of corn DM. The recommended dose (4.5 g per ton of rehydrated corn) of a microbial inoculant containing lactic acid bacteria (1×10^9 CFU/g; Silo Charger "D", NU-AG Bosko, Inc., Oskaloosa, IA) was applied to inoculant treatments. Experiment 1 compared DRY, WAT and ENS in a completely randomized designed. Data were analyzed using Proc Mixed of SAS with treatment as a Fixed effect. Experiment 2 compared WAT and ENS without or with exogenous protease addition (WATP and ENSP, respectively) in a completely randomized designed in a 2×2 factorial arrangements of treatments. Data were analyzed using Proc Mixed of SAS with ensiling, protease addition and their interaction as Fixed effects. Experiment 3 compared the effects of exogenous protease addition and inoculation in ENS corn (ENS, ENSP, ENSI, and ENSPI). In experiment 1, starch digestibility was greater for ENS (64.9%) than DRY and WAT (51.7% on average). In experiment 2, ensiling and exogenous protease addition increased ($P < 0.05$) starch digestibility, but exogenous protease addition was more effective in ENS than WAT (6.4 vs. 2.6% units increase). In experiment 3, starch digestibility was increased by the addition of protease ($P = 0.02$) but not inoculant ($P = 0.38$). Inoculation resulted in lower ($P < 0.05$) pH, acetate, propionate and ethanol concentrations, but greater lactate ($P = 0.001$) and total acid ($P = 0.09$) concentrations. Ensiling and protease addition increased starch digestibility in rehydrated corn.

Key Words: ensiling, protease, starch digestibility

1584 (M298) Forage type and exogenous fibrolytic enzyme application rate effects on the digestibility of dairy cattle forages. J. J. Romero[1], Z. Ma[*1], E. G. Macias[2], D. H. Garbuio[3], and A. T. Adesogan[1], *[1]Dep. of Animal Sciences, University of Florida, Gainesville, [2]Dep. de Zootecnia, Universidad Nacional Agraria La Molina, Lima, Peru, [3]Universidade Estadual Paulista, São Paulo, Brazil.*

The objective was to examine the effects of applying two *Trichoderma reesei* exogenous fibrolytic enzyme products (EFE) at different application rates on the in vitro DM (DMD) and NDF (NDFD) digestibility of bermudagrass silage, a 50:50 alfalfa-orchardgrass hay mixture and corn silage. Treatments were a Xylanase-rich EFE (XYL), a 25:75 mixture of XYL and a cellulase EFE (MIX), and an untreated Control. Endoglucanase and xylanase activities of MIX and XYL were 2087 and 2714 and 10,549 and 26,926 μmol/min per g, respectively. The EFE were diluted in water and applied in quadruplicate to the substrate at 0, 0.5, 1, 4, and 8 μL of EFE/g of DM. The suspensions were incubated at 25°C for 24 h before addition of buffered-rumen fluid (39°C) and further incubation for 24 h in two runs. Rumen fluid was obtained from three lactating dairy cows fed TMR containing all of the tested forages. Data were analyzed as a completely randomized design with a 2 × 5 × 3 factorial treatment arrangement. The optimal dose was defined as the application rate with the highest digestibility that was higher ($P < 0.05$) than lower doses. Optimal doses of XYL and MIX for improving bermudagrass silage DMD were 0.5 (58.2 vs. 55.2%) and 1 (58.4 vs. 55.2%) μl/g, and those for increasing NDFD were 4 (39.7 vs. 32.9%) and 0.5 (36.7 vs. 32.9%) μl/g, respectively. For alfalfa/orchardgrass hay, respective optimal doses for DMD were 1 (68.8 vs. 66.0%) and 0.5 (68.7 vs. 66.0%) μl/g and those for NDFD were 1 (29.6 vs. 22.9%) and 0.5 (27.2 vs. 22.9%) μl/g, respectively. For corn silage, the respective optimal doses for DMD were both 1 μl/g (62.8 and 64.1 vs. 60.7%) and for NDFD they were both 4 μl/g (25.5 and 25.3 vs. 16.3%). Both XYL and MIX increased the in vitro DMD and NDFD of bermudagrass silage, alfalfa/orchardgrass hay and corn silage. Optimal application rates for improving DMD and NDFD differed across substrates for each EFE. The XYL and MIX EFE increased milk production by dairy cows when applied 1 and 3.4 μl/g of TMR DM, respectively in a subsequent trial.

Key Words: forage, enzyme, dose

1585 (M299) A meta-analysis on the effect of fibrolytic enzyme treatment of dairy cow diets. K. G. Arriola[*1], A. T. Adesogan[1], and M. C. Giurcanu[2], *[1]University of Florida, Dep. of Animal Sciences, Gainesville, [2]University of Florida, Dep. of Statistics, Gainesville.*

The objective of this study was to use a meta-analysis approach to summarize the results of experiments that investigated effects of exogenous fibrolytic enzymes (EFE) treatment of diets on the performance of dairy cows. The study evaluated data from 20 studies and 30 experiments. Treatments were classified based on predominant enzyme activities listed by the authors, which included: Cellulase (C)-Xylanase (X) (C-X), Amylase (A), Cellulase-Xylanase-Amylase (C-X-A), Cellulase-Glucose oxidase-Lactobacillus (C-GO-Lac), C-GO-Lac-Amylase (C-GO-Lac-A), Ferulic acid esterase (FAE), Cellulase-FAE (C-FAE), Xylanase-Endoglucanase-Exoglucanase (X-En-Ex), Endoglucanase-Xylanase (En-X), Exogenous proteolytic enzyme (EPE). Data were analyzed with an analysis of covariance model that included effects of study, the EFE type x application rate effect, and the application method (EFE application to the TMR, concentrate or forage). Data were weighted using the inverse of the variance of each study. Among EFE, A increased DMI ($P = 0.029$); C-X increased ($P < 0.05$) DMI, milk yield, lactose yield and NDFD; C-X-A increased ($P < 0.05$) DMI, milk protein yield, DMD, and NDFD; and En-X and EPE increased ($P < 0.05$) only milk protein concentration and milk lactose yield, respectively. Tendencies ($P < 0.1$) were detected for FAE to increase DMI, for En-X to increase feed efficiency (FCM/DMI) and for EPE to increase DMD. Therefore, C-X and En-X were the only EFE that increased milk yield and feed efficiency, respectively. A unit increase in the rates of application of C-X and En-X increased milk yield ($P = 0.017$) and feed efficiency ($P = 0.057$) by 0.19 and 0.18 units, respectively. Applying EFE to the forage increased DMD ($P = 0.003$), whereas application to the concentrate or TMR increased milk lactose yield ($P < 0.001$). Effects of EFE on the performance of lactating dairy cows were equivocal and they depended on the EFE type x rate interaction and the method of application.

Key Words: fibrolytic enzymes, cellulase, xylanase

1586 (M300) Effects of forage particle size and corn oil supplementation related to milk fat depression in dairy cows consuming reduced-fat corn dried distillers grains with solubles. H. A. Ramirez Ramirez* and P. J. Kononoff, *University of Nebraska, Lincoln.*

Four ruminally cannulated Holstein cows averaging (± SD) 116 ± 18 DIM and 686 ± 52 kg of BW were used in a 4 × 4 Latin square with a 2 × 2 factorial arrangement of treatments to test the effects of forage particle size and dietary concentration of

corn oil on milk fat depression (MFD). Cows were housed in individual stalls, milked twice daily and fed once daily to allow ad libitum access to feed. In each 28-d period each cow was offered one of four TMR that differed in forage particle size by inclusion of grass hay (LONG) or grass hay pellets (SHORT) and 0 or 2% corn oil (OIL). Chewing activity was monitored visually every 5 min for 24 h on d 25. Total rumen evacuation was performed on d 27 and 28 of each period to determine rumen kinetics. Dietary treatments were: 0% oil + short particle size (OIL0+SHORT); 0% oil + long particle size (OIL0+LONG); 2% oil + short particle size (OIL2+SHORT); and 2% oil + long particle size (OIL2+LONG). Dry matter intake and milk yield were not affected by treatment averaging 26.5 ± 0.90 kg/d and 32.8 ± 3.25 kg/d, respectively. There was a decrease ($P < 0.01$) in 3.5% FCM due to oil inclusion resulting in 34.6 and 26.6 ± 2.6 kg/d for 0 and 2% oil diets. An oil × size interaction ($P = 0.03$) resulted in 2.26, 3.02, 3.62 and 3.62 ± 0.23% milk fat for OIL2+SHORT, OIL2+LONG, OIL0+SHORT and OIL0+LONG. Fat yield was reduced ($P < 0.01$) from 1.22 to 0.81 ± 0.09 kg/d with 2% oil diets. An oil × size interaction ($P < 0.01$) affected yield of *trans*-10, *cis*-12 conjugated linoleic acid (CLA) resulting in 0.35 g/d for OIL2+SHORT and 0.11 g/d for OIL2+LONG. Long particles increased ($P = 0.02$) eating time from 169 to 198 ± 15 min/d, rumination time ($P < 0.01$) from 400 to 504 ± 35 min/d and reduced ($P = 0.02$) rate of passage of DM from 3.38 to 2.89 ± 0.42%/h. These results demonstrate that dietary manipulations that modify rumen kinetics also impact milk fat production in dairy cows consuming TMR supplemented with corn oil, the effects of corn oil on MFD were less severe when cows consumed long particle size.

Key Words: rumen kinetics, biohydrogenation, chewing activity

---

1587 (M301) Impact of forage inclusion rate in a dry total mixed ration on the behavior and growth of growing dairy cattle. M. J. Groen[1,2], M. A. Steele[3], and T. J. DeVries[*1], *[1]University of Guelph, Kemptville, ON, Canada, [2]Wageningen University, Netherlands, [3]Nutreco Canada, Guelph, ON.*

The objective of this study was to determine the impact of forage inclusion rate in a dry TMR on behavior and growth of young dairy cattle. Ten Holstein bull calves (90.5 ± 2.4 d of age, weighing 136.0 ± 12.3 kg) were assigned to one of two treatments, a TMR containing (DM basis) either: 1) 85% concentrate and 15% chopped straw for 10 wk (wk 1 to 10); or 2) 85% concentrate and 15% chopped straw for 5 wk (wk 1 to 5), then 70% concentrate and 30% chopped straw for 5 wk (wk 6 to 10). After 10 wk, all animals were transitioned to a TMR containing (DM basis) 42.3% corn silage and 57.7% haylage for 2 wk (wk 11 to 12). DMI was recorded daily and BW was recorded 2x/wk. Feeding behavior was scored from digital video recordings 3 d/wk. Samples of TMR and orts were taken for particle separation 3 d/wk. Sorting was calculated as: actual intake of each particle fraction expressed as a % of its predicted intake. Data were averaged by week and analyzed in a repeated measures mixed effect model. DMI (5.5 ± 3.3 kg/d), ADG (1.7 ± 0.1 kg/d), feed efficiency (3.5 ± 1.4 kg DM/kg gain), and eating time (151.9 ± 8.8 min/d) were similar between treatments during wk 1 to 5. Calves on the 70% diet ate less DM (5.5 vs. 7.4 kg/d; SE = 0.4; $P = 0.006$), grew slower (1.3 vs. 1.6 kg/d; SE = 0.08; $P = 0.02$), sorted more against long forage particles (62.8 vs. 103.8%; SE = 6.3; $P = 0.01$), and spent a greater duration of time feeding (194.9 vs. 102.6 min/d; SE = 12.5; $P = 0.001$) during wk 6 to 10. A treatment × hour interaction ($P < 0.001$) in the analysis of feeding patterns indicated that this difference in feeding time occurred only during the first 8 h after feed delivery. Despite no differences in DMI (5.2 kg/d) or ADG (1.1 kg/d) in wk 11–12, there was a carryover effect on behavior. In wk 11 to 12, a treatment × hour interaction was detected ($P = 0.03$); calves previously fed the 70% diet continued to spend more time feeding immediately after feed delivery. Interestingly, during wk 11 to 12 those calves did not sort for or against long particles (103.6%), while the calves previously-fed the 85% ration sorted for (107.0%) those particles. These results show that feeding a dry TMR to weaned calves can promote high growth rates and efficiency. Further, altering forage content of such a TMR may have an impact on the expression and persistence of feeding behavior patterns.

Key Words: feeding behavior, forage concentration, straw

1588 (M302) Assessment of feeding high moisture corn grain with different qualities of alfalfa hay in high-forage lactation dairy diets. A. W. Kelley, K. Neal, A. J. Young, and J. S. Eun*, *Utah State University, Logan.*

This experiment was performed to test a hypothesis that quality of alfalfa hay (AH) would affect nutritive benefits of feeding high moisture corn (HMC) due to their associative effects on nutrient utilization efficiency. Eight multiparous lactating Holstein cows were used; four were surgically fitted with ruminal cannula. Days-in-milk averaged 184 ± 10.7 at the start of the experiment. The experiment was performed in a duplicate 4 × 4 Latin square design. Within each square, cows were randomly assigned to a sequence of 4 diets during each of the four 21-d periods (14 d of treatment adaptation and 7 d of data collection and sampling). A 2 × 2 factorial arrangement was used; fair quality AH (FAH; 39.6% NDF and 17.9% CP) or high quality AH (HAH; 33.6% NDF and 21.9% CP) was combined with steam-flaked corn (SFC) or HMC to form four treatments: FAH with SFC, FAH with HMC, HAH with SFC, and HAH with HMC. The AH was fed at 32% DM, whereas HMC was included at 17% DM. Quality of AH did not affect DMI, whereas feeding HMC decreased DMI ($P =$

0.04) regardless of quality of AH. While digestibility of DM increased by cows fed with HAH compared to those fed with FAH (70.1 vs. 67.6%; $P = 0.05$), NDF digestibility increased by feeding HMC (67.6 vs. 58.4%; $P = 0.03$) but not quality of AH. Starch digestibility decreased by feeding HMC with FAH (85.7 vs. 95.0%) but not with HAH, resulting an interaction between quality of AH and type of corn grain (CG; $P = 0.02$). Feeding different qualities of AH did not affect milk yield; however, feeding HMC numerically decreased milk yield in FAH diet, but increased milk yield in HAH (30.4 vs. 29.6 kg/d), causing an AH × CG interaction ($P = 0.05$). Efficiency of milk yield/DMI was improved due to feeding HMC regardless of quality of AH ($P = 0.05$). In addition, dietary N utilization for milk N tended to increase by feeding HMC ($P = 0.07$), but it was not influenced by quality of AH. Overall results in this experiment indicate that feeding HMC in high-forage diets improved feed efficiency as well as N utilization efficiency regardless of quality of AH.

Key Words: alfalfa hay, feed efficiency, high moisture corn

1589 (M303) Replacing corn with soyhulls for late-lactation cows fed high-forage diets. V. R. Moreira*[1], L. K. Zeringue[2], C. Leonardi[3], D. Schilling[2], and M. E. McCormick[2], *[1]Louisiana State University AgCenter School of Animal Sciences, Franklinton, [2]Louisiana State University AgCenter, Franklinton, [3]Louisiana State University, HSC– School of Public Health– Biostatistics, New Orleans.*

The objective was to evaluate performance of 48 late-lactation multiparous Holstein cows (27.6 ± 5.90 kg milk/d, 280 ± 79 DIM) fed rations gradually substituting ground corn (C) with soyhull pellets (SH). Treatments contained 17.4% of dietary DM as C, no SH (C100:SH0); 11.6% C, 5.8% SH (C67:SH33); 5.8% C, 11.6% SH (C33:SH67), and no C, 17.4% SH (C0:SH100). Other dietary ingredients remained similar in all treatments: bermudagrass hay (6.3%, diet DM), corn silage (56%), soybean meal (15.3%), urea (0.5%), calcium carbonate (0.5%), mineral (2.5%), salt (0.5%), and yeast (1%). Fixed ingredients except forages were premixed weekly. Treatments were mixed and offered once daily as TMR. Refusals were weighed and removed before next day feeding. Cows were randomly assigned to treatments for 7 wk following a 2-wk standardization period. Intake and milk yield were recorded daily. Milk samples were collected from one 48-h collection period (2 milkings/d) during pretrial and three collection periods during trial. Milk samples were analyzed for fat, protein, SNF, MUN and SCC. Body weights and body condition scores were recorded at the beginning and end of the experimental period. Two cows were removed before the end of the study because of mastitis (treatments C100:SH0 and C0:SH100). Means were analyzed using PROC MIXEDs (SAS, version 9.3) for main effects of treatment and contrasts were set to test for linear, quadratic and cubic effects of levels of soyhulls substitution for corn. Treatment diets contained 56.5% ± 0.2% DM, 17.0% ± 0.2% CP, 0.91% ± 0.04% Ca, and 0.39% ± 0.02% P as analyzed (average ± standard deviation), and 1.48 Mcal/kg DM as estimated with NRC (2001). Dry matter intake was not affected by treatments (means = 20.8 kg/cow/d; SEM = 0.81), ranging from 19.6 kg for cows fed C67:SH33 to 22.3 kg for those fed C100:SH0. Milk yield averaged 23 kg/cow/d (SEM = 1.55 kg/cow/d) and was not significantly different. Milk fat (3.9%), milk protein (3.3%) and MUNs (18 mg/L) did not differ statistically. There was no evidence supporting better NPN utilization for either feedstuff. Regardless of treatment, cows gained 0.5 kg body weight/d during the study, but body condition score changes in nearly 49 d of study were negligible, averaging 0.04 unit. This study suggests that soyhull pellets can replace corn in late-lactation cows' diets without significantly affect animal performance.

Key Words: ground corn, soyhull pellets, dairy cows

1590 (M304) Effects of different dietary forage sources on milk performance and amino acid profile in early lactating dairy cows. X. Q. Zhou[1,2], D. P. Bu[1], Y. D. Zhang[1], M. Zhao[1], P. Sun[1], and J. Q. Wang*[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Northeast Agricultural University, Harbin, China.*

The objective of this study was to evaluate the effects of different dietary forage sources on performance and milk amino acid profile in early lactation dairy cows. Thirty-two Chinese lactating Holstein cows with similar DIM (55 ± 15 d) and milk yield (31.4 ± 3.49kg/d) were randomly assigned to two groups and fed total mixed ration (TMR) using automatic feeding system. Diets contained similar concentrate mixtures with the same forage-to-concentrate ratio of 36:64 [dry matter (DM) basis]. Different forage sources were then added: 17.30% alfalfa hay and 18.77% corn silage (MF); 36.07% corn straw (CS).Experiment lasted for 90 d, including first 14 d dietary adaption. Animal health condition, milk yield, amount of feed offered and refused for individual cows were recorded every day in experimental period. Milk samples of each cow on 91 d were collected to analysis milk composition and amino acid profile in milk protein. MF group had increased daily DMI(21.35 vs. 17.43 kg/d, $P < 0.01$), milk yield (30.45 vs. 23.12 kg/d, $P < 0.01$), milk protein content (3.66 vs. 3.32%, $P < 0.01$), milk protein yield(1.11 vs. 0.75 kg/d, $P < 0.01$), milk fat yield (1.36 vs. 1.01 kg/d, $P < 0.01$) and milk lactose yield (1.47 vs. 1.13 kg/d, $P < 0.01$) compared with CS group. The content of Thr (3.79 vs. 3.71 g/100 g AA, $P < 0.01$), Ser (4.48 vs. 3.36, $P = 0.03$), Met (3.50 vs. 3.38, $P = 0.02$), Lys (7.71 vs. 7.55, $P < 0.01$) and Arg (3.35 vs. 3.31, $P = 0.02$) in milk protein were elevated significantly in MF group while the two kinds of BCAA (Leu 11.72 vs. 11.88, $P = 0.02$ and

Val 5.98 vs. 6.09, $P < 0.01$) showed an opposite trend. Otherwise, the concentrations of amino acids in milk were greater ($P < 0.01$) in response to MF group compared with CS group. But no difference was observed in content of milk fat and milk lactose between two treatments ($P > 0.05$).

Key Words: forage, milk performance, amino acid

1591 (M305) The partial replacement of corn silage by sugarcane silage plus crude glycerin and the effect of sensory feed additives for dairy cows.

O. F. Zacaroni*[1], F. F. Cardoso[1], A. C. S. Melo[1], R. F. Lima[1], R. A. N. Pereira[2,3], and M. N. Pereira[1,2], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]Better Nature Research Center, Ijaci, Brazil, [3]Empresa de Pesquisa Agropecuaria de Minas Gerais, Lavras, Brazil.*

Crude glycerin may compensate for the energy loss during the ensiling of sugarcane. The partial replacement of corn silage (CS) with an iso-NDF amount of sugarcane silage plus crude glycerin (SG), added or not of sensory feed additives (SA), was evaluated. Thirty-two Holsteins (182 DIM) were individually fed a standardization diet for 2 wk and a treatment for 44 d. The main statistical model contained covariate, block, forage, additive, interaction, time, and its two and three term interactions. Treatments were (% of DM): CS (30.2%) or CS (15%), sugarcane silage (10%), and crude glycerin (3.3%); with or without SA (Luctarom SFS-R 3386-Z and 1353-Z. Lucta, Spain) added to corn and then to forages in the mixer. Diets also contained 9.2% sorghum silage, 4.4% Tifton hay, and 24.5 ± 0.5 forage NDF. SA reduced milk yield in CS (32.2 vs. 31.1 kg/d) and increased in SG (30.3 vs. 31.7 kg/d) ($P < 0.01$ interaction); yields of lactose and solids followed the same trend ($P < 0.05$). SG increased DMI (22.6 *vs.* 21.9 kg/d, $P < 0.01$), while there was a trend for decreased DMI in response to SA (22.5 vs. 22.0 kg/d, $P = 0.07$). The ratio of milk to DMI had a greater positive response to SA in SG (1.34 vs. 1.43) than in CS (1.44 vs. 1.46) ($P = 0.03$ interaction). SG increased the contents of fat ($P = 0.01$) and protein ($P = 0.08$), improving milk solids ($P = 0.03$). There was no effect on feed sorting from 0700 to 1300 h ($P > 0.38$). From 1400 to 1900 h, SG induced selection in favor of particles > 19mm ($P = 0.05$), and, when added to CS, SA induced the rejection of 8- to 19-mm particles and consumption of < 8-mm particles, but had no effect when added to SG ($P < 0.01$ interaction). The intake rate from 0700 to 1300 h was faster in SG ($P < 0.01$), and it tended to be slower when SA was added to CS ($P = 0.05$ interaction). Plasma glucose content was reduced by SA in CS and increased in SG ($P = 0.01$ interaction). PUN did not respond to treatments ($P > 0.39$). There was a trend for reduced plasma γ-glutamyl transferase on SG ($P = 0.09$). Chewing activity was similar across treatments ($P > 0.49$), as well as the daily excretion of urinary allantoin ($P > 0.11$), ruminal fluid pH ($P > 0.24$), and protozoa count ($P > 0.48$). Total tract apparent digestibility was not determined by treatments ($P > 0.39$) neither the intake of digestible OM ($P > 0.72$). The partial replacement of CS by SG plus SA was a plausible alternative for feeding dairy cows.

Key Words: glycerin, sugarcane silage, sorting

1592 (M306) Relative excretion of nitrogen from alfalfa silage, corn silage, corn grain and soybean meal in urine and feces by lactating dairy cows.

M. J. Powell[1], T. Barros[2], M. A. C. Danes[2], M. J. Aguerre*[2], and M. A. Wattiaux[2], *[1]USDA–Agricultural Research Service, U.S. Dairy Forage Research Center, Madison, WI, [2]University of Wisconsin–Madison, Madison.*

The main objective of this trial is to determine the partitioning of nitrogen (N) from different feed ingredients in milk, feces and urine. This abstract focuses on relative excretion of N in feces and urine. Twelve multiparous late lactation Holstein cows (means ± SD; 264 ± 18 DIM) were fed a pretreatment TMR once a day for 11 d containing (DM basis) 35.5, 28.6, 20.3, 12.9 and 2.6% of corn silage (CS), alfalfa silage (AS), corn grain (CG), soybean meal (SBM) and a mineral and vitamin premix, respectively. On d 12, cows were grouped by milk yield and randomly assigned to one of four dietary treatments corresponding to each feed ingredient at natural abundance of ^{15}N being replaced by its homologue ingredient enriched with ^{15}N (except for CS treatment for which only 75% of the unlabeled CS was replaced by ^{15}N enriched CS). After 4 d feeding the ^{15}N-enriched TMR's, cows were fed the pretreatment non-enriched TMR during d 16 to 19. Total fecal and urinary collection was conducted on each cow every 6 h during d 12 to 19. Feed intake and lactation performance were also measured from d 12 to 19. Data were analyzed as a complete randomized design with treatment as a fixed effect and cow as a random effect. Corn silage and CG had the highest ^{15}N enrichment (atom % ^{15}N of 1.857 and 2.040, respectively) whereas AS and SBM had the lowest (atom % ^{15}N of 0.730 and 1.385, respectively) due to ^{15}N dilution by the atmospherically-fixed N by these legumes. Feeding ^{15}N-enriched ingredients had no effects on DMI (23.2 ± 2.4 kg/d, $P = 0.39$), milk yield (26.1 ± 5.2 kg/d, $P = 0.85$), N intake (601 ± 61 g/d, $P = 0.41$), protein yield (0.89 ± 18 kg/d, $P = 0.80$) and N use efficiency (milk N/N intake; 0.23 ± 0.05, $P = 0.86$). Cumulative ^{15}N recovery (% of total ^{15}N fed) in feces between d 12 and 19 was similar ($P = 0.61$) between AS and CS treatments (29.8 vs. 28.2%), which were greater ($P < 0.05$) than CG (21.5%) and SBM treatments (12.5%). Although not significantly different ($P = 0.12$), greater cumulative ^{15}N recovery (%) in urine was measured in AS (27%), it was intermediate in CS and CG (21.6 and 19.4%, respectively) treatments, and smallest in the SBM (17.0%) treatment. Results from this study suggested that AS and CS contributed most to fecal N excretion and AS contributed most to urinary N excretion.

Key Words: N partitioning, N use efficiency, ^{15}N

1593 (M307) A sensory additive improves performance of dairy cows under heat stress. F. Bargo*[1], S. Muñoz[2], M. Candelas[2], J. Vargas[1], and I. Ipharraguerre[1], [1]*Lucta S.A., Barcelona, Spain,* [2]*Nuplem, Durango, México.*

Five hundred seventy Holstein dairy cows (280 primiparous and 290 multiparous; 194 DIM and 34.4 kg/d milk) from the commercial dairy farm El Trébol (Durango, México) were used to evaluate the effect of a sensory additive (ProEfficient, Lucta S.A.) on dry matter intake, milk production, and feed conversion efficiency under heat stress conditions in a completely randomized design. Cows were grouped by parity (primiparous vs. multiparous) in four free-stall pens and randomly assigned to two treatments: control TMR or the same TMR supplemented with 30 g/d of ProEfficient (PE). The TMR (52:48 concentrate: forage; 18.2% CP, 29.1% NDF, 42.1% NFC) was offered twice daily and PE was top-dressed at each feeding during 34 d starting on June 25ᵗafter 2 wk of adaptation. Daily dry matter intake of each pen and individual milk yield (Alpro, De Laval) were measured. Data were analyzed by ANOVA with a mixed model with repeated measures using the PROC PROC MIXED of SAS (1999) where pen nested within treatment was considered as random effect. During the experimental period, maximum and minimum temperatures averaged 38.9 and 20.4°C, respectively. Dry matter intake increased 1.2 kg/d (23.6 vs. 24.8 kg/d; $P < 0.05$) with the inclusion of the PE additive. Cows fed the TMR with PE produced 2 kg/d more of milk (35.2 vs. 33.2 kg/d; $P < 0.05$) with similar feed conversion efficiency (1.42 kg milk/kg DMI; $P > 0.05$). Based on previous findings from studies with PE, the milk response to this additive could have been related to changes in ingestive behavior (meal size and frequency) and/or positive modulation of hormonal signals associated with the control of feed intake (e.g., ghrelin). Feeding a sensory additive under heat stress conditions increased dry matter intake and milk production of dairy cows fed a TMR.

Key Words: sensory additive, heat stress, intake and milk production

1594 (M308) Performance and health of calves pre- and post weaning fed milk replacers with supplements for heat abatement in the summer months. H. Chester-Jones*, *University of Minnesota Southern Research, and Outreach Center, Waseca.*

Two studies were conducted in the summer of 2012 and 2013 to evaluate pre- (d 1 to 42) and post-weaning (d 43 to 56) calf performance and health when fed milk replacers (MR) with supplements to aid in heat abatement. Calves were fed a non-medicated 20% fat:20% CP MR at 0.284 kg in 1.99 L water (12.5% solids) 2x/d for the first 35 d and 1x/d from d 36 to weaning at 42 d. From d 1 to 14, 1:1 neomycin:oxytetracycline was added to the MR solution to provide 22 mg/kg BW daily. Calf starter (CS; 18% CP) and water were fed free choice d 1 to 56. In study 1, 51 (2- to 4-d-old) individually fed Holstein heifer calves (38.5 ± 0.96 kg) were assigned to MR supplements as follows: SA1 = none; SA2 = B-complex vitamin premix fed at 1.42 g/calf daily and SA3 = betaine fed at 5 g/calf daily. There were no treatment differences in pre- and post-weaning ADG or total hip height (HH) gain which averaged 0.64 kg and 9.63 cm, respectively. There was a trend ($P < 0.10$) for increased 56-d CS intake when calves were fed the SA2 or SA3 compared to SA1 MR (0.81 vs. 0.72 kg DM/d). There were no differences in BW gain, total DMI, gain/feed or scouring days across treatments. Calves fed SA2 had higher ($P < 0.05$) daily health treatment costs vs. SA1 calves but were not different from SA3 calves ($P = 0.07$). In study 2, 75 (2- to 4-d-old) individually fed Holstein heifer calves (39.4 ± 0.65 kg) were assigned to MR supplements SB1, none; SB2, B-complex vitamin premix fed as in study 1 and SB3, B-complex vitamins as in SB2 plus an electrolyte mix fed at 28 g/calf daily. There were no treatment differences in ADG and HH gain (0.68 kg and 10.85 cm, respectively over the 56-d study). Pre-weaning gain/feed was higher ($P < 0.05$) for SB3 compared to SB1 or SB2 calves. There were no differences in health parameters. A heat index of 90 or more occurred on 34 d in 2012 and 26 d in 2013 studies, respectively. Under the conditions of these studies, heat abatement supplements added to MR did not consistently enhance calf performance.

Key Words: milk replacers, heat abatement supplements, performance

1595 (M309) Performance and health of calves pre- and post weaning fed milk replacers with supplements for heat abatement in the summer months. D. Schimek*[1], B. Ziegler[1], D. Ziegler[2], H. Chester-Jones[2], and M. Raeth-Knight[3], [1]*Hubbard Feeds Inc., Mankato, MN,* [2]*University of Minnesota Southern Research and Outreach Center, Waseca,* [3]*University of Minnesota, St. Paul.*

Two studies were conducted in the summer of 2012 and 2013 to evaluate pre- (d 1 to 42) and post-weaning (d 43 to 56) calf performance and health when fed milk replacers (MR) with supplements to aid in heat abatement. Calves were fed a non- medicated 20% fat:20% CP MR at 0.284 kg in 1.99 L water (12.5% solids) 2x/d for the first 35 d and 1x/d from d 36 to weaning at 42 d. From d 1 to 14, 1:1 neomycin:oxytetracycline was added to the MR solution to provide 22 mg/kg BW daily. Calf starter (CS; 18% CP) and water were fed free choice d 1 to 56. In study 1, 51 (2- to 4-d-old) individually fed Holstein heifer calves (38.5 ± 0.96 kg) were assigned to MR supplements as follows: SA1 = none; SA2 = B-complex vitamin premix fed at 1.42 g/calf daily and SA3 = betaine fed at 5 g/calf daily. There were no treatment differences in pre- and post-weaning ADG or total hip height (HH) gain which averaged 0.64 kg and 9.63 cm, respectively. There was a trend (*P*

< 0.10) for increased 56-d CS intake when calves were fed the SA2 or SA3 compared to SA1 MR (0.81 vs. 0.72 kg DM/d). There were no differences in BW gain, total DMI, gain/feed or scouring days across treatments. Calves fed SA2 had higher ($P < 0.05$) daily health treatment costs vs. SA1 calves but were not different from SA3 calves ($P = 0.07$). In study 2, 75 (2- to 4-d-old) individually fed Holstein heifer calves (39.4 ± 0.65 kg) were assigned to MR supplements SB1, none; SB2, B-complex vitamin premix fed as in study 1 and SB3, B-complex vitamins as in SB2 plus an electrolyte mix fed at 28 g/calf daily. There were no treatment differences in ADG and HH gain (0.68 kg and 10.85 cm, respectively over the 56-d study). Pre-weaning gain/feed was higher ($P < 0.05$) for SB3 compared to SB1 or SB2 calves. There were no differences in health parameters. A heat index of 90 or more occurred on 34 d in 2012 and 26 d in 2013 studies, respectively. Under the conditions of these studies, heat abatement supplements added to MR did not consistently enhance calf performance.

Key Words: milk replacers, supplements, performance

1596 (M310) Effect of supplementing heat stressed dairy cows with electrolytes on milk yield, composition, and blood metabolites. C. J. Cabrera*, S. H. Ward, and A. J. Geiger, *Mississippi State University, Starkville.*

The objective of this study was to determine the effect of supplementing electrolytes from -21 to 30 DIM to heat stressed cows on DMI, MY, and blood metabolites. A total of 104 Holstein and Jersey, cows and heifers, were utilized between August–September 2012 and August–November 2013. Before calving, all cows and heifers were fed ryegrass baleage in the morning and TMR in the evening (CON) or the same base ration plus 270 g of electrolyte (E+, Bovine Bluelite, TechMix, Inc; MN) providing balanced electrolytes (0.55% Ca; 0.30% P; 9.60% NaCl; 8.25% K; 0.14% Mg). Post-calving, CON cows were fed standard TMR and E+ cows received the same TMR plus 270 g of Bovine Bluelite. DMI, MY, rectal temperature, and respiration rate were monitored daily; while blood metabolites, body weight, condition score and frame (withers height, hip height, and heart girth) were measured weekly. Orts and feedstuffs were sampled weekly and subjected to proximate analysis. Milk samples were taken weekly and analyzed for fat, protein, solids, lactose content, and SCS. Blood samples were taken via jugular venipuncture, further analyzed for pH, HCO3, tCO2, pCO2, Anion Gap, Na^+, K+, and Cl^-, using an onsite IDEXX Blood Gas Analyzer, and for hematocrit utilizing a micro centrifuge. DMI was not different among treatments, however, during 2013 dry cows consumed more than in 2012 (8.33 vs. 7.09 kg/d; $P < 0.0001$). Cows fed E+ had lower MY than CON cows (29.64 vs. 34.99 kg/d; $P = 0.0042$). Holstein cows averaged greater MY than Jerseys (36.45 vs. 28.18 kg/d; $P < 0.0001$) but despite this expected breed effect, MY for CON and E+ cows only differed between Holsteins (40.90 vs. 32.00 kg/d, respectively; $P < 0.0001$), not between Jerseys (29.08 vs. 27.29 kg/d, respectively; $P = 0.6084$). Milk composition was not affected, however, E+ cows had increased fat content ($P < 0.001$) weekly for the first 4 wk, whereas CON cows decreased ($P < 0.001$) until wk 2. Respiration rate (57.12 vs. 55.30 bpm; $P = 0.1197$) and rectal temperature (38.7 vs. 38.7°C, respectively; $P = 0.9853$) were not influenced by treatment, but Holstein cows had greater respiration rates than Jerseys (58.63 vs. 53.78 bpm, respectively; $P < 0.0001$). No differences were observed in blood metabolites, nor in body weight change and condition score, except for withers height which was greater for CON cows (133.40 vs. 130.75 cm, respectively; $P = 0.0170$). Electrolyte supplementation did not increase MY, nor affect any of the other measured variables in the present study.

Key Words: dairy, electrolyte, transition

1597 (M311) Average daily gain among calves fed a high plane of milk replacer during the pre-weaning period is not associated with improved reproductive efficiency or lactational performance in Holstein heifers. M. D. Sellers*, C. R. Nightingale, and M. A. Ballou, *Texas Tech University, Dep. of Animal and Food Sciences, Lubbock.*

The objective was to determine if increased ADG while on a high plane of nutrition during the pre-weaning period is associated with improved reproductive efficiency as a heifer and improved reproductive efficiency or lactational performance as a primiparous cow. Seventy-two Holstein calves from a single herd in western Texas (2 ± 1 d old) were fed a high plane of nutrition (28/20 milk replacer fed at 756 g/d DM and 1010 g/d DM for the first wk and wk 2 through 6, respectively, with ad libitum access to calf starter grain during the pre-weaning period. Weaning was initiated at wk 7 with the removal of PM milk replacer feeding and was completed when starter intake was 800 g/d DM after d 53. Daily milk replacer and starter intakes were recorded, and ADG was calculated for the pre-weaning period (wks 1 to 7). All calves were returned to the dairy of origination 3 mo after weaning and were managed according to their standard procedures. Reproductive efficiency as a heifer, as well as first lactation reproductive efficiency and milk production were collected from DairyComp305 records. All descriptive data will be reported as [0, 25, 50, 75, and 100 percentile]. The pre-weaning ADG was [0.144, 0.491, 0.560, 0.636, and 0.827 kg/d]. There was no relationship between pre-weaning ADG and age at first calving [647, 672, 685, 721, and 776 d; $P = 0.14$]. Reproductive performance as a primiparous cow was not affected by pre-weaning ADG, as no relationship was observed for average days open [61, 83, 104, 173, 298 d; $P = 0.14$. In addition, there was no relationship between pre-weaning ADG and first lactation production metrics of peak milk [28.2, 35.9, 39.1, 41.8, and 50 kg; $P = 0.15$] and estimated 305 d mature

equivalent [8191, 10827, 11914, 13407, 16073 kg; $P = 0.32$]. Additional research is needed to evaluate the relationship between post-weaning heifer nutrition and health statuses and subsequent reproductive and lactational performance.

Key Words: calf, lactation performance, plane of nutrition

1598 (M312) Ruminal in situ DM and starch digestion descriptive statistics of corn silage and high moisture corn. C. R. Heuer*[1,2], J. P. Goeser[1,2], and R. D. Shaver[3], *[1]Dep. of Dairy Science, University of Wisconsin–Madison, Madison, [2]Rock River Laboratory, Inc, Watertown, WI, [3]University of Wisconsin, Madison.*

Starch comprises 20 to 35% of dry matter (DM) in diets for lactating dairy cows. Ruminal starch digestibility is highly variable across and within feed types. Our objective was to determine ruminal in situ starch digestibility (StarchD) for corn silage (CS; $n = 52$) and high moisture corn (HMSC; $n = 41$) samples. Samples were dried at 50°C in a forced air oven for 48 h and ground to pass through a 1-mm Udy Mill screen for DM and starch analysis, or a 6-mm Wiley Mill screen for ruminal in situ analysis. Rumen in situ samples were weighed with 3 g per bag in an Ankom 5x10-cm bag (50µm pore size) in triplicate. Bags were soaked in warm water before incubation. One bag was placed in three different ruminally-cannulated lactating dairy cows consuming a 58% forage diet with a 50:50 ratio of corn silage to legume (DM basis). Samples were incubated for 3 and 7 h; all bags were removed simultaneously. Following incubation the bags were rinsed until effluent was clear. Bags were dried at 50°C for 24 h and weighed to determine the DM digestibility (DMD). Residue samples were composited and ground to pass a 1-mm Udy Mill screen. Starch content was then determined according to a modified M.B. Hall 2008 procedure using an YSI2700 (YSI Life Sciences On-Line Biochemistry Analyzer), to determine glucose after samples were enzymatically digested, instead of theglucose oxidase–peroxidase procedure. StarchD was calculated as the difference in grams of starch remaining in the residue, relative to the grams of starch in the sample. DMD and StarchD descriptive statistics were analyzed using SAS JMPv10 and are presented in Table 1598. Ruminal in situ StarchD was highly variable for HMSC and CS.

Key Words: rumen, starch, digestion

Table 1598. Rumen in situ 3 and 7-h descriptive statistics of DMD and StarchD

Type	Hour	Mean	St.dev.	Min.	Max.	C.V
Dry Matter Digestion (%)						
HMSC	3	40.3	16.6	19.0	82.5	41.2
HMSC	7	50.6	12.8	28.8	86.6	25.3
CS	3	41.6	10.2	15.5	57.5	24.5
CS	7	48.4	8.4	22.3	66.9	17.4
Starch Digestion (%)						
HMSC	3	47.1	15.0	26.0	91.2	31.8
HMSC	7	58.2	12.9	36.6	91.3	22.2
CS	3	64.7	18.6	0.9	88.2	28.7
CS	7	77.0	14.5	16.8	93.8	18.8

1599 (M313) Response of rumen fermentation to urease inhibitor using dual-flow rumen simulation system. P. P. Wang[1], D. Jin[1], J. Q. Wang*[2], D. P. Bu[2], and S. Zhao[1], *[1]State Key Laboratory of Animal Science, Institute of Animal Science, Chinese Academy of Agricultural Science, Beijing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijng, China.*

The objective of this study was to investigate urea degradation using a novel dual-flow rumen simulation system. Eight fermentation vessels (1 L) were allotted to a 2 × 2 factorial arrangement of treatments with urea supplemented at 0 or 0.5% dry matter intake (DMI), and urease inhibitor equivalent to 0 or 450 mg/kg DMI. A total of 40 g of DM with urea were fed in two equal portions daily, while the urease inhibitor, contained approximately 98% (w/w) acetohydroxamic acid (AHA), was added in the artificial saliva infused into the vessels twice daily. The experimental period consisted of 6 d for adaptation and 3 d for sampling. On each sampling Day 15 mL fermentation fluids were obtained from each fermentation vessel by syringes at 0, 2, 4, 6, 8, and 10 h, respectively. Temperature (39°C), liquid, and solid dilution rates (8%/h and 200 mL/d, respectively) were maintained through the whole process. Both protozoa numbers and dry matter disappearance (DMD) ($P = 0.62$ for urea; $P = 0.47$ for AHA) from each fermentation vessel were not affected by urea or AHA supplementation. Urea supplementation significantly ($P < 0.01$) increased pH and ammonia-nitrogen (NH_3–N) concentration, and AHA addition increased ($P = 0.03$) urea-N concentration. There was no interaction between urea and AHA. The pH reached the peak value at 2 h with urea supplementation only, and the pH began to reduce at 4 h with both urea and AHA addition. NH_3–N concentration arrived at maximum at 2 h with urea and/or AHA supplementations, but it sharply ($P < 0.05$) decreased at 4 h with urea supplementation and at 6 h with both urea and AHA addition. Urea-N concentration of treatment with urea and AHA supplementation was sustainably higher than other

treatments until 6 h. It was concluded that AHA inhibited urea degradation but had no effect on ammonia formation.

Key Words: dual-flow rumen simulation system, fermentation, urease inhibitor

---

1600 (M314) Effects of four ruminant feed additives on in vitro ruminal fermentation kinetic gas production and degradability. J. Li[1,2], J. Q. Wang[1], P. Sun[1], F. D. Li[2], and D. P. Bu[*1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China.*

This experiment was designed to investigate the effects of four ruminant feed additives, *Bacillus subtilis*, *procreatin* (major ingredient was high-enriched live yeast), *Aspergillus oryzae* culture and fibrase (major ingredient was *Aspergillus oryzae, Aspergillus niger* and lactic acid yeast) on gas production (GP) kinetics of different doses of 0(control), 1.0, 2.0, 4.0mg/kg diet (DM), respectively. Ruminal fluid was collected approximately 2 h before feeding from three lactating Holstein dairy cows (BW = 558 ± 10 kg, DIM = 153 ± 16d) fed total mixed ration (C:F = 40:60) and mixed with McDougall's phosphate buffer (v/v = 1:2). 500mg diet substrates, which were consistent with the donor cows, were incubated with diluted buffered rumen fluids (75ml) for 72 h at 39°C. The batch completed in 2 experimental runs, and 4 fermentations per treatment were arranged in each run. All bottles were connected to gas channel inlets of Automated Trace Gas Recording System for Microbial Fermentation (AGRS, Beijing, China). Data on the cumulative gas production were fitted to a model: GP_t (ml/g DM) = $A/(1+(C/t)^B)$. Where GP_t was the cumulative gas production (ml/g DM) at t incubation time (h), A was the asymptotic gas production (ml/g DM), B was a sharpness parameter determining the shape of the curve and C was the time (h) at which half of A is reached. A, B and C were calculated by the nonlinear procedure of SAS. There was no difference of C in all treatments ($P > 0.05$). Regarding to *Bacillus subtilis*, the GP_{72} ($P = 0.08$), A ($P = 0.09$) tended to linearly decrease with increase of adding levels, while B tended to increase ($P = 0.06$). For procreatin, the GP_{72} ($P = 0.06$) tended to quadratically increase and A quadratically increased ($P < 0.05$), however, the doses did not affect B ($P > 0.05$). The addition of *Aspergillus oryzae* linearly increased the GP_{72} ($P < 0.01$) and A ($P < 0.01$) and had a tendency for B ($P = 0.09$). The GP_{72} ($P < 0.05$) and A ($P < 0.05$) linearly increased with the rise of fibrase addition levels and no difference in B. In vivo digestibility of animal feeds was estimated by measuring in vitro GP of feed samples incubated in ruminal fluid buffered. The results suggested that *Aspergillus oryzae* and fibrase addition could increase the extent and rate of feed degradation while *Bacillus subtilis* and procreatin addition had slightly effects.

Key Words: feed additives, gas production, in vitro

1601 (M315) Comparison of omasal and reticular sampling methods on ruminal nutrient outflow and digestion in lactating dairy cows. S. M. Fredin[*1], L. F. Ferraretto[1], M. S. Akins[2], and R. D. Shaver[1], *[1]University of Wisconsin, Madison, [2]University of Wisconsin, Platteville.*

An experiment was conducted to compare omasal and reticular sampling methods on ruminal nutrient outflow and digestion in lactating dairy cows fed normal- or reduced-starch diets. Eight ruminally-cannulated multiparous Holstein cows (96 ± 8 DIM at trial initiation) were randomly assigned to a 2 × 2 factorial arrangement of treatments in a replicated 4 × 4 Latin square design with 21-d periods. Treatments were finely (F; mean particle size = 552 μm) and coarsely (C; 1270 μm) ground dry shelled corn in normal (NS) and reduced (RS) starch diets fed as TMR. The NS and RS diets contained 27 and 18% starch (DM basis), respectively, by partially replacing corn grain with soy hulls. Continuous infusion of flow markers Cr-EDTA and YbCl began on d 15. Spot samples of omasal digesta were collected four times daily every 2 h on d 18 to 20, with a 6-h interval between sampling days to represent a 24-h feeding cycle. A 250-mL digesta sample was taken from the reticulum immediately after omasal digesta collection. Indigestible NDF, determined after a 288-h ruminal in situ incubation, was used as a large particle marker and digesta samples were reconstituted using the triple-marker system. Data was analyzed using Proc Mixed of SAS. Dry matter intake was 23.2 ± 1.6 kg/d across all treatments ($P > 0.43$). Marker concentrations were greater in omasal samples compared with reticular samples ($P < 0.001$), resulting in increased ($P < 0.001$) estimates of apparent ruminal digestibility of NDF (39.1 vs. 37.8%), and starch (83.5 vs. 78.9%) for omasal sampling. Outflow of starch from the rumen was greater ($P < 0.01$) for reticular sampling (1.0 vs. 0.8 kg/d), however outflow of NDF was similar ($P = 0.82$) between sampling methods (4.1 kg/d). Ruminal NDF digestibility was greater ($P < 0.001$) for RS compared to NS for omasal samples (43.4 vs. 34.9%, respectively). Unexpectedly, the diets containing C resulted in greater ruminal starch digestibility ($P = 0.02$) compared with F for omasal (85.0 vs. 82.2%, for C and F, respectively) or reticular samples (81.4 vs. 76.5%, for C and F, respectively). Although differences for ruminal nutrient digestibility estimates between sampling methods were observed, they were relatively minor. Therefore, reticular sampling appears to be an acceptable method to estimate ruminal nutrient outflow and digestibility.

Key Words: dairy cow, omasal sampling, reticular sampling

1602 (M316) Validation of a new approach to estimate total tract fiber digestibility from in vitro NDFD values. F. Lopes*[1], K. Ruh[1], D. K. Combs[2], L. F. Ferraretto[1], S. M. Fredin[1], C. Arndt[1], R. D. Shaver[1], and L. E. Armentano[1], *[1]University of Wisconsin, Madison, [2]Dep. of Dairy Science University of Wisconsin, Madison.*

The objective was to validate an in vitro model to predict the total tract fiber digestibility (TTNDFD) in dairy cattle. Nineteen diets from six different trials conducted at University of Wisconsin–Madison were analyzed for fiber digestibility using the in vitro standardized model (Goeser and Combs, 2009). Forages varied amongst diets (corn, alfalfa, tall-fescue and meadow fescue and wheat straw silages) and nutrient composition (NDF ranges from 22.5 to 32.1%, CP 15.8 to 18.9% and NFC 38.0 to 51.0%). Total NDF digestibility observed from the in vivo trials was calculated using indigestible NDF or lignin as marker analyzed in fecal, diet and orts samples. The in vitro TTNDFD model predicts total tract fiber digestibility from the rate of pdNDF degradation (kd, ranges from 1.5 to 4.8%/h), the rate of passage of pdNDF (kp, ranges from 2.5 to 2.8%/h) and the proportion of total NDF that is potentially digestible. The kd is calculated from in vitro NDFD measurements taken at 24, 30, and 48 h of incubation using first order kinetics model with an indigestible fraction (Mertens, 1993). Passage of potentially digestible fiber is predicted from a regression model (Krizsan et al., 2010) for iNDF which is adjusted to account for the selective retention of pdNDF (Lund et al., 2006). The pool of indigestible fiber was estimated from 240 h in vitro NDF residues. Data were analyzed using SAS procedure of logistic regression. The coefficient of determination (R^2) was used to measure the proportion of variation explained by the model. The range of in vivo TTNDFD was 26.3 to 55.6% compared to 33.8 to 52.8% for predicted in vitro TTNDFD. The relationship between predicted in vitro TTNDFD and in vivo TTNDFD was TTNDFD in vivo = −5.7531 + 1.1561 TTNDFD in vitro predicted with R^2 of 61.6%, Root-MSE of 4.3% and P-value of < 0.001. The in vitro test of diets from six different trials demonstrated that TTNDFD model can provide important insights into fiber utilization by dairy cattle that could be used in the field. The TTNDFD value can also be used as a stand-alone value to index forages, as already shown in other publications from our lab. The ability to predict total tract fiber digestibility from a model based on in vitro NDF degradation and incorporate this information into rations could improve our ability to optimize forage utilization and milk production.

Key Words: iNDF, fiber, digestibility

1603 The effects of supplementation with a blend of capsicum, cinnamaldehyde, and eugenol on milk production performance of dairy cows. R. Blanck*[1], K. Vecht[1], C. Oguey[2], and E. Wall[2], *[1]Bar-Magen, Emek Hefer, Israel, [2]Pancosma, Geneva, Switzerland.*

Essential oils are naturally-occurring chemicals in plants, and many of these molecules have been reported to influence production efficiency of dairy and beef animals. Previously, it was reported that a blend of capsicum, cinnamaldehyde, and eugenol increases feed efficiency of beef steers. Our objective was to determine if that same additive (EO; Xtract®-7065, Pancosma) would influence the milk production performance of lactating dairy cows during the summer months in Israel. In two consecutive field trials, Holstein dairy cows were assigned to no additive or supplementation with EO (1 g/d; n = 30 cows/treatment in trial one, 70 cows/treatment in trial two; n = 2 pens/treatment) for 4 mo. The EO was blended with ground corn meal and top-dressed; control cows received corn meal without EO. Dry matter intake (DMI) per pen was calculated daily and individual cow milk production, milk composition, and somatic cell count (SCC) were recorded monthly. Data were subjected to analysis of variance with repeated measures using pen as the experimental unit and trial as a random variable. Cow activity was monitored in the first trial using a pedometer (Afimilk, Isreal), and rumination minutes per day were measured in the second trial (SCR, Israel). Those data were analyzed using analysis of variance with repeated measures and cow as the experimental unit. Milk production was increased in EO cows (39.4 vs. 42.0 kg/d; $P < 0.01$) with no effect of EO on DMI (22.6 vs. 22.5 kg/d; $P > 0.70$). Consequently, there was an improvement in feed efficiency of EO cows (milk/DMI = 1.74 vs. 1.89; $P < 0.001$). There was no effect of EO on milk composition ($P > 0.50$), but there was an increase in energy-corrected milk with EO (40.1 vs. 42.2 kg/d; $P < 0.01$). In addition, there was a decrease in SCC of EO cows (306.1 vs. 242.4 cells*1000/ml; $P < 0.05$). In trial one, there was a decrease in activity of EO cows (165 vs. 137 steps/d; $P < 0.001$); however, in trial two, there was no effect of treatment on rumination time (425 vs 436 min/d; $P = 0.30$). We conclude that a blend of capsicum, cinnamaldehyde, and eugenol can increase milk production and feed efficiency of lactating dairy cows. Additional experiments are needed to confirm these observations and to understand the mechanism underlying the response of dairy cows to EO.

Key Words: essential oil, feed additive, phytonutrient

1604 (M318) Stochastic analysis of the effects of variation in corn silage composition on the supply of metabolizable energy and protein in lactating dairy cows. J. Ferguson*, Z. Wu[1], D. T. Galligan, L. Baker, and N. Thomsen, *University of Pennsylvania, Kennett Square.*

The UPENN Ration Balancer, based on CPMDairy and CNCPS 5.1 with modifications, was used to construct a stochastic model to evaluate the influence of variation in corn silage (CSG) composition on the supply of ME and MP and their allowable milk production. Proximate analysis of CSG samples (n = 514) from 63 PA farms defined the mean and range in nutrient composition (CP, soluble protein (SP), NPN as a percent of SP, NDF, starch, sugars, water soluble fiber, silage acids, fat, and ash) and NDF degradation rate (Kd) for model inputs. A diet was formulated using mean CSG nutrient content and Kd to meet the ME and MP requirements for a cow (675 kg BW) producing 45.0 kg/d milk with 3.7% fat and 3.1% true protein and a DMI of 24.1 kg/d with the following ingredients (% DM): CSG (41.54), alfalfa haylage (6.22), grass silage (8.30), corn grain (21.98), soybean meal (12.64), Soy Pass (5.51), Energy Booster (0.62), blood meal (1.02), minerals and vitamins (2.12), and an amino acid supplement (0.06). The basal diet composition was as follows (% DM): CP 17.7, NDF 29.0, starch 30.1, sugars 3.4, water soluble fiber 5.3, silage acids 4.2, fat 3.9, and ash 6.5. The mean, SD and nutrient correlation matrix of CSG composition was used to construct an @Risk model (Palisade Corporation, NJ) to exam the influence of stochastic variation in nutrient composition of CSG on ME and MP supply. Five thousand simulations were run varying CSG composition and consequently TMR composition. The influence of CSG nutrient content variation on ME and MP allowable milk was as follows: Lignin content of CSG had the major influence on both ME and MP supply followed by NDF kd and NDF and starch. Lignin and NDF digestion should be included in forage analysis of CSG.

Key Words: corn silage, production, nutrient content

Table 1604.

Nutrient (%DM)	CSG Content			Range in Allowable Milk, kg/d (in rank)			
	Mean	Min.	Man.	ME		MP	
Lignin	3.0	1.9	5.9	Lignin	3.32	Lignin	2.61
NDF Kd, %/h	3.8	1.3	6.6	NDF Kd	2.19	Starch	2.36
NDF	42.0	31.9	58.0	NDF	2.06	NDF	2.03
Starch	31.5	9.3	49.7	Starch	1.27	NDF Kd	1.37
Ash	3.7	1.6	8.8	Ash	1.07	SP	1.02
Fat	3.3	1.2	5.6	Fat	1.04	NPN, % SP	0.44
SP	4.4	1.6	7.4	SP	0.52	CP	0.41
CP	7.7	5.4	10.9	CP	0.37	FAT	0.22
NPN, % SP	60.5	20.9	100.0	NPN, % CP	0.16	Ash	0.20

1605 (M319) Extruded soybean meal increases feed intake and milk production in dairy cows. T. Frederick*[1], F. Giallongo[1], J. Oh[1], H. Weeks[1], A. N. Hristov[1], D. M. Kniffen[1], and R. A. Fabin[2], *[1]Dep. of Animal Science, Pennsylvania State University, University Park, [2]Fabin Bros. Farms, Indiana, PA.*

Extruded soybean meal (ESBM) has higher fat content and lower ruminal protein degradability than solvent-extracted soybean meal (SSBM), but information on its nutritive value for dairy cows is limited. A replicated 3 × 3 Latin square design trial with nine Holstein cows (*P*arity, 3.1 lactations; DIM and BW at the beginning of the trial, 161 ± 21 d and 637 ± 20.3 kg, respectively) and 28-d experimental periods was conducted to evaluate the effect of ESBM processed at two extruder temperatures, 149°C (LTM) and 171°C (HTM), on milk production and composition and blood plasma amino acid profile in dairy cows. The control diet contained 13% SSBM [53.8% crude protein (CP) with 71.4% ruminal degradability and 1.8% ether extract (EE)], which was replaced with equivalent amount (DM basis) of LTM (46.8% CP, 59.8% degradability, 10.0% EE) or HTM (46.9% CP, 41.1% degradability, 10.9% EE) ESBM in the two experimental diets (LTM and HTM, respectively). Other ingredients in the diets were (DM basis): 40% corn silage, 20% alfalfa haylage, 5% grass hay, 9% ground corn grain, 5% cottonseed hulls, 5% molasses, salt, urea (LTM and HTM diets only), and mineral-vitamin premix. The diets had 16% CP and met or exceeded the NE_L and metabolizable protein requirements of the cows (NRC, 2001). Both LTM and HTM tended to increase (P = 0.06) DMI compared with the control diet (28.3, 28.2, and 26.8 kg/d, respectively). This resulted in increased ($P < 0.001$) milk yield for both ESBM diets: 40.2 and 40.8 vs. 37.5 kg/d, respectively. Milk fat (3.38 to 3.60%) and milk true protein (2.86 to 2.95%) contents and milk fat yield were not affected by treatment. Milk protein yield tended to be increased (on average by 60 g/d; P = 0.09) by the ESBM diets. Plasma urea N and MUN were increased ($P < 0.03$) 18 and 13%, respectively, by the ESBM diets compared with the control. Blood plasma concentrations of His, Leu, and Val were increased ($P \leq 0.03$) by HTM compared with the control and LTM. Concentration of plasma Met was decreased (P = 0.05) and that of carnosine was increased (P = 0.02) by the ESBM diets compared with the control. This study demonstrated that replacement of SSBM with ESBM in the diet of lactating dairy cows increased feed intake, which resulted in increased milk yield, and increased milk protein yield.

Key Words: solvent-extracted soybean meal, extruded soybean meal, dairy cow

1606 (M320) Effect of inclusion of canola meal or wheat dried distillers grains with solubles on ruminal fermentation, omasal nutrient flow, and production performance in lactating Holstein dairy cows fed two levels of forage: concentrate. M. E. Walpole, G. E. Chibisa, and T. Mutsvangwa*, *University of Saskatchewan, Saskatoon, Canada.*

Canola meal (CM) and wheat distillers grains with solubles (W-DDGS) are high quality protein sources for lactating dairy cows, which are readily available for use in western Canada and parts of the U.S.A. When comparing the amino acid profile of CM and W-DDGS, CM generally has higher levels of lysine; however, ruminal degradability of CM is lower than that of W-DDGS. It is generally accepted that increasing ruminally-available N while increasing dietary ruminally-fermentable energy (e.g., by altering the forage:concentrate [F:C] ratio) can improve the rate of microbial protein synthesis in the rumen. Therefore, the objective of the current study was to examine the effects of differing F:C levels (45:55 vs. 55:45) when the main source of dietary protein was either CM or W-DDGS on milk production and composition, ruminal pH, and omasal nutrient flow. Eight lactating dairy cows (100 ± 58 DIM) were used in a replicated 4 × 4 Latin square design with 28-d periods (20 d adaptation + 8 d measurements) and a 2 × 2 factorial arrangement of dietary treatments. Four cows in one Latin square were ruminally-cannulated for measurements of ruminal fermentation and omasal nutrient flow. Diets were isonitrogenous (15.5% CP). Interactions between dietary source of protein x F:C ratio were not significant. Dietary treatment had no effect on DM intake ($P > 0.05$). Source of protein had no effect on milk yield and composition ($P > 0.05$); however, cows fed diets with the low F:C ratio tended to have higher milk ($P = 0.06$) and milk protein yields ($P = 0.07$), but had a lower milk fat content ($P = 0.04$) and milk urea nitrogen ($P = 0.02$) compared to those fed the high F:C ratio. Milk fat yield was unaffected by dietary F:C ratio ($P > 0.05$). Ruminal ammonia and mean pH were unaffected by dietary treatment ($P > 0.05$). Omasal DM flow was not affected by dietary treatment ($P > 0.05$). Apparent ruminal DM digestibility was numerically greater in cows fed the diet with the low F:C ratio when compared to those fed the high F:C ratio ($P = 0.11$). Total N intake, and omasal N flow were unaffected by dietary treatment ($P > 0.05$). In conclusion, both CM and W-DDGS are suitable protein sources when lactating dairy cows are fed diets varying in F:C ratio.

Key Words: canola meal, milk production, wheat dried distillers grains with solubles

1607 (M321) Analysis of dipeptidyl peptidase IV from microbial metagenomic library in the rumen of dairy cow. J. W. Zhao*[1], J. Q. Wang[2], S. G. Zhao[2], and D. P. Bu[2], [1]*College of Animal Science and Technology of Inner Mongolia University for the Nationalities, Tongliao, China,* [2]*State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

The study for sequence characteristics and enzymatic properties of dipeptidyl peptidases IV (DPP-IV), which is the key enzyme of oligopeptide degradation, will contribute to searching for it inhibit targets, reduce the dipeptide generating speed, and then decrease ammonia generation, thereby improve nitrogen efficiency. The DPP-IV gene of DP7 clone which could reduce the dipeptide activity of crude enzyme from microbial metagenomic library in the rumen of dairy cow was studied. Two primers were designed using DPP-IV gene (GenBank: JX466878) from DP7 clone, and plasmid of DP7 clone was direct sequenced. The structural feature of DPP-IV gene was analyzed by bioinformatics method and DPP-IV gene was expressed in BL21 competent cell. The DPP-IV gene expression sequence was obtained from PCR amplification of DP7 clones using sequence expression primer, and the target protein of DPP-IV was acquired by prokaryotic expression and purification. The analysis of DPP-IV gene sequence showed it had one open reading frame with 2298 bp length (756 amino acid residue) containing the characteristic catalytic domain GWSFGG found in all known DPP-IVs and the conserved region DWVYEEE. The results of BLASTP analysis showed the highest similarity of sequences derived from *Pontibacter sp* DPP-IV (46% identity), followed by *Sphingobacterium sp* (46%), *Solitalea canadensis* (46%), *Marinilabilia sp* (45%) and *Cecembia lonarensis* (45%). DPP-IV gene of DP7 had the identification of the catalytic triad (Ser-633, Asp-708 and His-740), and an inserted amino acid sequence from 422 to 445 compared with other organisms. The results demonstrated DPP-IV gene obtained from DP7 was a new sequence of DPP-IV. The molecular weight of target protein was consistent with the predicted molecular weight (78 kDa) indicating that the enzymatic properties of DPP-IV could proceed with further study.

Key Words: dipeptidyl peptidases IV, gene expression, sequence analysis

1608 (M322) Modification of the feeding behavior of dairy cows through live yeast supplementation. T. J. DeVries*[1] and E. Chevaux[2], [1]*University of Guelph, Kemptville, ON, Canada,* [2]*Lallemand Animal Nutrition, Milwaukee, WI*

The objective of this study was to determine if the feeding behavior of lactating dairy cows can be modified through live yeast supplementation. Twelve lactating Holstein dairy cows (2 primiparous and 10 multiparous) were individually

exposed to each of two treatment diets (over 35-d periods) in a replicated crossover design. Treatment diets were: 1) control TMR, and 2) control TMR plus $1x10^{10}$ cfu/head/d live yeast (*Saccharomyces cerevisiae* CNCM I-1077; Levucell SC20; Lallemand Animal Nutrition, Montreal, QC, Canada). Milk production, feeding, and rumination behavior were electronically monitored for each animal for the last 7 d of each treatment period. Milk samples were collected for the last 6 d of each period for milk component analysis. Data were analyzed in a general linear mixed model. DMI (28.3 kg/d), eating time (229.3 min/d) and rate (0.14 kg DM/min) were similar between treatments. With yeast supplementation, meal criteria were shorter (20.0 vs. 25.8 min; SE = 2.3; $P = 0.04$), translating into cows tending to have more meals (9.0 vs. 7.8 meals/d; SE = 0.6; $P = 0.07$), which tended to be smaller in size (3.4 vs. 3.8 kg/meal; SE = 0.2; $P = 0.09$). Meal length (33.9 min) was similar between treatments. Yeast supplemented cows also tended to ruminate longer (570.3 vs. 544.9 min/d; SE = 13.2; $P = 0.08$). Milk yield (45.8 kg/d) and efficiency of production (1.64 kg milk/kg DMI) were similar between treatments. There was a tendency for higher milk fat % (3.71 vs. 3.55%; SE = 0.08; $P = 0.09$) and yield (1.70 vs. 1.63 kg/d; SE = 0.04; $P = 0.1$) when cows were supplemented yeast. No differences in milk fatty acid composition were seen, with the exception of a tendency for a greater concentration of 18:2, *cis*-9, *cis*-12 fatty acid (2.71 vs. 2.48% of total FA; SE = 0.13; $P = 0.08$) when cows were yeast supplemented. Yeast supplemented cows had lower mean ruminal temperature (38.4 vs. 38.5°C; SE = 0.01; $P = 0.02$), spent less time with rumen temperature above 39.0°C (353.1 vs. 366.9 min/d; SE = 5.5; $P = 0.001$), and tended to spend less time with rumen temperature above 38.0°C (693.9 vs. 780.0 min/d; SE = 29.1; $P = 0.06$). The results suggest that live yeast supplementation had a beneficial impact on rumen fermentation as evidenced by improvements in meal patterns and rumination, milk fat production, and rumen temperature.

Key Words: live yeast, rumination, meal pattern

1609 (M323) The effect of supplementing dairy cows with a hydrolyzed yeast product (ProgutRumen) on milk production and somatic cell scores.

D. J. Gaffney*[1], M. R. Sheehy[2,3], J. A. Vuorenmaa[1], and A. G. Fahey[4], *[1]Hankkija Oy/Suomen Rehu, Hyvinkää, Finland, [2]Devenish Nutrition, Belfast, Northern Ireland, [3]School of Veterinary Medicine, University College Dublin, Ireland, [4]School of Agriculture and Food Science, University College Dublin, Ireland.*

The object of this study was to determine if supplementing Holstein-Friesian cows with hydrolyzed yeast product (ProgutRumen) had an effect on milk production and somatic cell score (SCS). Holstein-Friesian dairy cows ($n = 248$) were balanced for DIM, pre-experimental milk yield, and milk composition and assigned to either a control ($n = 127$) or hydrolyzed yeast (Progut, $n = 121$) treatment. Cows were put into two large pens and after each milking the cows were rotated into a new pen to account for environmental effects in the shed. Cows were individually fed the Control and Progut Rumen (10 g/cow/day) treatments in the milking parlor during the morning milking. Therefore, the cow was considered the experimental unit. The trial was performed over two seasons (for a 10-wk period and a 8-wk period) and on weekly intervals milk yield was recorded and milk composition (fat yield and %, protein yield and %, lactose yield and %) and somatic cell score was determined. The dataset was divided in three ways for the analysis; the entire dataset, all cows with an average daily milk yield > 24kg, and finally all cows with an average daily milk yield > 30kg. All data were analyzed in SAS with a repeated measures mixed model with the appropriate covariance structure determined by Bayesian Information Criterion. The fixed effects included treatment, season, parity (1 to ≥ 5), and week and the interactions between treatment and parity, and treatment and week with a random effect included for cow. There were no significant differences between the Control and Progut Rumen treatments for the milk composition traits. There was a significant increase in milk yield for the Progut Rumen treatment in the entire dataset ($P < 0.01$), > 24kg dataset ($P < 0.01$) and the > 30 kg dataset ($P < 0.05$). There was a significant decrease in SCS for Progut Rumen compared to the Control treatment in the entire dataset ($P < 0.01$), > 24kg dataset ($P < 0.05$) and the > 30 kg dataset ($P < 0.05$). In conclusion supplementing dairy cow diets with Progut Rumen did not alter milk composition, however it increased milk yield and decreased SCS indicating possible beneficial effects on the dairy cows' immune system.

Key Words: hydrolysed yeast, milk yield, somatic cell score

1610 (M324) Effect of live yeast vs. sodium sesquicarbonate supplementation on milk yield and milk components in dairy cows.

M. B. de Ondarza[1], E. Chevaux*[2] and A. Hall[2], *[1]Paradox Nutrition, LLC, West Chazy, NY, [2]Lallemand Animal Nutrition, Milwaukee, WI.*

The trial objective was to determine the effect of supplemental live yeast (LY) ($10x10^9$ cfu/cow/d; *Saccharomyces cerevisiae* CNCM I-1077) vs. sodium sesquicarbonate (SS) (227 g/cow/d) on milk yield, milk components, and DMI. Four pens of Holstein cows (200–230 cows/pen) in a freestall barn were paired as follows: Parity 1 and Parity 2+. Each pair was balanced pre-trial for parity, DIM, milk yield, and milk components. One pen per pair received LY and one pen per pair received SS. The study was 16 wk in length with 12 wk of diet adaptation and 4 wk of data collection. Parity 1 and Parity 2+ diets were similar except Parity 2+ contained 25% BMR corn silage and forage NDF was higher (24.26 vs. 23.45%).

Daily milk yield of individual cows was recorded. Individual milk components were assessed twice with a 2-wk interval between tests. Data was analyzed using JMP statistical software. Only cows remaining in study pens for the entire 16 wk were included (LY = 295 cows; SS = 279 cows). The statistical model for milk yield and components included treatment, DIM category, and pair as fixed effects with cow within pen as random. Pre-trial milk yield and componentswere included as covariates. Pair-wise comparisons were recalculated using JMP's contrast analysis which utilizes Student's *t* test. The statistical model for DMI used treatment and pair within treatment as fixed effects. Daily milk yield (kg/d) was unaffected by treatment. Weekly average daily milk yields around component test days tended ($P = 0.10$) to be higher for LY, especially in Parity 2+ cows (42.08 vs. 40.26 kg/d for LY and SS, respectively (SE = 0.56)) ($P = 0.01$). Percent milk fat and milk true protein were not affected ($P > 0.10$) by treatment. For all cows, yield of 3.5% FCM tended to be 1.29 kg higher with LY ($P = 0.08$) but for mature cows only, yield of 3.5% FCM was significantly higher with LY (45.66 vs. 43.56 kg/cow for LY and SS, respectively (SE = 0.63)) ($P = 0.01$). Live yeast improved ($P = 0.02$) overall milk true protein yield by 0.04 kg/d. Mature cows responded to LY with higher DMI (28.24 vs. 26.88 kg/d for LY and SS, respectively) ($P < 0.01$). Yield of milk and milk components was similar or higher with LY. Mature cows consuming a diet with more digestible forage NDF had a greater positive 3.5% FCM yield response to LY than first-lactation cows.

Key Words: live yeast, sodium sesquicarbonate, milk yield, milk components

---

1611 (M325) Milk production of dairy cows fed sugarcane silage based diets.
L. L. Cardoso, M. I. Marcondes*, K. G. Ribeiro, O. G. Pereira, G. F. Bayao, and M. M. D. Castro, *Universidade Federal de Viçosa, Minas Gerais, Brazil.*

This study aimed to evaluate the use sugarcane silage for Holstein high and medium producing cows. The treatments consisted of corn silage (CS) in forage: concentrate ratio 60:40, and four diets based on sugarcane in forage: concentrate ratio 40:60:fresh sugarcane (FSC), sugarcane silage control (SCC), sugar ane silage with *Lactobacillus buchneri* (SCLB), and sugarcane silage with *Lactobacillus plantarum* plus *Pediococcus pentosaceus* (SCLP). Fifteen cows were blocked for milk production (25, 30, and 35 kg/day), and were evaluated in five periods of 15 d. Animals were distributed in a randomized block design in a scheme of repeated measures. Data was analyzed according to the follow contrasts: CS vs. sugarcane diets; FSC vs. sugarcane silage diets; SSC vs. sugarcane silage with additives; SCLB vs. SCLP. DM, OM, NDF, NFC intakes did not differ between treatments ($P > 0.05$). The digestible OM intake was also not affected ($P = 0.05$). CP intake was greater ($P = 0.02$) for diets containing sugarcane silage. CS had higher DM ($P = 0.04$) and OM ($P = 0.03$) digestibility compared to diets containing sugarcane silage. It was also observed that digestibility of NDF in CS was greater ($P = 0.02$) than other diets, and SCLB promoted the lowest vules of NDF digestibility. We observed no differences ($P = 0.580$) for production of milk (25,8 kg/day), corrected milk 4% fat (23.19 kg/day), milk fat (3.34%), milk lactose (4.00%) and total solids (11.43%), whereas there was a higher crude protein content in milk ($P = 0.04$) for FSC (3.09%) and lowest level for SCLP (2.62%). Sugarcane diets contained higher levels of plasma urea nitrogen (*P*UN; 0.010), and FSC presented lower values compared to others sugarcane diets. Urea nitrogen in urine (UNU) and microbial efficiency (EFMIC) did not differ between diets ($P > 0.05$). The average daily gain (ADG) also did not differ ($P = 0.42$) between treatments (0.31 kg/day). It was concluded that diets with 60% concentrate added to sugarcane silage can allow support mean yields 25.8 kg/day of milk, similarly to other bulky sources.

Key Words: digestibility, milk, consumption

1612 (M326) Fecal sample starch content deteriorates over time after sampling.
K. Haerr*[1,2], J. P. Goeser[2,3], and C. R. Heuer[2,3], *[1]University of Illinois, Urbana, [2]Rock River Laboratory, Inc, Watertown, WI, [3]Dep. of Dairy Science, University of Wisconsin–Madison, Madison.*

Dairy and beef cattle fecal samples are typically taken from commercial dairies and feedlots to assess starch utilization. Greater fecal starch content is related to lesser ruminal and total tract starch degradation and animal performance. Fecal sample starch concentration may change during time in transit to analysis laboratory, which in some cases can be 5 d or more. Dairy cattle fecal samples (at least 10 250-g subsamples) were collected from manure piles at each of two commercial dairies in Wisconsin in July 2013. Subsamples were thoroughly mixed, immediately split on farm into air-tight plastic containers (250 g), and stored for 0 (control), 1, 2, or 5d. Samples stored for 1, 2, or 5d were also held at approximately 2°C (cold), 22°C (room), or ambient (variable, daily high 27°C) temperatures. The 0-h sample was processed on the same day samples were gathered. These combinations were organized in a factorial arrangement and chosen to simulate sample environment during shipping to analysis lab. Samples were oven dried (50°C for 48 h) and ground to 1 mm following treatment. Starch content (% of DM) was measured in each sample and total tract starch digestibility (% of starch, TTSD) was calculated using the Ferraretto and Shaver 2012 equation: 100 X (0.9997- 0.0125 × fecal starch). Data were analyzed with multiple linear regression using SAS JMPv10 and model effects chosen using forward selection. Temperature and time were entered as fixed effects and farm was random. Temperature ($P < 0.05$) and time ($P < 0.01$) were significantly related to fecal starch content and predicted TTSD. Fecal starch content

averaged 4.3, 5.4, 4.3, and 4.1% for control, cold, room, and ambient temperature exposures, respectively. The numerically greater starch content at cold-storage temp relative to control was unexplained, and warrants further evaluation. Fecal starch content raw data averaged 5.4 and 3.7% at 0 and 5d, respectively. Predicted TTSD data averaged 93.3 and 95.4% at 0 and 5 d, respectively. Model parameter slope estimates were -0.017 and 0.02 per h for fecal starch and TTSD, respectively. Results warrant further evaluation, but suggest fecal starch content and animal digestion estimates will change during extended time in transit. The amount of time between sampling and starch analysis should be considered and minimized.

Key Words: fecal, starch, digestion

1613 (M327) Effects of pH and incubation duration on the stability of the endoglucanase activity of seventeen exogenous fibrolytic enzyme preparations. A. F. Campos[1], B. Y. Coy[2], K. G. Arriola[*2], and A. T. Adesogan[2], *[1]São Paulo State University, Dep. of Animal Science, Brazil, [2]University of Florida, Dep. of Animal Sciences, Gainesville.*

This study examined effects of pH and incubation duration on the stability of the endoglucanase activity of various exogenous fibrolytic enzymes (EFE). Seventeen commercial EFE sourced from *Trichoderma reesei* or and *Aspergillus spp.* were assayed in triplicate for endoglucanase (EN) activity at pH 4.0, 5.0 and 6.0 after incubation for 0, 24, 48, and 168 h at 40°C. Endoglucanase activity was assayed in a 15-mL tube containing 1.0 mL of 1.0% (wt/vol) carboxymethyl cellulose as substrate and 0.9 mL of citrate-phosphate buffer (pH 4.0, 5.0 or 6.0). For the 0-h incubation, after a 10-min preincubation period, 0.1 mL of diluted EFE was added to cellulose to initiate the reaction and the suspension was incubated for 5 min. The reaction was terminated with 3 mL of dinitrosalicylic acid. For the other incubation periods, tubes were kept in a water bath at 40°C degrees for the respective durations. The unit of EN activity was the amount of EFE required to release 1 µmol of reducing glucose equivalents min^{-1} mg^{-1}. Treatments were arranged in a 17 (enzymes) × 3 (*P*H) × 4 (incubation duration) factorial layout and data were analyzed with a model including these terms and the interactions using the GLM procedure of SAS. Endoglucanase activity was greatest ($P < 0.0001$) for all EFE at pH 4.0 after 0 h of incubation except for one EFE, which exhibited the greatest activity at pH 6.0 after 0 h of incubation. For 13 of the 17 EFE, increasing the incubation duration or the pH quadratically ($P < 0.0001$) decreased EN activity. However, simultaneously increasing the pH and incubation duration linearly ($P < 0.0001$) decreased EN activity. Within 24 h of incubation, between 97.9 and 99.6% of the EN activity was lost from each EFE. Therefore, EN activity decreased substantially as the incubation duration increased. This study shows that the EN activities of the EFE decreased with increasing pH and or incubation time. Endoglucanase activities were much lower at the usual ruminal pH of lacting dairy cows than at those (pH 4 to 5) typically used to assay EFE activities in the laboratory.

Key Words: endoglucanase, exogenous enzyme, incubation duration, pH

1614 (M328) Evaluation of a source of α-amylase and a protease in the diet of lambs on nutrient intake and digestibility and blood parameters. *B*. Quintana[*1], L. C. Solorzano[2], and A. A. Rodriguez[1], *[1]University of Puerto Rico, Mayaguez, [2]DSM Nutritional Products, Parsippany, NJ.*

The effects of a commercial source of α-amylase and an experimental protease or their combination on nutrient intake and digestibility and blood parameters were determined in lambs fed 21% dietary starch. Twelve crossbred lambs (14.2 kg) were assigned to one of four diets; no additive (control) or diets containing α-amylase (RONOZYME RumiStar), an experimental protease, or their combination. Diets were offered daily at 4% of animal BW/DMB in four 28-d experimental periods consisting of 21 d of adaptation to the diet followed by 7 d of complete fecal collection. In each period, feed offered, orts, and feces were collected, quantified, and analyzed for DM, starch, CP, and NDF contents to determine intake and digestibility. Disease incidence was observed and recorded during the experiment. Blood samples were collected from each lamb at the end of each experimental period to determine glucose, BHB, NEFA, and insulin concentrations. Data were analyzed according to a 4 × 4 Latin Square experimental design. Treatments contrasts were performed using least squares means adjustment for multiple comparisons (Tukey-Kramer) between diets as follows: containing enzymes versus no enzymes, amylases versus no amylases, proteases versus no proteases, and amylases versus proteases. Adding proteases to the diet decreased ($P < 0.05$) starch consumption as compared to that of lambs fed without the experimental enzyme (248.5 vs. 255 g/d). Starch digestibility also tended ($P < 0.10$) to be higher in lambs fed with the protease than with α-amylase (98.9 vs. 98.5%). Adding enzymes to the diet tended ($P < 0.10$) to decrease BHB concentration (4.26 vs. 4.68 mg/dL). NEFA concentration tended to decrease ($P < 0.10$) for lambs fed α-amylase as compared to lambs fed diets without α-amylase (0.128 vs. 0.156 mEq/L). Insulin levels were lowered ($P < 0.05$) by addition of α-amylase in lambs diets as compared to those of animals fed with protease (73.3 vs. 80.3 pmol/L). Insulin level also tended ($P < .10$) to increase in lambs fed the experimental protease as compared to lambs fed the enzyme (80.3 vs. 78.7 pmol/L). In summary, adding the experimental proteases to lambs diets containing 21% dietary starch decrease starch consumption and tended to increase starch digestibility. Both exogenous enzymes influenced blood metabolites; however, a greater effect was observed in lambs fed with the experimental protease.

Key Words: enzymes, α-amylase, protease

1615 (M329) Evaluation of a source of α-amylase and a protease in the diet of lambs on nutrient intake and digestibility and blood parameters. B. Quintana*[1], L. C. Solorzano[2], and A. A. Rodriguez[1], *[1]University of Puerto Rico, Mayaguez, [2]DSM Nutritional Products, Parsippany, NJ.*

The effects of a commercial source of α-amylase, an experimental protease or their combination on nutrient intake and digestibility and blood parameters were determined in lambs fed a basal diet of 34% ground corn, 40% tropical grass hay, and 26% soybean meal providing 21% dietary starch. Twelve crossbred lambs (14.2 kg) were assigned to one of four diets: no additive or diets containing α-amylase (RONOZYMERumiStar), an experimental protease, or their combination. Diets (DM basis) were offered daily at 4% of animal BW in four 28-d experimental periods consisting of 21 d of adaptation to the diet followed by 7 d of complete fecal collection. In each period, feed offered, orts, and feces were collected, quantified, and analyzed for DM, starch, CP, and NDF contents to determine intake and digestibility. Disease incidence was observed and recorded during the experiment. Blood samples were collected from each lamb at the end of each experimental period to determine glucose, BHB, NEFA, and insulin concentrations. Data were analyzed according to a 4 × 4 Latin Square experimental design. Treatments contrasts were performed using least squares means adjustment for multiple comparisons (Tukey-Kramer) between diets as follows: enzymes versus no enzymes, amylase versus no amylase, protease versus no protease, and amylase versus protease. DM intake was similar across treatments (1106.1, 1087.5, 1104.8 and 1088.5 g/d for control, and diets containing α-amylase, experimental protease or their combination, respectively). Adding protease to the diet decreased ($P < 0.05$) starch consumption as compared to that of lambs fed without the experimental enzyme (248.5 vs. 255 g/d). Starch digestibility tended ($P < 0.10$) to be higher in lambs fed the protease than α-amylase (98.9% vs. 98.5%). Adding enzymes to the diet tended ($P < 0.10$) to decrease BHB concentration (4.26 vs. 4.68 mg/dL). NEFA concentration tended to decrease ($P < 0.10$) for lambs fed α-amylase compared to lambs fed diets without α-amylase (0.128 vs. 0.156 mEq/L). Insulin levels were lowered ($P < 0.05$) by addition of α-amylase in lambs diets as compared to those of animals fed with protease (73.3 vs. 80.3 pmol/L). Insulin level also tended ($P < .10$) to increase in lambs fed the experimental protease as compared to lambs fed the enzyme (80.3 vs. 78.7 pmol/L). In summary, adding the experimental protease to lambs diets containing 21% dietary starch decreased starch consumption and tended to increase starch digestibility. Both exogenous enzymes influenced blood metabolites, however a greater effect was observed in lambs fed the experimental protease.

Key Words: enzymes, amylase, protease

1616 (M330) Utilization of industrial enzymes in the evaluation of neutral detergent insoluble fiber content in high-starch samples. C. Batista Sampaio*[1], D. I. Gomes[2], E. Detmann[3], S. de Campos Valadares Filho[1], H. Valentim Nunes Machado[4], and M. de Oliveira Franco[1], *[1]Universidade Federal de Viçosa, Dep. of Animal Science, Minas Gerais, Brazil, [2]Universidade Federal do Pará, Parauapebas, Pará, Brazil, [3]Universidade Federal de Viçosa, Minas Gerais, Brazil, [4]Universidade Federal de São João Del Rei, Minas Gerais, Brazil.*

The method of analysis of fibrous components called "detergent system" was initially developed to evaluate forage and subsequently extended to other types of feeds. However, its application to analizing non-fibrous feeds is associated with some analytical problems, noticiably with high starch feeds. The use of a α-amylase is recomemended by AOAC International as a standard procedure to promote solubilization of the starch in feeds samples to obtain insoluble fiber with accuracy. Diferent amylases are available for industrial activities, which have, in general, certificated quality and activity. However, the type and amount of industrial enzymes that could potentially be used in evaluating the insoluble fiber have not established. It were performed two experiments to evaluate the utilization of industrial enzymes in the evaluation of neutral detergent fiber (NDF) contents in high-starch materials. In the first experiment, it was verified the accuracy of estimates of NDF obtained with the utilization of three industrial enzymes (Termamyl 2X, Liquozyme Supra 2.2.X, and Amylase AG 300L-Novozymes) at different volumes (50, 100, 250 or 500 μL/sample). Samples were simulated to contain starch at 0, 100, 300, 500, and 1000 g/kg using purified cellulose and starch ($n = 240$). Estimates of the bias of NDF contents were evaluated by analysis of variance, acording in a completely randomized design in a 3 × 4 × 5 (three types and four volumes of enzymes and five concentrations of starch). In the second experiment, samples of corn grain and sorghum grain were evaluated considering the same enzyme types and volumes used in the first experimente, also incluiding aliquots without using enzyme addition ($n = 104$). There was no significant bias of NDF recovery for simulated samples containing starch up to 300 g/kg ($P > 0.01$). Considering those samples, none difference among enzymes was observed ($P > 0.01$). The results obtained from the evaluation of corn and sorghum suggest the use of 250 μL volume and enzyme necessary for the extraction of starch. Therefore, it can be recommended the utilization of 250 μL the α-amylases evaluated.

Key Words: α-amilase; feed analysis; fiber

1617 (M331) In situ degradation and fermentation of a diet with an exogenous phytase for lambs.

L. H. Vallejo-Hernandez*[1], G. Buendia-Rodriguez[2], J. E. Ramirez-Bribiesca[3], L. A. Miranda-Romero[4], M. M. Crosby-Galvan[3], and S. S. Gonzalez[5], *[1]Universidad Autonoma del Estado de México, Toluca, [2]CENIDFyMA INIFAP, Queretaro, México, [3]Colegio de Postgraduados, Montecillo, México, [4]Universidad Autonoma de Chapingo, México, [5]Colegio de Postgraduados, Montecillo Estado de México.*

Close to 70% of phosphorus (*P*) from cereal grains and oleaginous seeds is linked to phytic acid as phytate, which is little utilized or not at all by non-ruminants. Diets containing more than 50% of the P as phytate will decrease hydrolysis of the phytate by rumen microorganisms. Therefore, the objective of this in situ trial was to evaluate the effect of an exogenous phytase added to a diet for lambs. Treatments were: 0, 540, and 720 g of phytase Ronozyme-HiPhos (DMS Nutritional Products, 5000 FTU/g) added to a 70% sorghum grain diet and fed to six Criollo lambs (40 ± 2 kg live BW) with ruminal and duodenal cannulas, and housed on individual metabolic cages during 45 d (plus 15 d for adaptation). The experimental design was a 3 × 3 Latin square repeated on time, data were analyzed using GLM procedure (SAS v. 9.2) and treatment means were compared with the Tukey test ($P \leq 0.05$). Variables were dry matter intake (DMI), pH and VFA concentration in ruminal fluid, NH_3–N and P concentration in ruminal and duodenal fluid, fecal and urine P, and plasma P; samplings were performed at 3, 6, 9, 12, 24, 48, and 72 h. Phytate of the diet was 67.74% of the total P. For 0, 540, and 720 g phytase, differences ($P \leq 0.05$) were found only for DMI (1053.32ab, 988.70b, 1141.32a g/day) and fecal P (2.32a, 2.01ab, 1.85b % P/g DM). Thus, it may be concluded that this exogenous phytase did not change pH, VFA, P in ruminal fluid, P in urine or plasma. But since fecal P excretion was reduced, soil contamination could be decreased.

Key Words: phytase, P excretion, lamb.

1618 (M332) Sources of sulfur in protein supplements and fiber degradability.

F. P. Leonel*[1], C. J. Silva[2], L. M. Moreira[1], J. C. Pereira[3], J. M. Carvalho[1], J. C. Carvalho[3], R. A. Vieira[4], and M. M. Assis[1], *[1]Federal University of São João del Rei (UFSJBrazil, [2]National University of Brasília, Brazil, [3]Federal University of Viçosa, Brazil, [4]Norte Fluminense State University, Campos dos Goytacazes, Brazil.*

The present work is focused on the evaluation of different sulfur sources in protein supplements for cattle. Crossbred steers were fed with *Brachiaria dictyoneura* hay, with different sulfur sources in the protein supplement: 70S elementary sulfur (ES70S); 98S elementary sulfur (ES98S); hydrated calcium sulfate (HCS); anhydrous calcium sulfate (ACS) and ammonium sulfate (AS). The nutritional effects observed to the steers in relation to the different sulfur sources were evaluated by means of different aspects, such as nutrient intake, apparent digestibility, fiber degradability and particle flow-rate. An 11:1 nitrogen:sulfur ratio was employed, being that five steers fistulated in the rumen and abomasum were utilized through distribution in a 5 × 5 Latin square. The different sulfur sources in the supplement did not affect ($P > 0.05$) the intakes of dry matter of hay; crude protein (CP); neutral detergent fiber corrected for ash and protein (NDFap); organic matter (OM); nonfiber carbohydrate (NFC); ether extract (EE); and total digestible nutrients (TDN). The respective sulfur sources do not generated significant alterations ($P > 0.05$) regarding the digestibility coefficients of NDFap and CP.

In this study, NDF degradation profiles were encountered in agreement with the solid transit kinetics parameters model and estimations. The data were adjusted to different double-compartment models (G1G1, G2G1, G3G1, G4G1, G5G1 and G6G1). The models G2G1, G3G1, G5G1, G4G1 and G3G1 were more efficient in accordance with the estimations of the following treatments: G2G1 to 70S elementary sulfur; G3G1 to 98S elementary sulfur; G5G1 to calcium sulfate (hydrated gypsum); G4G1 to calcium sulfate (anhydrous gypsum) and G3G1 to ammonium sulfate. It was possible to infer that the sulfur sources employed in the present work influenced slightly the ruminal fiber degradation.

Key Words: degradability, fiber, intake, nitrogen sulfur ration

Table 1618. Medium values and coefficients of variation (CV) for daily intake of dry matter (DM), crude protein (CP), neutral detergent fiber corrected for ash and protein (NDFap), organic matter (OM), total digestible nutrients (TDN), as function of sulfur sources in the protein supplements

Item	ES70S	ES98S	HCS	ACS	AS	CV(%)
			g/kg BW			
Hay DMI	17.08	17.31	16.71	17.18	17.11	4.66
			kg/day			
CP	0.48	0.47	0.47	0.47	0.45	7.46
NDFap	3.76	3.76	3.60	3.74	3.79	4.90
OM	4.19	4.17	4.00	4.14	4.18	5.14
NDT	3.04	3.15	2.73	2.51	2.62	17.67

1619 (M333) Effect of weight gain rates in the post-weaning phase and forage allowance in the finishing phase with high supplementation on performance of Nellore cattle. *V*. A. C. Mota[1], G. F. Berti[2], J. A. Alves Neto[3], R. M. Fernandes[4], P. H. Gonçalves[2], B. C. Carvalho[2], M. A. P. Alves[2], I. M. de Oliveira*[5], F. D. D. Resende[5], and G. R. Siqueira[5], *[1]UNESP/FCAV, Jaboticabal, Brazil, [2]Centro Universitário da Fundação Educacional de Barretos–Unifeb, Barretos, Brazil, [3]Universidade Estadual Paulista, Jaboticabal, Brazil, [4]UNESP-FCAV, Jaboticabal, Brazil, [5]APTA–Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil.*

The study analyzed the effect of forage allowance in the finishing phase of beef cattle fed high levels of supplementation and its interaction with the rate of weight gain in the post-weaning phase. Sixty four non-castrated Nellore cattle with an average body weight (BW) of 386.0 kg, were distributed into 16 paddocks (experimental units) of *Brachiaria brizantha* cv. Marandu and fed 2% of their BW in supplement containing 34% of corn, 51% of citrus pulp pellets and 15% of mineral mix. Treatments consisted of animals managed during the post-weaning phase on 15- or 35-cm-tall pastures receiving mineral mix 50 g/100 Kg BW and sub-divided into lots with low and high forage allowance in the finishing phase. In the post-weaning phase, the pasture height provided different ADG (0.761 kg d^{-1} for the 15 cm and 1.076 kg d^{-1} 35 cm pasture), and different forage allowances were obtained in the finishing phase, with the same stocking rate in the paddocks, with different initial masses (3.370 and 8.470 kg DM ha^{-1}) provided by the management of 15- and 35-cm-tall pastures during the post-weaning phase, respectively. The experimental period was 120 d, in a completely randomized blocks design in a 2 × 2 factorial arrangement, in which data were analyzed by using a mixed model through the PROC MIXED of SAS (SAS 9.2), significance at $P < 0.10$ by the *t* test. The animals that had the lowest weight gain and were in the treatment with the highest forage allowance in finishing had the greatest ADG (1.123 kg d^{-1}; $P = 0.02$), and the other nutritional strategies did not differ from each other ($P > 0.10$), averaging 0.929; 0.901 (biggest gain in post-weaning and low and high bid on finishing respectively) and 0.920 kg d^{-1} (lower gain in post-weaning and finishing in low supply). The supplement intake was affected by the post-weaning treatment ($P = 0.01$) and no effect of forage allowance in the finishing was observed ($P = 0.74$). Animals kept on 35-cm pastures in the post-weaning started the finishing heavier consumed more supplement (7.8 kg d^{-1}) than those reared on 15-cm pastures (7.3 kg d^{-1}). In relation the quantity of concentrate to gain 1 kg of BW, the animals on the lowest forage allowance level in the finishing showed an upward trend ($P = 0.15$; 7.7 vs. 8.9 kg supplement kg BW). *Supported by CAPES/UNESP/CONNAN.*

Key Words: gain, consumed, Marandu

1620 (M334) Nutritional evaluation of forage Kochia (*Kochia prostrata*) as an alternative forage for beef cattle using a dual-flow continuous culture system. E. Marostegan de Paula*, L. Galoro da Silva, T. Shenkoru, Y. L. Yeh, J. Bunkers, and A. Faciola, *University of Nevada.*

Forage Kochia (FK; *Kochia prostrata*) has the potential to be used as forage for beef cattle due to its high nutritional value and ability to grow well on soils with low moisture content. The objective of this experiment was to determine the nutritional value and rumen fermentation characteristics of FK as compared to alfalfa hay (AH) and orchardgrass hay (OH). Diets were randomly assigned to six dual-flow continuous culture fermenters (1200 to 1250 mL) in a replicated 3 × 3 Latin square arrangement with three 10-d experimental periods consisted of 7 d for diet adaptation and 3 d for sample collection. Fermenters were fed a total of 72 g of DM/d equally divided in 12 portions of one of three diets: 1) 100% AH, 2) 100% OH, and 3) 100% FK. Liquid and solid dilution rates were adjusted daily to 10%/h and 5%/h, respectively. A sample of 500mL from each fermenter was taken on d 8, 9, and 10. Two subsamples of 10ml were filtered through two layers of cheesecloth, and were preserved with 0.2 mL of 50% sulfuric acid and were centrifuged for subsequent ruminal NH_3–N and VFA analysis. Statistical analyses were performed using the GLM procedure in SAS. There were no differences ($P > 0.05$) among treatments for total VFA, molar proportion of acetate, propionate, butyrate, and branched-chain VFA (Table 1620). However, there were differences ($P < 0.05$) for NH_3–N. Ruminal NH_3–N observed was greater for FK compared with AH and OH, indicating a greater N availability for microbial growth; nevertheless, there were no significant differences between AH and OH. Results from this experiment indicated that FK may be a viable alternative for beef cattle producers. This is especially important for areas in which conventional forages may not grow well such as the U.S. Great Basin area.

Key Words: forage Kochia, alfalfa hay, in vitro fermentation

Table 1620.

	Treatment				
	AH	OH	FK	SEM	*P*-value
Diet Composition	——— %DM ———				
CP	15.7	10.3	20.9		
NDF	40.2	61.3	37.9		
NH3-N, mg/dL	1.23[b]	0.77[b]	2.76[a]	0.37	0.04
Total VFA, mmol	90.6	85.6	91.0	5.78	0.77
Acetate, %	74.8	72.0	73.9	2.72	0.77
Propionate, %	17.1	18.3	16.8	1.94	0.85
Butyrate, %	6.1	7.6	6.7	1.05	0.60
Isobutyrate, %	0.23	0.18	0.30	0.03	0.23
Valerate, %	1.37	1.47	1.44	0.25	0.95
Isovalerate, %	0.34	0.36	0.56	0.09	0.30
Acetate:Propionate	5.1	3.9	4.8	0.62	0.45
Total BCVFA, mmol	2.2	1.8	2.4	0.48	0.70

1621 (M335) Effect of using either barley straw or alfalfa hay on intake and digestibility in growing Simmental heifers fed high-concentrate diets.

A. Madruga*[1], E. Mainau[1], J. L. Ruiz[1], X. Manteca[1], M. Rodríguez[1], L. A. González[2], and A. Ferret[1], *[1]Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Centre for Carbon, Water and Food, Dep. of Plant and Food Sciences, Faculty of Agriculture and Environment, University of Sydney, Camden, Australia.*

The objective of this experiment was to compare the effects of using two different forage sources on intake and digestibility in growing heifers fed high-concentrate diets. Eight Simmental heifers (141 ± 15.5 d old and with an average initial BW of 147.4 ± 10.8 kg) were used in a crossover design experiment. Treatments tested were: a) total mixed ration with barley straw as forage source (BS), and b) total mixed ration with alfalfa hay as forage source (AH). Forages were coarsely chopped before their incorporation to total mixed ration. Diets were offered on an ad libitum basis, with a forage to concentrate ratio of 8:92, and formulated to be isocaloric (2.91 Mcal ME/kg DM) and isonitrogenous (15% CP on DM basis). The experiment was performed in two 28-d periods, and sampling was performed in the last week of each period. Heifers were weighed before feeding on two consecutive d at the beginning and at the end of the experiment, and the first and last d of the sampling week. Feed offered and refusal samples of each heifer were collected daily for 7 d in the sampling week for DM determination and chemical analysis. Dry matter digestibility was estimated using acid-insoluble ash as an internal marker. Fecal samples were collected from the rectum at d 6 and 7 of each sampling period. Differences were analyzed by using the PROC MIXED of SAS. The model contained the fixed effects of treatment, period and their interaction, and the random effect of heifer nested within sequence. Intake of DM, CP and NDF was unaffected by treatment, being on average 6.4, 0.8 and 1.6 kg/d, respectively. Average daily gain of heifers fed BS tended to be greater than that of heifers fed AH (1.7 and 1.5, respectively; $P = 0.10$). Gain to feed ratio tended ($P = 0.07$) to be greater in heifers fed BS than AH (0.29 and 0.27, respectively). Dry matter digestibility and intake of digestible DM was unaffected by treatment, being on average 63.5% and 4.1 kg/d, respectively. In conclusion, at 8% of incorporation, barley straw tended to result in a better performance than alfalfa hay when these forage sources were offered as total mixed ration to growing beef heifers.

Key Words: beef cattle, forage source, high concentrate diet

1622 (M336) Metabolism of nitrogenous compounds in beef cattle fed tropical forage supplemented with protein in the rumen, abomasum or both.

E. D. Batista*[1], E. Detmann[1], D. I. Gomes[2], L. M. A. Rufino[1], A. R. Lopes[1], S. C. Valadares Filho[1], M. F. Paulino[1], and E. C. Titgemeyer[3], *[1]Universidade Federal Viçosa, Minas Gerais, Brazil, [2]Universidade Federal Rural da Amazônia, Parauapebas, Pará, Brazil, [3]Kansas State University, Manhattan.*

Four Nellore steers, averaging 280 ± 10 kg BW, fitted with ruminal and abomasal cannulas were used in a 4 × 4 balanced Latin square design to evaluate the effect of protein supplementation in the rumen and/or abomasum on N metabolism in cattle fed tropical forage. The treatments were: 1) control (without supplementation); 2) ruminal supplementation (250 g/d casein); 3) ruminal plus abomasal supplementation (125 g/d casein in the rumen and 125 g/d in the abomasum); and 4) abomasal supplementation (250 g/d casein). Supplements and hay were provided twice per day at 0600 h and 1800 h. The animals were fed with Tifton-85 hay (9.9% CP; 71.5% NDFap) for ad libitum intake. Each period lasted 20 d, comprising 15 d of adaptation and 6 d for sampling. On d 16 through 19 of each period, eight spot samples of abomasal digesta and feces were collected, oven-dried, composited and subsequently analyzed. On d 20 total urine collection was performed. On d 21 blood samples and ruminal fluid were taken every 6 h (beginning at 0600 h) and composited on a daily basis. Supplementation increased ($P < 0.10$) N intake, N total digestibility, N balance, ruminal ammonia-N (RAN), serum urea-N (SUN), renal urea clearance (RUC), RUC proportion excreted, and urinary N and urea excretion. However, there were no differences ($P > 0.10$) between sites of supplementation, except for RAN, SUN, RUC, and urinary N and urea excretion which presented a negative linear effect ($P < 0.10$) by the displacement of supplementation rumen to the abomasum. Ruminal N digestibility, microbial N flow, as well as N retained/N intake were not affected by supplementation ($P > 0.10$). Intestinal N digestibility was increased ($P < 0.10$) by supplementation. Moreover, there was a positive linear effect ($P < 0.10$) on N intestinal digestibility when supplement was changed from the rumen to the abomasum. Fecal N excretion was not affected ($P > 0.10$) by treatments. These results indicate that protein supplementation either in the rumen or in the abomasum, exerts similar effects on efficiency of N utilization, but with different metabolic events.

Key Words: beef cattle, metabolism, nitrogen

1623 (M337) Effect of Amaferm on digestion of diets containing forages with high or low neutral detergent fiber digestibility. A. B. Chestnut*, J. M. Aldrich, W. Hu, W. B. Fokkink, and H. G. Bateman, *Provimi North America, Brookville, OH.*

Amaferm (AF), an extract obtained from fermenting *Aspergillus oryzae*, has been reported to stimulate fiber degrading ruminal fungi and bacteria. The objective of this study was to measure effects of AF on fermentation of typical lactation dairy cow rations containing forages with high NDF digestibility (NDFd) or low NDFd. Corn silage (CS) and alfalfa haylage (AH) with 30 h NDFd of 66.4 and 41.4% of NDF, respectively, were used as the only forages to formulate a high NDFd ration (HFd). A CS and AH with 30-h NDFd of 51.2 and 34.3% of NDF, respectively, were used as the only forages to formulate a low NDFd ration (LFd). Diets were formulated to contain (DM basis) 16.0% NDF from CS and 8.0% NDF from AH. Corn, soybean meal, urea, blood meal, Megalac and molasses were adjusted to equalize CP, soluble CP, starch, nonfiber carbohydrates and fat between diets. A completely randomized experimental design was used with a 2 × 2 factorial arrangement of diet forage NDFd (high or low) and level of AF (0.0 or 0.06% of DM). Diets were fermented in triplicate in continuous culture fermentors at the Rumen Fermentation Profiling Laboratory, West Virginia University, Morgantown, WV. Data on pH were reduced to daily means for each fermentor. Fermentation data were analyzed using the PROC MIXED of SAS with a repeated-measures model. Fermentor was treated as a random variable. First-order autoregressive structure type was selected as the appropriate covariance structure based on the goodness-of-fit criteria. Digestibility (%) of DM, NDF, and nonstructural carbohydrates (NSC) were, respectively, 67.8, 41.4, and 79.3 for HFd, 66.2, 34.8, and 77.5 for HFd + AF, 62.9, 34.9, and 79.3 for LFd and 65.8, 39.6, and 79.5 for LFd + AF. DM digestibility tended to be more for high NDFd vs. low NDFd treatments ($P = 0.08$). Digestibility of NSC was similar among treatments. Adding AF improved NDF digestion of LFd but reduced NDF digestion of HFd (forage NDFd x AF interaction; $P < 0.01$). Average fermentor pH for HFd, HFd + AF, LFd and LFd + AF were 6.03, 6.08, 6.31 and 6.24, respectively, with a main effect due to forage NDFd observed ($P < 0.01$). Adding AF improved NDF digestion of the LFd diet but not the HFd diet. The difference in response of HFd and LFd diets to AF may be related to differences in fermentor pH.

Key Words: Amaferm, NDF digestion

1624 (M338) Differences in forage utilization between *Bos taurus* and *Bos indicus* steers fed low-quality forage and supplemented soybean meal. M. de Oliveira Franco*[1,2], J. E. Sawyer[3], J. R. Baber[4], N. L. Bell[4], E. Detmann[5], and T. A. Wickersham[4], *[1]Universidade Federal de Viçosa, Dep. of Animal Science, Minas Gerais, Brazil, [2]sponsored by CAPES, Brasília, Brazil, [3]Texas AgriLife Research, College Station, [4]Texas A&M University, College Station, [5]Universidade Federal de Viçosa, Minas Gerais, Brazil.*

Five *Bos taurus* (Angus) and five *Bos indicus* steers (Brahman) fitted with ruminal and duodenal cannulae were used in concurrent 5 × 5 Latin squares to determine effects of protein supplementation with varying levels of low quality forage access. Treatments consisted of a control (CON; no supplement and ad libitum access to hay; 2.8% CP, 83.0% NDF) and four treatments arranged as a 2 × 2 factorial: two levels of hay intake (ad libitum and restricted, 1% of initial BW) and two levels of protein (50 and 100 mg N/kg BW, provided as soybean meal 48.5% CP). Periods were 14 d long, with 7 d adaptation and 7 d of sample collection. Data were analyzed using the PROC MIXED of SAS. Terms in the model included treatment, breed, period and treatment × breed, with steer as a random effect. The repeated statement was used for fermentation responses. There were no significant breed differences or treatment × breed interactions for hay intake, digestion, or ruminal fermentation ($P > 0.05$). Supplementation linearly increased ($P < 0.01$) hay intake, total OM intake, and total digestible OM intake in steers given ad libitum access to hay. Feeding 50 or 100 mg N/kg increased total digestible OM intake 34 and 54%, respectively versus CON. Ruminal N balance decreased linearly ($P < 0.01$) in ad libitum fed steers from 36.6 g/d for CON to -30.1 g/d for 100 mg N/kg, suggesting a net influx of urea into the rumen for CON and net absorption of ammonia from the rumen for 100 mg N/kg. When supplement was provided at 50 mg N/kg steers with ad libitum access to hay had greater ($P < 0.01$) ruminal N balance (11.2 g/d) than restricted steers (-3.6 g/d); however, there was only a tendency ($P = 0.09$) for a difference between ad libitum and restricted steers supplemented 100 mg N/kg. Ruminal ammonia N increased linearly ($P < 0.01$) with increasing protein supplementation and was greater ($P < 0.01$) when hay intake was restricted for both levels of N supplement. Similarly, total VFA concentrations were linearly increased ($P < 0.01$) with increasing supplementation; however, VFA concentrations were lower ($P = 0.03$) for both levels of supplementation when hay intake was restricted rather than ad libitum. These data suggest that the forage utilization response to supplemental protein was similar among the subspecies of cattle.

Key Words: low quality forage, protein, supplementation

1625 (M339) Impact of supplementation during the dry season on performance of young Nellore bulls in the post-weaning phase on pasture in the wet season. I. M. de Oliveira*[1], M. H. Moretti[2], A. D. Moreira[3], J. A. Alves Neto[3], R. M. Fernandes[2], P. H. Gonçalves[4], M. A. P. Alves[4], G. F. Berti[4], G. R. Siqueira[1], and F. D. D. Resende[1], *[1]APTA–Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [2]UNESP-FCAV, Jaboticabal, Brazil, [3]Universidade Estadual Paulista, Jaboticabal, Brazil, [4]Centro Universitário da Fundação Educacional de Barretos, Brazil.*

This study evaluated the impact of nutritional strategies on the performance of young Nellore bulls during the post-weaning phase. The experimental period was divided into dry (July to November 2012) and wet (November 2012 to May 2013) seasons. The design was completely randomized, using 60 young Nellore bulls which were distributed into 12 paddocks (experimental units) formed by *Brachiaria brizantha* pastures (5 animals/lot; 6 lots/treatment). In the summer, the paddocks were subdivided (three from each dry season treatment in each new wet season treatment). In the dry season, the animals were assigned to two treatments: a) protein supplement (1 g/kg of body weight; BW) and b) protein and energy supplement (5 g/kg of BW); in the summer were assigned to two treatments: a) mineral supplement ad libitum and b) protein and energy supplement (5 g/kg of BW). To determine the average daily gain (ADG), the animals were weighed at time zero (onset of the experiment) and subsequently every 28 d after being deprived of feed and liquids for 16 h. The data were analyzed as repeated measures over time using the PROC PROC MIXED of SAS. In the dry season, the protein and energy supplementation provided greater ADG (0.434 kg) as compared with the protein supplement (0.293 kg), resulting in heavier animals at the end of this season (225.38 and 208.87 kg, respectively; $P = 0.093$). In the summer, animals fed the protein and energy supplement gained more weight (0.972 kg/day; $P < 0.0001$) in relation to those fed mineral salt (0.623 kg/day). Although no interaction was found in ADG ($P = 0.4798$) between the nutritional plants of dry and wet seasons, the animals which received protein and energy supplementation in the dry season gained less weight (0.766 kg/day; $P < 0.001$) in comparison with those supplemented with protein (0.830 kg/day); this made it possible, at the end of the summer, to eliminate the difference in BW obtained during the dry season. At the end of the post-weaning phase, the young bulls fed protein and energy supplement in the summer completed the period heavier as compared with those fed mineral salt (286.75 and 261.76 kg, respectively; $P = 0.0045$). Protein and energy supplementation during the dry season had negative impact on the ADG in the summer, and increased the BW of the animals at the end of the dry and wet season by 7 and 9%, respectively.

Key Words: energy, performance, protein

1626 (M340) Use of modulators additives the ruminal fermentation in supplements high intake for finished bovines in pasture. J. A. Alves Neto[1], J. M. B. Benatti[1], M. H. Moretti[1], A. D. Moreira[1], R. C. Silva[1], I. M. de Oliveira*[2], P. H. Gonçalves[3], M. A. P. Alves[3], F. D. D. Resende[2], and G. R. Siqueira[2], *[1]Universidade Estadual Paulista, Jaboticabal, Brazil, [2]Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [3]Centro Universitário da Fundação Educacional de Barretos, Brazil.*

Performance of young grazing cattle has been improved by energy supplementation. Additionally, several antibiotics (monensin, lasalocid) have resulted in a consistent grown response. On the other hand, data concerning the effect of virginiamycin in grazing cattle are scarce. Therefore, 96 Nellore bull (480 ± 28 kg BW) were divided in five treatments with different level of supplement and additives blend (T1 = 0.5% BW, T2 = 2% BW, T3 = 2% BW + virginiamycin (25 ppm), T4 = 2% BW + virginiamycin (25 ppm) + monensin (20 ppm), T5 = 2% BW + virginiamycin (25 ppm) + salinomycin (10 ppm). Continue grazing was practiced in *Panicum maximum* cv. Tanzania pasture during dry-season. We used a randomized block design. Twenty paddock (four/treatment) were used divided two blocks (four bull/paddock). Average daily gain (ADG) was calculated using the initial and final individual live weight divided by the number of experimental days. Animals were slaughter in commercial slaughter room and hot carcass weights were obtained to calculate carcass dressing (CD). Statistic analyzer were determined according Proc Mixed SAS 9.0. Paddocks were used as experimental units. Treatments were considered fixed effect and, block aleatory effect. Treatments effects were tested using the following contrasts: 0.5 vs. 2% BW. Animals supplemented with 2% BW shown higher ADG ($P < 0.01$) and had highest CD when compared treatment 2% BW (1.313 vs. 0.534 and 58.4 vs. 53.9, respectively). The effect of virginiamycin and other treatments with 2% BW were tested using contrasts. There were difference ($P < 0.01$) for liveweight gain between treatments 2% BW + virginiamycin (25 ppm) (1.225 kg/d) and 2% BW + virginiamycin (25 ppm) + monensin (20 ppm) (1.505 kg/d), However, 2% BW and 2% BW + virginiamycin (25 ppm) + salinomycin (10 ppm) were not statistically different, the ADG for this treatments were 1.229 kg/d and 1.296 kg/d, respectively. Animals supplemented with virginiamycin ($P < 0.01$) had the highest carcass dressing (59.2) when compared with treatment 2% BW (57.8). Contrast with other treatments not shown statistic difference, achieved 58.7 and 58.0 for treatments 2% BW + virginiamycin (25 ppm) + monensin (20 ppm) and 2% BW + virginiamycin (25 ppm) + salinomycin (10 ppm), respectively. Therefore, increasing supplementation and use of additives may increase animal performance. *Acknowledgment: Phibro Animal Health Corporation.*

Key Words: monensin, pasture, virginiamycin.

1627 (M341) Effects of heights of Marandu pastures and sources of energy supplements on the intake, digestibility of nutrients by young Nellore bulls during the rainy season. A. A. Oliveira[1], M. V. Azenha[*2], S. S. Santana[2], A. L. S. Valente[2], J. P. R. Costa[2], T. T. Berchielli[2], A. C. Ruggieri[2], and R. A. Reis[2], *[1]UNESP, Jaboticabal, Brazil, [2]University of Sao Paulo State, Jaboticabal, Brazil.*

The study was conducted to evaluate the sward heights, and energy supplementation with different sources effects on the forage nutritive value, total DM intake, and digestibility of nutrients by young Nellore bull yearling in pastures of *Urochloa brizantha* cv. Marandu in continuous stocking grazing system during the rainy season. Effects of three sward heights (15, 25, and 35 cm) and three supplements (mineral mixture and two protein-energy supplements, based on corn and other on citrus pulp), were studied. Both energy/protein supplements contained 19.0% of crude protein were supplied at 0.3% of body weight/day. Forage mass, and animal body weight were determined monthly to calculate the forage allowance and the amount of supplement. Experiment was conducted from January to April, at this time forage was sampling by hand plucking methodology to evaluate the nutritive value. Fecal production was estimated using an external marker LIPE; (*Eucalyptus grandis* lignin isolated, purified and enriched). Individual supplement intake was estimated using titanium dioxide (TiO_2) as external marker. Experiment was conducted according to a randomized completely design whit a combination of three pasture heights and three supplements. The average value of NFC was 20.0, 20.0, and 18.9% in pastures of 15, 25, and 35 cm height. There was a linear increase in the levels of NDFap (52.9, 53.6, and 55.9%), and a reduction on the CP levels (16.3, 15.3, and 14.7%) in response to the pasture heights (15, 25, and 35 cm, respectively). Pasture maintained at 15 cm presented highest NPN of total nitrogen, and with 35 cm, showed highest values of N associated to NDF fraction. Intake of DM, OM, and NDF increased linearly in response to sward heights, however diet digestibility decreased. Citrus pulp supplementation as an energy source provided a greatest intake of DM, OM, CP, TDN and also increased the digestibility of DM, OM and CP compared to the others treatments. There was a reduction of NDF digestibility in response to corn supplementation. Swards grazed in lowest height, resulted in lower dry matter intake, but the CP and no fiber carbohydrate intake did not differ among heights, due to the greater proportion of these nutrients in the lowest pastures. It was concluded that swards grazed at lowest height provided forage with better nutritive value. Citrus pulp utilization as a source of energy of supplement increased the intake and digestibility of nutrients.

Key Words: beef cattle, citrus pulp, digestibility, tropical grass

1628 (M342) Within laboratory repeatability of the in situ nylon bag method. H. V. Laar* and J. Doorenbos*, Nutreco R&D, Boxmeer, Netherlands.*

The in situ nylon bag method is the basis of rumen degradation parameters for most feed evaluation models. In our laboratory, over a period of 10 yr all in situ rumen incubations contained a standard sample to study within laboratory repeatability. For raw materials (RM) the standard was a mix of corn, soybean meal and grass meal (1:1:1) to represent starch, crude protein (CP) and fiber fermentation, analyzed in 21 runs. For forage standards were two sequential grass (GS) and corn silages (CS) analyzed in 12 and 11 runs. Approximately 5 g of DM was weighed into 9x18-cm (inner size) nylon bags (40 µm pore size, 30% open surface, Radiometer, The Netherlands). Two or three bags were incubated in the rumen of three lactating fistulated dairy cows at eight time points (up to 336 h). After incubation bags were washed in a washing machine, along with four non-incubated bags per sample (0 h). Samples were pooled over cows by incubation time and analyzed for dry matter (DM), CP, starch and NDF. For each component, washable (W) and undegradable (U) fraction were equated to 0-h loss and 336-h residue. Degradation rate (k_d) was estimated by NLIN procedure of SAS. Effective degradability (ED) was calculated as $ED = W + (100\text{-}W\text{-}U)*(k_d/(k_d+k_p))$ with a k_p (*P*assage rate) of 0.06 for raw material and 0.045 forage standards. Coefficient of variation (CV) was used as measure of repeatability. For the forages CV was based on pooled variation and mean of both standards. Table 1628 shows the CV for ED of various components in RM, GS and CS. CV for NDF is numerically highest for all feeds. For RM, CV of DM is lowest, whereas for GS and CS, CV of CP and starch is lowest. For most components within feedstuff, CV of W, U and k_d(results not shown) was higher than that of ED. These results show that the lowest values for within laboratory repeatability of the in situ nylon bag method are in the range considered poor for analytical laboratory measurements, whereas repeatability values found for NDF are extremely high.

Key Words: In situ, repeatability, fermentation

Table 1628. Coefficients of variation (%) for effective degradation of chemical components of feedstuffs

CV% of ED	Raw Material	Grass Silage	Corn Silage
DM	3.9	5.0	12.2
CP	8.9	3.7	5.6
Starch	10.5	x	5.2
NDF	13.6	9.6	16.4

1629 (M343) Comparison of fermentation kinetics of four feedstuffs using an in vitro gas production system and the ANKOM gas production system.

J. G. L. Regadas Filho*[1], L. O. Tedeschi[2], M. A. Fonseca[2], and L. F. L. Cavalcanti[3], *[1]Universidade Federal de Viçosa, Brazil, [2]Texas A&M University, College Station, [3]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.*

The objective of this study was to perform a comparison between two computerized systems that are used to determine the fermentation kinetics of in vitro gas anaerobic incubation of feedstuffs. The evaluated systems were the ANKOM^{RF} Gas Production Systems (aIVGP) and the in vitro anaerobic fermentation system (tIVGP) as used at Texas A&M University. The aIVGP uses a wireless system, while the tIVGP a wired system to collect the measures. Four different samples of ground corn, alfalfa hay, dried distillers grain, and dried forage were used (n = 16). All components of the fermentation were maintained constant between the IVGP systems (sample: 0.20 g to tIVGP and 0.39 g to aIVGP; rumen fluid: 4.0 mL to tIVGP and 7.8 mL to aIVGP; media: 14.0 mL to tIVGP and 27.3 to aIVGP; and bottle volume: 158 mL to tIVGP and 307 mL to aIVGP). After 48-h, the concentrations of methane in the bottle's headspace was collected and analyzed using a gas chromatographer. The solution pH was measured and the profiles of the feedstuffs were interpreted using nonlinear model. The total gas production (ml/100 mg of DM), fractional production rate of gas (h^{-1}), pH of the solution and methane concentrations (µmole/ml of gas) were used to compare the systems. The levels of agreement between the IVGP systems were determined using the coefficient of determination (r^2) between both predictions (X axis = aIVGP and Y axis = tIVGP), bias correction (Cb); concordance correlation coefficient (CCC) and mean bias (MB). The IVGP systems had similar values for total gas production (mean X = 17.70; mean Y = 21.23; r^2 = 0.81; Cb = 0.85; CCC = 0.77; MB = 3.58; P = 0.2165), methane concentration (mean X = 2.15; mean Y = 2.66; r^2 = 0.89; Cb = 0.83; CCC = 0.79; MB = 0.51; P = 0.0787) and solution pH (mean X = 6.35; mean Y = 6.31; r^2 = 0.90; Cb = 0.98; CCC = 0.93; MB = -0.04; P = 0.6480). However, the estimated values of fractional production rate of gas were different (mean X = 0.1255; mean Y = 0.1031; r^2 = 0.44; Cb = 0.79; CCC = 0.52; MB = -0.022; P = 0.0032). The results suggest that both IVGP systems had similar fermentations patterns. The difference in the fractional production rate of gas between these IVGP systems may be due to difference in the headspace gas composition.

Key Words: gas production, headspace, in vitro systems

1630 (M344) The influence of source and quality of water and a water treatment system on the ruminal fermentation and nutrient digestibility of a total mixed ration using an in vitro gas production measurement system.

D. Casper* and I. P. Acharya, *South Dakota State University, Brookings.*

There is a wide range in water quality available in South Dakota and this variation could have an impact on the performance of lactating dairy cows. In addition, little is known regarding water treatment systems influence on ruminal fermentation. This study was to evaluate the water source and a water treatment system on the rate and/or extent of ruminal fermentation and nutrient digestibility. A standard TMR consisting of alfalfa haylage, corn silage, and a grain mix was dried at 55°C and ground through a ultracentrifuge mill having a 1.0-mm screen. One g of ground TMR was placed in a 50-µm dacron bag, heat sealed, and then placed in a 500-mL Ankom Gas Fermentation Bottle (GFB) to measure rate and extent of digestion. Treatments were: Control (C): laboratory distilled water; KCU: water taken from a local SD dairy operation before the water treatment system; KCT: water taken after treatment with H_2O_2 product; and DRTF: Municipal water used at the SDSU Dairy Research & Training Farm. Treatments were replicated four times as individual GFB and study was conducted in four blocks. Rumen fluid was collected from a ruminally cannulated lactating dairy cow fed the same TMR and strained through four layers of cheesecloth. Twenty mL of rumen fluid with 200 mL of buffer prepared from each of the water treatments were added to the GFB. Bottles were incubated in a circulating water bath at 39°C and gas measurements were collected every 5 min for 30 h. At the completion of 30 h fermentations, Dacron bags were removed, rinsed, and dried to calculate dry matter disappearance (DMD) and NDF concentrations to calculate NDF digestibility. The rate of gas production was greater (P < 0.01) for C (distilled lab water) compared to other treatments. (16.4, 9.50, 9.66 and 9.71%/h for C, KCU, KCT, DRTF, respectively). The DMD (82.0, 81.6, 80.8 and 81.6% for C, KCW, KCT, and DRTF, respectively) tended to be lower (P < 0.09) for KCT water compared to C water, with all other treatments being intermediate and similar (P > 0.10). The digestibility of NDF (60.0, 59.0, 58.3, and 59.6% of NDF) was similar (P > 0.10) for all treatments. The quality of water can influence rate of ruminal fermentation and the use of a water treatment system had minimal influence on ruminal fermentation and digestibility.

Key Words: gas production, nutrient digestibility, water quality

1631 (M345) Relationships between dry matter degradation, in vitro gas production and chemical composition of 15 feedstuffs. Y. J. Xu, M. Zhao, and D. P. Bu*, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

This study was designed to investigate the relationships of in vitro true digestibility of dry matter (IVTD) and in vitro gas production of feedstuffs. Fifteen ruminant feedstuffs were selected in Xinjiang province in China (corn, corn bran, bran, cottonseed meal, soybean meal, DDGS, urea gelatinized corn protein, corn gluten meal, monosodium glutamate residue, grape seed meal, cottonseed hulls, alfalfa meal, alfalfa hay, corn silage and tomato sauce residue). Gas production, volatile fatty acid (VFA) and IVTD at 24-h incubation were measured. Statistical analysis was performed using the PROC CORR procedure of SAS 9.1. The results revealed that strong negative correlation was observed between neutral detergent fiber (NDF) and IVTD ($r^2 = 0.81$, $P < 0.001$). Positive correlation was observed between non-fibern carbohydrate (NFC) and IVTD ($r^2 = 0.74$, $P < 0.001$). In vitro gas production at 24 h was negatively related with NDF content ($r^2 = 0.54$, $P < 0.05$) and positively related with NFC content ($r^2 = 0.92$, $P < 0.001$). In vitro gas production at 24h was positively related with total VFA production ($r^2 = 0.93$, $P < 0.001$). There was strong positive correlation between NFC content and total VFA production ($r^2 = 0.81$, $P < 0.001$). Therefore, chemical composition of feedstuffs were highly related with in vitro gas production, in vitro true digestibility of dry matter.

Key Words: chemical composition, in vitro gas production, in vitro true digestibility of dry matter

1632 (M346) In vitro gas production and dry matter degradability of a high concentrate diet: influence of exogenous enzymes level. D. López[1,2], J. F. Vázquez-Armijo[1], A. F. Z. M. Salem[3], J. Hernández[2], R. Rojo[*1], and J. Cedillo[1], *[1]Centro Universitario UAEM Temascaltepec, México, [2]Universidad Autónoma de Tamaulipas, Ciudad Victoria, México, [3]Universidad Autónoma del Estado de México, El Cerrillo Piedras Blancas, México.*

This study was conducted to evaluate the influence of an exogenous enzyme mixture on in vitro gas production (GP), in vitro dry matter degradability (DMD), metabolizable energy (ME) and short chain fatty acid (SCFA) production in growing lambs fed a high concentrate diet (219 g/kg CP), made with ground sorghum (550 g/kg), alfalfa hay (150 g/kg), soybean meal (220 g/kg), fishmeal (35 g/kg), salt (20 g/kg) and a mineral/vitamins premix (25 g/kg). ZADO (ENZ) is a powdered, commercially available multi-enzyme feed additive produced from *Ruminococcus flavefaciens*. Four levels of ENZ (i.e., 0, 5, 10, and 20 mg/g DM; or E0, E5, E10 and E20, respectively) were applied directly to the substrate inside the incubation bottles before addition of buffer medium and rumen fluid, and the treatments were assayed by triplicate in three runs for different weeks. Bottles were incubated at 39°C for 96 h. The volume of gas produced was recorded at 2, 4, 6, 8, 10, 12, 24, 48, 72, and 96 h after inoculation. A mathematical model was used for estimate lag time, asymptotic gas production and rate of gas production. DMD was determined at end of incubation by filtration of the residue. ME and SCFA were calculated. Data were analyzed as a randomized design and linear and quadratic effects were calculated at $P < 0.05$. Addition of ENZ linearly increased ($P < 0.05$) GP at 6 (74.5, 81.1, 83.7 and 87.5 mL/g DM) and 96 h (334.1, 336.1, 338.5 and 346.8 mL/g DM) of incubation and tended ($P = 0.08$) to linearly increase GP at 12, 48, and 72 h of incubation. Asymptotic GP (334.7, 336.6, 339.1 and 347.3 mL/g DM) was increased linearly ($P = 0.05$) as the level of ENZ increased and the lag time decreased linearly (2.34, 2.12, 1.78 and 1.73 h) ($P = 0.003$). Concurrently, DMD (709, 809, 820, 843 g/kg, repectively) increased linearly ($P < 0.001$) as the level of ENZ increased, but level of ENZ had no effect on SCFA and ME. Finally, level of ENZ had no influence on rate of gas production. Results suggest that this enzyme preparation has potential to improve efficiency of utilization of high concentrate diets fed to growing lambs.

Key Words: enzymes, degradability, gas production.

1633 (M347) In vitro ruminal fermentation with three sources of inoculum in diets containing *Acrocomia aculeate*. S. L. S. Cabral Filho[*1], L. S. Murata[1], R. A. Mandarino[2], C. Eufrásio de Souza[3], D. Leornadi Migotto[3], F. Lopes da Silva[3], J. Artemio Marin Beltrame[4], and J. H. Bernardes Pereira[3], *[1]University of Brasilia, Brazil, [2]Universidade Federal de Minas Gerais, Brasilia, Brazil, [3]Universidade de Brasília, Brazil, [4]Universidade Federal de Mato Grosso do Sul, Campo Grande, Brazil.*

The aim of this study was to determine the potential of different inoculum sources using in vitro gas production technique. Three different sources of inoculum were used for fermentation of gas production analysis: ruminal liquor from fistulated bovine grazing *Brachiaria brizantha* (LR); extracted from slaughtered pig cecum (CS); and cattle feces (FC) collected from the rectum and diluted with distilled water in 10% base. The substrate consisted in three diets content 100% of *Acrocomia aculeate* pulp (AA), 20% AA pulp + 80% of basal diet (20AA) and 10% AA pulp + 90% of basal diet. The basal diet was composed by soy bean meal and corn grains to attempt pig growth requirements. The cumulative volume of gas produced was measured at 0, 3, 6, 9, 12, 16, 24, 48, 72, and 96 h after incubation. The mathematical model used was described by France et al. (1993). The experimental design was one completely randomized blocks in factorial arrange-

ment with eight repetitions (8x3x3). All inoculums showed fermentative capacity and the time of colonization in each trial was lower ($P < 0.05$) for CS followed by LR and FC, was 2.5, 3.2 and 3.7 h, respectively. The substrate with higher potential of gas production was 20AA and presented lower value for FC (205.93 mL) and the difference between LR and CS ($P < 0.05$) (265.05 mL and 299.23 mL). The rates for gas production were: AAxCS, AAxFR, AAxLR (00014 mL.-1h, 0015 mL.-1h and 0028 mL.-1h), 10AAxLR, 10AAxCS, 10AAxFR (00276 mL.-1h, 00410 mL.-1h and 00437 mL.-1h) and 20AAxFR, 20AAxLR, 20AAxCS (00351 mL.-1h, 00365 mL.-1h and 00432 mL.-1h) showed no statistical difference $P > 0.05$). As a conclusion the CS inoculums can be used for the evaluation of gas production.

Key Words: gas production, alternative feed, biogas

1634 (M348) Relationship of protein structural conformation to protein functional property, buffer and water solubility, rumen digestive behaviors, and intestinal availability of common feeds in ruminants. Q. Peng[1,2], N. A. Khan[1], Z. Wang[2], X. Huang[*1], and P. Yu[1], *[1]University of Saskatchewan, Saskatoon, Canada, [2]Sichuan Agriculture University, Sichuan, China*.

The objectives of this study were to determine the relationship between the intrinsic molecular structures of protein feeds and their protein solubility, and rumen and intestinal digestibility in dairy cattle. The feeds investigated were barley, corn, oat, wheat, lentil, peas, canola meal, expeller meal (extruded canola meal), soybean meal, mill feeds (pelleted byproducts from cereal grains), lantic sugar beet pulp, blood meal and meat meal. The protein molecular structure makeup of the feeds was revealed using attenuated total reflectance-Fourier transform infrared molecular spectroscopy (ATR-FTIR). The spectral data on unique bands such as amid I, amide II, and protein secondary structures such as α-helix and β sheet and their ratios were analyzed for differences in intrinsic molecular structures. Moreover, multivariate analysis, agglomerative hierarchical cluster analysis and principal component analysis were computed on the molecular spectral data to distinguish the overall differences in intrinsic molecular structures among the feeds. The protein functional property, solubility, rumen and intestinal digestibility were determined directly using dairy cattle. The PROC MIXED of SAS was used to analyze the univariate spectra data, water-and buffer-based protein solubility, rumen and intestinal protein digestibility. Pearson correlation coefficients between the protein spectral data and protein digestibility were computed using the PROC CORR procedure. A stepwise multiple regression procedure of SAS was performed to determine which of the protein molecular structural features could be used to estimate protein solubility, degradability and digestibility of the prairie feeds. The stepwise option was used with variable selection criteria: SLENTRY = 0.05, SLSTAY = 0.05. The variance inflation factor (VIF) option was used to detect and avoid collinearity among the independent variables. The results showed a large variation in water-and buffer-based protein solubility; ruminal, intestinal and total protein digestibility; and in the inherent structure makeup of protein among the feeds. The protein structural conformation in terms of amide I-and II and protein secondary structures (α-helix and β sheet) were strongly correlated with protein solubility, and ruminal and intestinal digestibility in dairy cattle. The protein structure spectral parameters of amid II area and β sheet height could be used to predict protein intestinal and total digestible content of prairie feeds in dairy cattle. In conclusion, this study report a novel data on protein molecular structure and showed that protein structural makeup was associated with protein nutritional value and digestive behavior in dairy cattle.

Key Words: protein molecular structure, molecular spectroscopy, nutrient availability, metabolic characteristics of protein, ruminants

---

1635 (M349) Carbohydrate-protein matrix structure impacts protein and other primary nutrient digestion in common prairie feeds with different soluble and insoluble fractions. Q. Peng[1,2], X. Huang[*1], Z. Wang[2], and P. Yu[1], *[1]University of Saskatchewan, Saskatoon, Canada, [2]Sichuan Agriculture University, China.*

An experiment was conducted to investigate the relationship of carbohydrates molecular spectral characteristics to rumen degradability of primary nutrients in Prairie feeds in dairy cattle. In total, 12 different types of feeds were selected, each type of feed was from three different source with total 37 samples. Six types of them were energy-sourced feeds and the others were protein-sourced feeds. These feeds included various barley, corn, oat, wheat, lentil, peas, canola meal, expeller meal (extruded canola meal), soybean meal, mill feeds (*P*elleted byproducts from cereal grains), lantic sugar beet pulp, blood meal, meat meal etc. The carbohydrates molecular spectral intensity of various functional groups were collected using Fourier transform infrared attenuated total reflectance (ATR-FT/IR) spectroscopy. In the in situ study, the results showed that the rumen digestibility and digestible fractions of primary nutrients (DM, OM, NCP, and CP) were significantly different ($P < 0.05$) among the feeds. The spectral bands features were significantly different ($P < 0.05$) among the feeds. Spectral intensities of A_Cell, H_1415 and H_1370 were weakly positively correlated with in situ rumen digestibility and digestible fractions of DM, OM and NCP. Spectral intensities of H_1150, H_1015, A_1, and A_3 were weakly negatively associated with in situ rumen degradation of CP. Spectral intensities of A_1240 and H_1240, mainly associated with cellulosic compounds, were correlated with rumen CP degradation. The multiple regression analysis demonstrated that the spectral intensities of A_3 and H_1415

played the most important role and could be used as a potential tool to predict rumen protein degradation of feeds in dairy cattle. In conclusion, this study showed that the carbohydrates as a whole have an effect on protein rumen degradation, rather than cellulose alone, indicating carbohydrate-protein matrix structure impact protein utilization in dairy cattle. The non-invasive molecular spectral technique (ATR-FT/IR) could be used as a rapid potential tool to predict rumen protein degradation of feedstuffs by using molecular spectral bands intensities in carbohydrate fingerprint region.

Key Words: carbohydrate-protein matrix structure, rumen degradability, molecular spectral bands

1636 (M350) Performance and dry matter digestibility of finishing lambs fed diets with ground canola grains. N. I. Ortega-Alvarez[1], G. Buendia-Rodriguez[2], J. A. Cuaron-Ibarguengoytia[2], G. D. Mendoza-Martinez[3], and S. S. Gonzalez-Muñoz[*4], *[1]Universidad Nacional Autonoma de México, México D.F., [2]CENIDFyMA INIFAP, Queretaro, México, [3]Universidad Autonoma Metropolitana, Unidad Xochimilco, México D.F., [4]Colegio de Postgraduados, Montecillo, Estado de México.*

Canola seeds have 42–43% EE, 20% CP, and they can be used as a source of protein and energy for ruminants. The objective of this experiment was to evaluate the effect of ground canola grain (GCG) or canola meal (CM) and canola oilseed (CO) added to a concentrate diet (14.59% CP and 2.8 Mcal ME/kg DM) on finishing 21 Pelibuey x Texel lambs (32.09 ± 5.48 kg initial BW) housed in metabolic cages during 42 d. The experimental design was completely randomized with three treatments: T0: 4.6% CM, 67% sorghum grain, 19.5% alfalfa hay; T1: 7.5% GCG, 63.5% sorghum grain, 19.5% alfalfa hay; T2: 4.5% CM, 3% CO, 64% sorghum grain, 19.5% alfalfa hay (all diets contained 5% cornstalk, 2% cane molasses, 1% urea, 1% premix); and seven replications (lambs) per treatment. Variables were average daily gain (ADG, g), daily DM intake (DDMI, g), feed conversion (FC), carcass yield (CY, %) and DM digestibility (DMD, %). Data were analyzed using PROC MIXED (SAS v 9.0) and treatment means were compared with Tukey test ($P \leq 0.05$). Addition of ground canola grain to the diet did not change ADG (321, 382, 391 g; $P = 0.14$), DDMI (1796, 1671, 1790 g; $P = 0.54$), FC (5.75, 4.47, 4.64; $P = 0.09$), CY (54.13, 52.15, 52.16%; $P = 0.45$) and DMD (74.14, 78.80, 73.87%; $P = 0.13$). Since there were no differences among treatments, it may be concluded that ground canola grain can be used in diets for finishing lambs.

Key Words: canola grain, performance and digestibility, lambs

1637 (M351) Ruminal pH and epithelial function as affected by increasing compound feed supply in growing Holstein heifers. A. Navarro-Villa[1], M. A. Steele[*2], J. A. Metcalf[2], and J. Martin Tereso[1], *[1]Nutreco Research, and Development, Boxmeer, Netherlands, [2]Nutreco Canada Agresearch, Guelph, ON.*

Adaptation to high-concentrate diets involve changes in ruminal milieu and epithelium that remain largely undescribed. Changes in ruminal pH and epithelial function were studied by gradually introducing compound feed (CF)(from 0 to 8kg/d as-fed; Δ+0.5kg/d) in the diet of four fistulated Holstein heifers (8 ± 0.*32* mo of age) with ad libitum access to chopped barley straw. Loggers placed in the ventral rumen continuously monitored pH over 16 d. Cumulative time (min/d) spent below pH cut-off points was calculated for each animal and fitted to a logistic curve (AlZahal et al., 2007), where the slope (β_0; indication of daily pH range) and inflection point (β_1; median pH value) were calculated. Linear correlation between these parameters and CF supply was calculated. Rumen papillae samples were biopsied for RNA extraction and subsequent gene expression analyses when cattle consumed 0, 4, and 8kg of CF/d. Total DM intake was 5.8 ± 0.76, 6.9 ± 1.08 and 8.9 ± 0.71kg/d and straw intake 4.0 ± 0.76, 3.3 ± 1.08 and 1.7 ± 0.71kg/d for CF levels of 0, 4, and 8kg/d, respectively. The daily minimum pH was 6.4 ± 0.19, 6.0 ± 0.12 and 5.8 ± 0.17 at 0, 4, and 8kg/d CF, respectively. In contrast, no changes in daily maximum pH (from 7.3 ± 0.17 to 7.3 ± 0.31) and subtle decreases in daily mean pH (from 6.9 ± 0.1 to 6.7 ± 0.24) were observed with increasing CF intake. The slope of the logistic curve decreased ($P < 0.05$) as the intake of CF increased resulting in 8.7 ± 0.69, 6.6 ± 0.69 and 2.1 ± 0.69 for 0, 4, and 8kg CF/d, respectively. The inflection point decreased ($P < 0.05$) with CF supply but was not affected by CF dose (6.8 ± 0.13, 6.6 ± 0.11 and 6.3 ± 0.21 for 0, 4, and 8 kg CF/d, respectively). Slope correlated better to CF intake [$\beta_0 = 9.5(\pm 0.48)$-$0.6(\pm 0.10)\times$CF(kg); $R^2 = 39$] than inflection point [$\beta_1 = 6.8(\pm 0.06)$-$0.008(\pm 0.010)\times$CF(kg); $R^2 = 0.01$]. The relative mRNA expression of tight junction genes claudin1 (CLDN1) and claudin4 (CLDN4) were downregulated ($P < 0.05$) by 0.77 ± 0.03 and 0.85 ± 0.06-fold between 0 and 4 kg CF inclusion, respectively. Moreover, the relative mRNA expression from 0 to 4 and 0 to 8 kg CF supply was up-regulated ($P < 0.05$) for putative anion transporter 1 (PAT1) (1.25 ± 0.07; 1.39 ± 0.15) and carbonic anhydrase 1 (CA1) (1.20 ± 0.09; 1.30 ± 0.20). Based on the results of this study, adaptation to high-concentrate diets was associated more extreme fluctuations in rumen pH rather than obvious declines in average ruminal daily pH. In addition, adaption to high-concentrate diets involved changes in gene expression of key transport (PAT1), metabolic (CA1) and tight junction genes (CLDN1 and CLDN4) in the epithelium.

Key Words: rumen pH, adaptation, gene expression

1638 (M352) Metabolic characteristics of grazing Nellore bulls receiving concentrated supplementation with additives. J. A. C. Lima[*1,2], H. J. Fernandes[2], E. P. Rosa[2], L. S. Caramalac[2], K. A. Silveira[2], G. C. Silva[2], B. D. D'auria[2], and A. Aguiar[3], *[1]Federal University of Viçosa, Brazil, [2]State University of Mato Grosso do Sul, Aquidauana, Brazil, [3]University of Florida, Gainesville.*

The objective of this study was to evaluate the effect of a commercial concentrate supplement with additives in the metabolic characteristics of grazing bulls, during the dry/rainy transition season in Aquidauana–MS, Brazil. Twelve Nellore bulls (initial body weight of 370 ± 15 kg) were randomly assigned to twelve *Brachiaria decumbens* Stapf pastures (1.0-ha/pasture; one bull/pasture) on a completely randomized design. Treatments were: 1) concentrate supplement Lipomax with homeopathic additives (Convert H, Sodo 100, Figotonus) and Virginiamicina (Lipomax treatment), and 2) concentrate supplement with a similar protein content (18% CP), and without additives (Control treatment). Animals were feed daily at rate of 0.5% of the animal's body weight. After 53 d, when the animals achieved body weight of 426 ± 27.3 kg, urine "spot" and blood samples of the animals were collected, 4 h after the concentrate supplement was offered. Urine samples were analyzed for creatinine (for daily urine total production estimative), N-urea and total-N, and blood samples for serum urea. A significance level of 5% was adopted. Serum urea, and urine N-urea and total-N excretion of the grazing animals showed no difference ($P > 0.05$) when the additives were used in the concentrate supplementation (Table 1638). The low levels of these metabolic parameters for grazing animals indicated an efficient use of the diet metabolizable protein, and the use of additives could not increase this efficiency.

Key Words: grazing bulls, protein metabolism, tropical environment

Table 1638. Parameters of protein metabolism of Nellore bulls grazing brachiaria grass and receiving concentrated supplement with or without additives

	Treatments			
Item	Control	Lipomax	CV (%)	P-value
URbl[1] (md/dl)	15.1	14.7	10.3	0.690
Nururine[2] (g/d)	35.9	33.0	28.6	0.622
Ntotur[3] (g/d)	45.9	55.1	24.8	0.231

[1] URbl is the blood urea, mg/dl.

[2] Nururine is the N-urea in urine, g/d.

[3] Ntotur is the N total in urine, g/d.

1639 (M353) Productive parameters, metabolic and economic viability of dairy cows supplemented with different levels of urea in diets based on sugarcane. R. C. D. Souza[*1], R. B. Reis[2], F. C. F. Lopes[3], J. M. Leão[2], and M. H. F. Mourthé[4], *[1]PUC Minas, Betim, Brazil, [2]UFMG, Belo Horizonte, Brazil, [3]Embrapa Gado de Leite, Juiz de Fora, Brazil, [4]Universidade Federal dos Vales do Jequitinhonha e Mucuri, Diamantina, Brazil.*

Sugarcane has been recommended for dairy farms that utilize low-yielding cows, used in to feeding regimes that do not seek to obtain high lactating performance per animal. The utilization of sugarcane and other feedstuffs, should be based on dietary formulations that incorporate nutritional-model recommendations of practical use (NRC, 2001). Sugarcane was also considered adequate for dairy cattle producing 20 kg of milk per day. The sugarcane yield support potential, in balanced diets, must be defined more precisely to allow recommendations to be specifically targeted. No scientific data exist to support the use of sugarcane in diets formulated for high-performance lactating animals. Sugarcane has been used for animals of higher production due to its qualities, among them, the low cost of dry matter. However, the appropriate level of urea in to add to cane sugar diets feed to high production animal is still questionable. The objective of this study was to evaluate feed intake, nutrient digestibility, feed efficiency, production and milk composition, metabolic parameters and the economic viability of lactating cows fed diets based on sugarcane supplemented with increasing levels of urea: sulfate on dry matter basis (0, 0.5 and 1.0%). Twelve multiparous cows and six primiparous Holstein and Holstein x Gir, with 83 + 7 d of lactation, average milk yield of 21.3 ± 0.8 kg/d, average body weight of 580 + 18.3 kg, fed with total mixed ration 50:50, assigned to reversion assay type switch-back, 3 × 3. Cows fed the diet with 1.0% urea had lower ($P < 0.05$) dry matter intake (DMI) and organic matter intake (OMI), but feed efficiency higher on this diet. DMI, OMI and feed efficiency was 19.64, 19.66 and 18.33 kg/d, 18.24, 18.31 and 17.03 kg/d and 1.14, 1.17 and 1.71 kg/kg, respectively for diets containing 0.0, 0.5, and 1.0% of urea. There was no effect of diet

on nutrient digestibility, milk yield, milk composition and on plasma concentration of urea, glucose and insulin ($P > 0.05$). All diets had a positive balance if considered only cost with food, however the 1% urea diet showed the best outcome per cow. For dairy cows, with an average milk yield of 22 kg/d, sugarcane supplemented with 1% urea in green matter basis despite decreasing the dry matter intake, may be used, without causing any adverse effect on production and metabolic and improve parameters of cost.

Key Words: sugarcane, urea, productive parameters.

1640 (M354) Chia seed supplementation increases ruminal propionate concentration in alfalfa hay based diets evaluated in a dual-flow continuous culture system. J. Bunkers*, E. Marostegan de Paula, L. Galoro da Silva, T. Shenkoru, Y. L. Yeh, B. Amorati, D. Holcombe, and A. Faciola, *University of Nevada, Reno.*

Chia seed (CS) and flaxseed (FS) are rich in omega-3 fatty acids which may provide health benefits when added to animals' diets. However, data on the effects of CS supplementation on ruminal metabolism is scarce. The objective of this experiment was to determine nutrient digestibility, rumen fermentation characteristics, microbial protein synthesis, and long-chain fatty acids flow of supplemented alfalfa hay (AH) diet with either CS or FS. Diets were randomly assigned to six dual-flow continuous culture fermenters (1200 to 1250 mL) in a replicated 3 × 3 Latin square arrangement with three 10-d experimental periods consisted of 7 d for diet adaptation and 3 d for sample collection. Fermenters were fed a total of 72 g of DM/d equally divided in four portions. Diets consisted of (DM basis) 95% AH supplemented with: 5% Megalac (Diet A), 5% FS (Diet B), and 5% CS (Diet C). Liquid and solid dilution rates were adjusted daily to 10%/h and 5%/h, respectively. A sample of 500mL from each fermenter was taken on d 8, 9, and 10. Two subsamples of 10 mL were filtered through two layers of cheesecloth, were preserved with 0.2mL of 50% sulfuric acid and centrifuged for ruminal NH_3 and VFA analysis. Statistical analyses were performed using the GLM procedure in SAS. Ruminal metabolism data are presented in the table. Supplementing CS increased the molar proportion of propionate and decreased Acetate:Propionate ratio. There were no differences among treatments for ruminal NH_3 concentration, total VFA concentration, and molar proportions of acetate, butyrate, and branched-chain VFA. Results from this experiment indicate that CS supplementation may change ruminal metabolism by increasing ruminal propionate concentration which may be energetically beneficial for glucose synthesis in ruminants.

Key Words: dual-flow continuous culture, chia seed, flaxseed

Table 1640.

	Diet Composition %DM				
	Megalac	Flaxseed	Chia seed	SEM	*P*-Value
EE	5.6	5.6	5.6		
CP	18.5	19.2	19.4		
NDF	40.9	41.7	42.5		
NH_3–N, mg/dL	5.34	5.38	6.34	0.58	0.46
Total VFA, mmol	125.61	119.12	116.41	5.02	0.48

1641 (M355) Analysis of rumen motility patterns using a wireless telemetry system to characterize bovine reticuloruminal contractions. A. M. Egert*[1], K. R. McLeod[1], J. L. Klotz[2], and D. L. Harmon[1], *[1]University of Kentucky, Lexington, [2]USDA-ARS, FAPRU, Lexington, KY.*

The objective of this study was to characterize rumen motility patterns of cattle fed once daily. Eight ruminally-cannulated Holstein steers (BW = 321 ± 11 kg) were fed alfalfa cubes once daily at 1.5 × NE_m top-dressed with a TM-salt pre-mix. Three 24-h collection periods were conducted and each commenced immediately following feeding. A wireless telemetry system (emkaPACK*4G* telemetry system, emka TECHNOLOGIES USA, Falls Church, VA) was used to monitor real-time pressure changes in the rumen. Pressure transducers and transmitters were housed in a plastic container with screw-on lid that served as the cannula cap. A weighted (300 g), water-filled (1 L), balloon-tipped catheter was connected to the transducer through an adaptor and placed below the mat in the ventral sac of the rumen. Data were recorded and stored using iox2 software (iox 2.9.4.27, emka TECHNOLOGIES USA) which utilized a rhythmic analyzer to analyze the raw rumen pressure data, identify ruminal contractions, and calculate the following parameters for each contraction: baseline pressure, peak pressure, amplitude, frequency, time to peak, relaxation time, duration, and area under the curve. Mean results were calculated for each parameter (Table 1641). All parameters were affected ($P < 0.0001$) by animal and hour. Baseline and peak pressure of contractions increased through 14 h post-feeding, which may have been due to animals laying down more often. Amplitude of ruminal contractions was greatest the first 5 h post-feeding and then decreased quickly. Frequency, duration, and area decreased throughout the collection period, but increased shortly before the next feeding. Mean water intakes for the first and second 12 h post-feeding were 35.5 ± 2.19 L and 0.92 ± 0.26 L, respectively. These data demonstrate that wireless telemetry can be used to non-invasively monitor rumen motility patterns in freely moving steers. Feeding management impacts the values obtained and must be considered when designing experiments.

Key Words: forestomach, motility, rumen pressure

Table 1641. Means values and range between animals for rumen contraction variables measured

Item, units	Mean[1]	SEM[2]	Range[3]
Baseline, mmHg	22.99	2.35	8.35
Peak, mmHg	30.28	2.47	8.26
Amplitude, mmHg	7.29	0.40	1.04
Frequency, contractions/min	2.87	0.17	0.83
Time to peak, s	4.06	0.33	1.18
Relaxation time, s	5.22	0.47	1.14
Duration, s	9.28	0.62	1.74
Area, mmHg*s	30.41	2.43	6.35

[1] Mean = overall mean
[2] SEM = standard error of the mean, $n = 8$
[3] Range = range of means between the 8 animals

1642 (M356) Use of grouped samples of orts does not compromise feed intake data in studies of confined cattle. D. Zanetti[1], S. C. Valadares Filho*[1], M. V. C. Pacheco[1], L. F. Prados[1], E. Detmann[1], L. A. Godoi[1], F. C. Rodrigues[1], R. C. D. O. Ribeiro[2], J. M. D. Silva Júnior[1], and S. A. Santos[5], *[1]Universidade Federal de Viçosa, Minas Gerais, Brazil, [2]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil, [3]Universidade Federal da Bahia, Salvador, Brazil.*

The orts in the feed bunk are commonly analyzed as composited samples, which are collected within periods of 7 or 28 d for each animal. In this context, the use of only one grouped sample of orts per animal for the entire experimental period may reduce the labor and costs of laboratorial analysis. Therefore, this study aimed to compare samples of orts collected weekly with a grouped sample collected within 12 wk of feedlot. A total of 24 castrated cattle with average body weight of 397.3 kg were fed diets with 70:30 or 40:60 roughage:concentrate ratio using sugarcane as the only roughage source. Diets were provided, sampled and adjusted daily so the orts remained around 5% of the total offered. Orts were sampled daily and proportionally grouped weekly. Sample of orts were analyzed individually or as grouped samples, formed by grouping 12-wk samples of the experiment according to the proportion of orts in the feed bunk. Comparisons of nutrient intake were evaluated using the linear regression model of the values observed for the two sampling methods and the simultaneous hypothesis were tested as it follows: H_o: $\beta 0 = 0$ e $\beta 1 = 1$. Sampling methods were considered similar when the null hypothesis was not rejected. All the statistical analysis was performed by using SAS and differences were considered at $\alpha = 0.05$. The use of these diets allowed a great variation in the composition of orts where the levels of DM ranged from 25.06 to 82.21%, CP ranged from 4.01 to 14.11%, and NDF ranged from 32.52 to 77.06%. Comparisons of the estimates of nutrient intake are presented in Table 1642. In all cases, $H_0$was not rejected ($P > 0.05$) which indicates that dry matter and nutrient intake does not vary comparing orts collected weekly of a composite sample of 12 wk. We conclude that the use of a single sample of orts in the period of 12 wk for each animal is viable and reduces the time and cost of chemical analyzes.

Key Words: feedlot, nutrient intake, orts

Table 1642. Comparisons of estimates of nutrient intake (kg/day)

Treatment	Intake	Average	max	min
Weekly	DM	8.85 ± 1.84	12.58	5.87
	OM[1]	8.42 ± 1.74	11.95	5.60
	CP	1.11 ± 0.23	1.57	0.73
	NDF	3.99 ± 0.73	5.48	2.76
Grouped Samples	DM	8.84 ± 1.84	12.46	5.85
	OM	8.41 ± 1.74	11.84	5.58
	CP	1.10 ± 0.22	1.56	0.73
	NDF	4.00 ± 0.74	5.45	2.73

[1]Organic Matter

1643 (M357) Three dimensional imaging of rumen tissue for morphometric analysis using micro-computed tomography. M. A. Steele*[1], F. Garcia[2], M. Lowerison[3], K. Gordon[2], J. A. Metcalf[1], and M. Hurtig[2], *[1]Nutreco Canada AgResearch, Guelph, ON, [2]University of Guelph, ON, Canada, [3]University of Calgary, AB, Canada.*

Rumen development in calves has been evaluated microscopically by measuring papillae height, width and density. Although common in the literature, there are disadvantages such as large variations in rumen papillae size and shape, small numbers of total papillae being measured and the time required. The objective of this study was to develop a more effective technique for assessing rumen papillae using micro-computed tomography (micro-CT) and to compare this technique with microscopy. Rumen tissue was collected from the ventral sac of 20 bull calves at 55 d of age, immediately fixed in 10% Neutral Buffered Formalin for 48 h and stored in 70% ethanol at 4°C before the contrast enhancement. After evaluation of contrast enhancement protocols which included phosphotungstic acid, osmium tetroxide, and mercury chloride it was determined that mercury provided the most pronounced contrast for accurate micro-computed tomography imaging based on relatively density of the papillae. A 1 cm^2 tissue section from the ventral sac of all bull calves was tensioned on rapid prototype curved plastic holders and imaged at 45-µm resolution for 56 min using a GE Locus Explore micro-CT. MicroView V2.2 software created a three dimensional model of the entire sample. The height and width of 20 papillae per micro-CT section were measured three dimensionally and compared with measurements of 20 papillae under the light microscope taken from the same region using a mixed model equation with a random effect for calf. The length and width measurements using micro-CT (2.47 ± 0.12mm and 0.55 ± 0.01mm) compared to light microscope (2.96 ± 0.03mm and 0.86 ± 0.01mm) were significantly smaller ($P < 0.0001$). The difference may reflect a more accurate determination in the base of the rumen tissue with micro-CT or the specificity of mercury to bind only intact rumen tissue. The mean number of papillae per cm^2 viewed using micro-CT was 128.5 ± 33.9 with a total surface area of 681.8 ± 112.4 mm^2 and volume of 156.2 ± 33.2 mm^3 per sample. Micro-CT data showed that surface area and volume are positively associated ($P = 0.04$) and that papillae length was negatively associated ($P < 0.001$) with papillae per cm^2 and positively associated ($P = 0.02$) with total volume of tissue section as determined by Pearson Correlations. This study represents the first time that micro-CT has been being used to assess morphology of gastrointestinal tissue. Micro-CT has the potential to improve the accuracy and efficiency of rumen tissue measurements however more standardization of each factor involved in tissue preparation and imaging is required.

Key Words: rumen, morphology, development

1644 (M358) Kinetics of gas production of soybean meal, cotton seed meal and fish meal is affected using different zeolites. F. Kafilzadeh, M. Karimi Zandi, and G. Taasoli*, *Razi University, Kermanshah, Iran.*

An in vitro experiment was performed to study the effect of four types of zeolites (Clinoptilolite 1, Clinoptilolite 2, Clinoptilolite A and Heulandites) on kinetics of gas production of three different protein sources (soybean meal, cotton seed meal and fish meal). The cumulative gas production was measured at 2, 6, 10, 14, 18, 22, 24, and 48 h of incubation using a pressure transducer. Each sample was incubated in three replicates. The incubation inoculum was prepared by diluting the rumen liquor with a buffer solution (Tilley and Terry, 1963). Fifteen mL of buffered rumen fluid (20% rumen fluid + 80% buffer solution) prepared and were anaerobically dispensed in each tube at 39°C. All the tubes were crimped, placed in an incubatorat 39°C, and shaken at regular times. A factorial experiment within completely randomized design (CRD) was performed for data on gas production parameters from different protein sources and difference zeolites. All analyses were done on MSTATC program. The result of in vitro gas production showed that there were significant differences between total gas production and lag time of different protein sources ($P < 0.05$). Total gas production was affected by different zeolites ($P < 0.05$). A significant effect of feed × zeolite was observed for the rate at which gas was produced (c) ($P < 0.05$). The mean value for total gas production, lag time and the rate of gas production were 15.68 (ml/125 mg DM), 0.06 (%/h) and 0.31 (h), respectively. Fish meal, among the different protein sources and Clinoptilolite 2 among the different zeolites resulted in the highest gas production rate (0.08). Heulandites produced the highest cumulative gas production (17.41ml/125mg DM) as compared to the other zeolites.

Key Words: gas production, zeolites, protein sources

1645 (M359) Effects of zilpaterol hydrochloride on feedlot performance and carcass characteristics of hair-breed ram lambs. A. Mendoza-García[1], R. Rojo-Rubio[*2], U. Macias-Cruz[3], L. Avendaño-Reyes[4], A. F. Z. M. Salem[5], M. A. Jaime[1], and J. F. Vázquez-Armijo[1], *[1]Universidad Autónoma del Estado de México, Temascaltepec, [2]Universidad Autonoma del Estado de México, Temascaltepec, [3]Universidad Autonoma de Baja California, Mexicali, México, [4]Universidad Autonoma de Baja California, Calexico, [5]Universidad Autónoma del Estado de México, El Cerrillo Piedras Blancas.*

Twenty-one Dorper × Pelibuey croosbred ram lambs (39.01 ± 1.09 kg; 4 mo of age) were individually housed in pens equipped with shade, feed troughs and automatic waterer. Ram lambs were adapted to pens and basal diet, during a 20-d period. One wk before initiation of the experimental phase, lambs were individually weighed, stratified by BW and randomly assigned to treatments under a completely randomized design to evaluate effects of zilpaterol hydrochloride (ZH) levels (ZH; 0, 10, and 20 mg/Lamb daily; to ensure a total intake of ZH, 133.33 g was mixed with 19.1 kg of wheat meal, and 30 g/Lamb daily of mixture was offered to lambs before the morning feeding) on feedlot performance, carcass characteristics, and wholesale cut yield of ram lambs. After a 30-d feeding period, all lambs were harvested. Entire feeding period, ZH increased ($P \leq 0.05$) ADG and tended to increase ($P = 0.076$) feed intake. G:F was not affected ($P = 0.38$). In addition, ZH improved hot carcass weight, cold carcass weight, conformation (ranked 1: bad and 10: excellent), and dressing percent ($P \leq 0.05$). ZH don´t affected ($P \geq 0.05$) KPH fat, but tended ($P = 0.08$) to improved LM area (cm^2). ZH at 10 mg/Lamb dose increased ($P = 0.005$) carcass length (cm), but ZH at 20 mg/Lamb dose showed the highest leg perimeter ($P \leq 0.01$). ZH affected ($P \leq 0.05$) LM pH at 24 h postmortem ($P \leq 0.05$). All non-carcass components were not affected ($P \geq 0.05$) by ZH doses. Leg yield ($P = 0.01$) and plain loin ($P = 0.04$) decreased with ZH and yields of other wholesale cuts were not affected ($P \geq 0.1$). Inclusion of ZH improve some variables of feedlot performance and carcass characteristics of economic importance such as ADG, feed intake and LM area, carcass leg and leg perimeter.

Key Words: β-adrenergic agonist, feedlot sheep, growth rate, carcass characteristics

1646 (M360) Effect of particle size on dry matter intake and ruminal pH in goats fed with alfalfa hay and sorghum silage. D. Esparza[*1], R. Rodriguez[1], G. Veliz[1], C. Meza-Herrera[2], and P. Robles-Trillo[1], *[1]Universidad Autonoma Agraria Antonio Narro, Torreon, México, [2]Universidad Autonoma Chapingo, Unidad Regional Universitaria de Zonas Aridas, Bermejillo, México.*

The aim of this work was to evaluate the effect of particle size on dry matter intake and ruminal pH in Alpine goats. The experiment was designed as a 4 × 4 latin square with eight goats at the end of lactation. Treatments considered a 2 × 2 factorial arrangement; two forage particle lengths of alfalfa hay [short (1 ± 0.03 cm) and long (4 ± 0.05 cm)], combined with two different alfalfa hay and sorghum silage ratio (75:25 or 50:50). The forage:concentrate ratio was 60:40 for all rations. The particle size distribution of the diets was determined with the Penn State Particle Separator using the screen 2 and 3. Each period consisted of 11-d of adaptation stage and 3-d of experimental measurements. Subsequently, diets were exchanged during three periods. Offered food and orts were measured and recorded daily during the last 3 d of each period to calculate food intake. Ruminal fluid was collected on d 14 at 0700, 1100, 1500, 1900, 2300, and 0300 h and ruminal pH was immediately measured. According to our results, alfalfa hay particle

size did not affect voluntary intake (Table 1646), while silage can replace hay without affecting food intake or ruminal pH.

Key Words: goat, particle size, dry matter intake, ruminal pH

Table 1646. Dry matter intake and ruminal pH affected by alfalfa hay particle size

	50:50		75:25			
Diet	Long	Short	Long	Short	SE	*P*- value
DMI	1.39	1.44	1.45	1.53	0.38	NS
Ruminal pH	6.2	6.2	6.2	6.2	0.3	NS

1647 (M361) Milk composition of Murrah buffalo grazing on pasture in the Municipality of Taipu, Rio Grande do Norte, Brazil.

J. M. D. Silva Júnior*[1], T. D. S. Martins[1], R. M. D. Paula[1], L. C. Alves[1], D. Zanetti[2], J. A. D. C. Lima[1], L. F. Prados[1], L. N. Rennó[1], G. J. Melo[3], and W. G. D. Nascimento[3], *[1]Federal University Viçosa, Brazil, [2]Universidade Federal de Viçosa, Minas Gerais, Brazil, [3]Rural Federal University of Pernambuco, Garanhuns, Brazil.*

Brazil produces 27.75 billion liters of milk annually, with 92.3 million L coming from buffalo. There are 2500 establishments registered with the Brazilian Association of Breeders of Buffalo. It is estimated that the country has 2 million buffalo, with 82,000 contributing to milk production. Previous research indicates that buffalo-derived milk has numerically greater fat and total solids when compared to milk from dairy cattle, making it valuable for the dairy industry, especially in the production of mozzarella. The objective of this experiment was to evaluate the milk composition from buffalo within a herd at Tapuio Farm (Taipu, Rio Grande do Norte, Brazil) during the dry season (January to March). Total milk production was measured from 300 multiparous females each d over 1 wk. Samples of milk were collected from each female three times over the same wk. Immediately after collection, samples were sent to the Dep. of Animal Science at the Federal Rural University of Pernambuco for analysis. An overall average was obtained for milk production and composition from the entire herd. The milk composition results are shown in Table 1647 which compares the national average of buffalo, dairy cattle, and the results from this study. The farm's average milk production was 2500 kg/d, with an average individual animal production of 8.3 kg/d. This is above the national average of 7 kg/d for buffalo. However, numerically reduced values were observed for fat and total solids when compared to national averages for buffalo. This may have been due to poor pasture quality, caused by regional drought at the time of sample collection. These results reaffirm the superiority of the milk composition of buffalo compared to dairy cattle. With the improved milk composition of buffalo, it is possible to achieve a 40% yield improvement in the industrialization process when compared to the yield from cattle. This improvement in yield results in increased economic returns to the producer.

Key Words: buffalo, milk composition, yield

Table 1647. A comparison of milk composition between buffalo[1], cattle[1], and buffalo at Farm Tapuio

Nutrient (%)	Buffalo	Cattle	Farm Tapuio
Fat	7.15	3.5	6.42
Protein	4.15	3.6	4.56
Lactose	4.95	4.5	4.55
Total solids	16.86	11.9	16.52

[1] Results reported as a national average (Santos et al., 2001).

1648 (M362) Performance and morphometry of the gastrointestinal tract of goats kept on pasture during the dry period of the semiarid Pernambuco.

J. M. D. Silva Júnior*[1], K. P. Pereira[2], A. S. C. Veras[3], D. K. D. A. Silva[2], J. S. Lima[3], G. J. Melo[2], D. Zanetti[1], T. D. S. Martins[1], R. M. D. Paula[1], L. C. Alves[1], and L. N. Rennó[1], *[1]Federal University of Viçosa, Minas Gerais, Brazil, [2]Rural Federal University of Pernambuco, Garanhuns, Brazil, [3]Rural Federal University of Pernambuco, Recife, Brazil*.

The carcass length, your characteristics and of non-carcass components are directly related to the nutritional composition of the diet. The production of good quality protein also depends on the genotype and the environment in which the animal is held, which points to the importance of the use of supplementation, at the time of low rainfall, which creates food shortages, especially in native pasture, which is characterized by high variation in the chemical composition throughout the year, especially when it comes to semiarid region, Caatinga vegetation, which has its own characteristics, such as loss of leaves and disappearance of native species in the dry season. The experiment aimed to evaluate the endogenous losses in goats kept in grazing unrestricted with and without supplementation, and restricted grazing. Eighteen animals were used without pattern purebred (WPPB), neutered, with average live weight of 16 kg ± 0.22 BW with 90 d of age, undergoing an adjustment period for 15 d. The animals were divided into three treatments: grazing at will without supplementation to slaughter (GWS), grazing at will over supplementation with forage palm + soybean meal (GS) and restricted grazing (RG), with access to pasture during about four h/d, or according to the maintenance of BW. For statistical analysis was used the test F with 5% of probability. A significant difference was observed for slaughter weight ($P = 0.00023$) with higher means for the treatment GS (22.74 BW) when compared with others treatments, however there was no difference between the GWS (18.12 BW) and RG (16 BW) treatments. The same behavior was also observed for weight empty body (18.4 BW, 14.34 BW and 12.60 BW, respectively) ($P = 0.00026$). A significant

difference (P = 0.00965) was observed for rumen/reticulum, omasum, small intestine, and total gastrointestinal tract to the GS did not differing between GWS and RG. WPPB goats supplemented during the dry period had higher values of morphometric gastrointestinal tract in relation to goats kept on pasture only or restricted grazing.

Key Words: goats, growth, pasture

1649 (M363) Effects of replacing alfalfa hay and corn silage with corn straw in diets on milk production and composition of dairy cows. Y. Zhang[1,2,3], N. Zheng[1,2,3], D. P. Bu[3], M. Zhao[3], X. Q. Zhou[3], and J. Wang[*1,2,3], *[1]Ministry of Agriculture–Laboratory of Quality and Safety Risk Assessment for Dairy Products, Beijing, China, [2]Ministry of Agriculture–Milk and Dairy Product Inspection Center, Beijing, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China.*

A study was conducted to determine the effects of replacing alfalfa hay and corn silage as the only forage source with corn straw on milk production and composition. Thirty-two primiparous Holstein cows (55 ± 15 d, days in milk) were divided into two groups fed ad libitum a TMR containing either 17.30% alfalfa hay and 18.77% corn silage (control group) or 36.07% corn straw (CS group). The experiment period was 105 d with 14-d adaptation. Cows were fed individually with auto feeding system and food intake was recorded continuously using a computerized monitoring system (RIC system, Insentec B.V., Marknesse, Netherlands). Data were analyzed using the PROC MIXED of SAS (SAS 8.2; SAS Institute Inc., Cary, NC). Dry matter intake (21.35 vs. 17.43 kg/d, $P < 0.01$), crude protein intake (3.84 vs. 2.90 kg/d, $P < 0.01$) and consumption rate (103.25 vs. 68.65 g DM/min) were higher in the control cows, indicating more attractiveness to the cows. Higher milk yield (30.45 vs. 23.12 kg/d, $P < 0.01$), milk protein content (3.66 vs. 3.32%, $P < 0.01$) and yield (1.11 vs. 0.77 kg/d, $P < 0.01$), milk fat yield (1.34 vs. 1.02 kg/d, $P < 0.01$), milk lactose yield (1.47 vs. 1.13 kg/d, $P < 0.01$) were observed in the control cows, whereas milk fat content (4.46 vs. 4.38%, $P = 0.65$), and milk lactose content (4.86 vs. 4.80%, $P = 0.09$) were similar in the two groups. Feed efficiency (1.45 vs. 1.32%, $P < 0.01$), and milk N efficiency (29.68 vs. 26.67%, $P < 0.01$) were higher for control group compared with CS group. In conclusion, replacing alfalfa hay and corn silage with corn straw decreased milk production, and affected milk composition.

Key Words: milk composition, forage, dairy cow

1650 (M364) The use of favored or unfavored ingredients in starter feeds for preweaned calves. M. Terré[*1], and A. Bach[2], *[1]IRTA, Caldes de Montbui, Spain, [2]Dep. of Ruminant Production, IRTA, Caldes de Montbui, Spain.*

When calves are allowed to choose among different ingredients, soybean meal and wheat are the most consumed ingredients commonly used in starter concentrates, whereas canola and oats are among the least consumed. The objective of this study was to evaluate three different starter feeds containing ingredients of different acceptance by calves. Sixty-three (n = 21) Holstein male calves (41 ± 1.3 kg BW, 9 ± 0.9 d of age) were grouped in three treatments: a starter feed (18.6% CP, 21.4% NDF) based on soybean meal (17.5%), wheat (22%) and corn (24%), a starter feed (18.1% CP, 21.5% NDF) based on canola (15%), wheat (22%) and corn (18%), and a starter feed (20.3% CP, 18.5% NDF) based on soybean meal (18.5%), oats (24%) and corn (26.5%). All starter feeds were in a pellet form, and straw was also offered ad libitum. The milk replacer feeding program was the same for all three treatments: 4 L/d at 12.5% DM concentration from 1 to 7 d of study, 6 L/d at 12.5% DM from 8 to 35 d of study, and 3 L/d at 12.5% DM from 36 to 42 d (weaning). Animals were weighed weekly until the end of the study at 49 d, and milk replacer and starter feed intake measured daily. At 30 and 50 d of study, liquid rumen samples were obtained to determine rumen pH. Data were analyzed by PROC MIXED of SAS with repeated measures, being concentrate ingredients composition and week of the study, and their interaction the main effects, and initial BW as a covariate. Animals in all three treatments had similar performance and intake parameters (0.64 ± 0.045 kg DM/d of starter intake, 0.62 ± 0.027 kg/d of ADG). There were no differences in rumen pH (5.65 ± 0.084 pH) among the three treatments. In conclusion, the inclusion of a non-favored ingredient such as canola or oats in a pelleted starter feed did not affect performance parameters of preweaned calves.

Key Words: calf, ingredient composition, performance

RUMINANT NUTRITION II

1651 (T264) In vitro assessment of *Saccharomyces cerevisiae* cell fractions (YCF) using bovine epithelial cells and macrophages. Z. Li[*1], Q. You[1], F. Ossa[2], P. Mead[1], and N. A. Karrow[3], *[1]University of Guelph, Guelph, ON, Canada, [2]Lallemand Inc., Montreal, QC, Canada, [3]Dep. of Animal and Poultry Science, University of Guelph, ON, Canada.*

Since yeast *Saccharomyces cerevisiae* and its cell fractions (yeast cell fractions) are being used for the prevention and treatment of enteric diseases in different species, they may also be useful for preventing Johne's disease, a chronic inflammatory bowel disease of ruminants caused by *Mycobacterium avium* ssp. *paratuberculosis* (MAP). In this study, the adhesion of mCherry-labeled MAP to bovine mammary epithelial cells (Mac-T) co-cultured with CFs from two specific yeast strains (A and B)from the Lallemand culture collection was investigated. Additionally, bovine macrophages (BoMacs) were used to assess potential immunomodulatory properties of these yeast CFs by measuring BoMac viability, reactive oxygen species (ROS) production, and phagocytosis of mCherry-MAP. The Mac-T cells were treated for 6 h with the two CFs at different concentrations (0.25, 0.5, 1, 2, 4, 8, and 16 mg/ml). The highest concentration of CFs that did not affect the Mac-T cell viability was 4 mg/ml for the strain A, and 2 mg/ml for strain B. Non-cytotoxic concentrations of yeast CFs from both strains reduced MAP adhesion to Mac-T cells in a concentration-dependent manner. BoMac cell viability was also assessed after a 6-hour treatment with both yeast CFs, and concentrations $\leq$ 4 mg/ml were deemed non-cytotoxic. BoMac ROS production was measured at non-cytotoxic yeast CF concentrations, and a dose-dependent increase in ROS production was found for both yeast CFs, with strain A being more potent than strain B. Finally, BoMac phagocytosis of m-Cherry-MAP, assessed after 6 h, was prevented by co-culture with non-cytotoxic concentrations of yeast CFs. In summary, yeast CFs may be useful for preventing MAP adhesion to the gastrointestinal epithelium and for stimulating macrophage antimicrobial ROS production.

Key Words: prebiotic, immunomodulation, bovine mammary epithelial cells (Mac-T)

Table 1652. Digestibility of the diet of grazing Nellore bulls receiving concentrated supplementation with or without additives

	Treatments			
Item, %	Control	Lipomax	CV (%)	*P*-value
CDEE1	79.0a	67.9b	7.19	0.004
CDCP2	77.8	75.2	7.46	0.359
CDNDF3	68.2	67.8	7.88	0.817
CDNFC4	74.7	73.8	11.4	0.949
ME5 (Mcal/Kg)	2.488	2.395	4.68	0.187

[1] CDEE is the coefficient of digestibility of ether extract
[2] CDCP is the coefficient of digestibility of CP.
[3] CDNDF is the coefficient of digestibility of NDF.
[4] CDNFC is the coefficient of digestibility of non-fiber carbohydrates.
[5] ME is the metabolizable energy of the diet.

1652 (T265) Digestibility of the diet of grazing Nellore bulls receiving concentrated supplementation with additives. J. A. C. Lima[*1,2], H. J. Fernandes[2], M. F. Paulino[1], E. P. Rosa[2], L. S. Caramalac[2], K. A. Silveira[2], B. D. D'auria[2], and A. Aguiar[3], *[1]Federal University of Viçosa, Brazil, [2]State University of Mato Grosso do Sul, Aquidauana, Brazil, [3]University of Florida, Gainesville.*

The objective of this study was to evaluate the effect of a commercial concentrate supplement with additives in the digestibility of the nutrients on grazing bulls, during the dry/rainy transition season in Aquidauana–MS, Brazil. Twelve Nellore bulls (initial body weight of 370 ± 15 kg) were randomly assigned to 12 *Brachiaria decumbens* Stapf pastures (1.0 ha/pasture; one bull/pasture) on a completely randomized design. Treatments were: 1) concentrate supplement Lipomax with homeopathic additives (Convert H, Sodo 100, Figotonus) and Virginiamicina (Lipomax treatment), and 2) concentrate supplement with a similar protein content (18% CP), and without additives (Control treatment). Animals were feed daily at rate of 0.5% of the animal's body weight. After 45 d, when the animals achieved body weight closed to 420 kg, the digestibility trial started. Digestibility was estimated using the enriched and purified lignin (LIPE) as marker for fecal excretion estimation, and the indigestible neutral detergent fiber as internal marker. Forage nutritive value was estimated by hand-plucked sampling, and supplement intake was measured directly for each animal. A significance level of 5% was adopted. The coefficients of digestibility (CD) of the nutrients were obtained by the intake and composition of the forage and the supplement, and by analysis of feces, which was collected for five consecutive days. A significance level of 5% was adopted. The digestibility of the ether extract differed ($P < 0.05$), was greater in the Control treatment (Table 1652) and no other differences were significant. The similarity in composition between concentrated supplements, and the fact that the concentrate represented just around 10% of the diet of the animals influenced these results. The additives appears to work just in the animal's metabolism, without affecting the diet digestibility.

Key Words: additives, digestibility, grazing bulls

1653 (T266) Pre- and post-weaning performance and health of calves fed 24% crude protein and 20% fat milk replacer at different feeding rates.

B. M. Strayer*[1], D. Ziegler[2], D. Schimek[3], B. Ziegler[3], M. Raeth-Knight[4], H. Chester-Jones[2], and D. Casper[1], *[1]South Dakota State University, Brookings, [2]University of Minnesota Southern Research and Outreach Center, Waseca, [3]Hubbard Feeds Inc., Mankato, MN, [4]University of Minnesota, St. Paul.*

In our previous work, calves fed greater amounts of milk replacer (MR) and CP demonstrated improved growth. The current study was to evaluate the pre- (d 1 to 42) and post- (d 43 to 56) weaning performance and health of calves fed a 24% CP and 20% fat MR at different feeding rates (FR). One hundred four (1- to 5-d-old) individually fed Holstein heifer calves (40 ± 0.69 kg) were randomly assigned to one of four treatments in a randomized complete block design. The same all milk MR was fed at 14.7% solids with treatments being 1) Control (MR57): MR fed at 0.284 kg in water twice daily for 35 d; 2) MR71: MR fed at 0.34 kg twice daily from d 1 to 7 and at 0.34 kg twice daily from d 8 to 35; 3) MR85: MR fed at 0.34 kg twice daily from d 1 to 7 and at 0.43 kg twice daily from d 8 to 35; and 4) MR99: MR fed at 0.34 kg twice daily from d 1 to 7 and at 0.497 kg twice daily from d 8 to 35. All treatments were fed once daily MR from d 36 to weaning at d 42 with water and an 18% CP texturized calf starter (CS) offered free choice. Pre-weaning and overall ADG (0.78, 0.82, 0.83 and 0.85 kg/d for MR57, MR71, MR85, and MR99, respectively) were higher ($P < 0.05$) for MR99 calves vs. MR57 calves with other calves being intermediate. Overall d 1 to 56 CS intakes were higher for MR57 calves vs. other calf groups. There were no differences ($P > 0.05$) in total DMI. Pre-weaning gain/feed was lowest ($P < 0.05$) for MR57 calves. Gain/feed d 1 to 56 (0.49, 0.52, 0.52 and 0.54 kg/kg DM) was higher for MR99 vs. MR57 calves with other calves being intermediate. This study demonstrated that feeding higher FR of a 24:20 MR resulted in higher ADG's and feed conversions (gain/feed).

Key Words: milk replacers, feeding rate, calf performance

1654 (T267) Pre- and post-weaning performance and health of calves fed milk replacers with two protein concentrations and two feeding rates.

B. M. Strayer*[1], D. Ziegler[2], D. Schimek[3], B. Ziegler[3], M. Raeth-Knight[4], H. Chester-Jones[2], and D. Casper[1], *[1]South Dakota State University, Brookings, [2]University of Minnesota Southern Research and Outreach Center, Waseca, [3]Hubbard Feeds Inc., Mankato, MN, [4]University of Minnesota, St. Paul.*

One hundred eight (1- to 5-d-old) Holstein heifer calves (39.3 ± 0.66 kg) were randomly assigned to one of four milk replacers (MR) to evaluate pre- (d 1 to 42) and post- (d 43 to 56) weaning performance in a 2 × 2 factorial design of crude protein (CP) concentrations (20% (CP) and 24% (HP)) with feeding rates (FR; 0.57 (1) and 0.68 (2) kg/d). Treatments were MR fed at 15% solids of: 1) Control (CP1): a 20% CP:20% fat MR fed at 0.284 kg 2x/d for 35 d; 2) CP2: the 20:20 MR fed at 0.34 kg 2x/d for 35 d; 3) HP1: a 24:20 MR fed at CP1 rate; and 4) HP2: the 24:20 MR fed at CP2 rate. All MR's were fed at 1x/d from d 36 to weaning at d 42 with water and 18% CP texturized calf starter (CS) offered free choice through d 56. No significant ($P > 0.10$) interactions of CP by FR were detected for growth parameters. During d 1 to 14, calves fed CP2 and HP2 had the greatest ADG (0.36, 0.44, 0.36, and 0.45 kg/d for CP1, CP2, HP1 and HP2, respectively) compared to calves fed CP1 and HP1, but the interaction was nonsignificant ($P > 0.10$). Pre-weaning ADG's (d 1 to 42) were similar ($P > 0.10$). Calves fed HP2 had numerically greatest overall ADG d 1 to 56 compared to calves fed CP1 and HP1 with CP2 being intermediate. Intake of CS from d 1 to 56 was similar ($P > 0.10$) for calves fed MR with different CP concentrations (0.77 and 0.78 kg/d), while CS intake (0.81 and 0.74 kg/d) was reduced ($P < 0.05$) for calves fed higher MR FR. Feed conversions from d 1 to 56 were similar for calves fed different CP concentrations (0.54 and 0.55 kg/kg), but were improved when fed higher MR FR (0.53 and 0.56 kg/kg). However, a trend ($P < 0.11$) of CP by FR interaction from d 43 to 56 demonstrated calves fed CP2 having greater feed conversions (0.46, 0.53, 0.46 and 0.49 kg/kg for C-, C+, HP-, and HP+, respectively) compared CP1, HP1 and HP2 calves. Thus, indicating a carryover effect on post-weaning performance for CP2 calves. The results demonstrate calves fed a conventional MR at different FR with different CP concentrations performed similarly. Calves fed higher CP MR at higher FR had numerically the greatest ADG.

Key Words: milk replacers, protein concentration, feeding rate

1655 (T268) The effect of dietary supplementation of artificial sweetener on performance of milk-fed calves.

A. Siurana*[1], E. H. Wall[2], M. Rodríguez[1], L. Castillejos[1], A. Ferret[1], and S. Calsamiglia[1], *[1]Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Pancosma, Geneva, Switzerland.*

The small intestine contains nutrient receptors that react to changes in the composition of ingested feed. The feed additive Sucram (Pancosma, Switzerland) is an artificial sweetener that has been shown to increase absorption of glucose from the small intestine by activating sweet taste receptors in swine, this response results in improved animal performance. Recently, it was reported that a similar increase in glucose absorption was observed in calves supplemented with Sucram; however, it was unclear if there is a corresponding improvement in calf performance. Therefore, the current experiment was per-

formed to determine the effect of Sucram on performance of milk-fed calves. Sixteen male Holstein calves were assigned to two treatments (n = 8 per treatment): control (no additive), or Sucram (daily supplementation of 400 mg g Sucram per kg dry matter of milk replacer). All calves received 2 feeding/d of 2 L of milk replacer plus ad libitum commercial concentrate until weaning (50 d of age). Calves were weighed at the beginning and at the end of the experiment. Individual calf concentrate intake was measured weekly. Blood samples were collected the last day of the trial before feeding to analyze levels of insulin and glucose. Feed efficiency was calculated for each animal (total weight gain/average weekly concentrate intake from wk 2 to 5). Data were subjected to analysis of variance using the PROC MIXED of SAS. For body weight and concentrate intake, data for wk 1 were used as a covariate in the analysis. There were no effect of Sucram on final body weight (67.0 *vs.* 67.3 kg; P = 0.93), but there was a decrease in feed intake of Sucram calves (6.5 vs. 5.7 kg/wk; P = 0.10). Therefore, efficiency of feed was higher in animals supplemented with Sucram (gain/feed = 4.8 vs. 5.71; P = 0.10). There was no effect of Sucram on the concentration of serum insulin (0.23 vs. 0.21 µg/L; P = 0.74) or glucose (78.8 vs. 82.6 mg/dL; P = 0.45). We conclude that supplementation of milk-fed calves with artificial sweetener improves feed efficiency. However, additional experiments are needed to determine the mechanism underlying this response. The use of Sucram in milk replacer represents a potential management tool for dairy producers to increase feed efficiency of milk-fed calves and decrease the cost of animal rearing on commercial farms.

Key Words: sweetener, performance, milk-fed calves

1656 (T269) The effect of supplementation with a blend of capsicum, carvacrol, and cinnamaldehyde on performance of milk-fed calves. A. Siurana*[1], E. H. Wall[2], M. Rodríguez[1], L. Castillejos[1], A. Ferret[1], and S. Calsamiglia[1], *[1]Animal Nutrition and Welfare Service, Dep. of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Pancosma, Geneva, Switzerland.*

Plant extracts have antimicrobial properties that may reduce the risk of disease and improve the health and performance of young animals. The objective of this experiment was to study the effect of an essential oil feed additive (EO; XT-6930; Pancosma, Switzerland) on the performance of milk-fed calves. Eight male Holstein calves were randomly assigned to one of two treatments (n = 4 per treatment): control (no additive) or EO (115 mg/calf/d of XT-6930 added to milk replacer). Calves were housed in individual hutches and received 2 feeding/d of 2 L of milk replacer (22.4% CP, 20.6% fat) plus ad libitum access to commercial concentrate (16.9% CP; 5.3% crude fiber) until weaning (50 d of age). Calves were weighed at the start and the end of the experiment and concentrate intake was measured individually once a week. Feed efficiency was calculated for each calf as the ratio of body weight gain to average concentrate intake during the experimental period (wk 2 to 5). Blood samples were collected from the jugular vein on the last day of the experiment before feeding to analyze insulin and glucose concentrations. Average daily weight gain was higher (P = 0.02) in EO calves (0.83 kg/d) compared with control (0.63 kg/d) and feed intake was also higher (P = 0.01) in EO compared to control calves (7.23 vs. 5.71 kg/wk, respectively). The efficiency of feed conversion was not affected by treatment (gain/feed = 4.11 vs. 4.09 for EO and control calves, respectively; P = 0.95). There was no effect of treatment on serum concentrations of insulin (0.80 vs. 1.69 µg/L for control and EO, respectively; P = 0.31) or glucose (91.6 vs. 106.2 mg/dL for control and EO, respectively; P = 0.29). We conclude that supplementation of milk replacer with EO increased concentrate intake of milk-fed calves. Although there was no effect on feed efficiency, the increase in average daily weight gain has implications for decreasing costs associated with animal rearing. In addition, the increase in the intake of starter grain may enhance development of the rumen and subsequent animal performance.

Key Words: plant extracts, performance, calves

1657 (T270) Effect of milk replacer solids content on intake, growth and fecal characteristics of Holstein calves. J. D. Quigley*, T. M. Hill, H. G. Bateman, II, J. M. Aldrich, and R. L. Schlotterbeck, *Provimi North America, Brookville, OH.*

Increased energy intake during cold weather is required to maintain adequate calf growth. Many producers have limited ability to increase volume of liquid offered to calves; therefore, increasing solids content (SC) of the MR solution can increase energy content of milk replacer (MR). Common SC are 12 to 13%, but calves may be fed MR with SC up to 18% in some situations. It is unclear whether changing SC may affect performance, intake or health of young calves fed MR. Our objective was to compare different SC in calves fed MR to 56 d. Holstein bull calves (n = 48; initial BW = 45.4 ± 4.0 kg; 2 to 3 d of age) were assigned randomly to receive a commercial MR (Nurture Plus EZ, Provimi North America, Brookville OH) at 0.625 kg of MR powder from 0 to 39 d, then 0.313 kg/d until weaning at d 42. The MR (23% protein and 21% fat, DM basis) was diluted to 10.0, 12.5, 15.0, or 17.5% SC and offered twice daily in open pails. Amount of reconstituted MR offered was 6.25, 5.00, 4.17 and 3.57 kg/d for 10.0, 12.5, 15.0 and 17.5% SC, respectively. Texturized calf starter (CS; 20% CP, DM basis) and water were available for ad libitum consumption throughout the study. Data were analyzed as a completely randomized design using a repeated measures ANOVA. Orthogonal polynomials were used to determine linear and quadratic effects of SC. Pen was the experimental unit. There was no effect (P > 0.10) of SC on average daily gain (0.57 ± 0.027 kg/d), CS intake (0.74 ± 0.06 kg/d), MR intake (0.603 kg/d to weaning),

gain to feed ratio (0.48 ± 0.017 kg ADG/kg DM intake), or hip width change (0.1 ± 0.01 cm/d) from d 0 to 56. Number of abnormal fecal days and medical days preweaning declined linearly ($P < 0.05$) with increasing SC. Number of preweaning abnormal fecal days were 0.22, 0.13, 0.13 and 0.07 ± 0.039 and preweaning medical days were 0.32, 0.25, 0.19 and 0.08 ± 0.056, respectively, for calves fed 10.0, 12.5, 15.0, and 17.5% SC. Increasing milk replacer SC reduced abnormal fecal days and number of treatments.

Key Words: calves, milk replacer, growth

1658 (T271) Pre- and post-weaning performance and health of dairy calves fed all-milk protein milk replacers or partially replacing milk protein in milk replacers with plasma, wheat proteins and soy protein concentrate. D. Ziegler[*1], H. Chester-Jones[1], B. Ziegler[2], D. Schimek[2], M. Raeth-Knight[3], and D. L. Cook[4], *[1]University of Minnesota Southern Research and Outreach Center, Waseca,, [2]Hubbard Feeds Inc., Mankato, MN, [3]University of Minnesota, St. Paul, [4]Milk Products, Chilton, WI.*

One hundred five (2- to 5-d-old) individually fed Holstein heifer calves (39.8 ± 0.73kg) were randomly assigned to one of four treatments to evaluate pre- (d 1 to 42) and post weaning (d 43 to 56) calf performance and health when fed milk replacers (MR) with alternative protein sources. Calves were assigned to non-medicated MR with 1) All milk protein (AM), 2) 50% of total protein from wheat and plasma (WPL), 3) 50% of total protein from soybean protein concentrate (SPC) and plasma (SPL), and 4) 50% combination of wheat, SPC and plasma (SWP). All calves were fed a non- medicated 20% fat:20% CP MR at 0.284 kg in 1.99 L water (12.5% solids) 2x/d for the first 35 d and 1x/d d 36 to weaning at 42 d. Day 1 to 14, 1:1 neomycin:oxytetracycline was added to the MR solution to provide 22 mg/kg BW/d. Calf starter (CS; 18% CP) and water were fed free choice from d 1. Osmolality of the MR were 469, 421, 395, and 412 mOsm/L for AM, WPL, SPL, and SWP, respectively. There were no pre- ($P = 0.11$) or post ($P = 0.30$) weaning ADG differences. Calves averaged 0.74 kg/d gain for the 56-d study. There were no differences in CS ($P = 0.22$) or total DMI ($P = 0.33$) intake, which averaged 55.3 and 77.08 kg for the 56-d study, respectively. Pre-weaning gain/feed was higher ($P < 0.05$) in calves fed WPL vs. those fed SPL and SWP but similar to AM calves. There were no overall 56-d differences in gain/feed ($P = 0.19$). Across treatments, calves doubled their initial BW and gained > 10.2 cm in frame growth. Fecal scores d 1 to 14 and overall were higher ($P < 0.05$) for AM fed calves compared to WPL, SPL, and SWP treatments. The number of scouring d pre-weaning were also higher ($P < 0.05$) for AM calves vs. those fed SPL and SWP with WPL calves being intermediate. There were no differences in health treatment costs. Under the conditions of this study, replacing 50% of the total milk protein in MR with alternative sources resulted in calf performance and health similar to all milk protein.

Key Words: calf performance, milk replacers, alternative proteins.

1659 (T272) Effect of Radix Bupleuri herbal supplementation on diversity of the bacterial community and cellulolytic bacteria in the rumen of lactating dairy cows analyzed by DGGE and RT-PCR. L. Pan, D. P. Bu*, J. Q. Wang, J. B. Cheng, X. Z. Sun, and W. Liu, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*.

Numerous studies have been completed on use of herbal medicine in substitute for chemical feed additives to modify rumen fermentation. This experiment was conducted to investigate effects of *Radix Bupleuri* herbal supplementation (RBH) on diversity of the bacterial community and cellulolytic bacteria including *Fibrobacter Succinogenes, Ruminococcus albus* and *Ruminococcus flavefaciens* in the rumen of lactating dairy cows analyzed by DGGE and RT-PCR. Forty Holstein cows were assigned to one of 4 groups ($n = 10$) according to milk yield (37.5 ± 1.8 kg/d), day in milk (75 ± 15) and parity (1.7 ± 0.4) in a completely randomized block design. Four treatment diets consisted of supplemental RBH at 0, 0.25, 0.5 or 1.0 g/kg based on dry matter, which were randomly assigned to one of 4 groups. Cows were individually fed the treatment diets, and the experiment lasted for 10 wk in Shanghai. Rumen fluid samples were collected at 2 h post-feeding using stomach-tube on wk 6 of the trial. Rumen samples were strained through four layers of cheesecloth and frozen at -20°C until being analyzed. Rumen microbial DNA was extracted with CTAB plus bead beating and analyzed by DGGE with subsequent cluster and optimal density of the bands analysis. The copy number of rumen cellulolytic bacteria was detected by quantitative RT-PCR with species-specific PCR primers amplifying partial 16S rDNA regions. Diversity index values and data of copy numbers of 16s rDNA were analyzed using GLM procedure of SAS 9.2. DGGE profiles showed that the quantity of bands was similar, while the optimal density was different between control and treatment. The dendrogram of the DGGE fingerprint showed that they were assigned to different clusters by different supplemental levels with DGGE fingerprint similarity less than 0.54 overall. Shannon-Weiner index decreased ($P < 0.05$) especially with 1.0 g/kg RBH, while the dominance index increased ($P < 0.05$) especially at 0.25 and 0.5 g/kg levels compared with the control. RT-PCR revealed no difference in cellulolytic bacteria among groups. In total, RBH supplementation proved little effects on diversity of the bacterial community and cellulolytic bacteria in the rumen of lactating dairy cows potentially owing to gradual adaptation of rumen bacteria to the RBH supplementation.

Key Words: bacterial community, cellulolytic bacteria, Radix Bupleuri

1660 (T273) The effect of soluble propolis in milk on the performance of Holstein suckling calves.

P. Peravian*[1], K. Rezayazdi[2], and G. Nehzati[3], *[1]University of Tehran, Iran, [2]Dep. of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran, [3]University of Tehran, Karaj, Iran.*

This study was conducted to evaluate the effect of added soluble propolis in milk on the dry matter intake, body weight, digestibility and feed efficiency of Holstein suckling calves. Propolis in this experiment was come from Taleghan vicinity (near Tehran). Forty female Holstein calves with average 41 ± 1 kg birth weight were used from 14 to 65 d old. Calves were fed according to completely randomized design with four treatments (rations) and 10 replicates (calves) in each treatment. Treatments included: 1) Control (without Monensin in starter and without propolis in milk), 2) Starter without Monensin and 500ppm soluble propolis powder in milk, 3) Starter without Monensin and 1000ppm soluble propolis powder in milk, and 4) Monensin in starter and without propolis in milk. To reduce the stress of weaning, calves stayed in their boxes after weaning for 9 d. Individual dry matter intake was measured daily, and weight gain was measured each 14 d. Digestibility was measured with fecal sampling after weaning and the marker was acid insoluble ash (AIA). The results showed that dry matter intake had no significant differences among treatments in suckling period. But differences among dry matter intake of calves after suckling period were significant ($P = 0.01$). Means feed intake in whole period for treatments 1 to 4 were 1115.51, 1034.24, 1054.76, 920.81 g/d, respectively, and their differences were significant ($P = 0.04$). Means body weight for treatments 1 to 4 were 64.67, 60.84, 64.89, 62.25 kg, respectively, and there was a significant differences among treatments ($P = 0.01$). The feed efficiency for treatments 1 to 4 were 0.402, 0.393, 0.410, 0.404, and there were no significant differences among treatments ($P = 0.9$). Apparent digestibility of OM (76.76, 76.89, 78.03, and 78.11%), DM (78.97, 76.12, 77.32, and 77.42%) and NDF (57.99, 52.49, 52.89, and 52.60%) for treatments 1 to 4 respectively had no significant differences. The results showed the positive effect of propolis (biological additive) on the both dry matter intake and body weight in compare of Monensin (synthetic additive) which had the lowest dry matter intake and low body weight. Therefore, this study suggested that propolis could improve performance of calves.

Key Words: propolis, performance of calves, Monensin

1661 (T274) Supplementation of lysine and methionine for dairy calves on a step down milk-replacer feeding program.

J. T. Silva*, G. Santos, N. B. Rocha, E. Miqueo, T. Manzoni, and C. M. M. Bittar, *University of Sao Paulo, Piracicaba, Brazil.*

The aim of this study was to evaluate the performance of calves receiving starter concentrate or milk replacer supplemented with lysine and methionine to reach daily intakes of 17 g/d and 5.3 g/d, respectively. Forty-five newborn Holstein male calves were used in a randomized blocks experimental design and distributed into three treatments: 1) Control: no amino acid (AA) supplementation; 2) Starter concentrate: supplementation of lysine and methionine in the concentrate starter; 3) Milk replacer: supplementation of lysine and methionine in the milk replacer. Calves were housed in individual shelters, with free access to water, starter concentrate, and received milk replacer (20CP:16EE; 12.5% solids) according to the program: 4 L/d, until wk 2 of life; 8L/d from the 2 to 6 wk of life; and 4L/d from the 6 to 8 wk, when they were weaned. Calves were followed until the 10 wk of life. Starter concentrate and milk replacer intakes, as well as fecal scores were monitored daily. Body weight, withers height, heart girth and hip width were weekly measured. Supplementation of amino acids in the milk replacer resulted in lower total dry matter after weaning, which resulted on lower daily gain in the same period.

Key Words: amino acids, growth, weaning

Table 1661. Performance of dairy calves receiving starter concentrate or milk replacer supplemented with lysine and methionine

	Control	Starter concentrate	Milk replacer	SEM	$P <$
Body weight, kg					
Initial	36.3	36.3	37.4	2.06	0.267
At weaning	47.57	47.74	48.80	2.06	0.267
Final	54.55	54.73	56.1	2.07	0.267
Daily gain, g					
Before weaning	193.9	232.0	151.7	34.44	0.275
After weaning	553.5 ab	676.1 a	344.0 b	141.41	0.028
Starter intake, g/d					
At weaning	306.1	348.4	180.2	68.21	0.423
Final	1502.7	1615.61	1235.1	94.4	0.372
Total dry matter intake, g/d					
Before weaning	793.7	850.2	787.6	20.98	0.078
After weaning	1293.5 a	1341.3 a	950.6 b	90.69	0.009
Feed efficiency, daily gain/total intake	0.23	0.24	0.14	0.04	0.120
Fecal score	2.35	1.83	2.02	0.35	0.640
Height withers gain, cm/week	0.64	0.76	0.65	0.41	0.976
Heart girth gain, cm/week	1.09	1.44	0.96	0.18	0.184
Hip width gain, cm/week	0.33	0.30	0.31	0.03	0.889

[ab] means with different letters differ at $P < 0.5$

1662 (T275) Response of newborn calves to injectable vitamins A, D and E. D. B. Snider[*1], J. Gaska[2], D. E. Gockowski[3], and R. L. Stuart[4], *[1]Iowa State University, Ames, [2]Gaska Dairy Health Services, Columbus, WI, [3]North Ridge Veterinary Service, Sturgeon Lake, MN, [4]Stuart Products Inc, Bedford, TX*.

Due to poor placental transfer, newborn calves depend mainly on colostrum and milk to supply fat-soluble vitamin needs. If the dam has not received sufficient fat-soluble vitamins during gestation, colostrum may be deficient in these critically important vitamins resulting in deficiencies in the newborn. Weak-calf syndrome has been shown to be partly due to vitamins E and A deficiencies in calves. Injecting fat-soluble vitamins at birth is a method to enhance fat-soluble vitamin status during the first few weeks after birth. Two experiments were conducted to measure efficacy of a commercial product (VITAL E-Newborn, Stuart Products, Inc.) in newborn beef and dairy calves. The product contained 500 I.U. vitamin E, 50,000 I.U. vitamin A and 50,000 I.U. vitamin D per mL. In experiment 1, newborn beef calves (n = 4) were not injected and calves (n = 4) injected S.Q. with 5 mL VITAL E-Newborn. Serum samples were taken initially and Days 1, 2, and 7 post-injection and analyzed for α-tocopherol, total vitamin A (retinol plus retinyl-palmitate), and 25-OH-D3. In experiment 2, newborn dairy calves (n = 4) were not injected and calves (n = 7) were injected S.Q. with 5 mL VITAL E-Newborn. Serum samples were taken 62 h post-injection and analyzed for α-tocopherol, retinol and 25-OH-D3. For experiment 1, serum α-tocopherol concentrations in non-injected calves were 0.26, 0.46, 0.63, and 1.14 μg/mL; total vitamin A concentrations were 0.077, 0.126, 0.152, and 0.123 μg/mL; and 25-OH-D3 concentrations were 10.0, 9.0, 9.3, and 10.6 hg/mL, for d 0, 1, 2, and 7, respectively. Vitamin-injected calves had serum α-tocopherol concentrations of 0.40, 16.4, 12.6, 5.9 μg/mL; total vitamin A concentrations of 0.053, 0.262, 0.270, and 0.151 μg/mL; and 25-OH-D3 concentrations of 6.0, 23.0, 42.1 and 54.7 hg/mL for d 0, 1, 2, and 7, respectively. All post-injection serum vitamin concentrations between treatments were different (P < 0.001). Experiment 2 had similar results as experiment 1. At 62 h post-injection, average serum α-tocopherol concentrations were 1.30 and 10.20 (P < 0.001); average serum retinol concentrations were 0.128 and 0.154 μg/mL (P < 0.10); and average serum 25-OH-D3 concentrations were 24.2 and 78.6 hg/mL (P < 0.001) for control and injected calves, respectively. Injecting newborn calves with a bioavailable source of fat-soluble vitamins is an excellent method to assure that newborn beef and dairy calves have adequate levels of these critically important vitamins after birth.

Key Words: vitamin A, vitamin E, vitamin D, newborn, injectable

1663 (T276) Fecal scores, hemogasometry and blood metabolites of diarrheic calves fed concentrate containing sugarcane molasses or glucose syrup as a replacement for corn. M. C. Soares[1], G. G. O. Nápoles[1], C. E. Oltramari[2], J. T. Silva[1], M. R. De Paula[1], and C. M. M. Bittar[*1], *[1]University of Sao Paulo, Piracicaba, Brazil, [2]University of Santa Catarina State, Chapecó, Brazil.*

During the milk-feeding period, 32 calves were distributed into four treatments: 1) Control: starter feed containing corn as the main energy source (65% corn; 24% soybean meal; 10% soybean hulls, 1% minerals and vitamins, on dry matter basis); 2) 5SCM: 5% (DM) of sugarcane molasses replacing corn; 3) 10SCM: 10% (DM) of sugarcane molasses replacing corn; 4) 5GS: 5% glucose syrup (DM) replacing corn. Animals were individually housed, with free access to water and concentrate, and received 4 L/d of milk replacer (20:16; 12.5% solids). After the diagnosis of diarrhea, evaluations of fecal score and measurement of respiratory and heart beat rates as well as rectal temperature were performed 3x/d, during three consecutive d. Blood samples were collected for blood cells count, electrolytes, blood gases and biochemical parameters analysis. Concentrate composition had no negative effect (P > 0.05) on fecal score, which were higher than 2.5 during the first 4 wk and decreased thereafter for all treatments. There was a tendency (P < 0.09) for higher rectal temperature (39.1; 39.4; 39.5; 39.1 for Control, 5SCM, 10SCM and 5GS, respectively) and respiratory rate (36.2; 41.9; 46.3; 34.0 breaths/min for Control, 5SCM, 10SCM and 5GS, respectively) for calves fed both levels of molasses. Respiratory rate, heart beat rate and rectal temperature increased during the day, as temperature-humidity index also increased. Replacement of corn by co-products had no effect (P > 0.05) on total erythrocytes (6.87×10^6/μL), mean corpuscular volume (37.9 fL) and hemoglobin (8.99 g/DL), however hematocrit was increased (P < 0.05) as co-products were fed (23.0a; 26.4b; 28.9c; 25.1b for Control, 5SCM, 10SCM and 5GS, respectively). There were no concentrate composition effects on blood pH (7.33), HCO_3 (28.18 mmol/L), PCO_2 (52.6 mmHg), K and Na (4.9 and 135.7 mEq/L, respectively), anion gap (13.38 mmol/L) and base excess (2.33 mmol/L) concentration. Plasma metabolites were also not affected by replacement of corn by co-products in the concentrate, with values of BHBA (0.06 mml/L), glucose (82.5 mg/dL), total protein (6.8 g/dL), PUN (7.1 mg/dL) and total lactate (16.45 mg/dL) within the normal physiological range for dairy calves during the milk-feeding period. Replacement of corn with molasses or glucose syrup in the supplement did not affect animals' metabolism in response to the occurrence of diarrhea and can be used as an alternative for feeding dairy calves.

Key Words: byproducts, metabolic disorders, milk-feeding, starter feed

1664 (T277) Fecal scores, hemogasometry and blood parameters of diarrheic calves fed concentrate containing citrus pulp as a replacement for corn. M. C. Soares[1], C. E. Oltramari[2], J. T. Silva[1], M. R. De Paula[1], M. P. Gallo[1], and C. M. M. Bittar[*1], [1]*University of Sao Paulo, Piracicaba, Brazil,* [2]*University of Santa Catarina State, Chapecó, Brazil.*

During the milk-feeding period, 24 calves were distributed into three treatments: 1) Control: starter feed containing corn as the main energy source (64% corn; 26% soybean meal; 6% wheat meal; 3% limestone; 1% minerals and vitamins, on dry matter basis); 2) 50CP: 50% (DM) of citrus pulp replacing corn, 3) 100CP: 100% (DM) of citrus pulp replacing corn. Animals were individually housed, with free access to water and concentrate, and received 4 L/d of milk replacer (20:16; 12.5% solids). After the diagnosis of diarrhea, evaluations of fecal score and measurement of respiratory and heart beat rate and rectal temperature were performed 3x/d, during three consecutive days. Blood samples were collected for blood cells count, electrolytes, blood gases and biochemical parameters analysis. Concentrate composition had no negative effect ($P > 0.05$) on fecal score, which were higher than 2.5 during the first 4 wk and decreased thereafter. Respiratory and heart beat rates were not affected ($P > 0.05$), as well as rectal temperature, however values were always lower at 7 h as compared to 12 h and 19 h evaluations, suggesting high impact of environmental conditions for sick calves. Inclusion of citrus pulp in concentrate had no effect ($P > 0.05$) on hematocrit (23.9%) and total erythrocytes (6.93×10^6/μL), but affected the mean corpuscular volume, with the highest value for animals fed 50CP (40.3fL). Increase of total leukocytes and neutrophils suggests the occurrence of an infectious instead of an alimentary diarrhea. Blood gases, electrolytes and biochemical data did differ ($P > 0.05$) nor resulted in dehydration, acidosis, or any other metabolic disturbance in animals. There were no concentrate composition effects on blood pH (7.36), HCO_3 (27.16 mmol/L), PCO_2 (52.3 mmHg), K and Na (4.6 and 134.1 mEq/L, respectively), anion gap (12.2 mmol/L) and base excess (4.7 mmol/L). Plasma metabolites such as BHBA (0.057mml/L), glucose (85.6 mg/dL) and PUN (7.96 mg/dL) were not affected; however, total lactate and D-lactate were lower ($P < 0.05$) for calves fed 50CP (16.0; 9.17 mg/dL respectively), as compared to control (20.8; 14.7 mg/dL) and 100CP (23.8; 14.4 mg/dL); while L-lactate lowest for 100CP (9.42; 6.8; 6.1 mg/dL for 100CP, 50CP and control, respectively). Replacement of corn by citrus pulp in the concentrate did not affect animals' metabolism in response to the occurrence of diarrhea, being an alternative for feeding dairy calves.

Key Words: byproducts; metabolic disorders; milk-feeding; starter feed

1665 (T278) Effect of diet particle size on sorting, eating rate, rumen ph and digestibility in dairy heifers. F. H. Pino*, A. J. Heinrichs, and C. Castro, *Pennsylvania State University, University Park.*

Eight cannulated dairy heifers (19.3 ± 0.8 mo of age and 524.51 ± 10.01 kg of BW) were fed either long (62.7mm; LCS) or short (6.1mm; SCS) cut corn silage at 1.65% BW in individual stalls to determine eating behavior and digestion parameters. Diets consisted of 70% corn silage, 11% ground corn, 8% citrus pulp, 6% canola meal, 2% soy bean hulls, 1.2% Optigen and 2% mineral/vitamin mix fed once daily. Heifers were subject to a cross over design study with 18-d periods; 14 d adaptation 4 d sampling. Particle size of theTMR was measured at 0 and 2 h after feeding. Feces were collected (d 14 to 18) to determine DM digestibility. Rumen contents were sampled (d 17 to 18) to measure pH at 0, 1, 2, 4, 8, 12, 16, 20, and 22 h after feeding. Data were analyzed with PROC MIXED of SAS 9.4. The LCS ration had an increase of 91% of long (> 19 mm) feed particles 2 h after feeding with no change in feed particles on the SCS diet. Feed particles retained on the eight 4-mm and pan sieves decreased 7, 30, and 35%, respectively. The overall rate of eating was not different between treatments (2.75 vs. 2.37 kg/h SCS and LCS, respectively; $P = 0.47$). Rumen pH changed throughout the day from 7.1 to 4.7 from feeding to 8 h post feeding but was not different between treatments ($P = 0.55$). It is likely that these variables were not different because the heifers were fed a restricted diet (8.73 ± 0.19 kg of DMI) that was consumed by 4 h after feeding. The DM digestibility of diets (75.24 ± 2.2%) was not different ($P = 0.37$). In conclusion, there are no differences in rumen pH, eating rate and DM digestiblity with different particle size diets. Differences in the TMR particle size 2 h after feeding suggest that heifers sort the diets indicating selective consumption of the small particles and selective refusal for the long feed particles. This sorting could promote competition and selective consumption of feed particles by the more dominant heifers, which could lead to inappropriate and variable nutrition for heifers with group fed animals.

Key Words: heifers, sorting, DM digestibility

1666 (T279) Fatty acid profiles of *Longissimus dorsi* from Nellore cattle on pasture supplemented with crude glycerin and whole cottonseed. J. T. Zervoudakis[*1], A. J. Possamai[2], L. K. Hatamoto-Zervoudakis[1], A. S. Oliveira[3], L. B. D. Freiria[1], R. P. D. Silva[1], A. C. Barboza[2], and J. W. Koscheck[4], [1]*Federal University of Mato Grosso, Cuiaba, Brazil,* [2]*UFMT, Cuiabá, Brazil,* [3]*UFMT, Sinop, Brazil,* [4]*UNESP, Jaboticabal, Brazil.*

There is interest in the composition of fatty acids (FA) in beef for reduction of short-chain FA, with increment of medium-chain and omega-3 FA, by their anticarcinogenic and

immune-stimulatory effects. Nutritional strategies to improve meat quality should be studied to possibility better meat FA profile in this products. The aim of this experiment was to evaluate whole cottonseed and crude glycerin association in multiple supplements for 50 Nellore cattle in the fattening phase at *Brachiaria brizantha* pastures on longisssimus dorse FA profile. Animals were supplemented with 4 kg/d (21% of crude protein). The experiment was performed in a 2 × 2 factorial design (two levels of crude glycerin (0 and 15%) and two levels of whole cottonseed (0 and 25%). Orthogonal contrasts were used to evaluated the effect of crude glycerine, whole cottonseed and the interaction, adopting 0.05 to the critical level of probability. Inclusion of whole cottonseed reduced the quantity of hypercholesterolemic FA: C14:C19 ($P = 0.049$), C16:0 ($P = 0.038$), C16:C19 ($P = 0.006$) and C17:0 ($P = 0.028$). However, inclusion of crude glycerin increased C17:0 ($P = 0.002$) and C17:1 ($P = 0.003$). The cottonseed promoted an increase in the concentration of C18:0 ($P < 0.001$) possibly due to extensive biohydrogenation of isomers C18:1, C18:2 and C18:3 ($P < 0.001$). The glycerin promoted an increase in C18:2c9*t*11 conjugated linoleic acid ($P = 0.046$) due to reduction in lipolysis of FA in the rumen, with limited biohydrogenation. The C20:1 ($P = 0.02$) was reduced by feeding of cottonseed, due to the low concentration of this fatty acid in the ingredient. There was no influence of the inclusion of glycerin and/or cottonseed on the total of saturated FA, monounsaturated or polyunsaturated FA, as well as their relations ($P > 0.05$). The supply of glycerin and whole cottonseed modify the FA profile, because of ruminal biohydrogenation modulation by glycerine, for healthy meat production.

Key Words: meat quality, supplementation, stearic acid

1667 (T280) Performance and carcass attributes of Nellore heifers fed with zilpaterol hydrochloride.

N. R. B. Cônsolo[*1], R. S. Goulart[2], F. Rodriguez[1], M. O. Frasseto[1], J. M. Souza[1], L. F. P. Silva[1], and V. B. Ferrari[1], *[1]University of Sao Paulo, Pirassununga, Brazil, [2]MSD Saúde Animal, Sao Paulo, Brazil.*

Greater efficiency of production is mandatory in modern beef cattle industry, and use of feed additives, such as β-adrenergic agonists, have demonstrated positive results with *Bos taurus* cattle. However, there are no consistent data on the effects of these substances in Nellore (*Bos indicus*), which accounts for more than 70% of the Brazilian beef cattle. Therefore it was the objective of this study to evaluate the effects of zilpaterol hydrochloride (Zilmax) on the performance and carcass attributes of Nellore heifers. Seventy-two animals with 267 kg of BW and 18 mo of age were fed in a feedlot system for 135 d. Heifers were separated into two treatment groups: Control (C) and Zilpaterol (Z), which received the same diet containing 14% of crude protein, and formulated with corn silage, ground corn, soybean meal and mineral premix. The Z group received Zilmax at 8.3 mg/kg dry matter. Heifers were allotted to 18 pens ($n = 9$) and assigned in a completely randomized design. Animals were weighed at 21-d intervals after 16-h fasting to evaluate growth performance. Zilmax was administrated during the last 30 d of feeding, allowing 3 d of withdraw before slaughter. All animals were slaughtered in a commercial plant, according to proper welfare guidelines. Hot carcass weight, carcass yield, kidney, pelvic and abdominal fat weight were measured. Twenty-4 h later, longissimus muscle area and backfat thickness were measured at the interface of the 12th and 13th ribs. Zilpaterol administration increased ($P < 0.01$) final body weight (404 vs. 387 kg), average dairy gain (1.46 vs. 1.14 kg/d), hot carcass weight (224 vs. 208kg), and dressing percentage (56 vs. 54%) compared with control. However, no effects ($P > 0.10$) were noted in the longissimus muscle area (73.1 vs. 83.5 cm^2) and subcutaneous fat depth (5.2 vs. 4.8 mm) between C and Z group, respectively. In addition, there was a reduction in kidney and pelvic fat by zilpaterol administration compared with C (4.6 vs. 5.7% of hot carcass weight). In conclusion, zilpaterol treatment improved the performance and carcass characteristics of Nellore heifers in feedlot system.

Key Words: heifers, Nellore, zilpaterol

1668 (T281) Carcass characteristics of Nellore steers fed whole corn diets containing feed antibiotics.

B. J. M. Lemos[1], F. G. F. Castro[2], B. P. C. Mendonça[2], C. E. Dambros[1], D. B. Fernandes[2], A. L. Braga Netto[2], V. R. M. Couto[1], and J. J. R. Fernandes[*1], *[1]Universidade Federal de Goiás, Goiânia, Brazil, [2]AgroCria, Goiânia, Brazil.*

The objective was to investigate the effects of feed antibiotics on carcass characteristics of feedlot steers fed whole corn diets. Ninety-seven Nellore steers (302 ± 47 kg of BW and 24 mo of age) were assigned to a randomized complete block design experiment with four blocks (based on initial BW) and five treatments (Mon30: monensin 30 ppm; Virg25: virginiamycin 25 ppm; Mon20+Virg25: monensin 20 ppm + virginiamycin 25 ppm; Fla40: flavomycin 40 ppm; Mon20+Fla20: monensin 20 ppm + flavomycin 20 ppm). Pen was the experimental unit. The steers were slaughtered after a 100-d period of feeding. Steers were fed TMR (88.2% DM, 12.5% CP, 71.5% TDN) with 85% whole grain corn and 15% pelleted protein concentrate on a DM basis. Feed was supplied ad libitum. Steers were weighed after a 16-h fast on d 100 of the experimental period to determine final body weight. Hot carcass weight was determined after skinning and evisceration. Hot carcass yield was obtained at the time of slaughter. Subcutaneous fat thickness (FT) was measurement in *Longissumus dorsi*muscle at 12th rib. No carcass characteristic measures of feedlot Nellore steers fed whole corn diets were affected by the different feed antibiotics (Table 1668). Carcass characteristic values were higher than data reported previously for Nellore steers fed high-concentrate diets based on corn (267.0 kg HCW, 54.6% HCY), except by FT (3.9 mm) (Silva, 2009).

A relatively short number of animals ($n = 97$) was used in this experiment. It is not known if a higher number would have affected the variables studied.

Key Words: beef cattle, feedlot, finishing

Table 1668. Final body weight (BWf), hot carcass weight (HCW), hot carcass yield (HCY) and subcutaneous fat thickness (FT) of Nellore steers fed whole corn diets containing feed antibiotics

	Feed antibiotics						
Variable	Mon30	Virg25	Mon20 +Virg25	Fla40	Mon20 +Fla20	SEM	P Value
No. of pens (steers)	4 (19)	4 (20)	4 (19)	4 (19)	4 (20)	–	–
BWf (kg)	539	534	537	544	539	4.38	0.618
HCW (kg)	309.1	306.1	309.5	309.5	303.7	2.62	0.455
HCY (%)	57.4	57.3	57.6	56.9	56.2	0.45	0.267
FT (mm)	3.2	3.4	2.9	3.4	3.5	0.18	0.158

1669 (T282) Fatty acids ratio of loin from lambs fed with increasing levels of crude glycerin in feedlot.

C. M. Cunha[1], A. R. M. Fernandes[1], H. A. Ricardo[*1], L. V. C. Girão[2], R. O. Roça[3], L. O. Seno[1], M. A. P. Orrico Junior[1], J. C. S. Osório[1], and F. M. Vargas Junior[1], *[1]Grande Dourados Federal University (UFGD), Dourados, Brazil, [2]Uberlândia Federal University (UFU), Uberlândia, Brazil, [3]São Paulo State University (FCA/UNESP), Botucatu, Brazil.*

The crude glycerin (CG) has been successfully used in ruminant nutrition as energy concentrate substitute. The objective of the study was to evaluate the effect of increasing levels of CG on loin fatty acids (FA) ratio. Lambs (24) with a mean body weight of 20.0 kg were used. Animals used in the study belong to a group of native sheep of the State of Mato Grosso do Sul, Brazil, called Pantaneiros. The experiment was conducted in a completely randomized design with four treatments: 0, 2.5, 5.0, and 7.5% of CG inclusion as a % of diet dry matter (DM). Diets were formulated to be isonitrogenous and isocaloric only varying the inclusion of CG to replace coarse ground corn, to provide an average gain of 250 g/day. Oat hay was used as roughage and concentrate was composed of corn and/or CG, soybean meal, ground soybean and mineral mix, with a roughage:concentrate ratio of 25:75. Body condition (BC) was used as slaughter criterion. As soon animals had a BC between 3.0 and 3.5 slaughter was performed. After 24 h of chilling at 4°C, loin cuts obtained from deboned *Longissimus* between first and least lumbar vertebra of left side of the carcasses were used to determine FA profile (% of total FA) and ratio. There was no effect ($P = 0.1052$) of CG level on polyunsaturated (PUFA), monounsaturated (MUFA), saturated fatty acids (SFA), and ω6 percentages and on PUFA:SFA, and MUFA:SFA ratio. As CG increased, there was a linear decrease in unsaturated fatty acids (UFA) percentage ($P = 0.0304$; $R^2 = 0.16$; RSD = 2.49), and a linear decrease in ω3% ($P = 0.0084$; $R^2 = 0.26$; RSD = 0.13). UFA:SFA decreased linearly with the CG inclusion ($P = 0.0321$; $R^2 = 0.10$; RSD = 0.09) while ω6:ω3 had a linear increase ($P = 0.0289$; $R^2 = 0.18$; RSD = 1.58).

Key Words: crude glycerin, fatty acids ratio, lamb loin

1670 (T283) Performance and carcass yield of finishing lambs fed diets with safflower meal.

P. A. Meneses-Tapia[1], G. Buendia-Rodriguez[2], F. E. Martinez-Castañeda[1], C. G. Peñuelas-Rivas[1], and S. S. Gonzalez-Muñoz[*3], *[1]Universidad Autonoma del Estado de México, Toluca, [2]CENIDFyMA INIFAP, Queretaro, México, [3]Colegio de Postgraduados, Montecillo Estado de México.*

Studies about oilseed meals are important due to its relationship with fatty acids content and nutritive value of meat. So far, information is scarce about levels of fatty acids in tissues of lambs fed safflower meals. Therefore, the objective of this experiment was to evaluate the effect of a concentrated diet (30% sorghum, 30% corn grain, 15% alfalfa hay; 14.5% CP and 2.98 Mcal EM) plus three levels (treatments) of safflower meal: 0% (control), 10% and 15%, fed to 24 Dorper lambs (22.18 ± 2.6 live BW) housed in metabolic cages during 60 d. The experimental design was completely randomized with three treatments and eight replications. Data were analyzed using GLM procedure (SAS v9.2) and treatments means were compared with Tukey test ($P \leq 0.05$). Variables evaluated were daily dry matter intake (DDMI, g), average daily gain (ADG, g), feed conversion (FC), dry matter digestibility (DMD, %) and carcass yield (CY, %). Safflower meal (0, 10, and 15%) changed ($P \leq 0.05$) ADG (328^b, 367^a, 365^a g), DDMI (1534^b, 1621^a, 1573^b g) and CY (47.8^b, 51.0^a, $51.2\%^a$); however, it did not affect ($P > 0.05$) FC (4.68, 4.42, 4.30 g) neither DMD (65.87, 66.74, 64.89%). These results allow concluding that safflower meal increased average daily gain and carcass yield in finishing lambs.

Key Words: lambs, safflower meal, performance and carcass yield

1671 (T284) Quality traits of *Longissimus* muscle of two genetic groups fed with crude glycerin.

I. M. de Oliveira[*1], J. P. I. S. Monnerat[2], N. V. L. Serão[3], M. S. Duarte[4], V. R. M. Couto[5], S. C. Valadares Filho[4], M. L. Chizzotti[4], and P. V. R. Paulino[6], *[1]APTA– Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [2]Universidade Federal de Viçosa, Brazil, [3]Iowa State University, Ames, [4]Universidade Federal de Viçosa, Minas Gerais, Brazil, [5]Universidade Federal de Goiás, Goiânia, Brazil, [6]Nutron Alimentos Ltda., Campinas, Brazil.*

Quality traits of *Longissimus* muscle of two genetic groups: Nellore (NE) and F1 Red Angus x Nellore (NA), with 18 mo

of age, fed diets containing 5 and 15% of crude glycerin for 84 d, were evaluated. Higher concentration of blood glucose was observed in NE (P = 0.0097) than in F1 cross, and it was not affected by diet (P = 0.9573). No effects of genetic group (P = 0.0908) and crude glycerin (P = 0.0733) were observed on serum insulin, carcass pH and final temperature, frequency of muscle fiber type and size of type IIB fiber, beef color, shear-force, myofibrillar fragmentation index, purge loss, ether extract, ashes, and moisture content. The size of type I muscle fiber did not differ (P = 0.0521) among genetic groups and was larger in muscle from animals fed 15% of crude glycerin (P = 0.0244). The size of type IIA muscle fibers was greater in *Longissimus* muscle of F1 cross (P = 0.0002) than NE cattle, and in *Longissimus* muscle from animals fed 15% crude glycerin (P = 0.0068) compared to those fed diets with other levels evaluated. Collagen solubility was greater in meat of F1 cross (P < 0.0001) compared to NE cattle and was not affected by diet (P = 0.1146). There was interaction among genetic group and diet on total collagen amount (P = 0.0002) in beef. Greater crude protein level was observed on beef from animals fed 15% of crude glycerin (P = 0.0468). However, crude protein was not affected (P = 0.2197) by genetic group. The inclusion of crude glycerin in diets does not affect beef quality traits. These data show that it is possible to produce beef with desirable quality traits by using F1 Red Angus x Nellore and Nellore cattle.

Key Words: collagen, fiber, insulin

1672 (T285) Effects of corn processing method and dietary starch level on finishing performance of Nellore bulls.

M. Caetano[1,2], R. S. Goulart[3], S. Luz e Silva[4], J. S. Drouillard[5], P. R. Leme[4], and D. P. D. Lanna[*1], *[1]University of Sao Paulo/ESALQ, Piracicaba, Brazil, [2]University of Adelaide, Roseworthy, Australia, [3]MSD Saúde Animal, Sao Paulo, Brazil, [4]University of Sao Paulo/FZEA, Pirassununga, Brazil, [5]Kansas State University, Manhattan.*

The objective of this study was to evaluate flint corn processing method (CPM) and level of starch for finishing Nellore bulls with high-concentrate, corn-based diets. Nellore bulls (n = 112; 378.25 ± 21.28 kg) were used in a randomized complete block design in a 4 × 2 factorial arrangement. Four starch levels (30, 35, 40, and 45% of diet DM) were evaluated for two CPM: high moisture corn (HMC) and finely ground dry corn (FGC). Animals were offered ad libitum access to diets delivered twice daily in individual pens. Flint corn had 77.2% vitreousness, and corn geometric particle sizes were 1.30 and 5.84 mm for FGC and HMC, respectively. Bulls were adapted to the finishing diet over a 18 d period and fed a total of 75 d. To determine fecal starch (FS) concentration, each animal was sampled by rectal palpation on d 47 of the feeding period. The first derivative was solved of a second order polynomial to determine optimal dietary starch level (DSL). Interaction between CPM and DSL was observed for G:F (P = 0.04). Animals fed HMC 35% up to 45% DSL were more efficient than those fed HMC 30% DSL. However, G:F for bulls fed FGC 30% up to 45% DSL had no difference. DMI was 13.6% greater for FGC than those fed HMC (P < 0.01), but the final BW and ADG was not affected by CPM. Increases in the DSL resulted quadratic decreases in the DMI (P = 0.02) and linear decreases in the ME intake (P < 0.01). Interactions between CPM and DSL were found (P = 0.02), bulls fed HMC showed a linear increase in NEm (P = 0.02), NEg (P = 0.02) and ME (P = 0.02) when the DSL increased. However, NEm, NEg and ME for bulls fed FGC were not different with inclusions of DSL. Bulls fed HMC showed 2.75 times lower FS than those bulls fed FGC (P < 0.01), consequently the fecal pH was greater for HMC than FGC (P < 0.01). Fecal DM were 31.4% greater for FGC than HMC (P < 0.01), consequently the density was greater for FGC feces than HMC (1.120 vs. 1.098 g/mL; P = 0.02). In conclusion, HMC improved growth efficiency of Nellore cattle and the proportion of DSL required to optimize performance was dependent on CPM.

Key Words: feedlot, starch, Zebu

1673 (T286) Effect of wheat dried distillers grains with soubles inclusion and fibrolytic enzyme supplementation on ruminal fermentation and digestibility in beef heifers fed backgrounding diet.

Z. He[*1,2], N. D. Walker[3], T. A. McAllister[4], and W. Yang[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, [2]Key Laboratory for Agro-Ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, Chinese Academy of Sciences, Changsha, China, [3]AB Vista Feed Ingredients, Marlborough, UK, [4]Agriculture and Agri-Food Canada, Lethbridge, AB.*

A metabolic study was conducted to evaluate the effects of wheat dried distillers grain with solubles (DDGS) inclusion and fibrolytic enzyme (FE) application on digestibility, ruminal pH and fermentation in beef heifers. Six ruminally cannulated Angus heifers (averaged BW 794 kg) were used in a 6 × 6 Latin square design with 2 × 3 factorial arrangement. Treatments were control (CON; 50% barley silage, 10% grass hay, and 40% barley grain-based concentrate) and WDG (CON diet substituting 15% DDGS for barley grain) diets combined with 3 FE dosages (0, 1, and 2 mL FE/kg diet DM). Ruminal digestibility of wheat DDGS, barley silage and grass hay was measured using in situ technique and total digestibility was determined using Yb as external digesta marker. Heifers were fed at restriction of 90% ad libitum. Statistical analyses were conducted using the PROC MIXED of SAS with model including fixed effects of diet, FE and their interaction. In situ ruminal DM disappearance (DMD) of DDGS and grass hay

did not differ between WDG and CON after 12, 24, or 48 h of incubation, whereas in situ ruminal DMD (34.0 vs. 36.9%; $P = 0.01$) of barley silage was greater in heifers fed WDG than CON after 24 h of incubation. Increasing FE application quadratically ($P = 0.04$) changed in situ DMD (61.1, 63.1 to 59.3%) of DDGS after 24 h of incubation and linearly ($P = 0.03$) increased in situ NDFD of barley silage (14.9 to 18.9%) after 24 h of incubation. There was no interaction between diet and FE dosages on total digestibility and ruminal pH and VFA concentration. Inclusion of DDGS increased the digestibility (CON vs. WDG) of CP (58.9 vs. 67.6%; $P < 0.01$), NDF (32.7 vs. 37.4%; $P = 0.04$) and ADF (25.0 vs. 31.0%; $P = 0.03$). Increasing FE linearly ($P = 0.03$) increased CP digestibility from 61.8, 63.5 to 64.5% without affecting the digestibility of other nutrients. There were no effects of DDGS inclusion and FE dosages on ruminal pH and VFA concentration except the concentration of propionate was greater ($P = 0.04$) with WDG (19.5 m*M*) than CON (18.5 m*M*). These results indicate that inclusion of wheat DDGS or supplementation of FE in barley silage-based background diet improved ruminal and total digestibility of NDF and CP, and had potential to improve feed efficiency in beef cattle.

Key Words: backgrounding beef heifers, fibrolytic enzyme, wheat distillers grain

---

1674 (T287) Increasing condensed corn distillers solubles affects gene expression in rumen epithelial tissue. J. C. McCann[*1], S. Alqarni[1], J. R. Segers[2], D. W. Shike[1], and J. J. Loor[1], [1]*University of Illinois, Urbana,* [2]*University of Georgia, Tifton, GA.*

Five ruminally-fistulated steers were used in a 5 × 5 Latin square design to determine the effects of increasing dietary fat from corn distillers solubles (CDS) on the gene expression within rumen epithelial tissue. Treatments included a corn-based control (CON), and four levels of CDS (0, 10, 19, and 27%) in a coproduct-based (corn gluten feed and soybean hulls) diet. Fat concentrations were formulated to 3, 5, 7, and 9%, respectively, for diets containing CDS, and all steers were fed to ad libitum intake once daily. After 18 d of adaptation to the diet, ruminal epithelium tissue was collected and frozen in liquid N. Real-time quantitative PCR was used to determine dietary effects on expression of genes related to fatty acid oxidation, ketogenesis, transcriptional regulation, and monocarboxylic transporters. Data were analyzed using the PROC MIXED of SAS with treatment and period as fixed effects and steer as the random effect. Pairwise comparisons were implemented to separate means. Genes associated with long chain fatty oxidation (CPTIA, ACADS, and ACADS) were affected by treatment ($P \leq 0.01$). Steers fed 10% CDS diet had the least epithelial mRNA expression of CPTIA and ACADSB compared with all other treatments ($P < 0.01$). ACADS epithelial mRNA expression was decreased in epithelial tissues of steers fed 0 and 10% CDS diets. Among genes related to ketogenesis, HMGCS2 was affected by treatment ($P = 0.02$); epithelial mRNA expression remained similar for CON, 0%, 19%, and 27% CDS, but HMGCS2 was downregulated for steers fed 10% CDS diet. Although ACAT1 was affected by treatment ($P = 0.04$), CON and 10% CDS had less expression compared to 19% CDS treatment ($P \leq 0.01$). Expression of transcriptional regulation-associated genes (PPARA and RXRA) in rumen epithelium was not consistent. PPARA mRNA expression was the greatest for 27% CDS treatment and alternatively the least for 10% CDS. However, RXRA was affected by treatment ($P = 0.04$); epithelial mRNA expression was decreased at 10, 19, and 27% inclusion of CDS compared with the greatest expression for steers fed CON diet. SLC16A1, a monocarboxylic transporter-related gene, expression was increased for steers fed 0% CDS compared with 10 and 27% CDS treatments. Results indicate different concentrations of CDS alter the rumen epithelium transcriptome.

Key Words: rumen, epithelium, gene expression

1675 (T288) Crude glycerin as an energy source in finishing beef diets. P. Del Bianco Benedeti[*1,2], P. V. R. Paulino[3], M. I. Marcondes[1], A. Faciola[2], I. França Smith Maciel[1], and M. Custódio da Silva[1], [1]*Federal University of Viçosa, Viçosa, Brazil,* [2]*University of Nevada, Reno,* [3]*Nutron Alimentos Ltda., Campinas, Brazil.*

The objective of this study was to evaluate the effects of replacing dry ground corn with crude glycerin (CG) on DMI, digestibility, performance, and carcass characteristics of finishing beef bulls. An experiment in a completely randomized design with 25 d for adaptation and 95 d for sample collection was conducted, in which 3640 Nellore bulls (367 ± 37 kg) were blocked by BW and assigned to 20 pens. Animals were randomly assigned to one of four treatments: 0, 5, 10, and 15% (DM basis) CG in diet. All diets contained 85% concentrate and were formulated to meet NRC (2000) recommendations. Diets were isocaloric, isonitrogenous, and allowed 1.4 kg/d BW gain. Initially, 20 animals were slaughtered to serve as reference to estimate initial empty BW, which allowed carcass gain calculation. Bulls were weighted at the beginning and end of the experiment for performance calculation. Measurements of ribeye area (RA), back fat (BF) and rump fat (RF) were obtained by ultrasound. Data were analyzed using the PROC MIXEDs in SAS, and results are reported in the Table 1675. Intake of DM decreased linearly ($P < 0.01$) with CG inclusion. A quadratic effect was observed ($P < 0.01$) for DM and TDN digestibility. However, CG inclusion did not change ($P > 0.10$) ADG, final BW, carcass gain, carcass dressing, feed:gain ratio, RA, BF, and RF. These results suggest that CG may be included in finishing beef cattle diets without affecting performance and carcass characteristics.

Key Words: glycerin, feedlot, performance

Table 1675. Effects of replacing dry ground corn with crude glycerin on DMI, digestibility, performance, and carcass characteristics in finishing beef bulls

	Crude Glycerin (%)					P-value	
	0	5	10	15	SEM	L	Q
DMI, kg/d	10.5	10.1	10.2	9.6	0.15	< 0.01	0.60
DMI, % BW/d	2.4	2.4	2.3	2.22	0.14	< 0.01	0.42
DM Digest., %	62.6	60.2	64.1	69.7	0.86	–	< 0.01
TDN Digest., %	69.9	67.2	71.1	75.8	0.78	–	< 0.01
ADG, kg/d	1.41	1.37	1.35	1.34	0.02	0.20	0.77
Final BW, kg	510.1	498.7	503.8	497.1	2.18	0.19	0.45
Carcass gain, kg	89.2	84.2	82.7	83.1	1.41	0.33	0.07
Carcass dressing, %	56.9	56.7	56.6	56.5	0.33	0.64	0.92
Feed:gain	7.5	7.5	7.6	7.2	0.11	0.47	0.42
RA, cm3	83.0	82.2	82.1	80.9	0.40	0.06	0.88
BF, mm	4.6	4.4	4.4	4.5	0.08	0.04	0.04
RF, mm	6.6	6.4	6.4	6.4	0.06	0.09	0.25

1676 (T289) Ruminal fermentation of steers fed crude glycerin replacing starch- vs. fiber-based energy ingredients at low or high concentrate diets.

J. F. Lage*[1], A. F. Ribeiro[1], E. San Vito[1], C. S. Ribeiro Júnior[1], L. M. Delevatti[1], E. E. Dalanttonia[1], F. Baldi[2], R. A. Reis[3], and T. T. Berchielli[1], *[1]Universidade Estadual "Paulista Júlio de Mesquita Filho", Jaboticabal, Brazil, [2]Universidade Estadual Paulista "Júlio de Mesquita Filho", Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil, [3]University of Sao Paulo State, Jaboticabal, Brazil.*

Twelve ruminally cannulated Nellore steers (401.0 ± 41.5 kg) and 24 mo were used in a replicated truncated Latin Square arrangement of treatments with six animals in six treatments and four periods to evaluate the effect of crude glycerin (CG; 80.34% of glycerol) replacing starch- or fiber-based energy ingredients in the concentrate on ruminal pH, ammonia-N concentration and VFA's production of the steers fed in feedlot. Experimental periods were 15 d (14 d for adaptation and 1 d to sampling). Diets were: CO, without CG and corn as ingredient of concentrate; CGC, inclusion of CG (10% of DM) replacing corn in the concentrate; and CGSH, inclusion of CG (10% of DM) replacing soybean hulls (SH) in the concentrate. All three diets were offered at a low (LC) or high concentrate (HC; 40 or 60%). Ruminal contents were obtained at 0, 2, 4, 6, 8, 10, and 12 h after 0700 h feeding. Data were analyzed as a truncated Latin square using the PROC MIXED of SAS. The pH, ammonia-N and VFA, were analyzed as a repeated measurements. The least-squares means were generated and compared ($P \leq 0.05$) using Tukey's test. The pH was lower to animals fed HC diets than pH from animals fed LC diets ($P < 0.01$). No differences were detected in pH when animals were fed with CGC or CGSH. Animals fed diets CGSH had lower ammonia-N concentration than animals fed diets without CG or CGC ($P < 0.01$). The propionate concentrations ($P < 0.01$) and A:P ratio ($P < 0.01$) were affected by inclusion of CG in diets replacing corn or SH in the concentrate. Animals fed diets CGC or CGSH had higher propionate concentrations and lower A:P ratio in ruminal fluid ($P < 0.05$). There was an interaction between concentrate level and the diets for acetate ($P = 0.03$) and butyrate concentrations ($P = 0.05$). The decrease in acetate concentrations were observed in animals fed CGC or CGSH in LC than animals fed LC diets without CG. Butyrate concentrations were greater in diets CGC or CGSH, mainly in LC diets ($P = 0.05$). The inclusion of CG in diets did not alter the ruminal pH, but increase butyrate and reduces the A:P ratio as a result of increases of propionate concentrations.

Key Words: glycerol, propionate, ruminal pH

1677 (T290) Supplements containing different crude glycerin concentration does not affect the intake and digestibility of Nellore grass-fed beef.

E. San Vito*, L. Maneck Delevatti, E. E. Dalanttonia, J. F. Lage, M. B. Abra, C. S. Ribeiro Júnior, L. R. Simonetti, M. Machado, and T. T. Berchielli, *Universidade Estadual Paulista "Júlio de Mesquita Filho", Jaboticabal, Brazil.*

The aim of this work was to evaluate the effect of crude glycerin (CG)- 80% of glycerol- inclusion as a substitute to corn grain in the intake and digestibility (DM, OM, CP, NDF and TDN) of Nellore steers on pasture, supplemented in the dry season. Ten rumen-cannulated Nellore steers, with average body weight of 427 ± 15.76 kg were randomly assigned in double Latin square 5 × 5. The animals were distributed in five paddocks, of 0.4 ha each (two animals per paddocks). Treatments were constituted by five concentrations of CG in the supplement: 0, 70, 140, 210, and 280 g/kg dry matter of CG. Animals were supplemented individually, daily in a proportion of 300 g/100 kg of BW. The supplement was constituted of corn grain, soybean meal, urea, gluten meal and commercial premix, containing 300 g/kg DM of crude protein. Each experimental period lasted 14 d, so the first 10 d were for animal's adaptation and the remaining days to collect

samples. Intake and nutrient digestibility were estimated using two markers: isolated, purified and enriched lignin (LIPE) and indigestible neutral detergent fiber (iNDF), used for estimation of fecal excretion and forage intake, respectively. Fecal samples were collected directly from the rectum, 2x/d for 3 d, totaling six samples, with an interval of 2 h between collections. Data were analyzed in two simultaneous 5 × 5 latin squares by PROC MIXED of SAS (version 9.1), the effects of treatments were considered significant at $P < 0.05$. There was no statistical significance among the treatments, for intake of DM ($P = 0.239$), OM ($P = 0.183$), CP ($P = 0.076$), NDF ($P = 0.179$) and TDN ($P = 0.218$) with mean values of 7.59, 7.05, 1.24, 3.9 and 3.88, respectively. The inclusion of glycerin had no effect in the digestibility for DM ($P = 0.286$), OM (0.315), CP ($P = 0.339$) and NDF (0.270), with mean values of 44.26, 51.50, 57.20 and 43.04, respectively. The inclusion of crude glycerin until the level of 280 g/kg DM in the supplement did not affect the intake and digestibility of Nellore steers fed on tropical pasture in the dry season.

Key Words: pasture, co-product, biodiesel, glycerol

1678 (T291) Whole cottonseed and crude glycerin for Nellore cattle on pasture: Intake and digestibility of nutrients.

A. J. Possamai[1], J. T. Zervoudakis[*2], L. K. Hatamoto-Zervoudakis[2], A. S. Oliveira[3], E. R. Donida[2], P. I. J. L. R. Silva[1], A. C. Barboza[1], R. G. D. P. Junior[2], and J. W. Koscheck[4], *[1]UFMT, Cuiabá, Brazil, [2]Federal University of Mato Grosso, Cuiaba, Brazil, [3]UFMT, Sinop, Brazil, [4]UNESP, Jaboticabal, Brazil.*

Use of by-products in the beef cattle diets have important function to reduce production costs and needs to be evaluate in different production systems. The aim of this experiment was to evaluate intake and digestibility of nutrients in beef cattle diet with associations of whole cottonseed and crude glycerin in multiple supplements for Nellore cattle in the fattening phase at *Brachiaria brizantha* pastures in the rainy season. Animals were supplemented with 4 kg/d (21% of crude protein). The experiment was performed in a 5 × 5 (five supplements and five periods) Latin square design and structured in a factorial design 2 × 2 + 1 [two levels of crude glycerin (0 and 15%), two levels of cottonseed (0 and 25%) and supply of mineral mix (control)]. Orthogonal contrasts were used to evaluate effect of crude glycerine, whole cottonseed and interaction, adopting 0.05 to the critical level of probability. The supplementation increased dry matter intake at 2.25 kg/day ($P = 0.037$), due largest apparent digestibility of dry matter in function of fed supplements (65.83%) in relation to the control treatment (55.69%) ($P < 0.05$). Multiple supplements increased intake of ether extract (0.370 vs. 0.170 kg/d) ($P < 0.05$), crude protein (1.380 vs. 0.720 kg/d) ($P < 0.001$), and no fiber carbohydrates (3.715 vs. 2.07 kg/d) ($P < 0.001$), due to higher content of these nutrients in supplements when compared with only forage/mineral mix. Ether extract intake was still affected by the inclusion of whole cottonseed in supplement ($P < 0.05$) due high concentration of oil in this ingredient. Apparent digestibility of ether extract in the diets evaluated was affected by supplementation ($P < 0.05$) and whole cottonseed inclusion ($P < 0.05$) and assigning it lower contribution of endogenous excretion of ether extract when their content is high in diet. Intake and digestibility of neutral detergent fiber were not affected ($P > 0.05$), evidencing that extra supply of nutrients did not affect the cellulolytic microbiota, with appropriate digestibility of most abundant energy unit in grazing production system. By-products that reduce diets costs and improve voluntary dry matter intake are important in nutritional formulations because are responsible for most of the variations in productive performance.

Key Words: by-products, Nellore, pastures

1679 (T292) Crude glycerin in multiple supplements for beef cattle in grazing: pH and ammoniacal nitrogen.

R. G. D. P. Junior[*1], A. J. Possamai[2], J. T. Zervoudakis[1], L. D. S. Cabral[1], L. K. Hatamoto-Zervoudakis[1], A. C. Barboza[2], L. B. D. Freiria[1], J. B. Azevedo[3], and A. S. Oliveira[4], *[1]Federal University of Mato Grosso, Cuiaba, Brazil, [2]UFMT, Cuiabá, Brazil, [3]Federal University of Mato Grosso, Cuiabá, Brazil, [4]UFMT, Sinop, Brazil.*

Objective was evaluate the pH and concentration of ruminal ammoniacal nitrogen (NH_3–N) in beef cattle receiving multiple supplementation in grazing, with increasing levels of crude glycerin, in the rainy season. It has been utilized five Nellore beef cattle, male, non-castrated. The pastures were divided into five picket of 0.25 ha each, covered with *Brachiaria brizantha* cv. Marandu. The experiment was divided into 5 × 5 Latin square design, composed by five experimental periods of 19 d each and five animals. The strategy adopted was to provide 4 kg/animal/day of multiple supplements with four levels of crude glycerin (0; 8; 16 and 24%) and the mineral mixture (MM) was offered ad libitum(control). Ruminal liquid samples were collected for measuring the pH and quantification of NH_3–N by gavage, in two times (0 and 4 h after supplementation). The pH values for the time 0 and 4 h did not differ between the supplements ($P > 0.05$) (Table 1679), with average value of 6.83 and 6.59, respectively. It was verified decrease in measuring 4 h after the supplementation in comparison to time 0 ($P < 0.01$), demonstrating that there is a normal diurnal variation in the pH value without it being influenced by the multiple supplementation, important fact in the maintenance of ruminal fermentation. The content of NH_3–N has not been influenced by the supplementation before the concentration being supplied ($P > 0.05$) with average between the treatments of 4.98 mg/dL. It was observed at time four the raise in the content of NH_3–N for multiple supplementation regardless the formulation utilized ($P < 0.01$), while the control has not promoted such effect

($P > 0.05$). The average values of NH_3–N from animals receiving multiple supplementation was of 11.08 mg/dL, adequate for microbial development and ruminal fermentation.

Key Words: Nellore, rainy season, supplementation

Table 1679. Mean values of pH and concentration of NH3-N (mg/dL) in ruminal fluid

	Supplements					
Times	MM	0% GLYC[1]	8% GLYC[1]	16% GLYC[1]	24% GLYC[1]	SEM[2]
	Ruminal pH					
T 0	6.85^{Aa}	6.88^{Aa}	6.86^{Aa}	6.80^{Aa}	6.80^{Aa}	0.10
T 4	6.68^{Ab}	6.61Ab	6.65^{Ab}	6.51^{Ab}	6.53^{Ab}	0.14
	NH3-N					
T 0	3.72^{Aa}	6.08^{Ab}	5.68^{Ab}	5.03^{Ab}	4.40^{Ab}	1.57
T 4	5.46^{Ba}	15.64^{Aa}	11.57^{Aa}	12.25^{Aa}	10.50^{Aa}	3.73

Means followed by the same small letter in the column and same uppercase letter in row do not differ at 5% probability by SNK test.

[1] levels of crude glycerin.

[2] standard errors of the mean.

1680 (T293) Grain processing methods and concentration of corn silage NDF in the finishing diet of Nellore bulls.

C. Sitta*[1], D. A. Fleury[1], J. D. Souza[1], F. Batistel[2], W. F. Angolini[1], M. A. P. Meschiatti[1], N. C. G. Barbosa[1], G. G. Rosa[1], B. A. V. Arthur[1], P. D. Andrade[1], A. Paro[1], A. C. Aoki[1], M. R. R. Soares[1], and F. A. P. Santos[2], *[1]University of Sao Paulo, Piracicaba, Brazil, [2]University of São Paulo, Piracicaba, Brazil.*

Grain processing methods disrupt the protein matrix of starch granules and increase surface area allowing more starch to be digested and higher animal performance of cattle fed high concentrate diets. There are some interaction of grain processing and NDF concentration. Inadequate fiber concentration could result in metabolic disturbs decreasing animal performance. This study evaluated two grain processing methods (coarsely ground and steam flaked corn) and these methods interaction with four corn silage NDF concentrations (4, 7, 10, and 13%) on animal performance. Two hundred thirty-seven Nellore bulls (336 kg BW ± 1.53) were fed diets containing corn silage; corn; soybean meal; urea and a mineral and vitamin premix. The animals were blocked by initial BW and randomly allocated to 24 pens in groups of six animals and to eight pens in groups of 12 animals. The parameters evaluated were DMI, ADG and FE. The experiment lasted 117 d and the data was analyzed using PROC MIXED of the SAS package. Block was considered the random effect. Grain processing method, NDF concentration and grain processing method X NDF concentration were considered fixed effects. Linear and quadratic effects of NDF concentration were tested for each grain processing method. Animals fed flaked corn had higher FE than animals fed ground corn. From all concentrations of corn silage NDF, 7 and 4%, had higher FE for treatments containing ground corn and flaked corn, respectively. It was concluded that corn flaking is an efficient way to improve performance of Nellore cattle in feedlot in comparison to ground corn and that 4 to 7% of NDF from corn silage are efficient concentrations to obtain good results on animal performance.

Key Words: grain processing, NDF concentration, Nellore

1681 (T294) Effect of corn processing methods and dietary concentrations of sugarcane bagasse fiber on finishing Nellore bulls performance.

A. H. F. Melo*, D. F. A. Costa, C. A. B. Delveaux, J. D. Souza, F. Batistel, D. C. Basto, P. R. Gabarra, A. C. Aoki, and F. A. P. Santos, *University of Sao Paulo, Piracicaba, Brazil.*

The objective of this experiment was to evaluate processing methods of flint corn grain (ground corn, particle size: 3.18 mm and steam-flaked corn with bulk density of 360 g/L) combined with dietary contents of 4, 7, 10 or 13% roughage NDF (DM basis) using sugarcane bagasse as source of fiber on performance of Nellore bulls finished in feedlot. Two hundred forty Nellore bulls (initial BW = 350 ± 2.4 kg) were fed diets containing 76 to 86% corn and were randomly allocated to 32 pens in a factorial arrangement of 2 × 4. Animals were blocked based on initial BW. The parameters evaluated were dry matter intake (DMI), average daily gain (ADG), feed efficiency (ADG/DMI) and final BW after 120 d on feed. The data were analyzed using PROC MIXED of SAS and means were compared by F test considering the block as random effect and corn grain processing method, roughage NDF and corn grain processing method * roughage NDF effects. There

Table 1680. Performance of cattle receiving diets with two grain processing methods and different concentrations of corn silage NDF

Grain processing method	Ground corn						Flaked corn					
	Corn silage NDF concentrations				Contrast		Corn silage NDF concentrations				Contrast	
	4	7	10	13	L	Q	4	7	10	13	L	Q
IBW, kg	344.0	344.1	343.9	343.9	NS	NS	343.8	343.9	344.1	343.9	NS	NS
FBW, kg	512.1	518.2	527.2	517.6	0.05	0.001	520.3	517.5	521.1	535.7	0.01	0.001
DMI, kg	8.55	8.85	9.45	9.5	0.01	0.12	8.48	8.75	8.8	9.68	0.01	0.001
ADG, kg	1.44	1.49	1.57	1.48	0.05	0.002	1.51	1.48	1.51	1.64	0.01	0.001
ADG/DMI	0.168	0.169	0.166	0.157	0.01	0.15	0.181	0.172	0.172	0.169	0.04	0.38

was no interaction between the concentrations of sugarcane bagasse NDF and processing methods. Cattle fed steam-flaked corn diets presented less ($P < 0.05$) DMI (8.57 vs. 9.31 kg.d^{-1}), 26.3% greater ($P < 0.05$) final BW (509 vs. 493.3 kg), 12.3% greater ($P < 0.05$) ADG (1.37 kg.d^{-1} vs. 1.22 kg.d^{-1}) and 21.97% greater ($P < 0.05$) feed efficiency (0.161 vs. 0.132) than cattle fed coarsely ground corn. Increasing roughage NDF content of the diets caused a quadratic response ($P = 0.01$) for DMI (8.37, 9.13, 9.02 and 9.25 respectively), had no effect ($P > 0.05$) on cattle final weight (496.8, 506.3, 498.4 and 503.9 kg, respectively) and cattle ADG (1.26, 1.34, 1.28 and 1.31 kg.d^{-1}respectively) and it caused a linear decrease ($P = 0.04$) in feed efficiency (0.150, 0.148, 0.142 and 0.144 respectively). In conclusion, steam flaking of flint corn improved performance of finishing Nellore bulls in comparison to ground corn with particle size of 3.18 mm. Nellore bulls were mor efficient when diets containing 4% sugarcane bagasse NDF were fed compared to diets with greater roughage NDF contents.

Key Words: ground corn, steam-flaked corn, feedlot

1682 (T295) Predicting ruminal and total tract starch digestion as influence by changes in density of steam-flaked corn: Flake thickness, enzymatic reactivity, fecal starch. M. A. Franco[*1], J. F. Calderon-Cortes[2], L. Corona[1], A. Plascencia[2], and R. A. Zinn[3], *[1]UNAM, México City, [2]UABC, Mexicali, México, [3]University of California–Davis, El Centro.*

Six Holstein steers (153 kg ± 11) with cannulas in the rumen and proximal duodenum were used in a 6 × 6 Latin square design experiment to compare flake density (FD, kg/L), flake thickness (FT, mm), amyloglucosidase reactivity (AGR, %), and fecal starch (FS, %) as predictors of ruminal (RSD, %) and total tract (TSD, %) starch digestion. Based on FD, RSD = 92.5– 36.6FD ($r^2 = 0.76$) and TSD = 96.5 + 30.2FD– 68.6FD^2 ($r^2 = 0.99$). Based on FT, RSD = 88.9– 4.45FT ($r^2 = 0.83$) and TSD = 97.1 + 3.77FT– 1.43FT^2 ($r^2 = 0.99$). Based on AGR, RSD = 72.0 + 0.43AGR ($r^2 = 0.94$) and TSD = 90.9 + 0.695AGR– 0.0138AGR^2 ($r^2 = 0.91$). Based on FS, RSD = 85.9– 2.88FS + 0.204FS^2 ($r^2 = 0.97$) and TSD = 100.0– 0.40FS ($r^2 = 1.00$). Measures of fecal starch were the best single predictor of ruminal and total tract starch digestion in catte fed steam-flaked corn-based diets. Fecal starch has the additional advantage of being equally effective when data for dry rolled corn are included in the dataset. Whereas AGR was a good predictor of ruminal starch digestion, it was the least effective of the measures for estimation of total tract starch digestion. Due to the ease of its determination, flake thickness may be the more convenient and reliable measure for assessment of day-to-day process adequacy.

Key Words: starch, maize, digestion

1683 (T296) Intake and performance of crossbred dairy calves fed spineless cactus in transition. R. Gomes[1], M. F. S. Queiroz[*2], S. Gonzaga Neto[3], R. G. Costa[4], J. S. Oliveira[3], G. O. Mendes[4], R. L. Galati[2], and G. R. Beltrão da Cruz[4], *[1]University of Paraiba, CCA/UFPB, Areia, Brazil, [2]University of Mato Grosso–DZER/UFMT, Cuiabá, Brazil, [3]University of Paraiba–CCA/UFPB, Areia, Brazil, [4]University of Paraiba–CCHSA/UFPB, Bananeiras, Brazil.*

A study was conducted to evaluate the intake and performance of crossbred calves (Holstein x Zebu) in the transition from a liquid diet to a solid diet fed spineless cactus replacing Tifton 85 hay. Sixteen crossbred calves with initial body weight of 50.04 ± 6.3 kg were used. Calves were housed in individual hutches, and suckled artificially with 4 L of milk x d^{-1}until 30 d of life. After completing 31 d the experimental period was initiated in which the calves began to receive the liquid diet in the same amount (4 L) also solid foods according treatment. Treatments consisted of the replacement of Tifton 85 hay diet by spineless cactus (*Opuntia ficus indica*, MILL) as follows: T1 (DPA): 70% concentrate + 30% Tifton hay, T2 (SPV): 70% concentrate + 15% Tifton hay + 15% spineless cactus, T3 (STV): 70% concentrate + 30% spineless cactus, T4 (SCV): 50% concentrate + 17% Tifton hay + 33% spineless cactus. The experiment was analyzed as a completely randomized design with ANOVA being conducted with the GLS procedure of SAS and the averages compared by Tukey's test at 5% probability. The DMI, BW, body measurements, body score and fecal score were performed weekly until 67 d of life. The DMI (0.48 kg x d^{-1}), final BW (55.9 kg), body measurements (wither height: 84.2 cm; hip height: 88.0 cm and heart girth: 88.4 cm) and body score (2.4) of the animals were not affected by treatments ($P > 0.05$). The average daily weight gain was influenced ($P < 0.01$) by the treatments, the greatest gains were observed in the treatment SPV (421 g x d^{-1}), the DPA and SCV (388 g x d^{-1}) treatments were no longer different from other while the smaller ADG were obtained in treatment STV (289 g x d^{-1}). The fecal average scores observed during the entire experimental period shows that there was no incidence of diarrhea in animals. In conclusion the use of spineless cactus replacing the Tifton hay as roughage in the diet of crossbred calves in the transition phase from a liquid diet to a solid diet is indicated assisting in early weaning without affecting the growth and development of these animals.

Key Words: average daily gain, body score, body weight

1684 (T297) Carcass characteristics of crossbred dairy calves fed spineless cactus in transition. R. Gomes[1], M. F. S. Queiroz[*2], R. G. Costa[3], S. Gonzaga Neto[4], J. S. Oliveira[4], G. O. Mendes[3], G. R. Beltrão da Cruz[3], and J. Jordão Filho[3], *[1]University of Paraiba, CCA/UFPB, Areia, Brazil, [2]University of Mato Grosso–DZER/UFMT, Cuiabá, Brazil, [3]University of Paraiba–CCHSA/UFPB, Bananeiras, Brazil, [4]University of Paraiba–CCA/UFPB, Areia, Brazil.*

A study was conducted to evaluate the carcass characteristics of crossbred calves (Holstein x Zebu) in the transition from a liquid diet to a solid diet fed spineless cactus replacing Tifton 85 hay. Sixteen crossbred calves with initial body weight of 50.04 ± 6.3 kg were used. Calves were housed in individual hutches, and suckled artificially with 4 L of milk.d^{-1} until 30 d of life. After completing 31 d the experimental period was initiated in which the calves began to receive the liquid diet in the same amount (4 L) also solid foods according treatment. Treatments consisted of the replacement of Tifton 85 hay diet by spineless cactus (*Opuntia ficus indica*, MILL) as follows: T1 (DPA): 70% concentrate + 30% Tifton hay, T2 (SPV): 70% concentrate + 15% Tifton hay + 15% palm, T3 (STV): 70% concentrate + 30% palm, T4 (SCV): 50% concentrate + 17% Tifton hay + 33% palm. The experiment was analyzed as a completely randomized design with ANOVA being conducted with the GLS procedure of SAS and the averages compared by Tukey's test at 5% probability. The DMI, BW, body measurements, BS and fecal score were performed weekly until 67 d of life, when these animals were slaughtered to evaluate carcass yield. There was no significant difference ($P > 0.05$) in final BW (55.9 kg), hot carcass weight (30.4 kg) and chilled carcass weight (30.0 kg) with the replacement of Tifton by spineless cactus. As the treatments did not affect ($P > 0.05$) hot carcass yield (55.8%) and chilled carcass yield (54.1%). Measures of carcass, carcass length (72.4 cm), leg length (50.8 cm) and perimeter of cushion (44.4 cm) were not affected ($P > 0.05$) by treatments. Average of 20.9 cm for the areas of rib eye area, and 0.96 cm in the fat thickness were observed, both without influence of treatments ($P > 0.05$). In conclusion the use of spineless cactus replacing the Tifton hay in the diet of crossbred calves is indicated without affecting the carcass characteristics of these animals.

Key Words: forage cactus; rib eye area; veal

1685 (T298) Effect of chitosan and soybean oil combination on ruminal fermentation and milk yield and composition of dairy cows. *T*. A. Del Valle[*1], F. C. R. D. Santos[1], P. G. D. Paiva[2], E. F. Jesus[2], F. Zanferari[1], M. K. Kametani[1], A. G. B. V. B. Costa[1], and F. P. Rennó[1], *[1]School of Veterinary Medicine and Animal Science, University of São Paulo, Pirassununga, Brazil, [2]School of Agricultural and Veterinary Sciences of UNESP, Jaboticabal, Brazil.*

The aim of this study was to evaluate the effects of chitosan addition in mid-lactating dairy diet without or with soybean oil on ruminal fermentation and milk composition. Twenty-four Holstein cows (four ruminally cannulated), averaging 174.7 ± 53.1 DIM, were randomly assigned in six Latin square design with a 2 × 2 factorial arrangement of treatments. The diets contained Chitosan (150mg/kg of body weight) and soybean oil (3.3% of the diet DM). Each experiment period had a 14-d adaptation period and a 7-d for collection data. Sampling of milk was done on Days 16, 17, and 18 of each period to evaluate the composition. On d 21 of each period, rumen fluid samples were collected from cannulated cows in seven times to evaluate the effect of the diets on ruminal fermentation. The results of milk composition were subjected to analysis of variance, while fermentation data were analyzed as repeated measures, both by PROC MIXED of SAS. There was no interaction effect ($P > 0.05$) of factors and the time on ruminal fermentation. The addition of soybean oil in the diet increased the concentration of propionate and decreased acetate and the total concentration of short chain fatty acids (SCFA) in mmol.L^{-1}, however the ratio acetate:propionate was decreased. Those diets decreased ($P < 0.05$) the levels of milk fat in 5 g/kg on average. The addition of chitosan in the diet reduced the total concentration of SCFA, although ruminal fermentation and milk composition was not altered significantly. The protein contents in milk were on average 3.06% and were not affected by diets. There was interaction ($P < 0.05$) of the factors for milk yield. Milk yield was same in control and chitosan diets and was higher in diet with soybean oil than diet with chitosan and soybean oil, with averages of 33.87, 32.85, 32.86 and 31.26, respectively. In conclusion, the use of chitosan as a feed additive for dairy cattle was positive in increasing the milk production, when in diet of low lipids level, not altering, however, ruminal fermentation and milk composition.

Key Words: additive, milk fat, rumen

1686 (T299) Growth performance and total tract nutrient digestion for Holstein heifers precision-fed diets high in distillers grains with different forage particle size. R. D. Lawrence*, J. L. Anderson, T. J. Vanderwerf, A. K. Manthey, K. F. Kalscheur, and D. P. Casper, *South Dakota State University, Brookings.*

This study evaluated dairy heifer growth performance and total tract nutrient digestion when fed diets high in dried distillers grains with solubles (DDGS) with different forage particle size, achieved by utilizing alfalfa hay that was processed differently. An 8-wk randomized complete block design study was conducted using twenty-two Holstein heifers (123 ± 32 d of age; initial body weight (BW) of 140 ± 23.5 kg). Treatments were either 15% chopped (CHOP) or 15% pelleted (*P*ELL) alfalfa hay on a dry matter (DM) basis. Both diets also contained 30% DDGS, 53.75% corn silage, and 1.25% mineral mix. Rations were precision-fed for a dry matter intake (DMI) of 2.3% of BW. Frame sizes, BW, and body condition scores (BCS) were taken on two consecutive days during wk 0, 2, 4, 6, and 8. During wk 8, titanium dioxide was fed and fecal grab samples were collected to measure total tract nutrient digestion. Heifer DMI increased ($P < 0.01$) when fed CHOP versus PELL (4.42 and 4.19 kg/d for CHOP and PELL, respectively). Body weights (167.4 and 164.0 kg) and average daily gain (0.83 and 0.96 kg/d) were similar ($P > 0.05$) between treatments. Gain to feed was less ($P < 0.01$) in CHOP versus PELL (0.21 and 0.25). Hip height (110.7 and 110.9 cm), wither height (106.7 and 106.6 cm), and body length (95.1 and 94.9 cm) were similar between treatments. Paunch girth (153.6 and 150.4 cm), heart girth (122.4 and 120.4 cm), and hip width (30.2 and 29.6 cm) were greater ($P < 0.05$) for CHOP versus PELL. Body condition score was less ($P < 0.01$) for CHOP compared to PELL (3.03 and 3.09). For growth measurements there were no significant treatment by week interactions or differences in average daily changes. Total tract digestibility of DM (67.5 and 67.3%), neutral detergent fiber (51.2 and 50.1% of DM), and crude protein (68.3 and 67.9% of DM) were similar between treatments. Heifers fed diets containing 30% DDGS with 15% chopped or pelleted alfalfa hay had similar total tract nutrient digestion and growth performance, with some very minor differences in frame growth and feed to gain. Overall, this study demonstrated that feeding dairy heifers diets with different forage particle sizes, achieved by inclusion of chopped or pelleted alfalfa hay, does not affect utilization of DDGS.

Key Words: dairy heifer, distillers grains, particle size

1687 (T300) Comparison of efficiency of energy use in Holstein and Jersey dairy cows offered diets containing reduce fat distillers grains RFDDGS. G. Garcia Gomez*[1], A. Foth[1], P. J. Kononoff[1], T. Brown-Brandl[2], and H. C. Freetly[2], [1]*University of Nebraska, Lincoln,* [2]*ARS–USDA, Clay Center, NE.*

Fifty six energy balances were completed with eight Holstein (H) and eight Jersey (J) multiparous lactating cows to examine the effect of breed on the efficiency of milk production and energy use. Two dietary treatments were fed in a repeated switch back design to compare breeds. Dietary treatments consisted of 24.5% corn silage, 18.4% alfalfa hay, 6.9% grass hay, with either 22.9% rolled corn and 14.8% soybean meal or 4.51% rolled corn, 0% SBM, and 14.5% RFDDGS (dry matter basis). Diets were offered ad libitum for a 28-d adaptation period and 95% ad libitum for a 4-d collection period. During the collection days, ration digestibility and energy use was measured, indirect calorimeter respiration head boxes were used to determine heat production. Across the two treatments, Holstein cows had a significantly higher intake of gross energy (GE) (30 ± 3.96 Mcal/d; $P = < 0.01$), and higher energy output in feces, urine, methane, heat production (HP), and milk energy (6.5 ± 1.24, 0.11 ± 0.11, 1.2 ± 0.15, 8.95 ± 0.74, and 8.54 ± 1.27 Mcal/d, respectively; $P = < 0.01$) than did Jersey cows. Jersey cows produced milk with higher fat content (4.96% vs. 3.69% ± 0.19 for Jersey and Holstein, respectively; $P = < 0.01$), protein (3.75% and 3.20% ± 0.1 for Jersey and Holstein, respectively; $P < 0.01$), and energy concentrations, compared with those of the Holstein cows. Metabolizable energy (ME) and digestible energy (DE) intake as a proportion of GE intake were significantly higher for Holstein cows (0.03 ± 0.01 and 0.03 ± 0.007, respectively; $P = < 0.01$ and 0.02). However, breed had no significant effects on ME/DE (0.88 ± 0.01), HP/ME (0.56 ± 0.02), DE/DMI (2.78 ± 0.06), ME/DMI (0.45 ± 0.06), methane energy/DE (0.08 ± 0.004), and urine energy/DE (0.04 ± 0.002). No significant interaction was found between breed and treatment for any of the ratios of energy use examined. In addition, no significant differences in energy partitioning between milk (milk energy/ME intake) (0.40 ± 0.18), and body tissue (retention energy/ME intake) (0.04 ± 0.0034) were found between Holstein and Jersey dairy cows. In conclusion, breed had no effect on the overall production efficiency of dairy cows in terms of efficiency of ME use for lactation, and energy partitioning between milk and body tissue.

Key Words: energy efficiency, Holstein, Jersey.

1688 (T301) Effects of feeding canola meal (CM) and wheat dried distillers grains with solubles (W-DDGS) as the major protein source in low or high crude protein diets on ruminal nitrogen utilization, omasal nutrient flow, and milk production in dairy cows. T. Mutsvangwa[*1], and K. Doranalli[2], *[1]University of Saskatchewan, Saskatoon, Canada, [2]Evonik (SEA) Pte. Ltd., Singapore.*

The objective was to determine the effects of feeding CM or W-DDGS as the major source of protein in diets varying in CP content on ruminal N utilization, omasal flows, and milk production. Eight Holstein cows (109 ± 36 DIM) were used in a replicated 4 × 4 Latin square design with 28-d periods. Four cows in one Latin square were ruminally-cannulated to facilitate ruminal and omasal sampling. Treatments were: 1) source of protein (CM vs. W-DDGS); and 2) dietary CP content (15 vs. 17%). Interactions between source of protein x CP content were nonsignificant. Dry matter intake and milk yield were unaffected by diet ($P > 0.05$). Feeding CM increased milk lactose content compared to feeding W-DDGS ($P = 0.003$). Milk urea-nitrogen ($P < 0.001$) and ruminal NH_3–N ($P = 0.05$) concentrations were greater in cows fed the high CP compared to those fed the low CP diet. Dry matter apparently digested in the rumen was greater in cows fed the high CP compared to those fed the low CP diet, with the difference in DM apparently digested in the rumen being greater in cows fed W-DDGS as compared to those fed CM (interaction, $P = 0.02$). The RDP supply was greater in cows fed the high CP when compared to those fed the low CP diet when diets contained CM, whereas RDP supply was lower in cows fed the high CP when compared to those fed the low CP diet when diets contained W-DDGS (tendency for interaction, $P = 0.08$). The omasal flow of NH_3–N was greater in cows fed CM when compared to those fed W-DDGS ($P = 0.03$). The RUP supply was greater in cows fed the low CP when compared to those fed the high CP diet when diets contained CM, whereas RUP supply was lower in cows fed the low CP when compared to those fed the high CP diet when diets contained W-DDGS (tendency for interaction, $P = 0.06$). Omasal flows of threonine and tryptophan were greater ($P \leq 0.03$), whereas that of histidine and lysine tended ($P \leq 0.08$) to be greater, in cows fed CM when compared to those fed W-DDGS. In conclusion, when diets are formulated to contain 15 or 17% CP, CM or W-DDGS can support similar levels of milk production when used as the major protein source.

Key Words: canola meal, milk production, wheat dried distillers grains with solubles

1689 (T302) Performance, digestibility, and blood acid-base balance of dairy cows in response to the replacement of corn by crude glycerin. O. F. Zacaroni[1], F. F. Cardoso[1], R. A. N. Pereira[2,3], and M. N. Pereira[*1,3], *[1]Universidade Federal de Lavras, Brazil, [2]Empresa de Pesquisa Agropecuaria de Minas Gerais, Lavras, Brazil, [3]Better Nature Research Center, Ijaci, Brazil.*

This experiment evaluated the response of late lactation dairy cows to the partial replacement of corn by methanol rich, crude glycerin. The tallow derived glycerin contained 70.2% DM and 7.3% methanol on an as-fed basis. Twelve Holsteins (219 ± 57 DIM), three primiparous, were assigned to 35-d periods, 3 × 3 Latin squares. The isonitrogenous diets (15.8% CP) contained (DM basis): 11.8% finely ground mature corn and 17.2% soybean meal (T0); 4.9% glycerin, 5.9% corn, and 18.3% soybean meal (T5); or 9.7% glycerin and 19.4% soybean meal (T10). Other ingredients were: 31.9% corn silage, 28.2% sugarcane silage, and 6.2% high moisture corn. Statistical analysis was performed with PROC MIXED of SAS, with a model containing the random effect of cow and the fixed effects of period and treatment. Two contrasts were evaluated: Linear = T0 vs. T10, and Quadratic = T5 vs. (T0+T10). The replacement of corn by glycerin induced linear decreases in milk (22.2, 21.1, 20.0 kg/d, $P < 0.01$) and lactose secretions ($P < 0.01$), without affecting DMI (17.8 kg/d, $P = 0.53$), reducing feed efficiency ($P < 0.01$). Milk contents of fat (4.11, 4.33, 4.37%, $P = 0.01$) and protein (3.47, 3.64, 3.73%, $P < 0.01$) were linearly increased by glycerin, but daily secretions were similar ($P > 0.86$). Milk urea nitrogen was similar (13.8 mg/dL, $P = 0.51$), as well as chewing activity ($P > 0.32$), except the daily ingestion time, reduced by glycerin ($P = 0.05$). Total tract apparent digestibility of the non-NDF organic matter was linearly increased by glycerin (90.3, 91.4, 93.2% of intake, $P = 0.05$), but the intake of digestible organic matter was similar (10.6 kg/d, $P = 0.66$). The ratio of the daily milk energy secretion to the intake of digestible organic matter was linearly reduced by glycerin (1.58, 1.55, 1.42 Mcal/kg, $P = 0.05$). Rumen pH 12-h post feeding was similar (5.67, $P = 0.72$). The intake of crude glycerin was 1.24 kg/d in T5 and 2.5 kg/d in T10, methanol intake was 134 mg/kg of BW in T5 and 269 mg/kg of BW in T10. Health disorders were not observed. However, glycerin reduced the partial pressure of CO_2 ($P = 0.02$) and increased the saturation of hemoglobin with O_2 ($P = 0.05$) in jugular blood samples obtained 6-h post feeding, suggesting an induction of hyperventilation. Venous blood pH, bicarbonate level, base excess, and the partial pressure of O_2 were not affected by treatment ($P > 0.64$). The replacement of corn by crude glycerin reduced milk yield, feed efficiency, and the response was associated to low milk lactose secretion.

Key Words: digestibility, glycerin, methanol

1690 (T303) Effects of crude glycerin supplementation on fatty acids composition of milk fat from primiparous lactating cows on irrigated tropical pasture. M. C. A. Santana*[1], H. A. Santana Junior[2], M. P. Figueiredo[3], E. O. C. Santana[4], G. A. Filho[4], C. B. Figueiredo[2], M. S. Maciel[2], and J. I. Simionato[5], *[1]Emater, Goiânia, Brazil, [2]Universidade Estadual do Piauí, Corrente, Brazil, [3]Universidade Estadual do Sudoeste da Bahia, Vitória da Conquista, Brazil, [4]Universidade Estadual do Sudoeste da Bahia, Itapetinga, Brazil, [5]Universidade Estadual de Londrina, Brazil.*

The objective of this study was to evaluate the effect of different levels of crude glycerin suplementation on fatty acids composition of milk fat from primiparous lactating cows grazing on irrigated tropical pasture. The experiment was conducted at Rancho Santana farm, located in Jequié city, Bahia, Brazil, in the period from Dec. 21, 2010, to March 16, 2011. Ten 3/4 Holstein × 1/4 Dairy Gyr lactating primiparous cows, with 109 ± 24 d of lactation and a mean age of 30 ± 6 mo and mean body weight of 426.2 ± 68.29 kg were distributed into five treatments, using two simultaneous 5 × 5 Latin squares. Treatments consisted of inclusion levels (0, 94, 191, 289, 389 g/kg dry matter basis) of crude glycerin (CG) in the supplement. Fatty acid methyl esters were analyzed by Thermo Finnigan Trace-GC-Ultra gas chromatography. Results were statistically analyzed by variance and regression analyses at 0.05 probablity. Results showed effects on milk fat saturated fatty acids— caproic (6:0), caprylic (8:0), capric (10:0), lauric (12:0), pentadecanoic (15:0) and stearic (18:0)— when the crude protein concentrations in supplement increased. The increase of CG level in the supplement did not differ the polyunsaturated fatty acids ($P < 0.05$). To determine the ratio between pro- and anti-atherogenic acids, the atherogenic index (IA) and thrombogenic index (IT) were calculated, and difference was verified only for IA ($P < 0.05$). Treatments affected a few of the saturated and monounsaturated fatty acids. Overall, this data indicated that the addition of glycerin did not cause effects on the variables that express the milk quality, so the recommended crude glycerin level could be increased to 389 g (171 g glycerol) per kg of supplement.

Key Words: glycerol, biohydrogenation, biodiesel

1691 (T304) Effect of grain processing and fat supplementation on ruminal pH dynamics of cows grazing a tropical pasture. J. D. Souza*, F. Batistel, E. Miqueo, P. D. Andrade, M. M. V. Silva, C. Sitta, and F. A. P. Santos, *University of Sao Paulo, Piracicaba, Brazil.*

The objective of this experiment was to investigate the effects of grain processing and fat supplementation to dairy cows grazing a tropical pasture on ruminal pH dynamics and incidence of acidosis. Four rumen cannulated lactating cows (165 ± 32 DIM) were used in a Latin square design and subjected to the following treatments: a) fine ground corn without fat (FGC); b) fine ground corn + 400 g calcium salts of palm oil cow^{-1} d^{-1} (FGCCS); c) steam-flaked corn without fat (SFC); d) steam-flaked corn + 400 g of calcium salts of palm oil cow^{-1} d^{-1} (SFCCS). The fine ground corn had a particle size of 1.3 mm and steam-flaked corn a density of 360 g/L. Treatment periods were 24 d in length and cows grazed paddocks of *Pennisetum purpureum* and received 6.0 kg cow^{-1} d^{-1} (DM) of concentrate twice daily. Ruminal pH was continuously measured using a LRC pH measurement system. The in-dwelling electrode measured and recorded the ruminal pH every 10 min over the measurement period. Each electrode was standardized using pH 4.0 and 7.0 standards at the beginning and end of each period. The pH data were first summarized by day and then averaged across each measurement period as mean, maximum, and minimum pH and time in which pH was below 6.2, 6.0, and 5.8 as an index of severity of ruminal acidosis. Data were analyzed as repeated measures using a PROC MIXED model with period and animal as random effect and grain processing, fat supplementation and grain processing × fat supplementation as fixed effects. The means were compared by Tukey test at 5%. The mean pH, minimum pH and maximum pH were not affected by treatments. The mean pH was 6.63, 6.73, 6.68 and 6.64 for FGC, FGCCS, SFC and SFCCS, respectively. The minimum pH was 6.02, 6.10, 6.02 and 6.15 and the maximum pH was 7.04, 7.12, 7.02 and 7.06 for FGC, FGCCS, SFC and SFCCS, respectively. No pH measurements below 5.8 were observed. The time that the pH was below 6.0 was greater in steam-flaked compared with fine ground corn (5.2 vs. 2.6 h/d), and the time that pH was below 6.2 was also greater in steam-flaked diets (14.0 vs. 11.4 h/d). In conclusion, steam-flaked corn diets decreased the ruminal pH, but not below 5.8, which suggest no acidosis occurrence in dairy cows grazing a tropical pasture.

Key Words: steam-flaked corn, fat, tropical pasture

1692 (T305) Grain processing and fat supplementation on milk yield and milk composition of dairy cows grazing a tropical pasture. F. Batistel*, J. D. Souza, M. R. R. Soares, C. S. M. Motta, E. Miqueo, and F. A. P. Santos, *University of São Paulo, Piracicaba, Brazil.*

The objective of this experiment was to investigate the effects of grain processing and fat supplementation to early lactation dairy cows grazing a tropical pasture on milk production and composition. Forty early lactation cows (15 ± 4 DIM) were used in a randomized block design and subjected to the following treatments: a) fine ground corn without fat; b) fine ground corn + 400 g calcium salts of palm oil cow^{-1} d^{-1}; c) steam-flaked corn without fat; d) steam-flaked corn + 400 g of calcium salts of palm oil cow^{-1} d^{-1}. Treatment periods were 90 d in length and cows grazed paddocks of *Pennisetum purpureum* and received

9 kg cow^{-1} d^{-1} (DM) of concentrate twice daily. Milk yield was measured every 2 d and milk composition was analyzed every 6 d. Data were analyzed as repeated measures using a mixed model with block as random effect and grain processing, fat supplementation and grain processing × fat supplementation as fixed effects. The means were compared by Tukey test. Steam-flaked corn increased (P = 0.001) milk yield compared with fine ground corn (23.9 vs. 22.2 kg/d) and supplementation with fat also increased (P = 0.0001) milk production (24.7 vs. 21.3 kg/d). Milk fat content was reduced (P = 0.01) in steam-flaked corn in comparison with fine ground corn diets (3.22 vs. 3.30%). There was a pronounced increased (P = 0.0001) in milk protein content in steam-flaked corn compared with fine ground corn diets (3.41 vs. 3.15%). In addition, milk casein content was increased (P = 0.0001; 2.47 vs. 2.33%) and milk urea nitrogen was decreased (P = 0.002; 12.1 vs. 16.3 mg/dL) in steam-flaked diets indicating greater efficiency of N utilization in these treatments. Total solids content was reduced (P = 0.05) by fat supplementation (12.19 vs. 12.05%), which is associated with the tendency of reduction in milk protein content (P = 0.10; 3.29 vs. 3.22%). Milk fat yield was unaffected by grain processing (P = 0.18; 0.75 vs. 0.77 kg/d for fine ground corn and steam-flaked corn, respectively), but fat supplementation increased (P = 0.001) milk fat yield (0.80 vs. 0.71 kg/d). Steam-flaked corn increased (P = 0.001) milk protein yield compared with fine ground corn (0.81 vs. 0.71 kg/d). In grazing dairy cows, steam-flaked corn increased milk yield and milk protein, and fat supplementation increased milk yield and milk fat yield, and when combined (steam-flaked corn + fat) allowed the greatest milk yield, milk fat yield and milk protein yield.

Key Words: palm oil, flaked corn, tropical pasture

1693 (T306) Effect of grain type (corn versus milo), particle size (600 versus 1000 microns) and steam-flaked corn on productive and metabolite responses of early lactating Holstein cows. E. Mahjoubi[1], J. R. Johnson[*2], B. J. Bradford[2], and M. J. Brouk[2], [1]*Dep. of Animal Science, University of Zanjan, Iran,* [2]*Dep. of Animal Sciences and Industry, Kansas State University, Manhattan.*

Ten early lactation Holstein dairy cows (five multiparous and five primiparous) were used in a duplicated Latin square design to evaluate diets that differed in grain type (corn vs. milo) and grain particle size (fine vs. coarse roller-milled); a steam-flaked corn (SF-C) diet was also included for comparison. Periods were 21 d with 17 d for adaptation and 4 d for data collection, and data were subjected to PROC MIXED model analysis with contrasts used to evaluate effects of grain type, particle size, and processing method. Mean particle size of fine and coarse rolled corn, fine and coarse rolled milo and SF-C was 724, 1087, 636, 980, and 3356 microns, respectively. Daily dry matter intake was not influenced (P > 0.05) by treatment (26.6, 26.6, 27.8, 26.6 and 26.4 ± 1.7 kg, respectively), nor was milk yield (41.5, 41.5, 40.5, 40.9 and 41.6 ± 3.2 kg, respectively). Treatment did not affect (P > 0.05) milk component concentrations or yields except that when fed corn, cows yielded greater (P = 0.03) amounts of milk protein due to numerically greater milk yield and milk protein concentration. Efficiencies of milk production, energy correct production and fat corrected production were not impacted by treatment. However, feeding corn resulted in a trend for greater (P = 0.06) milk production efficiency when compared to milo. Milk urea nitrogen (MUN) was decreased (P = 0.05) when feeding corn compared to milo. Similar blood glucose levels were observed pre and post feeding for all treatments. Circulating NEFA was higher (P < 0.05) for rolled corn diets versus SF-C and milo diets. Period changes in body weight and body condition score were unaffected by treatment (P > 0.05). Data demonstrates that rolling corn or milo to 600 or 1000 microns resulted in similar milk production and milk production efficiency as compared to SF-C. Processing corn or milo to a particle size smaller than 1000 microns did not result in increased milk production or efficiency of production suggesting that it is not necessary to reduce particle size of corn or milo below 1000 microns when included in a total mixed ration (TMR) resulting in reduced processing expense. Similar milk production and production efficiency for milo versus corn suggests that relative pricing should be utilized to determine if corn or milo should be included in lactating dairy cow diets when corn or milo is processed to a similar particle size and fed in a TMR.

Key Words: grain processing, particle size, sorghum

1694 (T307) Effect of concentrate source (cottonseed vs. barley) on milk performance and fatty acids profile of spring calving Holstein-Friesian cows feeding an indoors silage regime. A. I. Roca-Fernández* and A. González-Rodríguez, *Agrarian Research Centre of Mabegondo, La Coruña, Spain.*

Milk performance and fatty acids (FA) profile of spring-calving Holstein-Friesian cows (n = 36) at end of lactation (200 d in milk) were examined. Cows were fed indoors with a total mixed ration (TMR) containing: 70% silage (grass: maize, 36:64) and 30% concentrate. Two sources of concentrate were investigated: cottonseed (C) at two levels, low (5 kg DM/cow/d) or high (7 kg DM/cow/d), and barley (B) at high level (7 kg DM/cow/d). Animals were randomly assigned to one of three indoor (n = 12) feeding regimes (C5, C7 and B7), during 10 wk in autumn. The B and C concentrates were composed of corn flour (B, 43.1 vs. C, 31.0%), soybean hulls (B, 28.5 vs. C, 34.0%), soybean meal (B, 23.5 vs. C, 20.0%), barley flour (B, 1.4 vs. C, 0%), cottonseed (B, 0 vs. C, 12.0%) amender (B, 1.0 *vs.* C, 1.0%), calcium carbonate (B, 1.5 vs. C, 1.0%) and dicalcium phosphate (B, 1.0 vs. C, 1.0%). Average chemical composition of B and C concentrates was: crude protein (166 vs. 168 g/kg DM), neutral detergent fiber (249 vs. 418 g/kg DM) and crude fat (31 vs. 49 g/kg DM), respectively. Daily

milk yield was higher ($P < 0.001$) at the high level of supplementation (B7, 18.1 and C7, 17.9 kg/cow/d) compared to the low level (C5, 15.7 kg/cow/d), and dairy cows at the high level of concentrate showed higher ($P < 0.05$) body weight values (B7, 605 and C7, 598 kg) compared to those at the low level (567 kg). Milk protein was lower ($P < 0.05$) at the high level of concentrate in the cottonseed (C7, 30.7 g/kg DM) than in the barley treatment (B7, 32.7 g/kg DM). There were no differences among treatments in milk fat and milk urea content. No differences were also found among treatments in short, medium and long chain FA. Despite this, higher ($P < 0.05$) content of polyunsaturated FA and linoleic acid were observed in the C7 compared to the C5 treatment (2.48 and 2.22 vs. 2.16 and 1.92 g/100 g of FA). These results might be explained by alterations in rumen biohydrogenation pathways of milk FA from dairy cows supplemented with cottonseed concentrate at high level. Linolenic acid was, however, higher ($P < 0.01$) in the B7 (0.27 g/100 g of FA) than in the C5 treatment (0.24 g/100 g of FA).

Key Words: dairy cow, lipid feed supplements, milk fatty acids composition

---

1695 (T308) Ruminal starch degradation of maize silage affected by ensiling time and dry matter content.

J. Doorenbos* and H. V. Laar, *Nutreco R&D, Boxmeer, Netherlands.*

Quantitative evaluation of rumen degradation of maize silage is relevant for accurate determination of its nutritional value. Our objective was to quantify combined effects of ensiling time and dry matter (DM) at harvesting on effective rumen degradation (ED) of starch, crude protein (CP) and NDF in maize silage. Maize silage (hybrid Nutreka) was harvested at 30, 35 or 40% DM with 2-wk intervals, allowing different maturity to develop in the same crop. Fresh samples were stored at -18°C. 25 L plastic vessels were filled with thin layers of material and compressed manually to remove air. Full vessels were sealed then stored for 4, 8 or 12 mo at ambient temperature. After opening, samples were stored at -18°C. Three fistulated mid-lactation Holstein cows fed a basal ration consisting of maize silage, grass silage, hay and compound feed, were used to incubate nylon bags. Bags (pore size 37 µm) were inserted at 0800 h and removed after 3, 8, 16, 32, 56, 96, and 336 h. All bags were machine washed, freeze-dried and weighed. Outliers were removed using Dixon Q-test. Residues were analyzed by NIRS for DM, starch, CP and NDF using calibration lines specifically developed for maize silage residues. Washable and undegradable fractions were based on residues after 0 and 336-h incubation, respectively. Rate of degradation (k_d) was calculated in SAS using PROC NLIN. ED was calculated as Washable + Degradable x (k_d/(k_d+ passage rate)) and analyzed in SAS using PROC MIXED for significant differences between treatments using ensiling time and DM as fixed factors and cow as random factor. Starch and CP ED increased with increasing time ensiled ($P < 0.0001$) from 63.3 to 85.4% and from 42.2 to 71.4%, respectively. Starch and CP ED decreased with increasing DM ($P < 0.0001$) from 82.3 to 71.7% and from 63.9 to 58.5%, respectively. Higher DM at ensiling led to a more pronounced effect of ensiling time on starch and CP ED ($P < 0.0001$ for interaction time x DM). NDF ED was not significantly affected by ensiling time or DM ($P > 0.10$). It can be concluded that ED of starch and CP in maize silage is affected by combined effects of ensiling time and DM at harvesting. These results can be applied in ration formulation systems for dairy cows to further optimize nutrient utilization and rumen conditions.

Key Words: maize silage, ensiling time, rumen starch degradability

---

1696 (T309) Relationship of in vitro starch digestion to corn kernel measurements from farms in Michigan.

D. Bolinger[1], L. Nuzback[2], and F. N. Owens*[2], *[1]DuPont Pioneer, Perrinton, MI, [2]DuPont Pioneer, Johnston, IA.*

With mature grain, increased kernel vitreousness and prolamin content reduce in vitro starch digestion. Does this apply for grain harvested at corn silage maturity? To answer this question, samples of whole plant corn silage and shelled grain from five Pioneer hybrids at silage harvest were gathered from 15 environmentally diverse locations in Michigan in 2013. Starch availability (7 h in vitro starch disappearance) and nutrient composition were evaluated at a commercial laboratory; vitreousness was appraised as kernel specific gravity by gas displacement. Impacts of hybrid and location on nutrient composition, starch availability, and vitreousness were evaluated by GLM procedures of SAS. Differences ($P < 0.01$) among hybrids were noted for DM, CP, fat, starch, and pycnometer density, and for starch availability ($P < 0.02$). Farm of origin also had an impact ($P < 0.02$) on every component except NDF content of grain. Across all samples, prolamin content was not closely related to in vitro starch availability ($r = -0.06$; $P = 0.63$) but increased as CP content of grain increased ($r = 0.74$; $P < 0.01$). Among all measurements, in vitro starch availability was predicted best but still poorly (R2 = 0.17) by the equation: Starch availability = 38.33– 0.124 × grain DM + 0.585 × grain starch percentage. As harvest DM increased, specific gravity and prolamin content tended ($P < 0.10$) to increase. Starch availability decreased as kernel specific gravity increased ($P < 0.05$). Perhaps because of its high dependence on kernel protein content, prolamin content was not closely related to starch availability of grain samples harvested when corn silage was harvested. Had all grain samples had been obtained from fields equal in N fertility, the relationship of prolamin to starch availability likely would have been closer. The range in starch digestibility among these silage hybrids was less than half the range among farms (2.9 vs. 6.3% points); this questions the accuracy of predicting starch availability from hybrid genetics alone. Low in

vitro starch digestion of dry vitreous hybrids may reflect high prevalence of larger particles from dry coarsely ground grain although other factors (e.g., fine grinding, fermentation) also will impact on in vivo starch availability.

Key Words: prolamin, starch digestion, vitreousness

1697 (T310) Effect of particle size and time of rumen fluid collection on in vitro starch digestibility of corn and sorghum. E. Raffrenato[*1,2], L. J. Erasmus[1], W. A. van Niekerk[1], and C. Engelbrecht[1], *[1]University of Pretoria, South Africa, [2]Stellenbosch University, South Africa.*

Starch digestibility affects rumen health and milk production in dairy cows. Corn and sorghum are among the most common starch sources, but the least digestible when unprocessed. Grinding is the preferred way to increase starch digestibility. However, time of rumen fluid collection is often not considered as source of variation when analyzing in vitro starch digestibility. In addition, interaction between particle size and time of feeding may further bias the digestibility results. Objectives of the study were to assess the effects of: 1) different particle sizes in corn and sorghum, 2) time of rumen fluid collection relative to feeding (ad libitum feeding, i.e., 8 h after first morning feeding, AL vs. collection after 8 h of fasting, FA), and 3) their interaction on in vitro starch digestibility (IVSD). Several cultivars of corn and sorghum were analyzed for starch and CP content and ground at 1, 2, 4, and 6 mm, using an ultra-centrifugal mill. Rumen fluid was collected from two cows fed a lactation diet containing 25% starch. Residual starch of the fermented samples were obtained at 0, 1, 2, 4, 6, 8, 12, and 24 h. Density of grains were also measured for all particle sizes and correlated with IVSD. Rates of starch digestion were computed assuming a first order decay and the parameters were estimated using PROC NLIN in SAS. Rates of digestion were on average higher for the FA rumen fluid ($P < 0.05$) compared to the AL rumen fluid with 0.21 vs. 0.16 and 0.14 vs. 0.10 h^{-1} for corn and sorghum, respectively. Furthermore, interaction between particle size and rumen fluid was highly significant ($P < 0.001$). Finer corn and sorghum had in fact consistently higher rates of starch digestion, increasing with decreasing particle size ($P < 0.001$), only within the AL rumen fluid. When using the FA rumen fluid, particle size did not have any influence on starch digestibility ($P = 0.67$). Both density and CP were also negatively correlated (-0.65 and -0.78, $P < 0.05$) with IVSD. This proves the importance of time of collection of rumen fluid but it could also imply important consequences for rumen health when feeding starch separately, after hours of fasting.

Key Words: in vitro starch digestibility, rumen fluid, rumen health

1698 (T311) Effect of reducing dietary starch on intake, lactation performance, and ruminal parameters of dairy cows: A meta-analysis. S. M. Fredin*, L. F. Ferraretto, and R. D. Shaver, *University of Wisconsin, Madison.*

A meta-analysis was conducted to determine the effect of feeding reduced-starch diets on intake, lactation performance, and ruminal parameters of dairy cows from a data set comprising 131 treatments means from 56 peer-reviewed trials from 1993 to 2014. Reduction in dietary starch was achieved by partially replacing cereal grains with non-forage fiber sources, forages, or sugars. Dependent variables were calculated as the difference between observations on the higher starch (% of DM) diet and observations on the reduced-starch diet(s) within trial. The higher starch concentration was used as a covariate within trial when $P \leq 0.15$. Data were analyzed using PROC MIXED of SAS with treatment as a Fixed effect and trial as a Random effect. Dietary CP and NDF contents (% of DM) were (mean ± SD) 17.8 ± 2.3 and 31.8 ± 5.5%, respectively, across all trials. The higher starch diet and reduced-starch diets contained (mean ± SD) 28.9 ± 5.0% and 21.5 ± 4.8% starch, respectively, across all trials. Dry matter intake was 24.3 ± 2.6 kg/d across all trials, and decreased 0.1 kg/d per %-unit (DM basis) decrease in dietary starch content ($P < 0.001$). Milk yield (kg/d) decreased 0.2 kg/d per %-unit decrease in dietary starch content ($P < 0.001$). Fat- and energy-corrected milk followed a similar pattern ($P < 0.001$). Feeding reduced-starch diets decreased milk fat (7 g/d), protein (9 g/d), and lactose (12 g/d) yields per %-unit decrease in dietary starch ($P < 0.001$). Milk fat concentration was unaffected by reduced dietary starch ($P = 0.60$), whereas milk protein (0.005%) and lactose (0.004%) concentrations were decreased per %-unit decrease in dietary starch ($P \leq 0.01$). There was a trend for lower feed conversion (kg milk/dkg DMI) on reduced-starch diets ($P = 0.06$). Total ruminal VFA concentrations were decreased 0.4 m*M* per %-unit decrease in dietary starch ($P = 0.03$), however, ruminal acetate and butyrate (mol/100 mol) concentrations ($P \geq 0.41$) were unaffected. There was a trend for a decrease of 0.09 mol/100 mol for ruminal propionate concentration on reduced-starch diets ($P = 0.09$), and rumen acetate: propionate ratio was increased ($P = 0.03$) on reduced-starch diets. Rumen ammonia (mg/dL) and pH ($P \geq 0.32$) were unaffected by reducing dietary starch content. Dry matter intake, milk, and component yields were decreased for dairy cows when fed reduced-starch diets.

Key Words: dairy cow, lactation, starch

1699 (T312) Effect of rehydration and silage storage period of corn with medium vitreous endosperm on chemical composition and dry matter in situ degradability. M. A. Arcari, C. Martins, J. Gonçalves, D. Sousa*, T. Tomazi, L. F. P. Silva, and M. Veiga dos Santos, *University of São Paulo, Pirassununga, Brazil.*

The aim of this study was to evaluate the effects of rehydration process and storage period of milled, rehydrated and ensiled corn (MREC) with medium vitreousness (67 ± 3%) on chemical composition and in situ DM degradability. Corn grains were harvested with 83% DM concentration and dried to obtain 87% DM concentration. After dried, corn grains were milled (2 mm), rehydrated to 67% DM, and ensiled (silo density of 880 kg/m^3) in mini-silos. Furthermore, the MREC samples were evaluated in different storage periods (3 to 330 d). The MREC were analyzed for nutrient contents, fermentation products and in situ DM degradability. The data were modeled according to Mehrez and Ørskov (1977), and the effects of MREC storage time on degradability were evaluated by the PROC MIXED of SAS ($\alpha = 0.05$), in a completely randomized design with two replications. No effect of ensiling period was observed for MREC DM and CP content. The ensiling period reduced the MREC starch content ($P < 0.001$). The MREC starch content was 2.4% points lower in the silos with 330 d of storage compared to the silos with 3 d of storage. The MREC with 330 d of storage had greater ($P < 0.001$) concentrations of NH_3–N, ethanol, lactate, acetate, propionate, and butyrate were increased by 8.5, 2.4, 3.45, 4.1, 1.7, and 2.8-folds, respectively. Likewise, the storage time of MREC increased ($P < 0.001$) in situ DM degradability. The percentage of rapidly degradable DM fraction (fraction A), the degradation rate of the slowly degradable DM fraction (fraction C) and the potentially degradable DM (PD) were increased by 3.04, 2.42 and 1.009 folds after 330 d of storage. The C fraction (slowly degradable DM fraction) from the MREC stored for 330 d decreased by 1.91-fold in comparison to the MREC stored for 3 d. The effective DM degradability, which was adjusted for rumen passage rates of 0.02, 0.05 and 0.08%/h, increased ($P < 0.001$) from 81 to 93.3%, from 66.6 to 88.6%, and from 57.6 to 84.9%, respectively. In conclusion, the storage period affected the chemical composition and increased the in situ DM degradability of MREC with medium vitreous endosperm.

Key Words: ensiling, in situ degradability, vitreousness

1700 (T313) Factors affecting 7-hour starch digestibility on conventional corn silage, BMR corn silage, and high moisture corn grain. A. J. Miner*[1], M. Tetreault[2], C. J. Sniffen[3], and R. Ward[4], *[1]Poulin Grain Inc., Newport, VT, [2]Poulin Graing Inc., Newport, VT, [3]Fencrest, LLC, Holderness, NH, [4]Cumberland Valley Analytical Services Inc., Hagerstown, MD.*

Previous research has shown that there appears to be a relationship between time after ensiling and starch digestibility in lactating dairy cows. The objective of this study was to measure how time after ensiling and other factors affect 7-hour starch digestibility in conventional corn silage, BMR corn silage, and high moisture corn grain. Samples were taken monthly on 16 farms in New York and Vermont from November 2010 to October 2011. All samples were sent to Cumberland Valley Analytical Services to have 7-hour starch digestibility and dry matter analysis determined on all samples. Linear analysis was performed on samples grouped by physical characteristics (Conventional vs. BMR vs. High Moisture Corn) comparing impact of time after ensiling and other factors on the 7 h starch digestibility of the starch in the feedstuffs. The analysis of the conventional corn silage demonstrated that time after ensiling has the largest impact on 7 h starch digestibility ($P = 0.0007$) however dry matter and farm that sample was taken from also has an impact. When time after ensiling, dry matter, and farm name was accounted for analysis showed a linear realtionship ($R^2 = 0.17$; $P = 0.11$). For the bmr corn silage there appeared to be a strong relationship for time after ensiling on 7-hour starch digestibility ($P > 0.99$); however, when dry matter and farm were applied to the data, there was a linear relationship ($R^2 = 0.54$; $P = 0.01$). It appears that the farm the sample came from had the biggest impact on the 7-hour starch digestibility of the BMR corn silage ($P = 0.04$). On the high moisture corn grain again there was a time after ensiling effect with a good relationship with 7-hour starch digestibility ($P < 0.01$). Dry matter and farm also have a linear relationship ($R^2 = 0.47$; $P = 0.01$). In conclusion time after ensiling has a significant impact on 7-hour starch digestibility of both the conventional corn silage and high moisture corn grain; it does not have a significant impact on BMR corn silage. The variation that was accounted for by the farm that the samples came from indicates that other factors such as soil type, corn hybrid, amount of processing, and other farm factors can have an impact on 7-hour starch digestibility.

Key Words: starch digestibility, time after ensiling, corn silage

1701 (T314) Glycerol exacerbates effects of sorghum-based tannins extract on in vitro fermentative activity of mixed ruminal microorganisms.

E. San Vito*[1], T. J. Herald[2], P. Gadgil[2], and J. S. Drouillard[3], [1]*Universidade Estadual Paulista Júlio de Mesquita Filho–UNESP, Jaboticabal, Brazil,* [2]*USDA–ARS, Grain Quality and Structure Research Unit, Manhattan,* [3]*Kansas State University, Manhattan.*

Tannins have been observed to impact ruminal metabolism, affecting protein degradation, predisposition to bloat, and production of methane and conjugated linoleic acid; however, these effects on rumen modulation and animal performance have not been consistent. Glycerin is a by-product from biodiesel production and is a major component of distiller's grains, and thus is frequently present in diets of finishing cattle. The aim of this work was to evaluate interactive effects of sorghum-derived tannins and glycerol on fermentative activity (in vitro dry matter digestibility, IVDMD; ammonia, NH3; and volatile fat acid, VFA profiles) of in vitro cultures of mixed ruminal microorganisms. Tannins were prepared from sorghum bran by extraction with acetone and lyophilized. For in vitro fermentations, 40 mL of modified McDougall's buffer (no urea) were placed into 100 mL plastic bottles along with 20 mL of strained ruminal fluid and 2 g of substrate. Ruminal fluid was obtained from fistulated cattle fed a diet consisting of approximately 50:50 forage:concentrate (alfalfa hay, corn silage, corn flake, dry distilled grain, mineral mix). Substrate for in vitro fermentations consisted of finely ground (< 1 mm) corn and soybean meal in a 90:10 ratio (C) or partial replacement of corn with glycerol (G; 10% of substrate), tannin (T; 1%) or a mix (TG). After incubating 24 h at 39C, IVDMD and concentrations of NH3 and VFA were measured. Data were analyzed as a randomized complete block design by using the PROC MIXED of SAS, and results are summarized below. Shifts in concentrations of ammonia and VFA in cultures fed glycerol generally were exacerbated by the presence of tannins. The observed interaction between glycerol and tannin may explain the varying results found in studies that use glycerol as a substitute for cereals grains in diets of ruminants.

Key Words: glycerin, tannin, sorghum

Table 1701. Effect of glycerol and sorghum-based tannins extract on in vitrofermentative activity of mixed ruminal microorganisms

	Treatment					
Item	C	G	T	TG	SEM	*P*-value*
IVDMD, %	55.2	53.7	53.1	52.5	0.91	0.104
Ammonia, mM	2.45[a]	2.31[a]	1.96[b]	1.59[c]	0.157	< 0.01
Acetate, mM	34.86[a]	33.74[b]	33.59[b]	32.31[c]	0.55	< 0.01
Propionate, mM	20.69[b]	23.30[a]	20.15[c]	22.92[a]	0.42	< 0.01
Butyrate, mM	6.57[a]	6.50[a]	6.21[b]	6.22[b]	0.16	< 0.01

*Means in the same row without a common superscript letter are different; $P < 0.05$.

1702 (T315) Use of byproducts from corn industry and citric acid on dairy heifer diet. I. D. C. Hermisdorff, R. M. Dos Santos*, M. F. Gonçalves, A. M. França, M. Visoná-Oliveira, H. Nogueira, A. Santos and I. C. Ferreira, *Universidade Federal de Uberlândia, Uberlândia, Brazil*

The use of byproducts in animal nutrition is an interesting alternative. Besides minimizing cost of livestock production, is a way to absorb part of the growing residue of industrial production, thus improving environmental conditions. By-products of sugar production, such as mycelium, precoat, and rafinate have become available for use. The mycelium is composed of cellular material from the fermentation of sugar by the fungus *Aspergillus niger*. The rafinate results from the purification process of the citric acid, the principal product formed from the fermentation of sugar. The precoat filter is derived from the step of glucose syrup production. The aim of this study was to evaluate performance of crossbred dairy heifers fed diets with wet byproducts. Forty heifers weighing on average 240 kg were randomly assigned to four treatments receiving control diet ($n = 10$) and diets containing: precoat ($n = 10$), mycelium ($n = 10$) and rafinate ($n = 10$). The control diet was formulated with sugar cane bagasse, and wet corn gluten feed (WCGF), corn gluten feed (CGF) and cracked corn. The other diets were formulated with the same ingredients, but with the inclusion of byproducts cited in their respective treatments. The average dry matter intake (DMI) was estimated by the difference between dry matter offered and orts, divided by the number of animals in treatment. Samples of offered and orts were collected daily and sent for chemical analysis. The design was randomized and analyzed variables were subjected to statistical analysis, considering significance at 5% probability. There were significant differences in dry matter intake (DMI) ($P < 0.01$), where mycelium showed the highest and control the lowest intake. There were no significant differences in consumption of neutral detergent fiber by the animals, initial and final body weight, total and average daily gains and feed efficiency (FE) of the heifers ($P > 0.05$). Control and rafinate groups showed better FE ($P < 0.01$) compared to the mycelium, whereas precoat performed equally to all treatments. The inclusion of wet byproducts mycelium, precoat and rafinate in the diet of crossbred dairy heifers at 5.5, 3.4 and 4.8% of fresh matter, respectively, provides satisfactory performance of the animals. However, more studies are needed to determine the economic viability of using these byproducts in ruminant diet.

Key Words: mycelium, precoat, rafinate, dry matter intake

1703 (T316) Monensin increases endotoxin concentration in an in vitro rumen fermentation model. N. Reisinger[1], S. Schaumberger[*2], I. Dohnal[1], C. Emsenhuber[1], C. Stoiber[1] and G. Schatzmayr[1], *[1]Biomin Research Center, Tulln, Austria, [2]Biomin Holding GmbH, Herzogenburg, Austria.*

Administration of antibiotics (e. g. Beta-lactam), which effect gram-negative bacteria, can lead to an increased concentration of endotoxins in the rumen. This increase can lead to endotoxin associated effects like inflammation, immune response and diseases risks, e.g. mastitis, endometritis and laminitis. Monensin has a wide range of application indications in ruminants: coccidiosis, ketosis, pulmonal edema, pneumonia, and is even used as growth promoter. This ionophore inhibits the growth of gram-positive bacteria, but there is no literature available on the effects on endotoxin release by increase of gram-negative bacteria. The objective of this study was, therefore, to test the effect of monensin on the ruminal endotoxin concentration in an in vitro rumen fermentation model. Rumen fluid was incubated under anaerobic conditions at 39°C and a continuous flow of synthetic saliva for 336 hours. Fresh feed (50% chopped hay; 50% cereal nutrient) was supplied in nylon bags every 24 hours. Six reactors were treated with monensin (10 mg/L), the other six reactors served as untreated control. Samples of the rumen fluid were taken after 24 and 336 hours. Samples were centrifuged; heat inactivated and filtrated before dilution with endotoxin free water. Endotoxin concentration was measured with the chromogenic *Limulus-Amebocyte* Lysate assay, according to manufacturer's instructions. Total bacterial count was performed with the flow cytometer. There was no significant difference in the endotoxin concentration of the control reactors (895 EU/ml) compared to the monensin treated reactors (1.715 EU/ml) after 24 hours ($P > 0.05$). In contrast, after 336 hours incubation, the endotoxin concentration in monensin-treated reactors (12.485 EU/ml) significantly ($P < 0.05$) increased compared to the control reactors (1.471 EU/ml). The total bacterial count was also significantly increased after 336 hours in the monensin-treated reactors compared to the control reactors ($P < 0.05$). Results of this in vitro experiment showed that monensin led to an increase of endotoxins in rumen fluid. This might be a result of the expected bacterial shift from gram-positive to gram-negative bacteria. Further investigations are necessary to verify these results and to clarify the mechanism of monensin in the in vitro rumen fermentation model. In addition, it will be useful to test other antibiotics, to avoid negative effects on bacterial populations and increase of endotoxins.

Key Words: endotoxins, monensin, rumen

1704 (T317) Effect of a calcareous algae and monensin on feed intake and rumen parameters of cattle fed abruptly high concentrate diets. R. Ferreira Carvalho[1], A. P. S. Silva[1], M. Rezende Mazon[2], C. A. Zotti[1], L. Silva Oliviera[1], S. Luz e Silva[*1] and P. R. Leme[1], *[1]University of Sao Paulo/FZEA, Pirassununga, Brazil, [2]University of Sao Paulo, Pirassununga, Brazil*

Additives are used in high concentrate diets to prevent metabolic disorders. The use of calcareous algae (*Lithothamnium calcareum*), a natural and renewable product, may be an alternative. The effect of a calcareous algae product (Top Buffer Sanphar, Campinas, Brazil) and monensin (Bovensin Phibro, Guarulhos, Brazil) on feed intake, rumen pH, short chain fatty acids, lactate and ammonia nitrogen concentration in the rumen of Nellore steers transitioned abruptly to a high concentrate diet was evaluated.. On d 1, the diet of all animals was abruptly changed from hay to a high concentrate diet (82.41% corn, 7.75% sugar cane bagasse, 6.78%, soybean meal, 1.29% urea and 1.77% mineral mixture). The diet was provided once a day during four periods of 21 days, and treatments consisted of different additives: limestone 7.1 g/kg DM, calcareous algae product 7.4 g/kg DM, limestone and monensin 30mg/kg DM and calcareous algae product and monensin 30mg/kg. Rumen pH was measured continuously from d -3 to d 21 through an indwelling pH probe (Dascor, Escondido, Canada) inserted in the rumen. Rumen samples were taken six hours after feeding on days -1, 4, 7 and 14. Feed intake was adjusted daily, allowing ten percent orts. There was no interaction ($P > 0.050$) between calcium source and monensin for feed intake, ruminal pH and total concentration of short chain fatty acids. There was no influence ($P > 0.050$) of calcium sources on feed intake, total concentration of short chain fatty acids, acetate:propionate ratio, lactate and ammonia nitrogen concentration. Diet with the calcareous algae product resulted in higher ($P = 0.040$) average rumen pH than limestone (6.09 vs. 6.01, respectively) and lower ($P < 0.001$) time bellow pH 5.2 (1hr29min vs. 2hrs43min). Treatments with the presence of monensin resulted in higher ($P = 0.008$) concentration of ammonia nitrogen (4.69 vs. 3.94 mg/dL without monesin) and lower ($P = 0.023$) time bellow pH 5.2 (1hr45min vs. 2hrs27min without monensin). Calcareous algae product was more efficient in controlling rumen pH than limestone without influencing feed intake and the concentration of short-chain fatty acids. Monensin was also beneficial in preventing rumen disorders.

Key Words: Nellore, additives, acidosis

1705 (T318) Effect of post-extraction algal residue supplementation on the rumen microbiome of steers consuming low-quality forage.

J. C. McCann*[1], M. L. Drewery[2], W. E. Pinchak[3], J. E. Sawyer[4] and T. A. Wickersham[2], [1]*University of Illinois, Urbana,* [2]*Texas A&M University, College Station,* [3]*Texas A&M Agrilife Research, Vernon,* [4]*Texas AgriLife Research, College Station*

Cattle consuming low-quality forages require protein supplementation to increase forage utilization and ruminal fermentation. Production of algal biomass for biofuel would result in large quantities of post-extraction algal residue (PEAR, 17.9% CP) which has the potential to elicit similar low-quality forage utilization responses to cottonseed meal (CSM, 42.9% CP); however, its effect on ruminal bacterial communities is unknown. Five ruminally and duodenally cannulated Angus steers in a 5 × 5 Latin square had ad libitum access to oat straw (4.5% CP, 80% NDF). Treatments were infused ruminally and consisted of an unsupplemented control (CON), PEAR at 50, 100, and 150 mg N/kg BW, and CSM at 100 mg N/kg BW. Rumen samples were collected 4 h after supplementation on d 14 of each period and separated into liquid and solid fractions. After DNA extraction, amplification of the V4-V6 region of the 16S rRNA gene and 454 pyrosequencing was performed on liquid and solid rumen samples. After denoising, chimera checking, and quality trimming, 8364 ± 2745 sequences were generated per sample. Weighted UniFrac analysis and Morisita-Horn index demonstrated different community composition between liquid and solid fractions. Greater homogeneity was observed within solid samples. At the phyla level, *Bacteroidetes* characterized more than 75% of sequences in the solid fraction, while relative abundance of *Firmicutes* in the liquid fraction increased linearly with PEAR supplementation ($P = 0.02$). *Prevotella* represented over 25% of sequences in all treatments and decreased in the solid fraction with increasing PEAR provision (linear, $P = 0.01$). *Lachnospiraceae*, *Ruminococcaceae*, and *Clostridiaceae* increased in the liquid fraction with greater PEAR supplementation (linear, $P \leq 0.03$). *Fibrobacter* and *Treponema* decreased in the liquid fraction with increasing PEAR (linear, $P < 0.10$). Bacterial community composition was similar between CON and 100 mg N/kg BW CSM treatments. Results suggest increased forage utilization from PEAR supplementation may be linked to changes within the liquid fraction of the rumen microbiome.

Key Words: microbiome, post-extraction algal residue, supplementation

1706 (T319) Effect of concentrate diets contrasting in fatty acid profiles on lamb performance, carcass characteristics, fatty acid composition and wool production.

S. J. Meale[1,2], A. V. Chaves[1], M. He[2] and T. A. McAllister*[2], [1]*The University of Sydney, Sydney NSW, Australia,* [2]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*

Knowledge of the health benefits associated with the consumption of *n*-3 PUFA has led to the selective inclusion of dietary lipids in ruminant diets in attempts to increase tissue incorporation. Increasing the *n*-3 fatty acid content of ruminant tissues requires the inclusion of dietary lipids that contain unsaturated fatty acids capable of withstanding ruminal biohydrogenation. Tasco a commercial algal product manufactured from the brown alga *Ascophyllum nodosum* (TA; 2% DM) was compared to canola (CO), flax (FO) and safflower oils (SO) for effects on performance, fatty acid profiles of skirt muscle, subcutaneous and perirenal adipose tissues and wool yield and quality characteristics of Canadian Arcott lambs. Fifty-six lambs were randomly assigned to four diets. Diets consisted of a pelleted, barley-based finishing diet with lipid sources included at 2% DM. Feed deliveries and orts were recorded daily with lambs weighed weekly and slaughtered once they reached ≥ 45 kg LW. Carcass characteristics and rumen pH were determined at slaughter. Dye-bands were used to determine wool growth, micron and staple length. Data were analyzed using mixed procedure in SAS. No effects were observed on intake, growth, feed efficiency or carcass characteristics. An increase ($P < 0.05$) in staple strength of CO lambs was the only effect observed in wool. Supplementing Tasco at 2% DM in the diet of Canadian Arcott lambs increased ($P \leq 0.002$) the SFA/PUFA ratio in skirt muscle and subcutaneous and visceral adipose tissues in comparison to the supplementation of oils. Additionally, Tasco supplementation did not improve concentrations of long chain *n*-3 PUFA or total *n*-3 concentrations in skirt muscle or adipose tissue when compared to lambs fed canola, flax or safflower oils. In contrast, supplementing FO increased total *n*-3 accumulation and reduced the *n*-6/*n*-3 ratio in all tissues ($P < 0.001$), suggesting that the supplementation of Tasco did not beneficially alter the FA profile of lamb tissues in comparison to other dietary lipids.

Key Words: fatty acids, lambs, micro-algae

1707 (T320) Feed value for ruminants of newly developed black and yellow type of canola seeds.
K. Theodoridou[*1], P. Yu[2,3], H. Xin[1] and X. Huang[1], *[1]University of Saskatchewan, Department Animal and Poultry Science, Saskatoon, SK, Canada, [2]Department of Animal Science, Tianjin Agricultural University, Tianjin, SK, China, [3]University of Saskatchewan, Saskatoon, SK, Canada*

Canola is one of the most valuable agricultural crops in world trade and a major oilseed crop in western Canada. The objective was to evaluate the nutritive value of canola seed, for ruminants, in terms of: 1) nutritional profiles, 2) degradation kinetics, 4) in vitro intestinal protein digestibility, and 4) energy values. Yellow (CS_Y) and black (CS_B) canola seeds (n = 4) were collected from two harvest years (2010, 2011). Three dry Holstein cows with rumen cannula were used in an *in situ* trial; then a three-step in vitro procedure was conducted to determine protein intestinal digestibility. According to this procedure the dried ground rumen residues, (contain 15 mg of N) after 12h of ruminal incubation, were exposed to HCl solution containing pepsin. The pH was neutralized with NaOH and phosphate buffer (pH 7.8) containing pancreatin, which were added to the solution and incubated. After 24h incubation, trichloroacetic acid (TCA) was added to precipitate undigested proteins. The samples were centrifuged and the supernatant was analyzed for N. Protein digestibility was calculated as TCA-soluble N divided by the amount of N in the 12h residue sample. The non-protein N (NPN) was analyzed by precipitating of true protein with tungstic acid and calculated as the difference between total N and the N of the residue after filtration. Soluble CP (SCP) was determined by incubating the sample with bicarbonate-phosphate buffer and filtering. The study revealed that the CS_Y was lower in NDF (122.1 vs. 154.5 g kg^{-1} DM, $P < 0.05$), ADF (60.7 vs. 98.6 g kg^{-1} DM, $P < 0.05$), NPN (g kg^{-1} SCP), ADICP (g kg^{-1} DM), soluble protein fraction (28.59 vs. 34.11, $P < 0.05$) and higher (67.28 vs. 59.02, $P < 0.05$) in degradable protein fraction and in vitro intestinal digestibility (56.6 vs. 44.6 g kg^{-1} CP in ruminally incubated residues, $P < 0.05$) than the CS_B. CS_Y contain lower amount of total phenolics compared to CS_B (626.0 vs. 718.0 mg/100g). No significant differences were obtained between the two canola varieties, for the total fatty acids (902.0 vs. 910.7 mg FA/g, SEM 5.17, $P > 0.05$), the CP (g kg^{-1} DM) and the SCP (7.0 vs. 8.5, $P > 0.05$). Total digestible nutrients, metabolizable and digestible energy was higher ($P < 0.05$) for the CS_Y than for the CS_B. Overall, the results demonstrated that the yellow-seeded canola has the potential to be a greater source for energy and protein supply for ruminants compared to the black canola seed.

Key Words: canola, protein supply, ruminal and intestinal digestion

1708 (T321) Could lactic acid treatment decrease in-vitro gas production of barley grain.
M. Dehghan banadaky[*1], A. Zali[2], M. Ganjkhanlou[2], K. Rezayazdi[3], M. Nematpoor[2] and A. Laki[2], *[1]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran, [2]University of Tehran, Karaj, Iran, [3]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran*

The aim of present study was evaluation the effects of treatment barley grain with lactic acid on gas production characteristics. Rolled barley steeped in an equal quantity (wt/vol) of tap water containing 2.5, 5 and 7.5 mL lactic acid (LA) per liter for 24 h. Treated barley were dried and was ground through a 1-mm screen. Then 300 mg of ground barley pre-loaded into 125-ml serum vials. Ruminal fluid was collected from three fistulated Holstein cows. Cow's ruminal fluid mixed in equal quantity and mixed Menke and sreingass, 1988 buffer solution. Inoculums was dispensed anaerobically (40 ml/vial) under a steam of 0_2–free with co_2, followed immediately by sealing and affixing to incubator at 39 ^{0}c. Triplicate vials containing no substrate were also prepared as blank controls. Gas produced was measured at 2, 4, 6, 8, 10, 12, 24 and 48 h of incubation. Cumulative gas production data were fitted to a model of $Y = b (1\text{-}e^{-ct})$; Y = potential of gas production at time t; b = the asymptotic gas volume (ml); c = gas production constant rate (ml/h); t = incubation time (h). Data analyzed by GLM procedure of SAS (2003). According to the result of this study steeping barley in water containing 7.5 gr LA for 24 h decreased gas volume in the early time of incubation and gas production constant rate in comparison to dry rolled barely. On the other hands, it showed that treated barley grain with 7.5 gr LA decreased barely grain digestibility until 6 h of incubation and may be decrease acidosis in ruminant.

Key Words: rolled barley, lactic acid and steeping

1709 (T322) Microwave irradiation induced changes in protein inherent structure, protein chemical profile, protein subfractions and digestive behavior of different types of new hulless barley in the rumen and intestine of dairy cows.
X. Yan[1,2], N. Khan[1], X. Huang[*1] and P. Yu[1], *[1]University of Saskatchewan, Saskatoon, SK, Canada, [2]Jilin Academy of Agricultural Sciences, Jilin, China*

The objectives of this study were to evaluate microwave irradiation (MIR) induced changes in nutritive value of three types of hulless barley (*Hordeum vulgare*) in ruminant nutrition, and to quantify the MIR induced changes in protein molecular structures in relation to protein chemical profiles and digestive behavior in the rumen and intestine of the dairy cow. In this study, three barley varieties with in two consecutive years from 2009 to 2010 were chosen. All samples were cultivated and harvested from the university testing farm. The

grains were either kept as raw or irradiated in a microwave, operated at a power of 900 W with irradiation frequency of 2450 MHz, for 3 min (MIR3) or 5 min (MIR5). Mixed procedure of SAS was performed to analyze data with a RCBD model. PROC CRRR was adopted to determine the correlation. Tukey was used to compare treatment means. Significance was declared at $P < 0.05$. Compared to non-irradiated grains, MIR5 markedly decreased (50.8 to 17.6%) soluble protein and increased NDIP (13.3 to 26.2%) and ADIP (1.0 to 5.3%) in total CP ($P < 0.05$). As consequence, the CNCPS CP rapidly degradable fraction substantially decreased (45.2 to 6.4% CP) with a simultaneous increase in the intermediately degradable (35.8 to 56.2% CP), slowly degradable (12.4 to 20.9% CP) and non-degradable (1.0 to 5.3% CP) fractions ($P < 0.05$). The MIR for 5min decreased soluble CP fraction (6.5 to 0.0%) and degradation rate (8.2 to 3.5%/h) of potentially degradable fraction ($P < 0.05$). As a consequence the RDP markedly decreased (55.7 to 34.1% CP) with a concomitant increase (43.3 to 65.9% CP) in RUP supply to the post-ruminal tract ($P < 0.05$). Except the CNCPS rapidly degradable and in situ soluble fraction, the MIR3 did not alter protein chemical profiles, CNCPS subfraction, rumen degradability and intestinal digestibility of RUP. However, the MIR5 decreased (79.4 to 67.9% RUP) intestinal digestibility of RUP. The molecular structure study revealed that MIR for 3 and 5 min consistently decreased the spectral intensities of amide I and II, α-helix and β-sheet, and increased their ratios. The changes in protein spectral intensities were strongly correlated with the changes in protein chemical profiles, CNCPS subfractions and in situ degradation characteristics. Our results showed that MIR for a short period with a lower energy input can improve the nutritive value and utilization of protein in barely grains.

Key Words: different hulless barley, microwave irradiation, nutrient availability, protein molecular structure

1710 (T323) Protein and energy availability of sorghum wet distiller grains without solubles in comparison to the parental grain. M. D. L. A. Bruni[1] and A. I. Trujillo[*2], *[1]Facultad de Agronomia Universidad de la Republica, Paysandu, Uruguay, [2]Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay*

Sorghum can be an alternative for ethanol industry in Uruguay and its by-product (SWDG) can be used as animal feed. An accurate characterization of protein fractions and energy is required for ruminant diets formulation. The chemical profile (in % ± standard deviation) of SWDG presented high values of moisture (66.7 ± 2.6), crude protein (CP, 31.4 ± 0.7), fat (11.0 ± 0.7) and neutral detergent fiber (70.2 ± 2.2).The objective of this study was to characterize the protein fractions and estimate energy digestible (ED) content of three batches of SWDG and its parental grain (SG). In addition, intestinal digestible protein (IDP) of SWDG was measured. Protein fractions were assessed according to the Cornell Net Carbohydrate and Protein System (rapidly protein degradable: A+B1; intermediate degradability: B2; slowly degradable: B3 and undegradable fraction: C, as percentage of CP). The rumen undegradable protein (RUP) was evaluated by in situ assay. Pepsin-pancreatin digestion of rumen pre-incubated (12 h) samples was used to estimate IDP. Digestible energy content was estimated using summative equation computed from digestibility's nutrients by chemical (NRC, 2001) or in situ (using 48 h of nutrient disappearance) approach. Data was analyzed with PROC GLM in a completely randomized design and compared with Tukey test. No differences were found between batches, neither in SWDG nor in SG. The SWDG presented lower ($P < 0.005$) values of A+B1 and B2 fractions than SG (2.3 vs. 4.2% and 36.3 vs. 60.5%) respectively; however B3 and C fractions were greater ($P < 0.018$) than SG (27.7 vs. 13.2% and 33.7 vs. 22.1%). The SWDG presented greater ($P < 0.05$) RUP (estimated using passage rate = 2%/h) compared with SG (75.5 vs. 42.2% CP). The IDP of the SWDG was 51.1 ± 4.5%RUP providing an average value of total digestible protein of 63.6%. Digestible energy estimations of SDWG were lower ($P < 0.003$) than SG (3.16 vs. 3.7 and 2.5 vs.3.7 Mcal/kg DM for chemical or in situ approach, respectively). The greatest difference between the two approaches was observed in SWDG which could be probably explained by estimation of truly digestible CP and NDF fractions. The potential supply of protein fractions of the SWDG was modified by the industrial process increasing slowly degradable and undegradable fractions. The potential of absorbable protein of SWDG was around half of a soybean meal while its ED content represent 70-80% of energetic value of SG.

Key Words: distillers grain, nutritive value, intestinal digestibility

1711 (T324) Effect of crude glycerin on dry matter and nutrient digestibility of feed ingredients in dairy cows. F. D. O. Scarpino van Cleef[*1,2], J. M. Bertocco Ezequiel[1], J. Borsari Dourado Sancanari[3] and E. H. C. B. Van Cleef[1,4], *[1]UNESP, Jaboticabal, Brazil, [2]CNPq, Brasilia, Brazil, [3]UCB, Jaboticabal, Brazil, [4]FAPESP, Sao Paulo, Brazil*

Rumen-cannulated Holstein cows ($n = 6$; 587 ± 39 kg BW; 114 ± 29 DIM; 20 ± 1.5 kg milk/d), were used to evaluate the effects of crude glycerin on in vitro digestibility of dry matter, and nutrients (CP and NDF) of feed ingredients. Cows were assigned to a replicated 3 × 3 Latin square. The three isoenergetic and isonitrogenous diets composed of corn silage, cracked corn grain, sunflower meal, corn gluten, urea, mineral premix, and 0 (G0), 15 (G15), or 30% (G30) crude glycerin. The experiment lasted 69 d, with three periods of 23 d each. For in vitro determinations, the Daisy II fermenter was used. The ingredients were ground (1 mm), and placed in F57 bags

(0.5 g/bag; 25 bags/treatment). At d 20 of each experimental period, rumen content was manually collected and strained with cheesecloth. Then, 400 ml of strained rumen content were placed in each fermentation jar, with 1330 ml buffer A and 266 ml buffer B. The jars were purged with CO_2, and incubated at 39°C for 72 h. When the incubation was completed 48 h, 8 g pepsin and 40 ml HCl 6N were added to each jar. The pH and ammonia-N (NH_3–N) were determined at 0, 48, and 72 h of incubation. Data were analyzed as mixed model with fixed effects of diet and period, and random effects of cow (diet) and residuals. Crude glycerin inclusion did not affect pH and NH_3–N concentration (pH = 6.5, 6.4, 3.4; NH_3–*N* = 20.5, 8.3, and 8.5 mg/dl, respectively for 0, 48, and 72 h incubation). The addition of 15% crude glycerin decreased ($P < 0.05$) IVDMD and IVCPD of sunflower meal, and corn grain. When 30% crude glycerin were added, a decrease in IVDMD was observed for corn gluten ($P < 0.05$), and in vitro NDF digestibility for corn silage ($P < 0.01$). No differences were observed on IVDMD and IVCPD of corn silage. The addition of up to 30% crude glycerin in lactating cows diets affected digestibility of feed ingredients. Caution should be taken when combining glycerin with roughages, due to the negative effect on NDF digestibility.

Key Words: dairy cow, digestion, glycerol.

1712 (T325) Positive effect of fat supplementation in the early postpartum period can continue throughout lactation after fat supplementation ceases.

M. Garcia*[1], L. F. Greco[2], W. W. Thatcher[2], J. E. P. Santos[2] and C. R. Staples[2], *[1]Department of Animal and Avian Sciences, University of Maryland, College Park, [2]Department of Animal Sciences, University of Florida, Gainesville.*

Objective was to determine whether increased milk yield detected during the period of fat supplementation in early lactation would continue throughout lactation after supplemental fat was removed from the diet. Three studies were conducted at the University of Florida dairy farm in which Holstein cows produced more milk in response to fat supplementation in the early postpartum period. Experiments 1 and 2 had the same dietary treatments. Cows consumed a control diet without fatty acid (FA) supplementation, a diet supplemented with mostly saturated free FA (SFA; 1.9% of dietary DM), or a diet supplemented with Ca salts enriched with essential FA (EFA; 2.4% of dietary DM). In the first experiment, cows (n = 74) were assigned randomly to treatments 56 d before calving and treatments were maintained until 90 DIM. In the second experiment, cows (n = 30) were fed the same 3 dietary treatments from 15 to 106 DIM. In experiment 3, Holstein cows (n = 39) were assigned to diets supplemented with a mixture of Ca salts of fish, safflower, and palm oils (1.4% of dietary DM) to create 3 supplemental ratios of 4, 5, or 6 parts of n-6 to 1 part of n-3 FA (R4, R5, and R6). Diets were fed from 15 to 105 DIM. Cows in experiment 2 and 3 had a covariate based on milk produced during the first 6 to 10 DIM. Milk production was recorded through 43 wk of lactation using AFI-MILK system. Orthogonal contrasts were used to test for effects of fat supplements during the fat-feeding period and for the complete lactation. In general, when fat supplementation improved or tended to improve milk production during the fat-feeding period, milk yield also was improved or tended to be improved for the whole lactation. Milk composition was minimally changed. Strategic feeding of FA during early lactation can benefit milk yield after fat is removed from the diet.

Key Words: dairy cow, fatty acids, milk yield

Table 1712.

	Treatments				*P*-value	
	Control	SFA	EFA	SEM	(SFA+EFA) vs. Control	EFA vs. SFA
	— Milk yield, kg/d —					
Experiment 1						
Fat supplement	31.6	31.8	34.3	0.99	0.28	0.06
Full lactation	29.1	28.0	30.6	1.00	0.85	0.05
Experiment 2						
Fat supplement	37.7	39.9	42.8	1.07	0.01	0.07
Full lactation	31.5	34.5	34.1	1.26	0.08	0.84
	Treatments				P-value	
	R4	R5	R6	SEM	Linear	Quadratic
	— Milk yield, kg/d —					
Experiment 3						
Fat supplement	46.4	44.7	43.0	0.98	0.02	0.98
Full lactation	36.7	35.2	33.5	1.33	0.10	0.97

1713 T326) Sources and levels of rumen protected fat on energy balance of dairy cows grazing a tropical pasture.

F. Batistel*[1], J. D. Souza[2] and F. A. P. Santos[1], *[1]University of São Paulo, Piracicaba, Brazil, [2]University of Sao Paulo, Piracicaba, Brazil*

The objective of this experiment was to investigate the effects of supplementation lactating cows grazing a tropical pasture receiving two levels of calcium salts of palm oil (CSPO) or calcium salts of soybean oil (CSSO) on energy balance. Five rumen-cannulated cows (115 ± 8.1 DIM) were used in a Latin square 5x5 and subjected to the following treatments: a) control (no fat); b) 400 g CSSO cow^{-1} d^{-1}; c) 700 g CSSO cow^{-1} d^{-1}; d) 400 g CSPO cow^{-1} d^{-1}; and e) 700 g CSPO cow^{-1} d^{-1}. Treatment periods were 24 d in length and cows grazed paddocks of *Pennisetum purpureum* and received 8 kg cow^{-1} d^{-1} (DM) of concentrate. Concentrate of treatment control was composed by ground corn (82.8%), soybean mean (12%), urea (0.2%), sodium bicarbonate (1%) and mineral/vitamin premix (4%) and fat supplementation replaced ground corn. To estimate fecal excretion, cows were orally dosed with titanium dioxide twice daily for 15 d. Forage intake was calculated from total

fecal excretion and feed digestibility. Indigestible NDF (estimated as NDF residue after 240 h of in situ incubation) was used as an internal marker to estimate digestibility. NE_L intake, milk NE_L and NE_L in empty BW gain was calculated according to NRC (2001). Data were analyzed using a mixed model with animal and period as random effects. The means were compared using a Tukey test. Both levels of CSPO increased NE_L intake (27.7 Mcal/d). There was no difference in NE_L intake between control and 400 g CSSO (26.1 vs. 26.0 Mcal/d), but both were greater than 700 g CSSO (25.4 Mcal/d). The milk NE_L (Mcal/d) was greater for 400 g CSPO (13.1) and 700 g CSPO (12.9) in comparison to control (12.1) and 400 g CSSO (11.6). The lowest milk NE_L was observed in 700 g CSSO (10.3), due to the lowest milk yield and milk NE_L per kg of milk observed in this treatment. The NE_L in empty BW gain (Mcal/d) was greater in 700 g CSSO (3.03) compared with 400 g CSSO (2.65), and both levels of CSPO (2.05 and 2.28 for 400 and 700 g, respectively). The control showed the lowest NE_L in empty BW gain (1.63) among the treatments. Dairy cows grazing tropical pasture supplemented with sources of fat increased energy intake with CSPO and the energy consumed was used differently according to the source of fat supplemented.

Key Words: palm oil, soybean oil

1714 (T327) Saturated fat supplementation interacts with dietary forage NDF concentration during the postpartum period in Holstein cows: Energy balance, nutrient digestibility, and metabolism.

P. Piantoni*, A. L. Lock and M. S. Allen, *Michigan State University, East Lansing*

Forty-eight multiparous cows were used in a randomized complete block design experiment with a 2x2 factorial arrangement of treatments. Treatment diets were offered from 1 to 29 d postpartum and contained 20% or 26% forage NDF (fNDF) and 0% or 2% saturated free fatty acid supplement (Energy Booster 100; FAT). The 2% FAT treatment increased total tract digestibility of OM and NDF in the low fNDF diet (67.6% vs. 65.9% and 44.0% vs. 40.1%, respectively), but not in the high fNDF diet (interactions $P \leq 0.08$). Overall, low fNDF vs. high fNDF and 2% FAT vs. 0% FAT increased digestible energy intake (DEI) (67.5 vs. 62.2 Mcal/d and 68.1 vs. 61.6 Mcal/d, respectively; both $P < 0.01$). An interaction between fNDF and FAT with time was detected for net energy balance (NEB): the low fNDF diet with FAT had higher NEB than the other treatments early but treatment differences diminished over time (interaction $P = 0.10$). Overall, low fNDF vs. high fNDF diets and 2% FAT vs. 0% FAT improved NEB (-13.0 vs. -16.3 Mcal/d and -12.0 vs. -17.3, respectively; both $P < 0.05$) but decreased efficiency of utilization of DEI for milk (Milk NE_L/DEI; 0.575 vs. 0.634 and 0.565 vs. 0.643, respectively; both $P < 0.05$). Low fNDF diets increased plasma insulin (0.308 vs. 0.137 µg/L) and glucose concentrations (50.5 vs. 45.7 mg/dL), and decreased concentrations of NEFA (606 vs. 917 µEq/L) and BHBA (9.29 vs. 16.5 mg/dL; all $P \leq 0.001$). The 2% FAT treatment tended to decrease plasma NEFA concentration (695 vs. 827 µEq/L; $P = 0.06$) compared with 0% FAT, but treatment differences diminished over time (interaction $P < 0.05$). The 2% FAT treatment increased maximum plasma insulin concentration during a glucose tolerance test in the low fNDF diet (84.5 vs. 44.6 µIU/mL) compared with the high fNDF diets (40.4 vs. 38.0 µIU/mL; interaction $P = 0.07$). FAT tended to interact with dietary fNDF concentration for insulin area under the curve: 2% FAT increased insulin area under the curve by 64% when included in the low fNDF diet (2586 vs. 1575 min*µIU/mL), but only by 5.1% when included in the high fNDF diet (1307 vs. 1243 min*µIU/mL; interaction $P = 0.12$). Supplementation of FAT and low fNDF diets increased DEI and improved NEB, but decreased apparent efficiency of utilization of DEI for milk production in the postpartum period.

Key Words: energy balance, postpartum, prilled fat

1715 (T328) Production performance parameters of early lactation Iranian Holstein cows fed diets containing high levels of palmitic acid or Ca-salt of unsaturated fatty acids.

H. Khalilvandi-Behroozyar[1], M. Dehghan Banadaky*[2], K. Rezayazdi[2] and M. Ghaffarzadeh[3], *[1]Department of Animal Science, Urmia University, Urmia, Iran, [2]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [3]Chemistry and Chemical Engineering Research Center of Iran, Tehran, Iran*

Fat supplements can improve energy balance, feed efficiency, and the yields of milk and milk fat. However, the effects of different FA profiles have not yet been adequately studied. The aim of this study was to evaluate the milk fatty acid profile in early lactating dairy cows supplemented with protected unsaturated fatty acids sources and prilled source of palm fatty acids. Twenty four multiparous Iranian Holstein cows were assigned to diets with different fatty acid profiles and supplemented through 30 days prior to expect calving date to 50 days in milk. Dietary treatments consisted of (1) Prilled Pam fatty acids (PO) [Energizer RP10 , 2 and 2.25% DM in pre- and postpartum, respectively]; (2) Ca-salts of sunflower oil (SO) [Persia Fat- SO]; (3) Ca-salts of fish oil (FO) [Persia Fat- FO] and (4) equal amounts of Persia Fat- FO and Persia Fat- SO. Calcium salts were supplemented as 2.2 and 2.5% of dietary DM in pre- and postpartum period, respectively Milk yield and the dry matter intake were measured daily throughout the experimental period. The milk samples were obtained weekly (2 consecutive days, 3 daily milking, Individual milk samples were analyzed for fat, true protein, and lactose concentration by mid-infrared spectroscopy by the Iranian Dairy Herd Improvement Association. Yields of 3.5% FCM, ECM, and milk components were calculated using milk yield and component concentrations for each milking. Data were analyzed using PROC MIXED of SAS 9.1 according with re-

peated measures in time function. Milk and milk component yields were greater with Persia Fat than with palmitic fatty acid prill. However feed efficiency was not statistically different (1.84 kg FCM/kg DMI vs. 1.89, 1.88 and.86, for treatments 1 to 4, respectively). Cows fed Persia Fat had greater DMI than those fed Palm oil fatty acids (20.17 kg DM vs. 23.56, 22.25 and 22.53, for treatments 1 to 4, respectively). Milk protein concentration was higher for PO compared with Persia Fat (3.27% vs. 3.14, 3.12 and 3.08, for treatments 1 to 4, respectively), but Persia Fat fed cows produced more milk protein per day. Based on results we conclude that different fatty acids have different digestibilities, absorption and/or differing biological effects post absorption.

Key Words: PUFA, palmitic acid, FCM

1716 (T329) Characterization of the role of long-chain fatty acids in the regulation of lipogenic gene expression via LXRα in goat mammary epithelial cells. W. Zhao*[1,2], J. Luo[1], P. Dovc[3] and J. J. Loor[2], *[1]Northwest A&F University, Yangling, China, [2]University of Illinois, Urbana, [3]University of Ljubljana, Domzale, Slovenia*

In dairy cows and goats, liver X receptor α (*LXRα*) is a nuclear receptor considered as a potentially important regulator of de novo long-chain fatty acid (LCFA) synthesis. Previous data in bovine MacT cells indicated that activation of *LXRα* with the agonist T0901317 (T09) up-regulates the expression of some lipogenic target genes, hence, could play a role in de novo FA synthesis regulation. In vitro, long-chain fatty acids (LCFA) could have an agonistic capacity on *LXRα*, thus, serving as an alternate mechanism for regulating milk fat synthesis. In order to characterize the roles of *LXRα* and LCFA in the regulation of lipid synthesis in goat mammary epithelial cells (GMEC), primary mammary cells isolated from mammary gland of Saanen dairy goats cultivated in lactogenic medium were cultured in triplicate and for 12 h with 50 μM of the specific *LXRα* agonist T0901317 (T09) or the specific *LXRα* antagonist GGPP (GP), 100 μM of several LCFA (16:0, 18:0, t10,c12- conjugated linoleic acid (CLA), docosahexaenoic acid (DHA), and eicosapentaenoic acid (EPA)), and a combination of GP with 100 μM of several LCFA (16:0, 18:0, t10,c12-CLA, DHA, and EPA) (for a total of 7 treatments excluding controls). Expression of 17 genes involved in LCFA plus 3 internal control genes was detected using qPCR. Data were statistically analyzed using the GLM of SAS. The multiple comparisons were corrected using Tukey's test and accepted as significant at $P < 0.05$. Although T09 did not alter *LXRα*, data from the cells treated with GP alone revealed that a minimum activation of *LXRα* is essential for the up-regulation ($P < 0.05$) of *INSIG1, LPIN1, FASN, SREBF1*, *AGPAT6,* and *SCD*. The marked up-regulation ($P < 0.05$) of *SREBF1*, *FASN*, *ACACA*, and *SCD* with T09 vs. control suggests their expression is partly controlled by *LXRα* as reported in MacT cells. Expression of *PPARG* did not respond to T09 or GP but when the LCFA were combined with GP, its expression was up-regulated ($P = 0.0001$) by 13-18 fold over the control. Both 16:0 and 18:0 when combined with GP up-regulated ($P < 0.05$) *SREBF1*, *INSIG1*, *SCD*, *ACSS2*, *AGPAT6*, and *LPIN1* but had no effect on *ACACA* or *FASN*. Data obtained with the combination of GP and LCFA revealed a complex scenario. However, data indicate that the LCFA effect could have been driven partly via *PPARG* as demonstrated previously in MacT cells. Overall, data suggest that LCFA could partly act as competitive agonists of *LXRα* in GMEC.

Key Words: nutrigenomics, milk fat synthesis, nuclear receptor

---

1717 (T330) Effects of feeding protected unsaturated fatty acids (Persia Fat)on milk fatty acid profile of Iranian Holstein dairy cows. H. Khalilvandi-Behroozyar[1], M. Dehghan Banadaky*[2] and M. Ghaffarzadeh[3], *[1]Department of Animal Science, Urmia University, Urmia, Iran, [2]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [3]Chemistry and Chemical Engineering Research Center of Iran, Tehran, Iran*

In recent years, consumer concerns about contribution of milk and dairy products to total intake of saturated fatty acids has driven extensive research about effectiveness of protected fatty acid sources in modification of milk fatty acids. The aim of this study was to evaluate the milk fatty acid profile in early lactating dairy cows supplemented with protected unsaturated fatty acids sources and prilled source of palm fatty acids. Twenty four multiparous Iranian Holstein cows were assigned to diets with different fatty acid profiles and supplemented through 30 days prior to expected calving date to 50 days in milk. Dietary treatments consisted of (1) Prilled Pam fatty acids (PO) [Energizer RP10 , 2 and 2.25% DM in pre- and postpartum, respectively]; (2) Ca-salts of sunflower oil (SO) [Persia Fat-SO]; (3) Ca-salts of fish oil (FO) [Persia Fat- FO] and (4) equal amounts of Persia Fat- FO and Persia Fat- SO. Calcium salts were supplemented as 2.2 and 2.5% of dietary DM in pre- and postpartum period, respectively Milk yield and the dry matter intake were measured daily throughout the experimental period. The milk samples used for evaluating fatty acids profile were obtained weekly (2 consecutive days, each sample coming from the 3 daily milking, and were quantified by gas chromatography (Varian CP-3800, FID detector, 100 m CP-Sil88 column, GLC 463). Data were analyzed using PROC MIXED of SAS 9.1 with repeated measures in time function. Cows fed PO produced milk with higher saturated (69.90 vs. 58.14, 56.45 and 56.74, for treatments 1 to 4, respectively) and lower monounsaturated (23.37 vs. 32.22, 32.54 and 32.36, for treatments 1 to 4, respectively) polyunsaturated (2.80 vs. 7.13, 7.58 and 6.98, for treatments 1 to 4, respectively) fatty acid concentrations than cows fed diets with unsaturated fatty

acid sources. All of the differences between PO and Persia Fat sources were statistically significant, but not between unsaturated fatty acid sources. Feeding Persia Fat increased the milk concentration of C18:0, whereas that of C16:0 was increased by PO supplementation (39.13 vs. 25.92, 23.60 and 23.72, for treatments 1 to 4, respectively). Supplementation with PO significantly increased C16 and < C16 fatty acids, whereas decreased > C16 fatty acids in milk fat. Highest (statistically significant) n-3 and n-6 fatty acids contents were belong to Persia Fat- FO and Persia Fat- SO, respectively.

Key Words: PUFA, palmitic acid, omega-3,omega-6

1718 (T331) Milk yield and milk fat responses to increasing levels of stearic acid supplementation of dairy cows. J. P. Boerman* and A. L. Lock, *Michigan State University, East Lansing*

Dose-dependent effects of a stearic acid-enriched fat supplement on feed intake, production responses, and the maximum amount of stearic acid that can be incorporated into milk fat were evaluated. Multiparous Holstein cows (n = 32; 145 ± 66 DIM) with a wide range in milk yield (25– 70 kg/d) were blocked by milk yield and assigned to replicated 4 x 4 Latin squares. Treatments were diets supplemented with a stearic acid-enriched fat (SA; 87% C18:0) at 0, 0.8, 1.6, or 2.4% of diet DM. Periods were 21 d with the final 5 d used for data and sample collection. The corn silage and alfalfa silage-based diets were formulated to contain 25.8% forage NDF and 17.0% CP. The statistical model included the random effect of cow and the fixed effects of treatment, period, and their interaction. Linear, quadratic, and cubic contrasts were used to determine the effects of increasing doses of SA. Intake of DM increased as SA supplementation increased (28.4, 29.0, 29.5, and 29.9 kg/d; linear, P = 0.02). Milk fat concentration was 3.78, 3.73, 3.74, and 3.82% for increasing doses of SA (quadratic, P = 0.10). Treatment had no effect on milk yield (38.2 kg/d, P = 0.54), milk fat yield (1.41 kg/d, P = 0.75), milk protein yield (1.32 kg/d, P = 0.51), or milk protein concentration (3.49%, P = 0.88). Feed efficiency (ECM/DMI) was 1.43, 1.39, 1.36, and 1.36 for increasing doses of SA (linear, P = 0.0003). Supplementation of SA had no effect on BW or BCS (P > 0.23). The yield of C18:0 plus *cis*-9 C18:1 in milk fat was increased by SA supplementation (linear, P = 0.005); however, the increase from 0 to 2.4% SA was only 17 g/d resulting in no effect of SA supplementation on yield of total preformed milk FA (> 16-carbons, P = 0.69). The yield of de novo (< 16-carbons) and 16-carbon FA in milk fat were also unaffected by SA supplementation (P = 0.72 and P = 0.33, respectively). In conclusion, although increasing SA supplementation increased DMI it had no effect on the yield of milk or milk components. While SA supplementation increased the yield of C18:0 plus *cis*-9 C18:1 in milk fat, it had no overall effect on the yield of de novo or preformed FA in milk.

Key Words: fat supplementation, milk fat, stearic acid

1719 (T332) Effect of different dietary fatty acid profiles on individual milk fatty acid yields by dairy cattle fed diets with less than 3% total fatty acids. C. M. Stoffel and L. E. Armentano*, *University of Wisconsin-Madison, Madison.*

Dietary fatty acid (FA) composition can affect milk fat yield but also relative yields of different FA. This study examined the effects on yield of individual milk FA resulting from different dietary FA profiles at FA levels below 3% of diet dry matter (DM). Trial design and production performance data were discussed in a 2013 ADSA abstract. Briefly, 60 cows were paired (within parity) to form 30 experimental units. Pairs were fed six diets in five 6x6 balanced Latin squares with 21-d periods. There were two control diets: a corn control diet (CC) containing 1.8% FA and a low oil control (LOC) containing 1.2% FA. A portion of the food grade corn starch in LOC was replaced with 1.7% diet DM of a 50/50 blend of corn and high linoleic safflower oils (CO), high oleic sunflower oil (OO), palm oil (PO), or 1.8% diet DM calcium salts of palm FA (ML, Megalac) to create four treatment diets that were enriched in either linoleic (CO), oleic (OO), or palmitic acid (PO and ML). Milk FA composition was measured on d 20, and milk yield and fat concentration were measured for the last 5 d of each period; these data were combined to determine yield of individual milk FA. There were significant treatment effects on the yield of 31 out 53 milk FA measured including 10 out of 14 C18:1 isomers (P < 0.05). Palmitic acid (C16) yield was lower for CO compared to other treatments (P < 0.01) and C18:1 and total C18 yield were higher for OO when compared to PO and ML (P < 0.01, P < 0.01). Trans-10 C18:1 yield was higher for CO when compared to the other treatments (P < 0.01) and for OO compared to PO and ML (P = 0.01). Trans-10, cis-12 yield was also higher for CO when compared to all other treatments (P < 0.01). Linear regression analysis was also conducted to examine the effect on milk FA yield of the increased dietary linoleic, oleic, and palmitic acid concentrations of the treatment diets over LOC. Dietary linoleic decreased short chain (< C16) and C16 FA yield (P = 0.02, P < 0.01), dietary oleic increased total C18 yield (P < 0.01), and dietary palmitic increased C16 yield (P < 0.01). These differences in milk FA profile are consistent with the idea that linoleic acid depresses short chain and C16 FA, resulting in milk fat depression even at dietary FA levels below 3%.

Key Words: biohydrogenation, milk fat depression, milk fatty acid

1720 (T333) Effect of specific essential oil blend on performance of Nellore young bulls in feedlot.

A. L. D. S. Valente*, J. M. Serra, E. Romanzini, R. A. Reis, R. Barbero, T. Araujo, S. Santos, L. Delevatti and F. Souza, *Unesp, Jaboticabal, Brazil*

The European Union has prohibited the use of growth-promoting antibiotics in animal feeds. These restrictions, based around concerns that the use of antibiotics for livestock can give rise to transmissible resistance factors that may compromise the therapeutic use of antibiotic in humans (Casewell et al., 2003). In this sense, natural plant products such as essential oils (EO) become an alternative to manipulate rumen fermentation (Iason, 2005). Chao et al., 2000 suggested that gram-negative bacteria's shows a trend to have higher resistance to essential oils than gram-positive bacteria. Decreasing gram + bacteria may improve animal performance. Therefore, seventy two Nellore bulls (375 ± 14 kg BW) were fed 15% of sugar-cane bagasse and 85% of concentrate for 81d in individual pens. The treatments compound different combinations of essential oil blend or monensin (M) or both (1*: 100mg EO; 2*: 20 mg of M + 100 mg of EO; 3*: 20 mg of M + 200 mg of EO; 4*: 200 mg of EO; 5*: 20 mg of M and 6*: 10 mg of M + 100 mg of EO). Treatment mixes were incorporated into the concentrate ration, which was composed by corn, soybean meal and citrus pulp. Diets were isoenergetic and isonitrogenous. Throughout the entire experimental period, the provided feed amounts were adjusted to allow approximately 100g/kg residue comparing with the total consumed on previous day. Average daily gain was calculated using the initial and final individual live weight divided by the number of experimental days. Data was subjected to analysis of variance compared by orthogonal contrast. Animals fed 20mg of M had the greatest liveweight gain (1.242 kg/d), treatments 20mg of M + 100mg of EO and 100mg of EO achieved 0.909 and 0.910kg/d, respectively. Animals supplemented with 10mg of M + 100 mg of EO and 20mg of M + 100mg of EO had lower average daily gain than 5* but higher than 2*. However, 6* and 3* were not statistically different, the ADG for this treatment were 1.174 kg/d and 1.008 kg/d, respectively. The data of feed conversion (kg DM/ADG) shown for treatment 1* feed intake of 9.278 kg DM/d to gain 1kg liveweight, and the treatments 2*, 3*, 4*, 6*; 9.196, 8.398, 8.244, 8.385, respectively. Animals the treatment 5* had the lower intake (7.137). Therefore, strategic use of essential oil did not improve the animal performance.

Key Words: essential oil, feedlot, monensin

1721 (T334) Effect of coconut oil and lauric acid on omasal nutrient flow and microbial protein synthesis in dairy cows.

A. Faciola[*1] and G. A. Broderick[2], [1]*University of Nevada, Reno,* [2]*Broderick Nutrition* and *Research, LLC, Madison, WI*

Ruminal protozoa (RP) contribute to ruminal bacterial turnover. Previously, feeding lauric acid (LA; C12:0), sharply decreased RP. However, despite reducing RP, LA reduced DMI and milk yield. In this trial, we tested coconut oil (CO), which contains about 50% LA, as a practical defaunating agent and assessed its effects on nutrient and microbial omasal flow. Six cows fitted with ruminal cannulae were blocked by DIM into 2 blocks of 3 cows and randomly assigned within blocks to 3 dietary treatments in a 3X3 replicated Latin square with 21 days of adaptation and 7 days of sampling. The basal diet contained (DM basis) 50% alfalfa silage, 10% corn silage, and 40% concentrate (corn, molasses, and soybean), 16% CP and 29% NDF. Diets A and C provided the same amount of fat: A) 3% Megalac and C) 3% CO. Diets B and C provided the same amount of LA (287g/d). Data were analyzed using the mixed procedure in SAS. Results are reported in Table 1721. DMI was similar among treatments; however, diet B increased NDF flow at the omasal canal and decreased ruminal NDF apparently digestibility. There were trends for reduced DM flow at the omasal canal, ruminal N digestibility and RDP supply, and increased RUP omasal flow, when diet B was fed.

Key Words: coconut oil, omasal flow, protozoa

Table 1721. Ruminal metabolism and omasal flows

Item	Control	LA	CO	SEM	*P*-value
DM intake, kg/d	22.8	22.4	23.0	1.0	0.14
DM flow, kg/d	14.1	13.6	14.2	0.7	0.06
DM apparently digested in the rumen, kg/d	8.68	8.77	8.76	0.82	0.21
NDF flow, kg/d	4.61[b]	4.82[a]	4.64[ab]	0.19	0.05
NDF apparently digested in the rumen, kg/d	1.87[a]	1.61[b]	1.89[a]	0.16	< 0.01
Total NAN[1] flow, g/d	523	522	525	25	0.19
N truly digested in the rumen, g/d	414	404	423	23	0.07
RDP supply, kg/d	2.52	2.46	2.58	0.15	0.09
RUP flow kg/d	1.15	1.17	1.13	0.06	0.08
NMNAN[1] flow, g/d	173	176	169	15	0.16
FAB-NAN[1] flow, g/d	152	149	155	10	0.13
PAB-NAN[1] flow, g/d	198	196	201	16	0.16
Total microbial NAN flow, g/d	350	345	356	19	0.12
Microbial efficiency, g of NAN/kg of OMTDR[1]	26.0	25.7	26.1	0.7	0.12

[a-b] Within the same row with different superscripts differ ($P < 0.05$).
[1] NAN = non-ammonia N; NMNAN = nonmicrobial NAN; FAB- and PAB-NAN = fluid- and particle-associated bacterial NAN; OMTDR = OM truly digested in the rumen.

1722 (T335) Supplementation of lemongrass oil and a mixture of garlic and ginger oil improved in vitro feed digestion. A. Nanon[1], W. Suksombat[1] and W. Yang*[2], [1]*Suranaree University of Technology, Muang, Thailand,* [2]*Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*

Lemongrass has shown antibacterial, antioxidant, and anti-hyper-NH_3–producing ruminal bacterial activities. However, the lemongrass, especially its essential oil (EO) has little been evaluated on its effect on ruminal fermentation. The objective of this study was to investigate the effect of lemongrass oil (LMO) and a mixture (1:1) of garlic and ginger oil (CEO) on gas production (GP) and feed digestion in batch culture. Four feeds: wheat distillers dried grains with solubles (DDGS), barley grain, grass hay, and a total mixed ration (TMR) were used as substrate with varying EO dosages from 0, 100, 200 to 300 mg/kg substrate DM. The TMR consisted of 35% grass hay, 15% alfalfa hay, 20% barley grain, 10% corn DDGS, 10% wheat DDGS, 5% canola meal, and 5% vitamin and mineral supplement. GP was measured at 3, 6, 12, 24, 36, and 48 h post incubation, and disappearance of DM (DMD) and neutral detergent fiber (NDFD) were determined at 24 and 48 h of incubation, respectively. There was no interaction on in vitro DMD and NDFD between the EO source and EO dose. DMD (% of input) were greater ($P < 0.05$) with CEO compared to LMO for wheat DDGS (48.6 vs. 47.9) and barley grain (61.5 vs. 60.3), but less ($P < 0.03$) for TMR (40.9 vs. 41.8) after 24 h of incubation. Increasing dosage of either CEO or LMO linearly ($P < 0.01$) increased DMD and NDFD of grass hay and TMR at 24 and 48 h of incubation, whereas increasing CEO or LMO dosages linearly ($P < 0.01$) increased only DMD of wheat DDGS and barley grain at 24 h of incubation. Cumulative GP was affected ($P < 0.03$) by both LMO and CEO in a quadratic manner after 24, 36 or 48 h of incubation with greatest GP at 200 mg/kg grass hay or TMR. These results suggested that the LMO and CEO appeared to be more effective to improve the DMD of fibrous feeds and modulated the digestive microorganisms in a dose-dependent manner. The EO used in the present study could be potentially developed as rumen modifier to improve feed digestion in ruminant.

Key Words: dry matter disappearance, in vitro, lemongrass oil

1723 (T336) Use of lemongrass oil for manipulation of ruminal fermentation using Rusitec technique. A. Nanon[1], W. Suksombat[1] and W. Yang*[2], [1]*Suranaree University of Technology, Muang, Thailand,* [2]*Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*

Supplementation of lemongrass powder or meal has revealed a positive impact on ruminal fermentation in beef cattle. However, lemongrass essential oil (LMO) has little been evaluated on its effect on ruminal fermentation. A study using Rusitec technique was conducted to investigate the effect of increasing dose of LMO supplementation on fermentation characteristics of a dairy cow diet. Experiment was a completely randomized design with 4 replications in each treatment and consisted of 10 d of adaptation and 6 d of data collection. The substrate consisted of 35% grass hay, 15% alfalfa hay, 25% barley grain, 20% wheat dried distillers grains with solubles, and 5% vitamin and mineral supplement. Four treatments were: 1) control (no additives), 2) low LMO (100 mg LMO/kg DM), 3) high LMO (200 mg LMO/kg DM), and 4) monensin (30 mg/kg diet DM). Increasing LMO supplementation affected neither volatile fatty acid (VFA) concentration (averaged 26.0 m*M*) nor molar proportion (mol/100 mol) of acetate (49.0), propionate (23.3) or butyrate (16.2). However, increasing LMO linearly ($P < 0.01$) increased large peptide N from 2.6, 3.1 to 3.3 mg/mL and small peptide N from 3.3, 4.1 to 4.5 mg/mL, and linearly ($P < 0.01$) reduced ammonia N concentration from 8.8, 8.3 to 7.9 mg/mL in fermentation media. Increasing LMO addition also linearly ($P < 0.02$) increased bacterial protein production from 66.3, 66.2 to 70.1 mg/d N, and tended ($P = 0.10$) to improve bacterial efficiency from 12.7, 12.9 to 13.3 g N/kg digested OM. However, digestibility (% of input) of DM (52.8), NDF (41.9), starch (76.5), and CP (59.0) was not affected by increasing LMO addition. Supplementation of monensin did not affect fermentation characteristics, feed digestion, and bacterial protein production. These results suggest that supplementation of a dairy cow diet with LMO inhibited deamination process by possibly altering microbial populations such as proteolytic bacteria.

Key Words: fermentation, lemongrass oil, Rusitec

1724 (T337) Effect of tea oil and sunflower oil on rumen fermentation, milk composition and rumen microbial population in water buffaloes fed elephant grass-based diets. C. Yang*, X. Liang, S. Wei, X. Liang, S. Li, C. Zou, B. Yang and L. Li, *Buffalo Research Institute, Chinese Academy of Agricultural Sciences, Nanning, China.*

The objective of this study was to investigate the effect of tea oil and sunflower oil on rumen fermentation, milk composition and rumen microbial population in water buffaloes fed elephant grass-based diets. Thirty two lactating water buffaloes were allocated at random to 1 of 4 treatments composed of elephant grass and concentrates containing no additional oil (Control group), or supplemented with 200g of sunflower oil(SF group), 200 g tea oil(TO group), 200 g sunflower oil and tea oil (SF:TO = 1:1, ST group). On d 7, 14, 21, 28, samples of milk were collected for milk composition analysis using GC and a MilkoScan FT120. On day 28, rumen fluids was collected by stomach tube and used for pH, VFA, NH_3–N determination and DNA extraction. Total bacteria, Methanogens, fungi, protozoa, *R. flavefaciens*, *F. succinogenes*, and

Butyrivibrio group were quantified by relative real-time PCR. Compared with the control, dietary supplements of 200 g tea oil or sunflower oil alone or in combination with each other decreased the concentration of NH_3–N and milk production significantly ($P < 0.05$). Concentrations of milk fat and total solids were greater than control group after oil supplementation ($P < 0.05$). Oils supplementations have no effect on concentrations of milk protein and lactose. Acetate: propionate ratios were significantly increased after oils supplementation ($P < 0.05$). Concentrations of acetate, propionate, butyrate and total VFAs were not affected by oils supplementation. C18:2 and c9t11-CLA were increased by sunflower oil or the combination of sunflower and tea oil ($P < 0.05$). Only Cis9 C18:1 was increased after tea oil supplement alone ($P < 0.05$). Inclusion tea oil resulted in greater concentration of milk fat, Cis9 C18:1 and total solids and less concentration of NH_3–N and milk production. Methanogens, fungi, protozoa, *R. flavefaciens*, *F. succinogenes*, and *Butyrivibrio* group populations were not influenced by oil supplementation. In conclusion, tea oil or sunflower oil manipulated ruminal fermentation and milk composition without effect on abundance of fibrolytic bacteria and *Butyrivibrio* group when water buffaloes were fed elephant-grass based diets.

Key Words: water buffalo, rumen, milk composition

1725 (T338) Effects of echium and flaxseed oil on ruminal fatty acid metabolism in vitro.

L. Jin[*1,2], C. Li[2], M. He[2], Y. Wang[2], T. W. Alexander[2] and T. A. McAllister[2], *[1]Department of Animal Science and Technology, Northeast Agricultural University, Harbin, China, [2]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada.*

Echium oil (EO) contains high level of γ-linolenic acid (*c*6, *c*9, *c*12) and stearidonic acid (*c*6, *c*9, *c*12, *c*15) and is considered to be a more desirable source of n-3 fatty acids (FA) than flaxseed oil (FO). However, there is little information on the metabolism of EO in the rumen. An in vitro study was designed as 2 × 2 (oil type × dose) + 1 (control) to assess the effect of EO and FO on ruminal FA profiles. A mixture of barley silage, barley grain and minerals and vitamin supplement (75:22:3, DM basis) was incubated with 0 (control), 3 or 6% of EO or FO in serum vials with rumen fluid. Each treatment was triplicated and incubated for 0, 3, 6, 24, and 48 h. The experiment was repeated (run) three times. The statistical model included run and treatments for the fixed effects and vial as unit. The whole content was freeze-dried and extracted for total FA which was used to determine the individual FA profile by GC. Percentage of C18:0 (g/100g total FA) was lower ($P < 0.001$) for 6% EO treatment than in other treatments at both 24 and 48 h of incubation. Both oil treatments had higher ($P < 0.001$) *cis* 15-C18:1 percentage than control. Inclusion of 3% and 6% FO resulted in higher ($P < 0.001$) *cis* 15-C18:1 than EO at 6, 24 and 48 h. However, incubation with 6% EO yielded FA with the highest ($P < 0.001$) *trans* 9-C18:1 and *trans* 11-C18:1 percentage at 24 and 48 h. *Cis*-9, *trans*-11-C18:2 was increased ($P < 0.001$) by both oil treatments. The total unsaturated FA and *trans* FA were higher ($P < 0.01$) with the addition of oil groups and 6% EO was the greatest ($P < 0.001$). The increased *trans* 11-C18:1 with EO but not FO suggests that EO is more desirable in that it produced more *trans* 11-C18:1, the precursor of *cis*-9, *trans*-11-C18:2 which has been reported to benefit human health.

Key Words: echium oil, fatty acids, in vitro

1726 (T339) Effects of linseed oil and propolis additives on protozoa population in dairy cows.

E. H. Yoshimura[1], L. M. Zeoula[*1], R. Franzolin[2], N. W. Santos[1], E. Machado[1], B. C. Agustinho[1], L. D. M. Pereira[1] and F. Alves[1], *[1]Universidade Estadual de Maringá, Maringá, Brazil, [2]Universidade de São Paulo- Faculdade de Zootecnia e Engenharia de Alimentos, Pirassununga-SP, Brazil*

Although the role of protozoa in the rumen fermentation is unquestionable, the truth is that its elimination may represent, in some cases, an additional benefit to the ruminant as increased microbial N outflow. The objective of this experiment was to examine the effect of linseed oil and additives on the population of ciliate protozoa in the rumen of dairy cow. Four lactating Holstein cows were used in a 4X4 Latin square design. Diets were composed of 600:400 forage:concentrate (dry matter basis-DM). The treatments were: basal diet (C); basal diet + linseed oil (25 $g.kg^{-1}$ DM) (LO); basal diet + linseed oil + propolis (10 mg $flavonoids.kg^{-1}$ DM) (LOP); basal diet + linseed oil + propolis + vitamin E (375 $UI.kg^{-1}$ DM) (LOPE). Samples of rumen contents were obtained (2 days in each period) manually through the fistula approximately 30 min before feeding and were fixed by diluting with an equal volume of formalin solution (18.5% formaldehyde final concentration). Total counts and generic distribution of protozoa were made in 100 microscopic fields at a magnification of 100x according to Dehority (1993). Statistical analyses were performed by analysis of variance ($P < 0.05$) and orthogonal contrasts to compare effects of 1) Linseed oil (C vs. LO, LOP and LOPE), 2) Propolis (LO vs. LOP and LOPE); 3) Vitamin E interaction (LOP vs. LOPE). There were no effects of linseed oil on the species of *Entodinium* ($P = 0.097$), *Isotricha* ($P = 0.143$) and total protozoa population ($P = 0.092$). In general, the *Endodinium* species was represented by the largest proportion (99.69%) and a lower *Isotricha* species (0.30%). However, the Diplodiniinae subfamily was not identified. It can be conclued that linseed oil and propolis additives do not change protozoa population.

Key Words: microbiology, omega-3, additives

Table 1726.

	Treatments					Orthogonal contrasts[1]		
Parameters	C	LO	LOP	LOPE	SEM	1	2	3
	—— Nx10^5 ciliates/mL ——							
Entodinium	4.894	3.731	4.097	3.026	0.403	0.097	0.813	0.226
Isotricha	0.024	0.008	0.011	0.008	0.004	0.143	0.879	0.792
Total	4.918	3.739	4.108	3.034	0.405	0.092	0.814	0.222
	———— % Total ————							
Entodinium	99.58	99.83	99.76	99.60	0.111	0.633	0.635	0.678
Isotricha	0.41	0.16	0.24	0.39	0.111	0.633	0.635	0.678

[1] *P*-value.

1727 (T340) Effect of linoleic and linolenic acid sources supplementation on in vitro rumen fermentation characteristics and microbial diversity.

S. M. Amanullah[1], S. C. Kim[*1], D. Kim[1], H. Lee[1], Y. Joo[1] and I. H. Choi[2], *[1]Division of Applied Life Science (BK21Plus, Insti. of Agri.* and *Life Sci.), Gyeongsang National University, Jinju, South Korea, [2]Department of Companion Animal and Animal Resources Science, Joongbu University, Geumsan-gun, South Korea*

An in vitro experiment was conducted to estimate the effects of oil sources on rumen fermentation characteristics and microbial diversity. Oil sources were corn oil (CO), linseed oil (LSO) and Ca-salts of linoleic acid (CaSalt). Rumen fluid was collected from 2 canulated Hanwoo steers fed rice straw and concentrate mixture in 2:8 ratio. Incubation was performed in 50 ml glass serum bottles containing 150 mg of synthetic diet (411 g cellulose, 411 g starch, and 178 g casein/kg DM), 7 mg (µl) of either oil sources, and 15 ml of incubation medium (rumen fluid + Van Soest medium = 1:2) at 37 °C for 0, 3, 6, 12 and 24 h with 5 replications and 5 blanks for each time period. After 24 h of incubation, total gas volume and the concentrations of ammonia-N and total VFA were unaffected ($P > 0.05$). The pH was higher ($P = 0.024$) in CaSalt with a concomitant lower in lactate concentration ($P = 0.001$). Acetate concentration was significantly higher in CaSalt ($P = 0.013$), but propionate concentration was higher in CO than that in others ($P = 0.007$). Concomitantly, acetate to propionate ratio was higher in CaSalt than in CO ($P = 0.016$). The real time PCR analysis was conducted for relative quantification of microbial DNA. At 12 and 24 h of incubation, *F. succinogens*, *R. flavefaciens*, and *R. albus* were significantly higher ($P < 0.05$) in CaSalt than those in CO and LSO. However, *S. bovis*was observed higher in LSO at both of those time periods ($P < 0.05$). On the other hand, after 24 h, Methanogenic archaea and ciliate protozoa was highest in LSO and CO, respectively ($P < 0.005$). It is concluded that CaSalt showed lowered rumen methanogenic archaea and ciliate protozoa, while less toxic effects on fibrolytic bacteria compared to other oil sources, as also evidenced from higher acetate production in this treatment.

Key Words: corn oil, linseed oil, Ca-salts of linoleic acid, rumen fermentation, rumen microbes

1728 (T341) Intake and daily gain of grazing Nellore bulls receiving concentrated supplementation with additives.

J. A. C. Lima[*1,2], H. J. Fernandes[2], M. F. Paulino[1], E. P. Rosa[2], L. S. Caramalac[2], K. A. Silveira[2], G. C. Silva[2] and A. Aguiar[3], *[1]Federal University of Viçosa, Viçosa, Brazil, [2]State University of Mato Grosso do Sul, Aquidauana, Brazil, [3]University of Florida, Gainesville, FL*

The objective of this study was to evaluate the effect of a commercial concentrate supplement with additives in the intake and daily gain of grazing bulls, during the dry/rainy transition season in Aquidauana-MS, Brazil. Twelve Nellore bulls (initial body weight of 370 ± 15 kg) were randomly assigned to twelve *Brachiaria decumbens* Stapf pastures (1.0 ha/pasture; one bull/pasture) on a completely randomized design. Treatments were: 1) concentrate supplement Lipomax with homeopathic additives (Convert H, Sodo 100, Figotonus) and Virginiamicina (Lipomax treatment), and 2) concentrate supplement with a similar protein content (18% CP), and without additives (Control treatment). Animals were feed daily at rate of 0.5% of the animal's body weight. The animals were weighed (shrunk body weight) at beginning of the experiment and 104 d after, to evaluate the weight gain. After 45 days, a trial for estimated intake was made using the enriched and purified lignin (LIPE) as marker for fecal excretion estimation, and the indigestible neutral detergent fiber as internal marker. Forage nutritive value was estimated by hand-plucked sampling, and supplement intake was measured directly for each animal. A significance level of 5% was adopted. The forage (DMfor), supplement (DMsuppl), total dry matter, crude protein and TDN intakes showed no difference ($P > 0.05$) between treatments (Table 1728). However, DMsuppl intake was 50% higher when using additives (Lipomax treatment) with similar quantity reduction on DMfor. The lack of significance, in this case, could be explained by the high coefficient of variation of DMsuppl. The average daily gain was higher ($P < 0.05$) when using concentrate supplement with additives. In conclusion, additives in concentrate supplement increased the efficiency of nutrient use for grazing animals.

Key Words: grazing bulls, intake, performance

Table 1728. Intake and daily gain of Nellore bulls grazing brachiaria grass receiving concentrated supplementation with or without additives

Item	Treatment		CV (%)	*P*-value
	Control	Lipomax		
	kg/d			
DMfor[1]	8.418	7.988	15.1	0.561
DMsuppl[2]	0.844	1.269	51.0	0.205
DMtot[3]	9.261	9.258	12.7	0.996
CPint[4]	0.848	0.835	22.0	0.797
TDN[5]	6.374	6.134	16.3	0.746
ADG	0.811	1.107	19.2	0.028

[1]DMfor is dry matter intake of pasture.
[2]DMsuppl is dry matter intake of supplement.
[3]DMtot is the total dry matter intake.
[4]CPint is crude protein intake. [5]TDN is total digestible nutrients intake.

1729 (T342) Effects of concentrate level and combined use of virginiamycin and salinomycin on nutrient intake and digestibility of Nellore steers.
A. J. C. Nuñez[1], V. V. Almeida[2], I. E. Borges[1], F. Pinese[1], F. T. Mercado[1], S. L. Silva[*1], P. R. Leme[1] and J. C. M. Nogueira Filho[1], *[1]Department of Animal Science- FZEA/USP, Pirassununga/SP, Brazil, [2]Department of Animal Science- FCAV/UNESP, Jaboticabal/SP, Brazil*

Eight ruminally cannulated Nellore steers (434 ± 35 kg initial BW) were allotted to a 4x4 replicated Latin square design (21-d periods) to evaluate the effects of concentrate and virginiamycin levels in diets containing salinomycin on nutrient intake and digestibility. Treatments were arranged as a 2x2 factorial, with 2 concentrate levels (70C and 90C diets had 70 and 90% concentrate, respectively) and 2 virginiamycin levels (0 and 15 ppm) in the diet DM. Steers were fed once daily at 0800 and salinomycin was included in all diets (13 ppm). The 70C diet contained 33% starch, 16% CP, and 31% NDF, whereas the 90C diet contained 47% starch, 16% CP, and 19% NDF on DM basis. Dry matter, CP, NDF, and starch intakes were calculated as the difference between the amount of nutrient offered and refused. Apparent digestibilities of nutrients were determined by total fecal collection for 3 d on each experimental period. Statistical analyses were performed using the MIXED procedure of SAS. No interactions between concentrate and virginiamycin levels were observed for any analyzed variable. Steers receiving the 90C diet showed greater ($P \leq 0.01$) DM (7.73 and 8.23 ± 0.19 kg/d for 70C and 90C, respectively), CP (1.24 and 1.32 ± 0.03 kg/d for 70C and 90C, respectively), and starch intakes (2.58 and 3.78 ± 0.13 kg/d for 70C and 90C, respectively), whereas NDF intake was greater ($P \leq 0.01$) for steers fed the 70C diet (2.28 and 1.57 ± 0.07 kg/d for 70C and 90C, respectively). Intake variables were not affected by virginiamycin inclusion. Animals receiving the 90C diet showed greater ($P < 0.01$) apparent digestibilities of DM (66.21 and 73.70 ± 0.94% for 70C and 90C, respectively) and CP (71.23 and 77.35 ± 0.83% for 70C and 90C, respectively), whereas NDF and starch digestibilities did not differ between concentrate levels. Steers fed only salinomycin showed greater ($P = 0.05$) starch digestibility in comparison with those receiving both additives (90.90 and 88.98 ± 0.78% for 0 and 15 ppm virginiamycin, respectively). There were no effects of virginiamycin inclusion on DM, CP, and NDF digestibilities. In conclusion, nutrient intake and apparent digestibility of Nellore steers are affected by dietary concentrate levels, whereas the effects of the combined use of virginiamycin and salinomycin on these variables are less pronounced.

Key Words: antibiotic, ionophore, Zebu cattle

1730 (T343) A meta-analysis of effects of feeding nitrate on toxicity, production, and enteric methane emissions in ruminants.
C. Lee* and K. A. Beauchemin, *Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*

Nitrate is usually considered an undesirable compound in ruminant feeds due to its potential toxicity (methemoglobinaemia). Despite this concern, nitrate has recently received attention as an electron acceptor in the rumen that could possibly reduce enteric methane emissions. It was also proposed that nitrate might be a useful non-protein nitrogen source as a substitute for urea. Therefore, a meta-analysis was conducted to investigate the effects of feeding nitrate on its toxicity and effects on animal production and enteric methane emissions. Data were collected from published literature (PubMed, ScienceDirect and CAB direct) and analyzed using the MIXED procedure of SAS with study as a random effect. When nitrate was fed without a gradual acclimation (stepwise increases in nitrate in diets) or infused into the rumen, blood methemoglobin levels (MetHg, % of total hemoglobin) linearly responded to nitrate levels [9 studies with 25 treatments; MetHg (%) = 41.3 × nitrate (g/kg BW/d) + 1.2; $R^2 = 0.76$, $P < 0.001$]. However, when nitrate was fed using a gradual acclimation, the potential toxicity of nitrate was considerably lowered [3 studies with 11 treatments; MetHg (%) = 4.2 × nitrate (g/kg BW/d) + 0.4, $R^2 = 0.76$, $P = 0.002$]. Animals fed nitrate reduced enteric methane emissions in a dose–response manner [8 studies and 25 treatments; CH_4 (g/kg DMI) = −8.3 × nitrate (g/kg BW/d) + 15.2, $R^2 = 0.80$, $P < 0.001$]. Three studies examined the persistent efficacy of nitrate on reducing enteric methane emissions (54, 90, and 92 d, respectively). Animals fed nitrate (2.1 to 2.7% of dietary DM) reduced methane emissions persistently by 16.5 to 35.4% (treatments × time, $P > 0.31$). However, dry matter intake (DMI) and live weight gain (LWG) of cattle were not affected by nitrate (DMI, 20 studies and 46 treatments; $R^2 = 0.007$, $P = 0.65$; LWG, 12 studies and 35 treatments; $R^2 = 0.03$, $P = 0.31$). In conclusion, the potential toxicity of nitrate can be reduced by acclimatizing the animals to nitrate gradually. Nitrate is a potential feed additive to re-

duce enteric methane emissions and its efficacy is persistent. However, lowering methane production using nitrate may not re-direct additional metabolizable energy towards animal production. This meta-analysis, however, needs to be interpreted with caution because of the small number of studies used.

Key Words: meta-analysis, nitrate, ruminants

1731 (T344) Methane production of Nellore young bulls on pasture in the rainy season supplemented with crude glycerin associated energy sources.

A. José Neto*[1], L. G. Rossi[2], A. F. Ribeiro[1], B. R. Vieira[3], I. Pena Carvalho de Carvalho[2], E. E. Dalanttonia[4], A. S. Gómez I[3] and T. T. Berchielli[4], *[1]Universidade Estadual Paulista "Julio de Mesquita Filho", Jaboticabal, Brazil, [2]Universidade Estadual Paulista, Jaboticabal, Brazil, [3]Universidade Estadual Paulista Júlio de Mesquita Filho, Jaboticabal, São Paulo, Brazil, [4]Universidade Estadual Paulista Júlio de Mesquita Filho- UNESP, Jaboticabal, Brazil*

The objective of this study was to evaluate the effect of adding 28% crude glycerin (CG) in the supplement (DM basis), replacing corn or soybean hulls, with or without a source of oil, on enteric methane emission, average daily gain (ADG) and daily carcass gain (GC) of young bulls in the pasture. A total of 36 young Nellore bulls with an average initial BW of 333.20 ± 41.60 kg were distributed in a completely randomized design (three animals per paddock and three paddocks per treatment) with nine replicates. Treatments were arranged as a 2x2 factorial (high or low starch, with or without a source of oil). Paddock was the experimental unit, and the model effects included treatment. These animals were grazed on *Brachiaria brizantha* cv. Xaraés in the rainy season (January 2013 to May 2013), with the same treatments and supplemented at the rate of 500 g/100 kg BW. The supplements were: T1- CG with high starch (corn), T2- CG with low starch (soybean hulls), T3- CG with high starch associated to a source of oil (corn and soybeans) and T4- CG with low starch associated to a source of oil (soybean hulls in soybean grain). The sulfur hexafluoride (SF_6) tracer method for measuring eructated CH_4 was used in this study (Johnson et al., 1994). To determine daily carcass gain, eight animals were slaughtered as a reference at the beginning of the experiment and after 133 days of the experiment, eight more animals were slaughtered. Data were analyzed using the SAS PROC GLM, considering the significance of $P < 0.05$. Daily carcass gain (GC, kg.day^{-1}) and average daily gain (ADG, kg.day^{-1}) of the animals was evaluated. The methane emission were expressed in kilogram of methane emitted per year (kg CH_4.yr^{-1}), gram per day (g CH_4.day^{-1}), kilogram per kilogram of carcass produced (kg CH_4.kg CAR^{-1}) and kilogram per kilogram of average daily gain (kg CH_4.kg ADG^{-1}). Differences were not detected ($P > 0.05$) between treatments, with average values of 0.54 kg.day^{-1}, 0.88 kg.day^{-1}, 44.03 kg.yr^{-1}, 120.64 g.day^{-1}, 0.22 kg.kg CAR^{-1} and 0.16 kg CH_4.kg ADG^{-1}, respectively. Crude glycerin associated with high or low levels of starch, with or without a source of oil, did not alter the methane production of Nellore bulls on pasture supplemented during the rainy season.

Key Words: energy, environment, ruminant

1732 (T345) Effects of encapsulated nitrate on toxicity, feed intake and feed consumption rates in beef cattle.

C. Lee*[1], R. C. Araujo[2,3], K. M. Koenig[1] and K. A. Beauchemin[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]GRASP Ind.* and *Com. LTDA, Curitiba, Brazil, [3]EW|Nutrition GMBH, Visbek, Germany.*

Slow-release encapsulated nitrate [EN; 66.9% nitrate in DM; GRASP Ind. and Com. LTDA, Paraná, Brazil] was investigated for its effects on toxicity threshold, feed intake, and feed consumption rates in 2 experiments. In Exp. 1, 5 beef heifers were fed once daily a diet (55:45 forage:concentrate) at 75% of ad libitum intake. The proportion of EN in the diet was increased by 1% every 4 days to 1.0, 2.0, 2.9, 3.9, 4.8, and 5.8% of dietary DM (10.3 to 15.6% CP at 0 to 5.8% EN). In Exp. 2, 8 beef heifers were used in a replicated 4 × 4 Latin square design and fed ad libitum once daily diets (iso-nitrogenous, 12.7% CP; 55:45 forage:concentrate) containing 0, 1, 2, and 3% EN (DM basis) using a 21-d stepwise adaptation. In Exp. 1 with restrictive feeding, a heifer was removed due to rapid feed consumption causing nitrate-poisoning at 3% EN and another due to refusal to eat the 2% EN diet. Comparing 0% with 5.8% EN, feed consumption from 0 to 3 h after feeding was decreased (70.3 to 48.6% of total; $P = 0.03$), that from 12 to 24 h was increased (0.6 to 22.6%; $P = 0.01$), and feed consumed over 24 h was decreased (100 to 92.3%; $P = 0.01$). Animals showed negligible blood methemoglobin levels (< 1%; MetHb, % of hemoglobin) at 1% EN. However, MetHb levels were greater (avg. 8.6 vs. 3.3% and max. 23.6 vs. 13.6% at 3 h) at 2.0 and 2.9% EN than at 3.9% or more EN because of sorting of the concentrates containing higher levels of EN. The MetHb level peaked 3 h after feeding for all EN levels and the magnitude of the peak was dependent on the amount of feed consumed from 0 to 3 h. In Exp. 2 with ad libitum feeding, feed consumption rates were not different (41.8% of total from 0 to 3 h) among EN levels. Although MetHb levels increased ($P < 0.01$) with increasing EN level, the magnitude was lower for Exp. 2 compared with Exp. 1 (avg. 2.8 vs. 8.4%; max. 7.2 vs. 23.6% at 3% EN). Sorting of the EN diets was not observed in Exp. 2. In conclusion, MetHb responses to EN levels were dependent on feed consumption rates after feeding. Offering a diet containing EN for ad libitum intake minimized risks of nitrate toxicity.

Key Words: encapsulated nitrate, methemoglobin, beef cattle

1733 (T346) Effects of the combined use of virginiamycin and salinomycin on rumen fluid kinetics of Nellore steers. A. J. C. Nuñez[1], V. V. Almeida[2], F. Pinese[1], I. E. Borges[1], F. T. Mercado[1], S. L. Silva[*1], P. R. Leme[1] and J. C. M. Nogueira Filho[1], *[1]Department of Animal Science- FZEA/USP, Pirassununga/SP, Brazil, [2]Department of Animal Science- FCAV/UNESP, Jaboticabal/SP, Brazil*

Two experiments were conducted to evaluate the combination of dietary virginiamycin and salinomycin on rumen fluid kinetics of Nellore steers fed high concentrate diets. In experiment one, 8 Nellore steers (322 ± 26 kg initial BW) were allotted to a replicated 4x4 Latin square design (21-d periods), in a 2x2 factorial arrangement of treatments, with 2 salinomycin concentrations (0 and 13 ppm) and 2 virginiamycin concentrations (0 and 15 ppm) in the diet DM, which contained 80% concentrate. In experiment two, 8 Nellore steers (434 ± 35 kg initial BW) were allotted to the same experimental design, with 2 concentrate inclusions (70C and 90C diets had 70 and 90% concentrate, respectively) and 2 virginiamycin concentrations (0 and 15 ppm) in the diet DM. Salinomycin was included in all diets (13 ppm). In both experiments, on d 20 of each period, 300 g of polyethylene glycol 4000 (PEG) were diluted in 600 mL of deionized water and infused into the rumen of each steer at 0800. Rumen fluid samples were collected before infusion and at 1.5, 3, 6, 12, and 24h after infusion, and PEG concentrations were determined by colorimetry. Ruminal fluid rate of passage (RP; %/h) and volume (FV; L) were calculated from linear regression of the natural logarithm of PEG concentration on time. Fluid retention time (RT; h) was determined as the inverse of RP, whereas flow rate (FR; L/h) was calculated as RP multiplied by FV. Statistical analyses were performed using the MIXED procedure of SAS, and the model included the random effects of animal, period, and Latin square, and the fixed effects of salinomycin or concentrate, virginiamycin, and the two-way interaction. No interactions were observed for any variable. In experiment one, rumen fluid kinetics variables were not affected by treatments. In experiment two, steers receiving the 70C diet showed greater ($P \leq 0.02$) RP (9.90 and 7.92 ± 0.48%/h for 70C and 90C, respectively), FV (39.07 and 31.47 ± 1.89 L for 70C and 90C, respectively), and FR (3.69 and 2.55 ± 0.23 L/h for 70C and 90C, respectively), whereas RT was greater ($P < 0.01$) for steers fed the 90C diet (9.77 and 13.24 ± 1.15 h for 70C and 90C, respectively). No effects of virginiamycin were observed for any variable. In conclusion, rumen fluid kinetics of Nellore steers is affected by dietary concentrate inclusion, but not by the combined use of virginiamycin and salinomycin.

Key Words: antibiotic, ionophore, Zebu

1734 (T347) Monensin, virginiamycin and functional oils on rumen health of Nellore cattle fed high concentrate diets without adaptation. A. P. dos Santos Silva[1], R. Ferreira Carvalho[2], C. A. Zotti[2], M. Rezende Mazon[1], L. Silva Oliviera[2], S. Luz e Silva[*2] and P. R. Leme[1], *[1]University of Sao Paulo, Pirassununga, Brazil, [2]University of Sao Paulo/FZEA, Pirassununga, Brazil*

Feed additives and adaptation strategies are used to prevent metabolic disorders in feedlot cattle. The extent on how additives can contribute to rumen health of Zebu cattle that are not adapted to high grain diets is still unknown. To evaluate the different feed additives on rumen health, 48 Nellore bulls (322 ± 23 kg of BW, 20 months old) were submitted to a diet change, without adaptation, from grass pasture to a high concentrate diet (92% grains) fed ad libitum during 120 days. The treatments were different feed additives added to the basal diet: monensin at 30 mg/kg DM (M30), monensin at 40 mg/kg DM (M40) fed during the first 14 days, decreasing to 30 mg/kg after this period, monensin at 30 mg/kg DM + virginiamycin at 25 mg/kg DM (MV) and functional oils (a blend of castor oil and cashew oil) at 400 mg/kg DM (FO). After 120 days animals were slaughtered and the livers were examined for abscesses. Rumen pH was measured and the incidence of ruminites (IR) was classified according to a 0 to 10 scale. Fragments of 3 cm^2 were taken from the cranial sac of the rumen and kept in buffer solution for the measurements of papillae number (PN), papillary area (PA) and absorption surface (AS). PN was counted by 3 evaluators and PA and AS were measured on the UTHSCA Image Tool free software. Animals fed FO diet had higher ($P = 0.01$) daily DMI than M30 and MV. However, there was no difference ($P = 0.22$) between OF and M40.There was no difference among treatments for ADG ($P = 0.13$), final BW ($P = 0.16$) and G:F ($P = 0.10$). No difference ($P = 0.86$) was verified for rumen pH (6.37 ± 0.51). There was no incidence of liver abscesses and low IR ($P = 0.61$; 1,09 ± 1,42). No differences ($P = 0,90$) were found on PN (53.18 ± 14.25), on PA ($P = 0.60$; 0.7 ± 0.26) and also on AS ($P = 0.82$; 38.07 ± 17.89). No metabolic disorders occurred and there was no decrease in animal performance indicating a relative protection of the additives and the possibility of feeding high concentrate diets to Nellore cattle without adaptation. Also, FO, a natural product, may substitute ionophores and antibiotics as additives for rumen protection when high concentrate diets are fed.

Key Words: feed additives, Zebu, feedlot

1735 (T348) Effects of grain source and monensin level on site and extent of digestion in feedlot heifers.

W. Yang*[1], L. Xu[2], Y. Zhao[1,3] and T. A. McAllister[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Bao Tou Light Industry Vocational Technical College, Bao Tou, China, [3]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China.*

Many feedlot producers include wheat grain into the rations due to increasing supplies of feed wheat in North America, whereas few studies have documented the effects of wheat source on animal response. A study was conducted to examine feed intake and site and extent of digestion by substituting wheat grain (soft or hard) for barley and to determine whether increasing monensin level would improve feed digestion in feedlot heifers. Five ruminally and duodenally cannulated beef heifers were used in a 5 × 5 Latin square design with 2 × 2 + 1 factorial. Treatments were barley (10% barley silage, 90% barley-based concentrate, and 28 mg/kg monensin), and diets substituting soft or hard wheat for barley combining with 28 (low) or 44 (high) mg/kg monensin. The barley diet is a standard feedlot diet used in western Canadian feedlots. Contrasts were generated to compare barley vs. wheat diets in low monensin; soft vs. hard wheat; and low vs. high menensin in wheat diets. Intake of DM was affected neither by grain source (8.3 kg/d) nor by wheat source (7.7 kg/d), whereas increased monensin level reduced ($P < 0.02$) DMI from 8.1 to 7.3 kg/d. Inclusion of wheat in place of barley grain did not affect the flows of OM to the duodenum (3.8 kg/d) and digestibility (% of intake) of OM in the rumen (64.2%) and in the total tract (80.5%). However, digestibility of NDF (barley vs. wheat; 60.6 vs. 48.3%; $P < 0.01$) and that of starch (barley vs. wheat; 95.5 vs. 97.6%; $P < 0.03$) in the total digestive tract were different. Feeding soft vs. hard wheat delivered lower ($P < 0.03$) OM (soft vs. hard; 3.4 vs. 3.6 kg/d) and non-ammonia N (soft vs. hard; 164 vs. 178 g/d) to the duodenum with no differences in ruminal and intestinal digestibility of OM. Increased monensin supplementation decreased ($P < 0.05$) duodenal flows of OM from 3.7 to 3.3 kg/d, total N from 182 to 168 g/d, and microbial N from 99 to 87 g/d without affecting the site and extent of feed digestibility. These results indicated that wheat exhibited similar feed value to barley; high level monensin may potentially alleviate ruminal acidosis by reducing DMI of finishing cattle.

Key Words: feedlot heifers, grain source, digestibility

1736 (T349) Effects of different doses of sodium monensin on rumen tissue histology of feedlot cattle.

A. L. Rigueiro*[1], A. C. J. Pinto[1], M. C. Pereira[1], D. H. Watanabe[1], C. A. Oliveira[1], T. V. Carrara[2], D. D. Estevam[2], D. P. Silva[1], F. T. Pereira[1] and D. D. Millen[1,3], *[1]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [2]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [3]São Paulo State Foundation (FAPESP), São Paulo, Brazil*

This study, conducted at the São Paulo State University feedlot, Dracena Campus, Brazil, was designed to determine the effects of different doses of sodium monensin on rumen tissue histological variables of feedlot cattle. The experiment was designed as a completely randomized block, with 12 replications per treatment, in which 60 20-mo-old yearling Nellore bulls (402.52 ± 33.0 kg) were fed in individual pens for 84 days according to the different doses of monensin (DM basis): 1) 0 ppm (D0); 2) 9 ppm (D9); 3) 18 ppm (D18); 4) 27 ppm (D27), and 5) 36 ppm (D36). The adaptation program consisted of ad libitum feeding of two adaptation diets over period of 14-d with concentrate level increasing from 68% to 84% of diet DM. The finishing diet contained: 71.5% cracked corn grain, 16.0% sugarcane bagasse, 7.7% soybean meal, 3.0% supplement, 1.2% urea, and 0.6% limestone (DM basis). At harvest, a 1-cm^2 fragment of each rumen ($n = 60$) was collected from ventral sac for histological assessment. Histological sections were stained with hematoxylin and eosin, embedded in paraffin wax, and sectioned. Morphometric measurements, such as papillae surface area, papillae height, papillae width, keratinized layer thickness, and mitotic index, were determined in four papillae per animal using computer-aided light microscope image analysis. Orthogonal contrasts were used to evaluate linear, quadratic, cubic and quartic relationship between doses of monensin and the dependent variable. The use of different doses of sodium monensin did not affect ($P > 0.10$) keratinized layer thickness. However, as doses of sodium monensin increased, papillae width in mm (D0 = 0.46; D9 = 0.42; D18 = 0.44; D27 = 0.45; D36 = 0.38), papillae surface area in cm^2 (D0 = 2.43; D9 = 2.12; D18 = 2,25; D27 = 2.68; D36 = 1.72) and mitotic index, as % of basal cells (D0 = 2.57; D9 = 3.15; D18 = 2.92; D27 = 2.71; D36 = 3.11) were affected ($P < 0.05$) cubically. The papillae height in mm (D0 = 4.98; D9 = 5.42; D18 = 5.04; D27 = 6.21; D36 = 4.71) was affected ($P = 0.05$) quadratically as dose of sodium monensin increased. Thus, increasing doses of sodium monensin affected histological variables of rumen tissue. The feeding of either 9 ppm or 27 ppm of sodium monensin seemed to be the best options in this study.

Key Words: Nellore, mitosis, papillae

1737 (T350) Effects of different doses of sodium monensin on DMI variation and selective consumption by feedlot cattle. D. H. Watanabe*[1], M. C. Pereira[1], J. Silva[1], T. V. Carrara[2], A. L. Rigueiro[1], L. A. Tomaz[1], D. P. Silva[1], D. V. Vicari[1], A. C. J. Pinto[1], D. D. Estevam[2], M. D. Arrigoni[2] and D. D. Millen[1,3], *[1]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [2]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [3]São Paulo State Foundation (FAPESP), São Paulo, Brazil*

This study, conducted at the São Paulo State University feedlot, Dracena Campus, Brazil, was designed to determine the effects of different doses of sodium monensin on DMI variation and selective consumption (sorting) of diets by Nellore cattle. The experiment was designed as a completely randomized block, replicated 12 times, in which 60 20-mo-old yearling Nellore bulls (402.52 ± 33.0 kg) were fed in individual pens for 84 days according to the following treatments (DM basis): 1) 0 ppm (D0); 2) 9 ppm (D9); 3) 18 ppm (D18); 4) 27 ppm (D27), and 5) 36 ppm (D36). The adaptation program consisted of ad libitum feeding of two adaptation diets over period of 14-d with concentrate level increasing from 68% to 84% of diet DM. The finishing diet contained: 71.5% cracked corn grain, 16.0% sugarcane bagasse, 7.7% soybean meal, 3.0% supplement, 1.2% urea, and 0.6% limestone (DM basis). The DMI variation was calculated for each individual pen as the difference in intake, expressed as % of variation, between consecutive days throughout the study. Samples of orts and diets were collected on days 10 and 40 of the study for particle size distribution determination, which was performed by sieving using the Penn State Particle Size Separator and reported on as-fed basis. Values equal to 1.0 indicate no sorting, < 1.0 show selective refusals, and > 1.0 indicate preferential consumption. Orthogonal contrasts were used to assess linear, quadratic, cubic and quartic relationship between doses of monensin and the dependent variable. During the period of adaptation, DMI variation was affected (P = 0.02) quadratically as dose of sodium monensin increased (D0: 15.3%; D9: 14.6%; D18: 13.6%; D27: 13.5%; D36: 18.5%); however, the use of different doses of sodium monensin did not affect (P > 0.10) DMI variation during the finishing period. Increasing doses of sodium monensin only affected particle sorting during the adaptation period, in which as dose of sodium monensin increased, sorting for screens one (diagonal opening = 19.0 mm; D0 = 0.986; D9 = 0.962; D18 = 0.947; D27 = 0.928; D36 = 1.021), two (diagonal opening = 8.0 mm; D0 = 0.992; D9 = 1.013; D18 = 1.014; D27 = 0.936; D36 = 0.932), and three (diagonal opening = 1.18 mm; D0 = 1.001; D9 = 1.015; D18 = 1.065; D27 = 1.043; D36 = 0.993), and bottom pan (D0 = 0.938; D9 = 1.022; D18 = 1.020; D27 = 1.074; D36 = 1.016) were affected (P < 0.05) quadratically. Thus, the feeding of sodium monensin up to 27 ppm reduced DMI variation, but increased diet sorting during the adaptation period.

Key Words: fluctuation, Nellore, sorting

1738 (T351) Feeding monensin or essential oils in high corn or byproduct finishing diets for Nellore bulls. L. J. Chagas*[1], M. G. DOS Santos[1], A. H. De Melo[1], J. R. R. Dórea[2], D. F. A. Costa[2] and F. A. P. Santos[2], *[1]University of São Paulo- ESALQ, Piracicaba, Brazil, [2]University of São Paulo, Piracicaba, Brazil*

The objective of this study was to evaluate the effects of sodium monensin replacement for essential oils on behavior, DMI, ruminal pH and ammonium concentration in feedlot cattle. Sixteen Nellore bulls (339 ± 30 Kg initial BW) were allocated in individual pens to four 4 × 4 Latin square (LS) design, consisting of 21 d (including 14 d of adaptation). One of two basal diets used had 5% sugar cane bagasse, 50% wet corn gluten feed, 43.5% soybean hulls and 1.5% mineral and vitamin mix and the other had 80.6% ground corn, 12% sugar cane bagasse, 4% soybean meal, 0.9% urea, and 2.5% mineral and vitamin mix (DM basis). Each basal diet was used in two 4 × 4 LS. Feed additives were mixed within the mineral and vitamin mix according to treatments: 1) Control (CON), no additives;2) Monensin (MON), 25 mg/kg of DM (Rumensin); 3) Essential oil (EO), 0.5 g/kg of DM (commercial additive extracted from castor and cashew oils, Essential); and 4) Essential oil plus monensin (E+M), 0.3 g/kg of DM and 25 mg/kg of DM, respectively. There were no differences between the basal diets for DMI (8.2 kg/d), feeding and idle time (193 and 1104 min in 24 h), feeding frequency (9.5 feed/d) and meal size (22 min/feed). Supplementing essential oils at 0.5 g/kg of DM (EO) decreased (P < 0.05) rumination in 37% compared to control, 130 vs. 208, respectively. Essential oils only, or E+M increased (P < 0.01) ruminal pH and ammonia nitrogen, 6.06 and 6.01 vs. 5.79 and 5.89 mg/dL, respectively for EO, E+M, CON and MON. Feeding frequency was the only parameter affected (P < 0.05) when byproducts were used, with 12.9 and 8.1 meal/d, for CON and MON, EO and M+E, respectively. In conclusion, castor and cashew essential oils have some beneficial effects on cattle physiology in the short time, such as the 21 days adaptation period to high grain diets.

Key Words: feedlot, feed additives, ionophores

1739 (T352) The effect of a citrus extract rich in flavonoids (Bioflavex) and its main components on rumen fermentation and microbial population under in vitro system using steers fed high concentrate diet as rumen liquor donors.

A. R. Seradj[1], J. Crespo[*2], M. Fondevila[3] and J. Balcells[1], *[1]University of Lleida, Lleida, Spain, [2]Interquim S. A. (Ferrer Health Tech), Barcelona, Spain, [3]University of Zaragoza, Zaragoza, Spain*

To evaluate the effect of flavonoids on rumen fermentation and microbial population an in vitro assay was designed. Four sets of incubation series (batches) were separately conducted using a complete randomized block design. Four steers fed high concentrate ration (90:10 comemercial concentrate:barley straw) were used as donors. Serum glass bottles (120 ml) were filled with 80 ml of an incubation solution under a CO_2 stream. A mixture of the same concentrate and barley straw (600:60 mg/bottle) was used as substrate. Bioflavex (BF) was tested against its main flavonoid components (Hesperidine [HS]; Isonaringine [IN]; Naringine [NG]; Neoeriocitrine [NE]; Neohesperidine [NH] and Poncirine [PC]) at 200µg/g DM, and the substrate without flavonoids was considered as a control (CTR). Bottles were incubated at 39 ± 1°C and two bottles per treatment opened after 12 h, and sampled for pH, NH_3–N, volatile fatty acids (VFAs) and microbiota analyses. The DNA was extracted using QIAamp DNA Stool Mini Kit. qPCR was used to quantify the protozoa and hydrogenotrophic methanogenic archaea (HMA) concentration, moreover specific primers were used to determine the relative abundance of *Streptococcus bovis*, *Selenomonas ruminantium* and *Megasphaera elsdenii* in relation to the total bacteria while HMA and the acetoclastic *Methanosarcina* spp. were refered to total archaea. The treatments did not alter pH and no differences were recorded in NH_3 nor in total VFA concentration. However, in relation to the CTR, the addition of flavonoids (except for HS), altered the VFA profile, reducing acetate and increasing propionate proportion. Ciliate protozoa concentration was reduced by BF, NG, NH and PC ($P < 0.05$). Flavonoids, did not alter the relative abundance of *S. bovis* as lactate producing bacteria, (except for NE) although they enhanced ($P < 0.05$) *M. elsdenii* propotion in relation to the CTR (except for HS, IN and NE). A clear inhibition of flavonoids on the relative abundance of HMA was observed although only PC, NH, NG and BF reduced the relative abundance of *Methanosarcina* spp. ($P < 0.05$). Flavonoids exert significant changes in the fermentation end products and also altered the concentration and composition of lactate-utilizing bacteria, methanogenic population and ciliate protozoa. However, the different tested flavonoids substances did not interact homogeneously against rumen population.

Key Words: absolute and relative microbiota quantifications, in vitro incubation and pure flavonoids

1740 (T353) Use of a citrus flavonoids extract (Bioflavex) to improve rumen fermentation efficiency and performance in steers consuming high concentrate diets.

A. R. Seradj[1], B. A. Refat[1], A. Jimeno[2], J. Crespo[*3] and J. Balcells[1], *[1]University of Lleida, Lleida, Spain, [2]University of Zaragoza, Zaragoza, Spain, [3]Interquim S. A. (Ferrer Health Tech), Barcelona, Spain*

To study the effects of a citrus ñavonoids extract (Bioñavex; BF) on fermentation and performance in steers fed high concentrate diets (90:10 Concentrate:Barley straw), two experiments were performed. In the first one, eight Friesian bulls (398 ± 12.2 kg BW) fitted with rumen cannula and were housed in individual pens and assigned to one of two treatments, they received the basal concentrate (CTR) or the basal concentrate supplemented with Bioflavex (450 mg/kg DM) in 2×4 cross over design. The trial lasted for 24 days and was divided in 2 experimental periods of 12 days, 10 days for dietary changeover followed by two sampling days. In the second experiment, 32 Friesian steers (395 ± 10.1 kg BW) were weighed and blocked in 2 homogeneous groups (BW basis) receiving the same treatments as Exp. 1 (CTR and BF) and were weighed at day 7 and 24 of the experiment. Concentrate and barley straw were offered ad libitum, once a day (0800 h) for 24 days. At the sampling days of 1st trial, rumen was sampled (at 0, 4 and 8 h post feeding) for pH, NH_3–N, volatile fatty acids (VFAs) and microbiota analyses. BF in the concentrate improved pH values (6.1 vs. 5.8 for BF and CTR; SEM 0.05; $P < 0.01$) and molar proportion of propionate (24. 2 vs. 22.5 SEM 0.60; $P = 0.05$). Flavonoids did not alter absolute abundances of total bacteria nor relative abundance of *Streptococcus bovis* while relative abundances of *Selenomonas ruminantium* ($P < 0.01$) and *Megaesphera elsdenii* ($P = 0.05$) were enhanced by the presence of BF in the concentrate. In the second trial no differences were observed neither in the final BW (425 vs. 420 kg SEM 10.9) nor in average daily gain (1.1 vs. 1.2 Kg/d SEM 0.14, for CTR and BF respectively) but feed conversion ratio was lower in BF than CTR steers (6.1 vs.6.8 SEM 0.8; $P = 0.05$). Flavonoid supplementation might be effective in improving rumen fermentation and animal's performance which may be explained changes induced by BF in the microbial flora.

Key Words: animal's performance, flavonoids and ruminal fermentation

1741 (T354) Effect of blend *Enterococcus faecium* plus *Saccharomyces cerevisiae* in different doses on intake and digestibility of steers in feedlot.

A. A. Oliveira, J. Koscheck*, A. L. D. S. Valente, F. Basso, C. Rabelo, U. Carneiro and R. A. Reis, *Unesp, Jaboticabal, Brazil*

The goal of this study was to evaluate the effect of different probiotic doses on the intake and partial digestibility of dry matter.

Were evaluated six Nellore steers fitted with ruminal cannulas and allocated to a double 3 x 3 Latin square design with three treatments and tree periods on two simultaneous repetitions. The blend of *Enterococcus faecium* (5 x 10^9 ufc/g of product) and *Saccharomyces cerevisiae* (5 x 10^9 ufc/g of product) in different doses (0, 1 or 2 g/day) were provided on the rumen. Steers were fed a diet containing 200 g/kg of corn silage and 800 g/kg concentrate. Within each experimental period, 18 days were to adaptation, DMI and digestibility were recorded from d 19 to 21. The statistical analyzes were conducted using PROC MIXED from SAS and means were compared using Tukey test ($P < 0.05$). Different doses of probiotic did not affect ($P > 0.05$) DMI, whereas the digestibility of OM (746.4, 697.9, 689.2 g/kg), and carbohydrates (757.4, 715.8, 706.6 g/kg) showed a quadratic response to 0, 1 and 2 g/day, respectively.

Key Words: concentrate, digestibility, probiotic

1742 (T355) Effect of doses at *Enterococcus faecium* and *Saccharomyces cerevisiae* on ruminal parameters responses of feeder cattle.

A. A. Oliveira, J. Koscheck*, A. L. D. S. Valente, F. Basso, C. Rabelo, U. Carneiro and R. A. Reis, *Unesp, Jaboticabal, Brazil*

This study aimed to evaluate the effect of doses of *Enterococcus faecium* and *Saccharomyces cerevisiae* on the pH, ruminal ammonia nitrogen (RAN) and short-chain fatty acids (SCFA) in beef cattle in feedlot. Six Nellore steers fitted with ruminal cannulas, with initial average body weight of 460 kg were used in a double Latin square 3 x 3. Within each experimental period, 18 days were to adaptation and three days for sampling. Steers were fed a diet containing 200 g/kg of maize silage and 800 g/kg of concentrate. The following treatments: 0, 1 or 2 g/day of a blend with *Enterococcus faecium* (5 x 10^9 cfu/g of product) and *Saccharomyces cerevisiae* (5 x 10^9 cfu/g of product) provided in the rumen were evaluated. The statistical analyzes were conducted using PROC MIXED from SAS and means were compared using Tukey test ($P < 0.05$). Different doses of probiotic did not showed statistic difference ($P > 0.05$) for the variables evaluated, however, statistical difference were achieved to the time of sampling ($P > 0.05$). The pH was highest up to 6 hours after feeding the animals. Highest level of ammonia nitrogen (36.28 mg/dL) was observed 3 hours after feed supply. Concentrations of acetic acid was highest (72.59 mmol/L) 9 hours after feed supply ($P < 0.05$), however the highest level of propionic (22.94 mmol/L) occur after 12 hours ($P < 0.05$), and butiric acid had highest level 15 hours after feed supply ($P < 0.001$). The use of different doses of the blend with *Enterococcus faecium* and *Saccharomyces cerevisiae* did not affect the ruminal parameters.

Key Words: feedlot, probiotic, ruminal parameter

1743 (T356) Influence of soybean meal supplementation with tannins extracted from pistachio hulls on performance and feed efficiency of Holstein bulls.

A. Jolazadeh[1], M. Dehghan banadaky[*2] and K. Rezayazdi[2], *[1]University of Tehran, Karaj, Iran, [2]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran.*

The objective of this study was to examine the effects of soybean meal (SBM) supplementation with pistachio concentrated extract (PEC) on performance and feed efficiency of Holstein bulls. The sun dried pistachio hulls was grounded through a 0.5 mm screen and soaked with ratio of 1:10 in (pistachio: water). Filtered extract was concentrated by heating at 95 ℃. The SBM was treated with PCE containing 11.14% total phenol and 7.13% total tannin/DM of extract. The experiment duration was 14 weeks and involved 28 growing young bulls (256 ± 56 kg BW) in a completely randomized design. The study lasted 94 d (10 d adaption). Treatments included: (1); control (SBM without PEC) (2); SBM with 5% PEC (3); SBM with 10% PEC and (4); SBM treated with 15% (kg PEC/100kg DM SBM). Diets were formulated to meet nutrient requirements according to NRC (1996) and to be isocaloric and isonitrogenous, with forage concentration ratio of 30:70. The TMRs were supplied ad-libitum to bulls in two equal meals (08.00 and 17.00) and bulls had free access to fresh water. Body weight (BW) of each calf was recorded every 28 days before the morning feeding. Results indicate that, tannin supplementation did not affect ($P < 0.05$) final BW and dry matter intake but there were significant differences among treatment 15% and control in average daily gain (1.25 Vs. 1.06 consequently, $P < 0.01$) and feed efficiency (gain: feed) (6.62 Vs. 7.82 consequently, $P < 0.05$). So it seems that the high level of PCE can improve performance and feed efficiency of Holstein bulls.

Key Words: Holstein bulls, pistachios hulls, soybean meal, tannin

1744 (T357) Depression of rumen ammonia and protozoal population of Holstein bulls fed soybean meal treated with tannins extracted from pistachio hulls.

A. Jolazadeh[1], M. Dehghan banadaky[*2] and K. Rezayazdi[2], *[1]University of Tehran, Karaj, Iran, [2]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran.*

An experiment was conducted to determine the effects of soybean meal (SBM) supplementation with tannins extracted from pistachio hulls (TEP) on some ruminal parameter such as: pH, rumen ammonia and protozoal population of Holstein growing bulls. Twenty-eight Holstein young bulls (average initial weigh 256 ± 63kg) were used in a completely randomized design with four treatments and seven replicates for 94 days. Tannin were extracted from pistachio hulls (TEP) and

contained 11.14% total phenol and 7.13% total tannin/DM of extract. Treatments included: (1); control (SBM without TEP) (2); SBM with 5% TEP (3); SBM with 10% TEP and (4); SBM treated with 15% (kg TEP/100kg DM SBM. Rumen fluid was collected via stomach tube 4h after morning feeding. The pH was determined in ruminal samples immediately after sampling and then Protozoa were counted using Burker counting chamber on days 83 and 85. Rumen fluid was transported to the laboratory and frozen for ammonia analysis. According to results, there was a significant decrease ($P < 0.05$) in the rumen ciliate protozoa population caused by feeding 15% levels of TEP. On the other hand, there was a significant decrease ($P < 0.05$) of tannin supplementation on ammonia concentrations and pH among treatment 15% TEP and control. This result indicates that tannin are able to reduce protein degradation in the rumen and increase bacterial flow to the duodenum by effecting defaunation in male bulls.

Key Words: Holstein young bulls, pistachios hulls, protozoal, rumen ammonia,tannin

---

1745 (T358) Could soybean meal supplementation with crude extract of pistachio hulls change the blood metabolites of Holstein male bulls? M. Dehghan banadaky*[1], A. Jolazadeh[2], K. Rezayazdi[1] and N. Vahdani[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran,* [2]*University of Tehran, Karaj, Iran.*

An experiment was carried out to determine the effect of soybean meal (SBM) supplementation with crude extract of pistachio hulls (CEP) on blood metabolites of Holstein bulls. CEP were extracted from hulls of pistachio containing 7.13% total tannin/DM of extract. Twenty-eight bulls 256 ± 63kg (mean ± SEM) were assigned randomly to one of the four treatment groups with seven replicates in a completely randomized design for 94 days. The bulls were housed in individual tie stalls and had free access to water. They were fed twice daily at 08:00 and 17:00 h. Four iso-energetic and iso-nitrogenous diets were offered to the experimental animals. Treatments included: (1); control (SBM without CEP) (2); SBM with 5% CEP (3); SBM with 10% CEP and (4); SBM treated with 15% (kg CEP/100kg DM SBM). Blood samples were taken from each bull at end of each month prior to morning feeding via coccygeal venipuncture and immediately chilled. According to results, Plasma total protein and albumin concentration was greater ($P = 0.001$) for bulls fed SBM with 15% CEP compared with other levels and Control. Plasma Glucose, BUN and Triglycerides concentrations were not affected by treatments ($P > 0.05$). Probably, in this experiment tannin able to reduce protein degradation in the rumen by formation tannin-protein complex and bypass them to the small intestine and increase digestive utilization of dietary protein is the reason for increase Plasma albumin and total protein concentration ($P < 0.001$) in bulls. It was therefore concluded that CEP could be used as chemical additives for improving the digestive utilization of protein-rich feeds in Holstein bulls.

Key Words: blood metabolites, pistachios hulls, tannin

1746 (T359) Effect of Saikosaponin on rumen gas production, volatile fatty acid concentrations and microbial populations in vitro. L. Pan*, D. P. Bu, J. Q. Wang, J. B. Cheng and X. Z. Sun, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

There has been increasing interest to exploit bioactive saponins for improving rumen metabolism. This experiment was conducted to investigate effects of Saikosaponin (SSA) on rumen gas production, volatile fatty acid concentrations and microbial populations using batch cultures in vitro. It was anaerobically incubated in triplicates together with 0.5 g TMR, 50 mL basal media and 25 mL rumen fluid obtained from rumen-cannulated lactating Holstein dairy cows. Four treatments consisted of supplemental SSA at 0 (control), 0.25, 0.5 and 1.0 mg/g of dry matter,which were assigned randomly to 5 of 20 incubation bottles. Cumulative gas production (GP) was continuously measured in an automated trace gas recording system (AGRS-III, Beijing) at 39 °C during 48 h of incubation, after which the pH values were measured immediately and 10.0 mL of culture fluid sample were kept for analysis of volatile fatty acids (VFAs) by a gas chromatographic and the copy number of rumen bacteria populations by quantitative RT-PCR with species-specific PCR primers amplifying partial 16S rDNA regions. Data were analyzed using GLM procedure of SAS 9.2. Results revealed that SSA did not affect GP kinetics and fermentation gas pattern, while the increase of SSA addition improved the total gas production (131.78^{a}, 112.56^{ab} and 123.50^{ab} vs. 107.50^{b} ml/g DM, $P < 0.05$) and dry matter degradability (53.49^{a}, 50.36^{ab} and 51.83^{ab} vs. 48.67^{b} %, $P = 0.07$) compared with the control. The concentrations of acetate (54.88^{a}, 53.82^{a} and 54.00^{a} vs. 52.13^{b} mmol/L, $P < 0.05$), propionate (20.83^{a}, 20.32^{ab} and 20.25^{ab} vs. 19.74^{b} mmol/L, $P < 0.05$) and total VFA (91.58^{a}, 89.19^{a} and 89.34^{a} vs. 86.53^{b} mmol/L, $P < 0.05$) were increased, whereas molar proportions of acetate to propionate ratio were not influenced by supplementing SSA. There was no treatment effect on Ruminococcus flavefaciens and Butyrivibrio fibrisolvens, while the relative copy number of the following bacterial species: Ruminococcus albus, Prevotella ruminicola, Anaerovibrio lipolytica, Streptococcus bovis and Fibrobacter succinogene were increased ($P < 0.05$) compared to the control. Overall, SSA supplementation improved gas production, VFA concentrations and major microbial species in the culture fluid in vitro, therefore Saikosaponin may be beneficial to manipulate rumen microbial fermentation in vitro.

Key Words: microbial populations; Saikosaponin; volatile fatty acid

1747 (T360) Methane production from dairy cows fed red clover- or corn silage-based diets supplemented with linseed oil. C. Benchaar*[1], F. Hassanat[1], R. Gervais[2] and R. Martineau[1], [1]*Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada,* [2]*Université Laval, Québec, QC, Canada*

The objective of this study was to examine the effect of linseed oil (LO) supplementation on enteric CH_4 emissions from dairy cow fed red clover-(RC) or corn silage (CS)-based diets. Twelve lactating, multiparous Holstein cows (DIM = 91 ± 25; milk yield = 45.2 ± 4.7 kg) were used in a replicated 4 × 4 Latin square (35-d period; 14-d adaptation) with a 2 × 2 factorial arrangement of treatments. Cows were fed (ad libitum; 5% orts on an as-fed basis) a TMR (60:40, forage:concentrate ratio) not supplemented or supplemented with 4% LO (DM basis) and with the forage portion of the TMR consisting of either RC or CS. Production of CH_4 was determined (3 consecutive days) using respiration chambers, while milk performance was determined over 6 consecutive days. Main effects of forage source, LO supplementation and interactions (LO × forage source) were determined using the MIXED Procedure of SAS and significance was declared at $P \leq 0.05$. Significant interactions between LO and forage source were observed for DM intake, and yield of fat-corrected milk, which were not changed by adding LO to RC-based diets but decreased when LO was added in CS-based diets. Similarly, CH_4 production (g/d or as a proportion of gross energy intake) was unaffected by supplementing LO to RC-based diets, but declined by 25% when LO was included in CS-based diets (LO × forage source interaction; $P < 0.01$). When expressed on FCM yield basis, CH_4 production decreased with LO addition regardless the source of forage used (12.7 vs. 14.4 g CH_4/kg FCM). Results of this study show that 4% LO had no effect on CH_4 production when supplemented to RC-based diets, but decreased daily CH_4 emissions and CH_4 energy losses if supplemented to CS-based diets.

Key Words: dairy cow, methane, corn silage, red clover silage, linseed oil

1748 (T361) Replacing alfalfa with panicled-tick clover or sericea lespedeza in a dairy diet decreases ruminal methane but not total gas production. H. D. Naumann*[1], S. A. Armstrong[2,3], M. A. Fonseca[4], B. D. Lambert[5,6] and L. O. Tedeschi[4], [1]*University of Missouri, Columbia,* [2]*Prince Agri Products, Inc, Quincy, IL,* [3]*Oregon State University, Corvallis,* [4]*Texas A&M University, College Station,* [5]*Texas A&M AgriLife Research, Stephenville,* [6]*Tarleton State University, Stephenville, TX*

Enteric methane (CH_4) emissions by ruminants represent a decrease in gross-energy intake by the animal. Biologically active forage plant polyphenols, condensed tannins (CT), are known to suppress enteric CH_4 production in ruminants that consume them. However, consumption of these forages alone, or in too great of quantities could result in antinutritional effects, negatively impacting ruminant efficiency and growth. The objective of this study was to determine the effects of replacing the forage component of a traditional dairy diet (50% corn grain, 50% alfalfa; CRN:ALF) with that of forages containing CT on enteric methane and total gas production. *Desmodium paniculatum* (panicled-tick clover; PTC) and *Lespedeza cuneata* (sericea lespedeza; SL) were evaluated as an alfalfa replacement at levels of 15%, 30% and 45%. Methane production was determined using an in vitro gas production technique. In a randomized complete block design, replications consisted of two fermentation events, 06/25/2012 and 09/16/2012, where each diet was fermented in each of two fermentation chambers. Fermentation chamber was considered a random variable, whereas fermentation flasks within each fermentation chamber were considered random factors. Two ruminally-cannulated steers not adapted to forage containing CT were used for rumen fluid collection. Forages were individually fermented anaerobically in rumen fluid for 48h. Methane concentrations were determined by gas chromatography following fermentation. LS-means were determined and a value of $P < 0.05$ was considered significant. There was no difference in CH_4 production among PTC 15%, SL 15% and CRN:ALF (130.5, 132.2 and110.8 g/kg fermentable-organic matter; FOM, respectively). Fermentation of PTC 30% and SL 30% produced 85.5 and 89.7 g CH_4/kg FOM, respectively, which did not differ from CRN:ALF. However, fermentation of PTC 45% resulted in the least amount of CH_4 produced (38.1 g/kg FOM), which was 54% less than that of SL 45% (84.0 g/kg FOM; $P = 0.0022$) and 65% less than that of CRN:ALF ($P < 0.0001$). Total gas production did not differ among treatments compared to the CRN:ALF control. Results from this study suggest that 45% replacement of alfalfa with PTC or SL will suppress ruminal CH_4 with no compromise in total gas production (i.e. FOM).

Key Words: condensed tannin, legume, ruminal fermentation

1749 (T362) Effects of forage source and NDF concentration on methane emissions and milk production of dairy cows. K. J. Hammond*, A. K. Jones, D. J. Humphries, L. A. Crompton and C. K. Reynolds, *University of Reading, Reading, United Kingdom*

Strategies to mitigate greenhouse gas emissions from dairy cows are unlikely to be adopted if production or profitability is reduced. Dietary manipulation to reduce methane emissions can be readily used and may benefit productivity. The objectives of this study were to examine the effects of silage type and diet NDF concentration on methane emissions and milk production of dairy cows. A 12-week randomized block con-

tinuous design was used with 40 mid-lactation Holstein cows (74 DIM ± SEM 2.57) assigned to one of 4 treatments (10 cows each) according to calving date, parity and milk yield. Milk production and DMI were measured daily and milk composition measured weekly (weeks 3 to 12), and methane emissions estimated using a GreenFeed automated head chamber (weeks 10 to 12). Four isonitrogenous diets were fed as total mixed rations (TMR) containing 50% silage (DM basis) offered ad libitum. Silage was comprised of either 25:75 (MS) or 75:25 (GS) grass silage:maize silage on a DM basis, without or with additional NDF from chopped straw and soy hulls (+ 47 g NDF/kg TMR DM). A commercial calf pellet was included in the TMR (weeks 1 to 8) or provided via the GreenFeed (weeks 9 to 12). Data (weeks 10 to 12) were analyzed using mixed models for effects of silage, NDF, and their interaction. Cows fed MS had a greater milk yield ($P < 0.01$; 34.5 vs. 29.0 kg/d), milk protein yield ($P < 0.001$; 1076 vs. 926 g/d), DMI ($P < 0.001$; 24.6 vs. 19.3 kg/d), lower milk fat concentration ($P < 0.001$; 3.59 vs. 4.19%) and lactose yield ($P < 0.01$; 1540 vs. 1286 g/d), and lower methane yield ($P < 0.001$; 17.7 vs. 24.1 g/kg DMI), compared to GS. Added NDF increased methane production (410 vs. 461 g/d) and yield (16.5 vs. 18.9 g/kg DMI) when MS was fed, but not GS (460 g/d and 24.0 g/kg DMI, respectively), as indicated through a silage by NDF interaction ($P < 0.10$). Effects of silage type and NDF on methane emissions may be attributable to changes in rumen digesta dynamics, including rumen outflow and retention time, and warrants further investigation.

Key Words: methane, dairy cows, forage NDF

1750 (T363) Changes of rumen methanogen diversity associated with different types of forage and protein in diets. X. W. Wang, J. Q. Wang*, D. P. Bu and S. G. Zhao, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

The objective of this study was to compare the methanogenic community and number in the rumen of dairy cows fed with different types of forage and protein in diet. Forty-eight healthy Chinese Holstein dairy cows were randomly assigned into three groups according to milk yield and day in milking. The diets in three treatments were as follows: MF (alfalfa and corn silage, soybean meal), CSA (corn stover, soybean meal), CSB (corn stover, cottonseed and rapeseed meal). The cows were fed with different diets (MF, CSA, CSB) for 91 days. Rumen fluid samples were collected before and after feeding using stomach-tube on d 91. Mothur software was used to assign clones to operational taxonomic units (OTUs) based on a 94% sequence identity cutoff. The results showed that the copy number of total methanogen of CSA was greater than that of CSB ($P = 0.049$). However, there was no difference between CSA and MF ($P = 0.67$). A total of 739 clones isolated from six methanogen mcrA gene clone libraries (samples from MF, CSA and CSB groups before or after feeding) were assigned to 25 species-level OTUs. The average OTU coverage of clone libraries was 96% (from 95% to 97.6%). Libshuff analysis showed methanogenic community of CSA and CSB, MF and CSA were different ($P = 0.03$ and $P = 0.04$, respectively). MF (2.08) and CSB (2.24) had lower diversity of methanogen based on Shannon index, compared with CSA (2.31). Additionally, Rumen cluster C (RCC, 73.2%) and *Methanobacteriales* (26.3%) were the predominant methanogenic archaea in the rumen. However, OTU10 were only found in CSA and CSB, and OTU20 only in MF. Meanwhile, OTU11 was only found in CSA and MF, while OTU21 only in CSB. Taxonomy analysis showed that OTU10, OTU20, OTU11 and OTU21 were closely related to *Candidatus methanomethylophilus alvus Mx1201* (83%), *Thermoplasmatales archaeon BRNA* (100%), *Methanobrevibacter ruminantium M1* (94%) and *Methanomassiliicoccus luminyensis B10* (78%), respectively. In conclusion, soybean diet could promote the number of total methanogen and increase the diversity of methanogen compared with rapeseed diet in rumen, and the diet with corn straw had higher diversity than the alfalfa and corn silage diet.

Key Words: methanogen, forage, protein

1751 (T364) Effect of cashew nut shell liquid on lactation performance and rumen methane production in dairy cows. A. F. Branco[1], F. Giallongo*[2], T. Frederick[2], H. Weeks[2], J. Oh[2] and A. N. Hristov[2], *[1]Universidade Estadual de Maringá, Paraná, Brazil, [2]Department of Animal Science, The Pennsylvania State University, University Park*

Technical cashew nut shell liquid (CNSL) is a by-product of the cashew nut industry in tropical countries, and is known to exhibit a wide range of biological activities, including inhibitory effect against gram-positive bacteria. This study was conducted to investigate the effects of CNSL (73.3% cardanol, 16.4% cardol, and 3.0% metilcardol) on DMI, milk yield and composition, rumen fermentation and CH_4 and CO_2 production, and nutrient digestibility in dairy cows. Eight multiparous Holstein cows (DIM, 140 ± 14 d; BW, 669 ± 47.8 kg) were used in a crossover design trial with two, 21-d periods. The TMR was based on corn silage and alfalfa haylage, and was formulated to meet or exceed the NE_L and metabolizable protein requirements of the cows (NRC, 2001). The diet contained (DM basis): 15.5% CP, 32.0% NDF, and 1.53 Mcal/kg NE_L. Treatments were: control (no CNSL supplementation), or 30 g/cow/d CNSL. The daily dose of CNSL was mixed with about 2 kg of TMR and top-dressed. Dry matter intake (average 26.6 ± 1.0 kg/d), 3.5% FCM (38.8 ± 1.6 kg/d), and milk composition (fat 3.32 ± 0.28% and true protein 3.09 ± 0.05%) were not affected by CNSL. Milk yield was numerically increased ($P = 0.13$) by CNSL (40.9 kg/d) compared with the control (39.0 kg/d). Rumen CO_2 production, measured using GreenFeed (C-Lock Inc., Rapid City, SD), was

not affected by CNSL. Compared with the control, CNSL numerically decreased (P = 0.12) rumen CH_4 production (534 vs. 505 ± 39.6 g/cow/d, respectively) and CH_4 emission intensity (P = 0.16; 13.3 vs. 12.3 ± 1.05 g/kg milk) and tended to decrease (P = 0.08) CH_4 production per kg of DMI (20.3 vs. 19.1 ± 0.83 g/kg). CNSL did not affect total tract apparent digestibility of nutrients, except NDF digestibility tended to be increased compared with the control (P = 0.09; 36.8 vs. 34.2 ± 1.47%, respectively). Total urinary N, urea N, and urinary purine derivatives excretions were not affected by treatment. MUN concentration was numerically increased (P < 0.13) in cows receiving CNSL (8.57 vs. 7.50 ± 0.62 mg/dL, respectively). Plasma urea and glucose concentrations were not affected by CNSL. In this study, CNSL tended to decrease rumen CH_4production per kg DMI and numerically increased milk yield without affecting DMI in dairy cows.

Key Words: cashew nut shell liquid, methane, dairy cow

1752 (T365) Metabolism of dairy cows as affected by dietary starch level and supplementation with monensin during early lactation. M. M. McCarthy*[1], T. Yasui[1], C. M. Ryan[1], S. H. Pelton[1], G. D. Mechor[2] and T. R. Overton[1], *[1]Cornell University, Department of Animal Science, Ithaca, NY, [2]Elanco Animal Health, Greenfield, IN*

The objective of this study was to evaluate the impact of dietary starch level and monensin (M) on metabolism of dairy cows during early lactation. Primiparous (n = 21) and multiparous (n = 49) Holstein cows were fed high starch (HS; 26.2% starch, 34.3% NDF, 22.7% ADF, 15.5% CP) or low starch (LS; 21.5% starch, 36.9% NDF, 25.2% ADF, 15.4% CP) TMR beginning at parturition until 21 DIM with a topdress pellet containing 0 or 450 mg/d M in a completely randomized design with a 2 × 2 factorial arrangement of treatments. Prior to parturition all cows were fed a common controlled energy diet with daily topdress of either 0 or 400 mg/d M consistent with postpartum treatment. Postpartum blood samples were collected 3× per wk and liver biopsies were taken on d 7 ± 4. Cows fed HS had higher plasma glucose (57.5 vs. 53.9 mg/dL; P = 0.003) and insulin (0.26 vs. 0.19 ng/mL; P = 0.008), and lower NEFA (533.1 vs. 696.6 μEq/L; P = 0.002) than cows fed LS. Cows fed LS had elevated BHBA during 11 to 21 DIM compared to cows fed HS (starch × d; P = 0.04). There was no effect of M on postpartum plasma NEFA. Cows fed M had higher plasma glucose compared to controls (58.1 vs. 53.3 mg/dL; P < 0.001) which was driven by a M × parity interaction in which heifers fed M had greater plasma glucose concentrations than controls (62.0 vs. 54.2 mg/dL; P = 0.008). Cows fed M had lower plasma BHBA compared to controls (10.08 vs. 12.66 mg/dL) which was contributed to by a M × parity interaction in which heifers fed M had lower BHBA concentrations than controls (10.11 vs. 13.99 mg/dL; P = 0.03). There was no effect of starch treatment on overall liver triglyceride content. Heifers fed M had increased liver triglyceride content compared to control heifers and cows fed M had decreased liver triglyceride content compared to control cows (M × parity; P = 0.05). Cows fed LS with M had higher liver glycogen content than cows fed the LS without M, with no effect of M treatment for cows fed HS (starch × M; P = 0.008). Overall, animals fed HS postpartum and M throughout the transition period exhibited improvements in energy metabolism during early lactation.

Key Words: starch, monensin, metabolism

1753 (T366) Effect of dietary monensin supplementation and amino acid balancing on lactation performance by dairy cows. A. L. Hagen*[1,2], L. F. Ferraretto[1], R. D. Shaver[1] and R. Martin[2], *[1]University of Wisconsin, Madison, [2]Vita Plus Corporation, Madison, WI*

A continuous-lactation experiment was conducted to evaluate the effect of dietary monensin supplementation and amino acid balancing (Lysine and Methionine) on milk yield, composition, component yields, and feed conversions (kg actual or component-corrected milk/kg DMI). Multiparous (n = 96) and primiparous (n = 32) Holstein (n = 112) and Holstein × Jersey cross-bred (n = 16) cows were stratified by breed, parity, and DIM (104 ± 39 at trial initiation) and randomly assigned to 16 pens of 8 cows each. Pens were randomly assigned to 1 of 4 treatments in a 2 × 2 factorial arrangement of treatments: control (CN; no monensin or amino acid balancing), amino acid balanced (AA), CN plus monensin (CNMN), or AA plus monensin (AAMN) for a 2-wk covariate period with cows fed a common non-experimental diet followed by a 10-wk treatment period with cows fed their assigned treatment diet. The TMR contained on average (DM basis) corn silage (37.5%), alfalfa silage (23%), and concentrate mixture (39.5%). The AA and AAMN treatments were supplemented with blood meal and a ruminally-protected Methionine source (Ultramet, Vita Plus Corp.; contains MetaSmart, Adisseo) to achieve a 3:1 Lysine:Methionine ratio in the metabolizable protein. The MN and AAMN treatments were formulated using Rumensin 90 (Elanco Animal Health) to provide a monensin intake of 540 mg/cow/d. Data were analyzed using Proc Mixed in SAS with covariate, monensin, amino acids, monensin x amino acids, week, and treatment x week interactions as Fixed effects and pen within treatment as a Random effect. DMI was reduced by monensin (26.6 vs 28.1 kg/d; P < 0.01). Milk yield was unaffected (P > 0.10) by treatment. Actual milk feed conversion was greater for cows fed monensin (1.82 vs. 1.73 kg milk/kg DMI; P = 0.03). Milk protein percentage and yield were increased by amino acids (3.16% vs. 3.09% [P < 0.01] and 1.53 vs. 1.50 kg/d [P = 0.03]), respectively. Component-corrected feed conversions were greater (P < 0.05) for cows fed diets containing monensin. Monensin × amino

acid interactions were not ($P > 0.10$) detected for any of the parameters measured. Dietary monensin supplementation increased feed conversions, while milk protein percentage and yield were greater for cows fed the amino acid balanced diets.

Key Words: monensin, amino acids, dairy cows

1754 (T367) Effects of beta-extract of *Humulus lupulus* (hops) on fermentation by rumen microbes in continuous culture. S. W. Fessenden*, I. J. Salfer and M. D. Stern, *University of Minnesota, Saint Paul*

Beta-acids in hops (*Humulus lupulus*) have been shown to exhibit selective bacteriostatic properties toward Gram-positive and hyper-ammonia producing bacteria in pure and co-culture. Previous work with whole or ground hops in batch culture fermentations with rumen microbes demonstrated promising results toward altering microbial output, however confounding factors such as additional fermentable substrate and presence of condensed tannins in hops can be difficult to control. Use of hop beta-acid extract can eliminate major confounding factors and improve consistency of administration. The objective of this experiment was to evaluate effects of beta-acid extract from hops on microbial fermentation in continuous culture. Eight dual-flow continuous culture fermenters were used in two consecutive 10-d periods consisting of 7 d of adaptation followed by 3 d of sampling. A basal diet containing 44% corn silage, 14% alfalfa hay, 13% ground corn, 11% protein mix, 10% corn gluten feed, 5% cottonseed, and 3% liquid vitamin and mineral supplement on a DM basis was provided to the fermenters at a rate of 75 g of DM/L of fermenter volume/d. Hop beta-extract (BE) was added daily to the artificial saliva to supply 0, 600, 1200, or 1800 mg of β-acids/kg of diet DM/day. Effluents from sampling days were composited by fermenter within period, resulting in 4 reps/treatment. Beta extract inclusion had no effects on DM, OM or fiber digestion ($P > 0.05$). Volatile fatty acid production and N metabolism were not affected by BE inclusion ($P > 0.05$). Mean and maximum fermentation pH tended ($P = 0.09$) to increase linearly with increasing levels of BE inclusion. Time spent above pH 6.2 tended to increase linearly with greater BE inclusion ($P = 0.08$), while time spent between pH 5.8 and 6.2 tended to decrease linearly ($P = 0.07$). Changes in pH were less than biologically relevant levels. Increasing concentration of BE had very limited effects on fermentation measurements by rumen microbes using continuous culture fermenters.

Key Words: continuous culture, hops, beta-acids, rumen

1755 (T368) Evaluation of Celmanax SCP on lactational performance and ruminal fermentation of Holstein dairy cows fed corn silage based diets with a moderate starch content. H. M. Dann*[1], P. Ji[1], K. W. Cotanch[1], C. S. Ballard[1], R. J. Grant[1] and C. C. Elrod[2], *[1]William H. Miner Agricultural Research Institute, Chazy, NY, [2]Vi-COR, Inc., Mason City, IA*

Primiparous ($n = 21$) and multiparous ($n = 39$) Holstein cows averaging 123 ± 28 (SD) days in milk were used in a randomized complete block design (RCBD) study to evaluate the effect of supplemental yeast culture plus enzymatically hydrolyzed yeast cell wall (Celmanax SCP; Vi-COR, Mason, City, IA) on lactational performance and ruminal fermentation. Following a 2-wk covariate period with a yeast-free diet, cows (20/treatment) were fed a diet supplemented with 0, 3, or 5 g of Celmanax SCP per day for a 4-wk treatment period. The diet contained 30.8% bmr corn silage, 16.2% corn silage, 9.7% haycrop silage, and 43.3% concentrates with a nutrient content of 16.5% crude protein, 36.3% neutral detergent fiber, and 24.3% starch. Cows were fed individually, housed in freestalls, and milked 3× daily. Dry matter intake (DMI) and milk yield were measured daily and milk composition was measured weekly. Fifteen ruminally cannulated cows (5/treatment) were sampled during the last week of the covariate and treatment periods for ruminal pH (72-h period) and volatile fatty acids (VFA; 24-h period). Data from wk 3 and 4 of the treatment period were analyzed as a RCBD by ANOVA using the MIXED procedure of SAS. Least squares means were adjusted using data from the covariate period. On average, cows ate 27.3 kg DMI/d and produced 45.5 kg milk/d containing 3.88% fat and 3.21% true protein. There was a quadratic effect of supplementing Celmanax SCP on feed efficiency with feed efficiency highest at 3 g/d. Ruminal pH averaged 6.05 over a 24-h period with 308 min/d below 5.8. Celmanax SCP supplementation linearly increased the concentration of total VFA and acetate with no effect on propionate. Supplementation of Celmanax SCP improved feed efficiency potentially through changes in ruminal fermentation.

Key Words: yeast culture, dairy cow, lactational performance

Table 1755.

Item	0 g/d	3 g/d	5 g/d	SE	Linear *P*	Quadratic *P*
DMI, kg/d	27.4	27.1	27.4	0.2	0.87	0.20
Milk, kg/d	45.3	45.9	45.4	0.4	0.82	0.36
Solids-corrected milk, kg/d	44.8	45.4	44.6	0.6	0.80	0.33
Fat, %	3.88	3.90	3.86	0.05	0.78	0.54
True protein, %	3.23	3.20	3.20	0.02	0.35	0.69
Milk/DMI	1.66	1.70	1.66	0.01	0.82	0.01
SCM/DMI	1.64	1.69	1.63	0.02	0.87	< 0.01
Ruminal pH	6.11	6.02	6.03	0.08	0.38	0.70
Total VFA, m*M*	128.6	138.2	141.9	3.7	0.01	0.72
Acetate, m*M*	71.0	76.2	79.9	2.0	< 0.01	0.94
Propionate, m*M*	27.0	29.9	29.4	1.3	0.17	0.37

1756 (T369) Effects of *Bacillus subtilis* and yeast cell wall on diarrhea incidence and immune function of dairy calves. J. Freitas*, *University of Parana, Palotina, Brazil*

The effects of *Bacillus subtilis* spores and spray-dried yeast cell wall (YCW) on health of dairy calves in the first 60 d of age were evaluated using 30 animals in three treatments. In control treatment, dairy calves received 8 liter of milk/day, after the 2nd day of live and a 20% pellet ration fed "ad libtum", in treatment 2 the calves received the same ration of treatment 1 plus $3x10^9$ viable spores/calf/d of *Bacillus subtilis* (Calpis Co. Ltda, Tokyo, Japan), in treatment 3 it was offered treatment 2 + 4 g/calves/d of YCW (Alltech of Brazil, Brazil). The *Bacillus subtilis* spores and YCW were mixed with milk and fed directly to the calves. The animals were housed in individual pens, with free access to water, starter feed and milk (give three times a day) until weaning that occurs on 9th week of life. Fecal consistency (FC) was scored as 1 when firm, 2 when soft or of moderate consistency, 3 when runny or mild diarrhea, and 4 when watery and profuse diarrhea. The FC 1 and 2 were considered no diarrhea. The supplementation with *Bacillus subtilis* tended ($P = 0.08$) to increased number of calves without diarrhea (Table 1756). Dairy calves feeding with probiotic and YCW showed higher rectal temperature. However, there is no difference ($P > 0.05$) in the levels of serum *immunoglobulin* G (IgG). The use of *Bacillus subtilis* reduced diarrhea incidence of pre-weaning calves without effects on serum immunoglobulin levels.

Key Words: dairy calves, probiotic, immune function

Table 1756.

	Control	*B. subtilis*	*B. subtilis* +EPL	SEM	*P* Treat
RT mean[1]	38.71	38.75	38.87	0.039	0.02
RT % > = 39°C	26.58	28.44	36.81	3.7	0.14
FC < 3 (no diarrhea)[1]	25.3	33.20	27.80	-	0.08
FC < 3 (%)	61.76	75.22	68.61	-	0.34
IgG 20 d (mg mL^{-1})	25.50	21.00	24.38	-	0.51
Average IgG 20- 60 d (mg mL^{-1})	17.48	15.61	17.06	1.274	0.55
Weight weaning (kg)	77.55	81.60	78.20	3.102	0.61

[1] Rectal temperature, number of observation.

[2] Fecal consistency

1757 (T370) Effects of *Bacillus subtilis* and yeast cell wall on diarrhea incidence and immune function of dairy calves. J. A. Freitas*[1], V. Souza[2], J. C. De Souza[3], C. Nozawa[4] and P. Pinto[5], *[1]University of Parana, Palotina, Brazil, [2]University of Sao Paulo, Piracicaba, Brazil, [3]University of South of Mato Grosso, Aquidauana, Brazil, [4]University of Londrina, Londrina, Brazil, [5]University Federal of Parana, Palotina, Brazil*

The effects of *Bacillus subtilis* spores and spray-dried yeast cell wall (YCW) on heath of dairy calves in the first 60 d of age were evaluated using 30 animals in three treatments. In control treatment, dairy calves received 8 liter of milk/day and a 20% pellet ration, in treatment 2 calves received the same ration of treatment 1 plus $3x10^9$ viable spores/calf/d of *Bacillus subtilis* (Calpis Co. Ltda, Tokyo, Japan), in treatment 3 it was offered treatment 2 + 4 g/calves/d of YCW). *Bacillus subtilis* spores and YCW were mixed with milk and fed to calves. The animals were housed in individual pens, with free access to water, starter feed and milk (8 L, three times a day) until weaning. Fecal consistency (FC) was scored as 1 when firm, 2 when soft or moderate consistency, 3 when runny or mild diarrhea, and 4 when watery and profuse diarrhea. The FC 1 and 2 were considered no diarrhea. The supplementation with *Bacillus subtilis* tended ($P = 0.08$) to increased number of calves without diarrhea (Table 1757). Dairy calves feeding with probiotic and YCW showed higher rectal temperature. However, there is no difference ($P > 0.05$) in the levels of serum immunoglobulin G (IgG). The use of *Bacillus subtilis* reduced diarrhea incidence of pre-weaning calves without effects on serum immunoglobulin levels.

Key words: dairy calves, immune function, probiotic.

Table 1757. Rectal temperature (RT), feces consistence (FC), serum imunoglobulin at 20 day (mg mL^{-1}), average of serum IgG (20-60 day) and weaning weight (kg) for Holstein calves receiving B.subtilis and yeast

	Control	*B. subtilis*	*B. subtilis* +EPL	SEM	*P* Treat
RT mean[1]	38.71	38.75	38.87	0.039	0.02
RT % > = 39°C	26.58	28.44	36.81	3.7	0.14
FC < 3 (no diarrhea)[1]	25.3	33.2	27.8	-	0.08
FC < 3 (%)	61.76	75.22	68.61	-	0.34
IgG 20 d (mg mL^{-1})	25.5	21	24.38	-	0.51
Average IgG 20- 60 d (mg mL^{-1})	17.48	15.61	17.06	1.274	0.55
Weaning weight (kg)	77.55	81.6	78.2	3.102	0.61

1758 (T371) Effects of different doses of *Bacillus subtilis* Natto on in vitro rumen fermentation parameters.

J. Li[1,2,3], D. P. Bu[2], J. Q. Wang[*1,2], P. Sun[2] and F. D. Li[3], *[1]Heilongjiang Bayi Agricultural University, Daqing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [3]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China*

This experiment was conducted to investigate the effects of different doses (0 (contrl), 0.2×10^{11}cfu/ml (BSL),1×10^{11}cfu/ml (BSM), 5×10^{11}cfu/ml (BSH)) of *Bacillus subtilis Natto* culture (BSN) on rumen fermentation in vitro. Ruminal fluid was collected from three lactating Holstein dairy cows (BW = 558 ± 10 kg, DIM = 153 ± 16 d) fed diets contained (DM basis) Chinese wildrye (3.7%), Alfalfa hay (28.4%), Corn silage (26.7%), Corn (22.6%), Soybean meal (11.8%), Cottonseed fuzzy (5.1%), $CaHPO_4$ (0.6%), NaCl (0.5%), Premix (0.6%). Diets were mixed with phosphate buffer (1:2), incubated (90ml) anaerobically at 39°C for 0h, 12h, 24h, 36h and shaken at 50rpm. Each substrate (500mg DM basis) which had same concentrate mixture with donors was added to. Four sets of bottles were sealed anaerobically under CO_2 atmosphere with butyl rubber stoppers and capped with aluminum. One set (0h) were sampling immediately after mixed, other sets were incubated 12h, 24h, 36h respectively. Each set contained four levels of supplements, and for each level, three bottles were incubated. Statistical analysis was carried out by ANOVA (GLM) using SAS (SAS9.2). Medium pH was unaffected (P = 0.61) by BSN in all treatments, ammonia-N tended to increase linearly with increasing BSN dose ($P < 0.01$). Compared with the control, the molar proportion of acetate(46.66 vs 57.32, 60.96 and 68.17, $P < 0.01$), propionate (19.23 vs 22.88, 24.48 and 29.98 linear, $P < 0.01$), iso-butyrate (0.83 vs 2.18, 2.50 and 3.70, $P < 0.01$), iso-valerate (1.55 vs 4.50, 5.02 and 7.70, $P < 0.01$), valerate (1.52 vs 4.38, 5.04 and 6.89, $P < 0.01$) and total VFA (79.93 vs 102.77, 110.12 and 131.03, $P < 0.01$) was enhanced significantly with increasing concentrations of BSN. The molar proportion of butyrate of BSL treatment was increased ($P < 0.05$) and BSM and BSH treatment were increased significantly ($P < 0.01$). The molar proportion of acetate:propionate was increased ($P < 0.05$) in BSL and BSM treatment compared with control, however, decreased significantly in BSH treatment ($P < 0.01$). The results indicated that the *Bacillus subtilis Natto* culture can stimulated in vitro fermentation by increase the molar proportion of VFA and change the rumen fermentation type by change the molar proportion of acetate:propionate, and the diets should consist of a minimum of 10^{10}cfu/g (DM) of BSN to make sure it's effect.

Key Words: *Bacillus subtilis Natto*, in vitro, rumen fermentation

1759 (T372) An on-farm application of feed probiotics to increase total tract starch digestibility (TTSD) in high producing, lactating dairy cows.

W. L. Braman*, K. A. Bryan and J. E. Kurtz, *Chr. Hansen Animal Health and Nutrition, Milwaukee, WI*

With the increased cost of grains and forages in the USA, dairy producers have turned their attention to the feed efficiency of milk production. Two reviews of starch digestibility in lactating dairy cows have suggested that over 50% of TTSD takes place in the lower digestive tract. Low on-farm starch digestibility contributes to reduced feed efficiency. Several researchers have demonstrated that measuring fecal starch is highly correlated to TTSD in lactating dairy cows. Our previous studies using a dairy feed probiotic (Probios Complete, Chr. Hansen, Inc., Milwaukee, Wisconsin USA) demonstrated increases in TTSD, production performance, and feed efficiency in lactating dairy cows fed high starch + sugar diets (32% and 35%, respectively). To further validate this probiotic research, field trials were conducted to test a similar probiotic, Probios Precise containing 3 strains of *Enterococcus faecium* and live yeast, on fecal starch on farm. Total mixed ration and fecal samples were collected from the same pen at 30-d day intervals for 90 d on 10 commercial dairy farms averaging 2041 cows located in Wisconsin, Texas, New Mexico and Minnesota. Fresh floor fecal samples were collected from at least 20 cows per pen from cows less than 120 d-in-milk. Total mixed rations and fecal samples were analysed by Rock River Laboratories (Watertown, WI). Fecal components including starch (FS), protein, NDF, 120 h-indigestible NDF, fat, and ash (DM basis) were measured. Samples on d 0 were taken prior to adding Probios Precise to each herd's diet which averaged 23.7% starch (DM basis). Subsequent samples taken at 30, 60, and 90 d were analysed to measure the response from the probiotic treatment. The REG procedure of SAS was used to analyse the relationship between days fed Probios Precise and FS. As days fed the probiotic increased, there was a reduction in FS ($R^2 = 0.31$; $P < 0.001$; 5.41, 3.95, 3.09, and 3.04%, respectively for d 0, 30, 60, and 90 sampling times). These results suggest that feeding the probiotic decreased FS confirming earlier trials that indicated certain feed probiotics decreased FS and increased TTSD in early lactation dairy cows. Thus,

supplementing the dairy feed probiotics, Probios Complete and Probios Precise, can be a management tool to decrease FS, increase TTSD, with potential increase in feed efficiency.

Key Words: dairy, probiotics, starch

1760 (T373) Effect of feeding yeast culture (YC) on lactation performance of dairy cows fed diets differing in rumen fermentability. A. L. Dias*, R. A. Azevedo, J. A. Freitas, B. Micai, T. V. Silva, G. C. Gomes, E. S. Ribeiro, L. F. Greco, P. M. Leopoldo Junior and J. E. P. Santos, *Department of Animal Sciences, University of Florida, Gainesville*

Objectives were to evaluate the effect of feeding YC (*Saccharomyces cerevisiae*, Rumen Yeast, ICC, Brazil) on lactation performance of dairy cows fed diets with two concentrations of starch. Fifty-six Holstein cows at 42 d postpartum were blocked by parity and milk production and randomly assigned to 1 of 4 treatments, low starch no YC (22% starch and control; LSC), low starch and YC (22% starch and 15 g/d of YC; LSYC), high starch no YC (28% starch and control; HSC), and high starch with YC (28% starch and 15 g/d of YC; HSYC). The study lasted 13 weeks and milk yield, body weight, and dry matter intake were measured daily. Milk samples were collected weekly to determine concentrations of milk components and somatic cells. Data was analyzed by ANOVA for repeated measures using the MIXED procedure of SAS. Results are presented in Table 1760. Feeding high starch improved yields of milk and milk protein, whereas inclusion of YC improved yields of milk and all milk components regardless of starch in the diet.

Key Words: dairy cow, lactation, yeast culture.

Table 1760. Effect of YC and level of starch on lactation performance of dairy cows

	Treatment					*P*		
Variable	LSC	LSYC	HSC	HSYC	SEM	Starch	YC	Starch x YC
Milk yield, Kg/d	38.7	40.4	40.4	41.7	1.2	0.09	0.09	0.81
3.5% FCM, Kg/d	40.2	41.9	40.3	43.3	1.3	0.57	0.05	0.62
Milk fat, %	3.90	3.84	3.64	3.82	0.09	0.10	0.49	0.17
Fat yield, Kg/d	1.47	1.53	1.43	1.57	0.05	0.96	0.05	0.41
Milk protein, %	2.90	2.84	2.97	3.04	0.05	0.01	0.95	0.12
Protein yield, Kg/d	1.09	1.12	1.16	1.24	0.03	0.01	0.04	0.40
Milk NE_L, Mcal/d	27.2	28.2	27.5	29.4	0.9	0.28	0.04	0.51
Body condition	2.85	3.00	2.89	2.92	0.05	0.70	0.06	0.21

LSC: low starch and no YC; LSYC: low starch and YC; HSC: high starch and no YC; HSYC: high starch and YC.

1761 (T374) Milk fatty acid profile in cows fed red clover or alfalfa based diets differing in rumen-degradable protein supply. M. Leduc*[1], P. Y. Chouinard[1], R. Gervais[1], E. Baumann[1], Y. Lebeuf[1] and G. Tremblay[2], *[1]Université Laval, Québec, QC, Canada, [2]Agriculture and Agri-Food Canada, Soils and Crops Research and Development Centre, Quebec, QC, Canada*

Polyphenol oxidase in red clover silage (RCS) has been shown to reduce lipolysis and consequently protect its constituent fatty acid (FA) against biohydrogenation by ruminal microorganisms. Fatty acid biohydrogenation could be further inhibited by reducing the supply of nitrogen to ruminal bacteria. To compare the effects of RCS and alfalfa silage (AS) fed in diets differing in rumen-degraded protein (RDP) supply on milk FA profile, 8 multiparous Holstein dairy cows (72 ± 17 DIM) were used in a replicated 4×4 Latin square design (21-d periods, 14-d adaptation). Four treatments were compared in a 2×2 factorial arrangement with AS or RCS fed in diets formulated to provide 85% (RDP85) or 100% (RDP100) of calculated RDP requirements. Untreated and heat-treated (AminoPlus) soybean meals were used to adjust dietary RDP. No significant interaction of silage by RDP was observed on milk FA profile ($P > 0.05$). As compared with AS, feeding RCS increased ($P < 0.01$) c9c12c15-18:3 (6.89 vs. 4.26 mg/g fat) and c9c12-18:2 (18.64 vs. 16.50mg/g), but decreased ($P < 0.01$) t11-18:1 (5.87 vs. 6.75 mg/g; $P < 0.01$) and t11c15-18:2 (0.63 vs. 0.82 mg/g) concentrations in milk fat. As compared with AS, feeding RCS increased ($P < 0.03$) milk fat content of iso 13:0 (0.23 vs. 0.21 mg/g), iso 14:0 (1.23 vs. 0.89 mg/g), iso 15:0 (1.46 vs. 1.22 mg/g), iso 16:0 (2.25 vs. 1.84 mg/g), iso 17:0 (1.90 vs. 1.77 mg/g), anteiso 15:0 (4.01 vs. 3.57 mg/g), and anteiso 17:0 (3.58 vs. 3.10 mg/g), but decreased ($P < 0.01$) milk fat content of 11:0 (0.60 vs. 1.32 mg/g), 13:0 (0.98 vs. 1.83 mg/g), 15:0 (10.64 vs. 15.77 mg/g), 17:0 (4.99 vs. 5.87 mg/g), and c9-17:1 (1.65 vs. 2.05 mg/g). The supply of RDP had only minor effects on milk FA with higher concentrations ($P < 0.01$) of iso 13:0, iso 15:0, and iso 17:0 observed with RDP100 (0.23, 1.41, 1.91 mg/g, respectively) as compared with RDP85 (0.21, 1.28, 1.76 mg/g, respectively). In conclusion, cows fed RCS as compared with those fed AS produced milk with greater concentrations of major forage FA (i.e. c9c12c15-18:3 and c9c12-18:2) and lower proportions of intermediates (i.e. t11-18:1 and t11c15-18:2) that are produced during the ruminal biohydrogenation of these FA. Variations in milk fat concentrations of odd and branched chain FA, which are known to be synthesized in the rumen by various microbial populations, may reflect the effect of forage legume species on ruminal fermentation.

Key Words: biohydrogenation, odd and branched chain fatty acids, polyphenol oxidase

1762 (T375) Use of virginiamycin and monensin sodium in diets of confined beef steers. F. R. Camilo[1], A. M. Mobiglia[1], R. K. Grizotto[2], J. A. Alves Neto[3], M. Q. Manella[4], F. D. D. Resende[2], G. R. Siqueira[2] and J. J. R. Fernandes[*5], *[1]Escola de Veterinária e Zootecnia da UFG, Goiânia, Brazil, [2]APTA-Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [3]Universidade Estadual Paulista, Jaboticabal, Brazil, [4]Phibro Animal Health Corporation, Guarulhos, Brazil, [5]Universidade Federal de Goiás, Goiânia, Brazil*

Feed additives are used as tool of nutrition management to enable the supply of high concentrate diets. The association of antibiotics may improve the response of ruminal fermentation manipulation and increase performance. The objective of this study was to evaluate the isolated and combined effects of the virginiamycin (VM) and monensin sodium (MON) in diets of crossbreed steers in feedlot. The animals were kept in feedlot in group pens for 105-d with a 28-d adaptation period. Three hundred and thirty nine 1/2Nellore x 1/2 Guzera beef steers (402.7 ± 1.3 kg of initial BW) were used in a randomized complete block design with 5 treatments and 7 replicates. The blocks were defined by initial BW. Treatments were defined by levels of VM and MON (mg/kg of dry matter) as follows: 30MON; 15VM+30MON; 25VM+30MON; 34VM+ 30MON e 34VM. Animals were fed < *i* > ad libitum < /*i* > twice daily with isonitrogenous and isoenergetic diets, with a 88:12 concentrate:forage (sugarcane bagasse) ratio. Steers were weighed at the beginning, after the adaptation period and at the end of the trial. Data are shown in Table 1762. Dry matter intake (DMI), final BW and average daily gain (ADG) were not affected ($P > 0.05$) by treatments. However, effects ($P < 0.05$) were observed on DMI for percentage of body weight (BW) between 34VM and 25VM + 30 MON, with lower DMI/BW (%) for the intermediate association. The treatment 30 MON showed higher feed efficiency (FE) than 34VM. In conclusion, the MON showed higher FE in relation to VM, however, no effects were observed on treatments with different association levels of feed additives. Supported by Phibro/Minerva/FAPEG.

Key Words: feed additives, feedlot, performance

Table 1762. Performance of beef steers fed with different levels of feed additives

	Treatments					
Variables	30MON	15VM+ 30MON	25VM+ 30MON	34VM+ 30MON	34VM	SEM
Initial BW (kg)	402.7	401.2	402.7	402.4	404.6	1.3
Final BW (kg)	569.2	560.2	563.0	565.3	564.1	3.3
DMI (kg/day)	10.6	10.4	10.4	10.6	10.7	0.1
DMI/BW (%)	2.19^{ab}	2.17^{ab}	2.15^{b}	2.20^{ab}	2.22^{a}	0.02
ADG (kg/day)	1.602	1.527	1.541	1.564	1.531	0.031
FE	0.150^{a}	0.146^{ab}	0.148^{ab}	0.147^{ab}	0.143^{b}	0.002

Different superscripts indicate differences among treatments by t test at 5% of probability

1763 (T376) GLOBAL NETWORK for the development of nutrition-related strategies for mitigation of methane and nitrous oxide emissions from ruminant livestock. A. N. Hristov[*1], E. Kebreab[2], Z. T. Yu[3], C. Martin[4], M. Eugène[4], D. R. Yáñez–Ruiz[5], K. J. Shingfield[6], S. Ahvenjärvi[6], P. O'Kiely[7], C. K. Reynolds[8], K. J. Hammond[8], J. Dijkstra[9], A. Bannink[10], A. Schwarm[11] and M. Kreuzer[12], *[1]Department of Animal Science, The Pennsylvania State University, University Park, [2]University of California, Davis, Davis, [3]The Ohio State University, Columbus, [4]INRA, Clermont-Ferrand, France, [5]Estacion Experimental del Zaidin, CSIC, Granada, Spain, [6]MTT Agrifood Research, Animal Production Research, Jokioinen, Finland, [7]7Animal and Grassland Research and Innovation Centre, Teagasc, Dunsany, Ireland, [8]University of Reading, Reading, United Kingdom, [9]Animal Nutrition Group, Wageningen University, Wageningen, Netherlands, [10]Animal Nutrition, Wageningen UR Livestock Research, Lelystad, Netherlands, [11]ETH Zurich, Institute of Agricultural Sciences, Zurich, Switzerland, [12]ETH Zurich, Zurich, Switzerland*

Ruminant husbandry is a major source of anthropogenic greenhouse gases (GHG). There is a large body of existing nutrition-related GHG and ammonia (NH_3) mitigation data that are not well organized. The main objective of the GLOBAL NETWORK consortium, a 4-yr project funded through The Joint Programming Initiative on Agriculture, Food Security and Climate Change (FACCE-JPI), is to accumulate and analyze ruminant GHG mitigation data. The specific goals of this collaborative project are to: (1) Create, update, and expand animal and feed databases for the mitigation of enteric methane (CH_4); (2) Gain understanding of the contribution of genetic and microbial factors to the variation in enteric CH_4 production, digestion, and nutrient utilization; (3) Validate markers of enteric methanogenesis for the development and monitoring of CH_4 mitigation strategies in ruminants; (4) Create, update, and expand a database of mitigation strategies aimed at improving dietary N utilization and lowering N excretion and decreasing NH_3 and nitrous oxide (N_2O) emissions from manure; (5) Develop Standard Operating Procedures (SOP) and guidelines for conducting and assessing data from in vitro and in vivo studies designed to evaluate nutritional strategies for mitigation of CH_4, NH_3, and N_2O emissions; (6) Develop new and evaluate existing models for predicting CH_4 emission and N excretions under various nutritional, animal, and farm management scenarios; and (7) Identify and recommend CH_4, NH_3, and N_2O mitigation technologies that are both practical and feasible for implementation in various ruminant livestock production systems. These activities will be integrated with those of the "Network and Database on Feed and Nutrition in Relation to GHG Emissions" (FNN; http://animalscience.

psu.edu/fnn), which is an activity of the Livestock Research Group (LRG) of the Global Research Alliance (GRA) on Agricultural GHG. The newly created GLOBAL NETWORK consortium intends to fill important knowledge gaps and provide the much needed expert recommendations for future research priorities, methodologies, and science-based GHG mitigation solutions to governments and non-governmental organizations, advisory/extension networks, and the ruminant livestock sector. Animal scientists with an interest in GHG mitigation research are encouraged to contact members of the consortium to identify areas and opportunities for future collaboration and contribution of data.

Key Words: livestock, greenhouse gas, mitigation, database

1764 (T377) Effect of oat grain variety on methane emissions from mature sheep.

J. M. Moorby*, H. R. Fleming and S. A. Cowan, *Aberystwyth University, Aberystwyth, United Kingdom*

Methane emissions from ruminants are driven by DM intake and feeds characteristics such as oil concentration and OM fermentability; an oat breeding program at Aberystwyth aims to breed new varieties for livestock feeding that help reduce pollutant emissions by manipulating nutritional characteristics. To study the effect of feeding different varieties of oat grains on enteric methane emissions from sheep, eight mature barren ewes, four each of two breeds (Welsh Mountain and Welsh Mule; mean LW 41.5 ± 1.93 and 64.9 ± 1.46 kg respectively) were fed diets comprising ryegrass silage and oats in a 1:1 ratio (on a DM basis) in a Latin square changeover design experiment. Feed was offered at rates (i.e. restricted) designed to supply ME requirements for maintenance (according to AFRC 1992 guidelines). The same grass silage was used throughout, fed with 1 of 4 oat grain treatments: A) a husked oat, cv Balado, B) a naked oat, cv Racoon, C) a new breeding line husked oat, NewLine, and D) a 1:1 (fresh) mix of B and C, Mix. Each of the 4 periods of the experiment consisted of 14 days for diet adaptation and 6 days for measurements of feed intake, whole tract apparent diet DM digestibility, and methane emission. Methane emissions were measured for each animal for 3 days in open-circuit respirations chambers. There were no significant sheep breed effects on measurements except for LW and therefore DMI (grand mean 637 g/d). There were significant effects of oat variety on methane emissions, both in g/d and when expressed in relation to intake and metabolic LW. Differences in methane emissions from the sheep are likely to be related to differences in fiber and oil concentrations of the oat grains. In conclusion, the Mix treatment composition is a good breeding target for new varieties of oats.

Key Words: sheep, oats, methane

Table 1764.

	Oat treatment					
	Balado	Racoon	New-Line	Mix	SED	*P*
Oat CP, % DM	10.5	10.5	10.9	10.7	-	
Oat NDF, % DM	23.1	6.1	9.5	6.0	-	
Oat total oil, % DM	5.6	10.2	4.9	7.5	-	
CH_4, g/d	15.2[a]	14.7[a]	17.2[b]	14.7[a]	0.60	0.002
CH_4/DMI, g/kg	24.1[ab]	23.0[a]	26.9[b]	23.9[a]	0.96	0.003
CH_4/dig. DMI, g/kg	3.11[ab]	2.88[a]	3.45[b]	2.85[a]	0.227	0.001
$CH_4/LW^{0.75}$, g/kg	0.78[a]	0.74[a]	0.88[b]	0.75[a]	0.031	0.002
CH_4E/GE intake, %	7.3[ab]	6.9[a]	8.1[b]	6.9[a]	0.29	0.003

Values in rows with different superscripts differed significantly, $P < 0.05$.

1765 (T378) Effect of acetate, propionate and pH on aqueous concentration and gaseous methane and hydrogen production in continuous culture.

S. Ghimire*[1], B. A. Wenner[2], R. A. Kohn[3], J. L. Firkins[2] and M. D. Hanigan[1], *[1]Virginia Polytechnic Institute and State University, Blacksburg, [2]The Ohio State University, Columbus, [3]The University of Maryland, College Park*

Four continuous culture fermenters were used to determine the effect of varying volatile fatty acid concentrations and pH on hydrogen and methane production. The experiment constituted 4 treatments applied in 4 periods. Treatments were: control, 20 mmol/d acetate infusion (INFAC), 7 mmol/d propionate infusion (INFPR), and low pH (LOWPH). In LOWPH buffer flow was adjusted to lower pH by 0.5 units compared to control. The fermenters were fed 40 g of a pelleted 50:50 alfalfa: concentrate diet once daily. One week of adjustment occurred each period before sampling. Filtered liquid effluent (20 ml) from the fermenters was sampled at 0, 2, 4, 6, 8, 12, 16, and 22 h after feeding for measurement of aqueous hydrogen and methane concentrations. Daily cumulative gas production and hourly production rate were analyzed for headspace methane and hydrogen. The effects of treatments are shown in Table 1765. Headspace methane production was lower ($P < 0.05$) in LOWPH compared to other treatments. Methane production rate in LOWPH was lower ($P < 0.05$) than other treatments from 2 to 9 h, and was lower ($P < 0.05$) compared to INFAC and INFPR at 10 h. Aqueous methane concentrations were higher ($P < 0.05$) in LOWPH compared to control and INFAC, whereas in INFPR it was higher than control ($P < 0.05$). The differences were significant ($P < 0.05$) at 16 h. Headspace hydrogen production was higher in INFAC, followed by INFPR and control, and LOWPH ($P < 0.05$). Production rate of headspace hydrogen from INFAC was higher ($P < 0.05$) than others from 2 to 7 h. The effect of treatment on aqueous hydrogen concentration was not significant ($P > 0.05$). These results reveal that headspace methane and hydrogen was lowered by low pH, and acetate infusion increased the headspace hydrogen in a continuous culture. Aqueous hydrogen was unaffected

by the treatments, whereas aqueous methane was increased by low pH and propionate infusion.

Key Words: fermenter, hydrogen, methane

Table 1765. Effect of low pH, acetate infusion, and propionate infusion on gaseous production and aqueous concentration of methane and hydrogen in continuous culture

Gas production and concentration	Control	INFAC[1]	INFPR[2]	LOWPH[3]	SE	*P*-value
Aqueous methane (uM)	120[a]	130[a,b]	176[b,c]	187[c]	18	0.02
Headspace methane (umol/d)	9775[a]	11266[a]	9998[a]	5823[b]	2220	< 0.001
Aqueous hydrogen (uM)	2.25	1.74	2.01	1.47	0.31	0.35
Headspace hydrogen (umol/d)	65.6[a]	142.6[b]	76.9[a,c]	18.8[d]	29.7	< 0.001

[1] INFAC: Acetate infusion (20mmol/d).

[2] INFPR: Propionate infusion (7mmol/d).

[3] LOWPH: buffer adjusted to lower pH by 0.5 units.

1766 (T379) Ruminal parameters of confined steers fed with diets containing virginiamycin and monensin sodium. F. R. Camilo[1], A. M. Mobiglia[1], G. F. Berti[2], N. M. Jerônimo[2], R. K. Grizotto[3], M. Q. Manella[4], F. D. D. Resende[3], G. R. Siqueira[3] and J. J. R. Fernandes[*5], *[1]Escola de Veterinária e Zootecnia da UFG, Goiânia, Brazil, [2]Centro Universitário da Fundação Educacional de Barretos-Unifeb, Barretos, Brazil, [3]APTA- Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [4]Phibro Animal Health Corporation, Guarulhos, Brazil, [5]Universidade Federal de Goiás, Goiânia, Brazil*

Ionophore and non-ionophore antibiotics are known for their abilility to manipulate rumen fermentation and increase efficiency of high concentrate diets. The aim of this trial was to evaluate the effects on ruminal parameters of confined Nellore steers fed with diets using isolated and combined levels of virginiamycin (VM) and monensin sodium (MON). Fifteen Nellore steers (536 kg of BW) with ruminal cannula were used in a randomized complete block design with five treatments and three replicates. The blocks were defined by initial BW. The animals were kept in feedlot in individual pens for 28-d. Ruminal ammoniacal nitrogen (NH_3–N), short-chain fatty acids (SCFA) and ruminal fluid pH were measured before feeding (T0) and 6 and 12 hours after feeding (T6 and T12, respectively). Treatments were defined by levels of VM and MON (mg/kg of dry matter) as follows: 30MON; 15VM+30MON; 25VM+30MON; 34VM+ 30MON and 34VM. Animals were fed ad libitum twice daily with isonitrogenous and isoenergetic diets, with a 88:12 concentrate:forage (sugarcane bagasse) ratio. Data are shown in Table 1767. There were not effects ($P > 0.05$) on NH_3–N concentration between treatments. However, pH and SCFA presented differences in T0 for the treatments, with lower SCFA concentration in 34VM+30MON than in 34VM. Acetate:propionate ratio (A:P) did not show differences ($P > 0.05$) between treatments. In conclusion, the different levels of isolated and combined associations of VM and MON did not affect pH, NH_3–N, SCFA and A:P ratio, except for pH and SCFA measured at T0, when we observed differences between treatments. *Supported by Phibro/Minerva/FAPEG.*

Key Words: feed additives, feedlot, ruminal fermentation

1767 (T380) Ruminal parameters of young Nellore bulls in a feedlot fed Yea-Sacc8417 live yeast, monensin and their combination. J. M. B. Benatti[1], N. M. Geronimo[2], J. A. Alves Neto[1], I. M. de Oliveira[*3], A. D. Moreira[1], C. L. Francisco[4], G. R. Siqueira[3] and F. D. D. Resende[3], *[1]Universidade Estadual Paulista, Jaboticabal, Brazil, [2]UNIFEB, Barretos, Brazil, [3]APTA- Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [4]Universidade Estadual Paulista- FMVZ, Botucatu, Brazil*

The objective of this study was to analyze the ruminal parameters of young Nellore bulls in a feedlot for 109 days. The treatments consisted of a control diet with monensin sodium (27.0 mg kg DM^{-1}), a diet with Yea-Sacc^{8417} live yeast (2.0 g $animal^{-1}$) and a diet with the two additives combined. Diets (10.00% sugarcane bagasse, 73.60% ground corn, 6.40% cottonseed, 6.40% soybean meal, 0.26% corn gluten, 0.79% urea and 2.55% mineral mix) varied only in the inclusion of additives. We used 16 non-castrated Nellore bulls (422.00 ± 80.26 kg) cannulated in the rumen. The experiment was arranged in a completely randomized blocks design (four replicates) as a function of the initial body weight. Data were analyzed by the MIXED procedure of SAS software and means were compared by Fisher's test at 10% significance. The animals were kept in individual pens and were considered the experimental unit. Dry matter intake (DMI) did not differ among the studied diets (9.6 kg DM day^{-1}), and neither did ($P > 0.10$) the digestibility of DM (65.8%). The rate of intake was also not affected ($P > 0.10$) by inclusion of additives, and 90.4% was consumed in the first 12 hours after the 1st feed. Monensin sodium increased ($P = 0.0150$) the selectivity for concentrate (0.8% more concentrate) as compared with the other diets (0.3% more concentrate). Live yeast, alone or combined with monensin, elevated ($P = 0.0420$) the acetate content in the rumen (58.15%) in relation to control diet and the treatment of monensin alone (56.97%). Monensin not combined with yeast reduced ($P = 0.0373$) the acetate-to-propionate ratio in the rumen (1.79) over the other diets (2.05). When supplied separately, the additives monensin sodium and live yeast showed lower values ($P = 0.0345$) for the rumen pH (5.74 and 5.93 for monensin and yeast, respectively) compared with the other

diet (6.07). The combination of the additives live yeast and monensin sodium controlled ($P = 0.0376$) the decrease in the rumen pH 12 hours after the feed (6.08) as compared with the diet with these additives supplied alone. Sodium monensin not combined with live yeast increased ($P = 0.0367$) the daily fluctuations of rumen pH (0.19) in relation to the other treatments (0.10). The monensin reduces the acetate-to-propionate ration and yeast increase the acetate proportion. The use additives live yeast and monensin sodium combined has an additive effect on the rumen pH. *Supported by FAPESP and Alltech.*

Key Words: digestibility, intake, ruminal pH

Table 1767. Ruminal parameters of steers fed with diet containing different levels of feed additives

Treatments	30MON	15VM+-30MON	25VM+-30MON	34VM+-30MON	34VM	SEM
NH_3–N (mg/dL)						
T 0	16.16	16.71	14.96	14.97	17.11	1.1
T 6	16.51	18.23	16.27	19.13	20.80	2.8
T 12	18.46	21.32	19.45	19.03	21.72	3.1
SCFA (mM)						
T 0	105.27ac	113.08ab	97.72bc	93.45c	116.03a	5.6
T 12	148.98	138.60	135.03	139.37	140.74	7.1
A:P ratio						
T 0	3.34	3.48	3.10	3.46	4.03	0.3
T 12	3.30	3.27	3.22	3.58	4.04	0.3
Ruminal pH						
T 0	6.68ab	6.67ab	6.78a	6.85a	6.54b	0.1
T 6	5.94	6.24	6.24	6.23	6.08	0.1
T 12	5.67	5.80	5.88	5.91	5.81	0.1

Different superscripts indicate differences among treatments by t test at 5% of probability

1768 (T381) Optimal ration of combined origanum essential oils to reduce methane emissions under in vitro ruminal fermentation.

A. Castañeda-Correa*[1], A. Corral-Luna[1], F. A. Rodriguez-Almeida[1], L. De la Torre-Saenz[2], R. Silva-Vázquez[3], L. Carlos-Valdez[1], H. Gutiérrez-Bañuelos[4] and O. Ruiz-Barrera[1], *[1]Universidad Autonoma de Chihuahua, Chihuahua, Mexico, [2]CIMAV, Chihuahua, Mexico, [3]CIRENA, Salaices, Mexico, [4]Universidad Autonoma de Zacatecas, Zacatecas, Mexico*

Origanum (*Origanum vulgare*) essential oils (EO; thymol T and carvacol C) have been reported as potential anti-methanogenic additives for dairy cattle rations. An in vitro fermentation trial was conducted to determine the optimal T:C ratio (100:0, 80:20, 60:40, 40:60, 80:20 and 0:100) in an EO combined dose of 100 mg/L added to a total mixed ration (TMR; 65:35 concentrate:forage). The incubation was carried out in 60 mL flasks in triplicate for each T:C ratio and the control. The in vitro buffered solution was prepared anaerobically. Inside of anaerobic chamber 20 mL of buffered medium and 10 mL of rumen fluid were dispensed in each flask containing 200 mg of the ground substrate. The flasks were sealed with butyl rubbers and aluminum seals and incubated at 39 °C for 24 h with a constant shaking at 150 rpm. After 24h of incubation, gas production was recorded and sampled to determine its composition and 5mL of liquid content were taken from each flask and preserve with metaphosphoric acid to determine VFA. Gas composition and VFA concentration were determined by chromatography. Dry matter digestibility (IVDMD) was determined by the DAISY procedure. Data were analyzed by PROC GLM of SAS (SAS, 1992) by a complete randomized design considering the EO ratio as sole effect. Adding EO to the ration did reduce total gas production ($P < 0.0001$) in all C:T ratios (Table 1768). Also, methane production was decreased ($P < 0.05$) by the EO in all treatments. However, the 80:20 T:C ratio showed the greatest reduction ($P < 0.0001$). Total VFA concentration and IVDMA was not affected ($P > 0.70$ and 0.93, respectively) by EO addition. The molar proportion of acetate was decreased by the 60:40 T:C ratio. These results suggest that 80:20 T:C ratio has the best potential to decrease methane emissions of dairy cattle without DM digestibility decreases.

Key Words: thymol, carvacrol, methane

Table 1768.

Treatment (T:C ratio)	GAS (ml/200 mg DM)	Reduction (%)	Methane (ml/200 mg DM)	Reduction (%)
Control	36	–	7.55	–
100:0	32	11	6.48	14
80:20	28	22	5.84	23
60:40	32	11	6.73	11
40:60	35	3	7.29	3
20:80	30	17	6.40	15
0:100	32	11	6.51	14

1769 (T382) Effect of phytogenic feed additives on performance parameters and health of bull calves under commercial conditions.

C. Schieder*[1], T. Steiner[1] and M. Friedrichkeit[2], *[1]BIOMIN Holding GmbH, Herzogenburg, Austria, [2]Commercial farm, Reisenberg, Austria*

The increased emphasis on achieving a good health status for adequate growth rates in calves and the ban on sub-therapeutic antibiotics in the European Union in 2006 have resulted in growing interest in alternative feeding strategies. Phytogenic feed additives (PFA) exert strong anti-inflammatory, anti-oxidative and anti-microbial activities, and all of which offer potential benefits for improving performance and preventing intestinal disorders. The aim of the study was to evaluate the efficacy of PFA on growth performance, feed-to-gain ratio and number of medical treatments in commercial calves. During the trial period of 56 days, 53 calves with an average initial body weight of 93.2 kg were assigned to either the control ($n = 26$) or treatment group ($n = 27$) based on their initial body weight and breed (Simmental and Belgian Blue). Calves were housed in groups (1 pen/group) and were fed

twice a day receiving calf milk replacer (CMR), calf starter (CS), corn silage, hay and a concentrate mixture consisting of corn, cereals, soybean and rapeseed meal. Control calves received a standard non-medicated CMR and CS. Experimental calves received CMR and CS supplemented with two different mixtures of PFA including herbs, spices and plant extracts [Digestarom Milk in CMR (500 g/t) and Digestarom Calf in CS (300 g/t), BIOMIN Phytogenics GmbH, Stadtoldendorf, Germany]. Feeding CMR was restricted during the first 3 wk, whereas CS was offered ad libitum. Calves were weighed individually on d 1, 21, 42 and 56. Feed intake was determined per group on a weekly basis. Medical treatments were recorded throughout the trial. Data for body weight and weight gain was statistically analyzed with the independent *t* test using SPSS. Calves offered CMR and CS containing PFA were superior in average daily gain (1.33 vs. 1.23 kg; $P = 0.06$) and exhibited a higher average final body weight (168.1 vs. 161.2 kg; $P = 0.02$). Adding PFA resulted in a slightly increased average dry matter intake (2.46 vs. 2.41 kg) and improved feed efficiency (feed-to-gain ratio 1.86 vs. 1.97). Moreover, PFA supplementation positively influenced the health status of calves, as indicated by a reduced number of animals treated for health problems (fever and diarrhea). This led to reduced medication costs and higher farm profits. In conclusion, PFA supplementation in the CMR and CS is a suitable tool to improve growth rates and reduce medication costs in commercial beef calves.

Key Words: phytogenic feed additive, calves, performance

1770 (T383) Efficacy of *Propionibacterium* strains in mitigating methane emissions from beef heifers fed a high forage diet.

D. Vyas*[1], A. Alazzeh[1], S. M. McGinn[1], O. M. Harstad[2], H. Holo[2], T. A. McAllister[1] and K. A. Beauchemin[1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Department of Animal and Aquacultureal Sciences, Norwegian University of Life Sciences, Ås, Norway.*

The objective of this study was to test the efficacy of *Propionibacterium* strains to mitigate methane (CH_4) emissions in beef heifers fed a high forage diet. Sixteen ruminally cannulated beef heifers were used in a randomized complete block design with 21-d periods. Treatments included: 1) Control, 2) *Propionibacterium freudenreichii* T114, 3) *P. thoenii* T159, and 4) *P. freudenreichii* T54. Strains (10×10^{11} CFU) were administered daily directly into the rumen prior to feeding. All heifers were fed a basal diet consisting of 60:40 barley silage:barley grain. Environmental chambers were used for CH_4 measurements. No treatment effects were observed for overall DMI ($P = 0.76$) or DMI in chambers ($P = 0.67$). Mean ruminal pH averaged 6.17 and was not affected by treatments ($P = 0.62$). Likewise, both minimum and maximum ruminal pH were similar for all treatments ($P > 0.10$). No treatment differences were observed for total VFA ($P = 0.44$) or ammonia-N concentration ($P = 0.79$). However, proportions of individual VFA changed with acetate being reduced with *Propionibacterium* T159 (61.1 vs 63.8; $P = 0.02$), whereas ruminal isobutyrate (1.18 vs 1.00; $P < 0.01$) and acetate:propionate ratio (3.95 vs 3.40; $P = 0.04$) were greater with *Propionibacterium* T114, relative to the Control. Total daily enteric CH_4 production averaged 188 g/d and was not affected by *Propionibacterium* strains ($P = 0.57$). Enteric CH_4 emission intensity averaged 22 g/kg of DMI and was numerically greater with *Propionibacterium* T114; however, treatment effects were not significant ($P = 0.19$). In conclusion, *Propionibacterium* strains, T159 and T54, did not affect total enteric CH_4 production possibly due to their inability to increase ruminal propionate concentrations. On the contrary, *Propionibacterium* T114 numerically increased CH_4 emission intensity and the effects could be attributed to greater acetate:propionate ratio observed with the inoculated strain.

Key Words: beef, methane, *Propionibacterium*

1771 (T384) Effect of a commercially probiotic on in vitro gas production of alfalfa hay and barley grain.

S. Payandeh[1], F. Kafilzadeh[1], E. Maleki[1], G. Taasoli*[1] and A. Kamyab[2], *[1]Razi University, Kermanshah, Iran, [2]University of Columbia, Columbia*

Effect of addition of a commercial multi-strain probiotic (PrimaLac, Star Labs, St. Joseph, MO) was studied on Kinetics of fermentation of alfalfa hay and barley grain using in vitro gas production technique. Thirty six ml of buffered rumen fluid (30% rumen fluid + 70% buffer solution) was added to 300 mg of either ground alfalfa hay or barley grain with or without 20 mg PrimaLac. Each sample was incubated in three replicates. The pressure of gas produced in each tube was recorded using a pressure transducer (Manometer Digital testo 512) in barley grain and alfalfa hay at 2, 4, 6, 8, 12, 18, 24 and 48h after the start of the incubation and at 2, 4, 6, 8, 12, 18, 24, 48, 72 and 96h after the start of the incubation, respectively. The data were subjected to analysis of variance using General Linear Model procedure of SAS (2003). Mean separation was performed by the T-tests. Potential gas production (ml/300 mg DM) significantly ($P < 0.05$) increased in alfalfa hay and barley grain (75.85 vs 73.66 and 131.30 vs 113.55 respectively) due to the addition of the probiotic. Rate of gas production in half life (ml/h), lag time (h) and half-life (h, at which half of the total gas production is produced) was affected by PrimaLac both in alfalfa and barley grain ($P < 0.05$) Also, total rate of gas production (b) was increased significantly ($P < 0.05$) in Alfalfa hay (0.0162 vs 0.0082), but was not significant in barley grain. From the result of this experiment it appears that addition of PrimaLac at the level used has a pronounce effect on the fermentation of hay and grains.

Key Words: probiotic, Primalac, alfalfa hay, barley, in vitro gas production

1772 (T385) *Lactobacillus brevis* YM 3-30, a γ-aminobutyric acid producing bacteria, decreases blood endotoxin level of Hanwoo cattle.

S. S. Lee[*1], B. S. Ku[1], L. L. Mamuad[1], S. H. Kim[1], C. D. Jeong[1], Y. J. Choi[1], A. P. Soriano[1], K. Lee[2] and K. K. Park[3], *[1]Sunchon National University, Suncheon, South Korea, [2]The Ohio State University, Columbus, [3]Konkuk University, Seoul, South Korea*

This study was conducted to determine the effects and significance of *Lactobacillus brevis* YM 3-30, a γ-amino butyric acid (GABA) producing bacteria (GPB) on growth performance, meat quality and blood endotoxin level of Hanwoo cattle. Twenty seven Hanwoo steers (602.06 ± 10.13 kg) were subjected to a 129-day feeding trial and were fed daily with commercially available total mixed ration (TMR) supplemented with different inclusion rates of GABA produced by GPB: 3 g/kg (T1), 5 g/kg (T2) or non addition (Con) of GABA. The data gathered were gain in weight, feed conversion ratio (FCR), average daily gain (ADG), marbling score, and blood endotoxin. Hanwoo steers fed with GPB-produced GABA had superior weight performance than the control animals. Additionally, mean weight gains in T1 and T2 were 6.50 kg and 18.34 kg higher than those of the control, respectively, which resulted in higher ADG values in T1 (0.76 kg) and T2 (0.85 kg) than the control (0.71 kg). However, these differences were not statistically significant. The marbling score of meat from animals upon slaughter also did not differ significantly among treatments. However, animals in T1 and T2 had lower ($P < 0.05$) blood endotoxin levels of 17.23 and 16.42 EU/ml, respectively, than the control group at 29.23 EU/ml. Hanwoo cattle fed with GPB-produced GABA diet decreased the plasma endotoxin level and comparable ADG, FCR, and beef marbling scores upon slaughter.

Key Words: blood endotoxin, γ-amino butyric acid, Hanwoo cattle

1773 (T386) Probiotic levels, chemical composition and fermentative characteristics in the solid state fermentation of paper sludge for ruminant feeding.

O. Ruiz-Barrera[*1], Y. Castillo-Castillo[2], C. Rodriguez-Muela[1], L. M. Carrillo-Chan[3], C. Arzola-Alvarez[1], J. Lopez-Morones[3] and A. Corral-Luna[1], *[1]Universidad Autónoma de Chihuahua, Chihuahua, Mexico, [2]University of Ciudad Juarez, Cd. Juarez, Mexico, [3]University of Chihuahua, Chihuahua, Mexico*

Sludge from the paper industry could be used for animal feeding when treated with probiotics upon solid state fermentation process. This study assessed the effects of four probiotic levels (PT) on chemical and fermentative characteristics in SSF of the paper sludge (PS) at controlled temperature (30°C) in laboratory scale. The probiotic used in this experiment is a mexican commercial trademark (Prozoot15) rich in yeasts and lactobacilli, organic acids and vitamins. The tested treatments (T) were: T1 (0% PS), T2 (50 g/kg PS), T3 (100 g/kg PS) and T4 (150 g/kg PS), which were fermented at 0, 24, 48 and 72 h, according to a completely randomized design, in a 4 × 4 factorial arrangement with six repetitions per sampling. All treatments included (g/kg DM) 300 molasses, 15 urea, 20 ammonium sulfate, 9 calcium carbonate and 5 of vitamin and mineral premix, plus the PS which was substituted by the PT at 0, 50, 100 and 150 g/kg DM. The results showed a decrease in pH in all treatments at 24 h; however the lowest pH was at 72 h of fermentation. At 72 h of fermentation, the PT addition in T4 increased crude protein, true protein and yeast counts ($P < 0.05$), and decreased pH ($P < 0.05$). In all fermentation time, the PT addition increased ether extract, lactic acid and ammonia nitrogen ($P < 0.05$) and decreased dry matter, ash, NDF and ADF ($P < 0.05$). It was concluded that the addition of 150 g/kg of PT in SSF of paper sludge improves crude and true protein, ether extract, lactic acid, and ammonia. This treated byproduct may have a potential use in animal feeding.

Key Words: fermentation; paper sludge; yeast

1774 (T387) *Lactobacillus brevis* YM 3-30, a γ-aminobutyric acid producing bacteria, increases antioxidant concentration and reduces biogenic amines.

S. S. Lee[*1], B. S. Ku[1], L. L. Mamuad[1], S. H. Kim[1], C. D. Jeong[1], Y. J. Choi[1], A. P. Soriano[1], K. Lee[2] and K. K. Park[3], *[1]Sunchon National University, Suncheon, South Korea, [2]The Ohio State University, Columbus, [3]Konkuk University, Seoul, South Korea*

This study was conducted to determine the effects of *Lactobacillus brevis* YM 3-30, a γ-amino butyric acid (GABA) producing bacteria (GPB), on in vitro rumen fermentation. Also, evaluation of biogenic amines and antioxidant concentration were analyzed. Ruminal samples were collected from ruminally cannulated Hanwoo cattle and soybean meal was used as substrate at 1g dry matter (DM) per 100ml buffered rumen fluid. Different inclusion rates of GABA produced by GPB, *L. brevis* YM 3-30, were investigated using in vitro rumen fermentation. The following treatments were: 2 g/kg and 5 g/kg fresh GABA, 2 g/kg and 5 g/kg autoclaved GABA, and non addition of GABA and, hereafter referred to as treatments 2, 3, 4, 5, and 1, respectively. Fresh culture of GPB was added in treatments 2 and 3 while autoclaved GPB for treatments 4 and 5. The GPB was autoclaved at 121°C for 15 min prior to inclusion into the fermentation bottles. Addition of GABA produced by GPB had no significant effect on pH and total gas production, but did increase ($P < 0.05$) the ammonia nitrogen (NH_3–N) and reduce ($P < 0.05$) the total biogenic amines (TBA). Treatment groups containing GPB-produced GABA

(T2 and T3) having the lowest ($P < 0.05$) volumes of TBA with 10.62 mM to 11.21 mM. Additionally, histamine was produced in the highest levels in T1 at 15.99 mM. Acetate, propionate, and butyrate concentrations and acetate:propionate (A:P) ratio did not differ significantly among treatments. The volume of production of SOD and GSH-Px were significantly highest in treatments added with 5 g/kg GABA (T3) after 24 h of incubation with 76.60 U/ml and 38.51 U/ml, respectively. The addition of GABA produced by GPB improves in vitro fermentation by reducing biogenic amines production while increasing antioxidant activity and NH_3–N production.

Key Words: antioxidant, biogenic amines, γ-amino butyric acid

---

1775 (T388) Effects of lactobacilli and fibrolytic enzymes on chemical composition, ferementation traits, conservation characteristics and in situ digestibility of mixed cereal silage. L. Jin[*1], L. Duniere[1], Y. Wang[2] and T. A. McAllister[2], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*

Growing mixed cereal crops for silage offers benefits in terms of increased yields and enhanced disease resistance. Little information is available regarding the effects of silage additives on the conservation characteristics and nutritional value of mixed cereal crops. This study was to determine the effect of lactic acid-producing bacteria (LAB) and fibrolytic enzymes on chemical composition, conservation characteristics and in situ digestibility of a mixed cereal crop consisting of barley, oats and spring triticale seeded 1:1:1. Forage was harvested at the mid-dough stage, wilted to 33% DM, chopped to 1 cm and either not treated (Control) or inoculated with a mixture of esterase-producing *Lactobacillus buchneri*, *L plantarum* and *L casei* (T1), a mixture of non-esterase-producing *L. buchneri*, *L. plantarum* and *E. faecium* (T2) or T2 plus exogenous enzymes (Rovabio Excel LC, T3). The MIXED procedure of SAS was used for this study with completely randomized design. The fixed factors were bacteria treatment, run and cow for in ensiling, in vitro and in situ trials respectively. After treatment, forage was packed and stored in mini-silos for 90 d, prior to measurement of ensiling characteristics and in vitro and in situ digestibility. Both T1 and T2 silage had higher NDF ($P < 0.001$) than Control or T3. All inoculants increased populations of LAB ($P < 0.01$) but, reduced concentrations of water soluble carbohydrate ($P < 0.01$), ammonia ($P < 0.001$) and pH ($P < 0.001$) in mixed crop silage. Compared with Control, T1 silage had lower ($P < 0.001$) whereas T2 and T3 silage had higher ($P < 0.001$) concentrations of acetic acid and total VFA. Concentration of lactic acid was similar among all silages. All silages had similar DM disappearance and VFA production during 48-h of in vitro ruminal incubation. However, in situ NDF disappearance of T1 silage was higher ($P < 0.001$) than that of Control and T3 silage. Applying esterase-producing *Lactobacillus* at ensiling to a mixture of barley, oats and spring triticale has potential to improve fermentation traits and enhance the fibre digestibility of silage.

Key Words: *Lactobacillus,* mixed cereal silage, rumen digestion

---

1776 (T389) Use of Yea-Sacc8417 live yeast, monensin and their combination in diets for young Nellore bulls in a feedlot. J. M. B. Benatti[1], N. M. Geronimo[2], J. A. Alves Neto[1], R. C. Silva[1], I. M. de Oliveira[*3], C. L. Francisco[4], G. R. Siqueira[3] and F. D. D. Resende[3], *[1]Universidade Estadual Paulista, Jaboticabal, Brazil, [2]UNIFEB, Barretos, Brazil, [3]APTA- Agência Paulista de Tecnologia dos Agronegócios, Colina, Brazil, [4]Universidade Estadual Paulista- FMVZ, Botucatu, Brazil*

The objective of this study was to analyze the effects of different food additives administered solely or combined in diets for young Nellore bulls in a feedlot for 109 days. The treatments consisted of a control diet with monensin sodium (27.0 mg kg DM^{-1}), a diet with Yea-$Sacc^{8417}$ live yeast (2.0 g $animal^{-1}$) and a diet with the two additives combined. Diets (10.00% sugarcane bagasse, 73.60% ground corn, 6.40% cottonseed, 6.40% soybean meal, 0.26% corn gluten, 0.79% urea and 2.55% mineral mix) varied only in the inclusion of additives. We used 66 non-castrated Nellore bulls (387.24 ± 21.17 kg), 22 of which were slaughtered in the course of the experiment (6 at the beginning and 16 right after the adaptation period [25 days]) to measure the empty body weight (EBW) and served as reference animals. The experiment was arranged in a completely randomized blocks design (11 replicates) as a function of the initial body weight. Data were analyzed by the MIXED procedure of SAS software and means were compared by Fisher's test at 10% significance. The animals were kept in individual pens and were considered the experimental unit. The dry matter intake (DMI) was lower ($P = 0.0798$) (8.47 kg DM day^{-1}) in the treatments containing monensin in relation to control diet (10.20 kg DM day^{-1}). The yeast supplied alone did not interfere ($P > 0.10$) on DMI. The supply of net energy (NE) by the diet was greater ($P = 0.0055$) in the two treatments containing monensin (1.98 and 1.33 Mcal kg DM^{-1} for maintenance and gain, respectively) as compared with the control diet and with yeast alone (1.90 and 1.17 Mcal kg DM^{-1} for maintenance and gain, respectively). The average daily gain evaluated as body weight (BW) (1.47 kg day^{-1}) and as EBW (1.58 kg day^{-1}) did not differ ($P > 0.10$) among diets, but when evaluated as carcass, the diets with monensin reduced ($P < 0.10$) the values (0.89 kg day^{-1}) as compared with the others (1.04 kg day^{-1}). There was no difference ($P > 0.10$) among treatments regarding the final BW (521.01 ± 37.59 kg); however, the diets with monensin reduced ($P < 0.10$) the final carcass weight (293.37 kg) in relation to control

diet and the diet with yeast alone (304.96 kg). Live yeast does not change the DMI or performance of young Nellore bulls in a feedlot. Monensin reduces DMI and reduces the carcass weight. Supported by FAPESP and Alltech.

Key Words: carcass, empty body weight, performance

1777 (T390) Effects of lactobacilli and fibrolytic enzymes on ensiling as well as in vitro and in situ digestibility of of barley silage.

L. Jin*[1], L. Duniere[1], Y. Wang[2] and T. A. McAllister[2], [1]*Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada,* [2]*Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*

Lactobacilli-based inoculants have been shown to improve the ensiling and aerobic stability of barley silage and there is evidence that those with esterase activity may improve fibre digestion. This study aimed to compare the effects of esterase-producing lactobacilli-inoculant to non-esterase or exogenous fibrolytic enzymes inoculants on ensiling characteristic and in situ digestibility. Whole barley crop was cut at the mid-dough stage, wilted to 33% DM and chopped to 1 cm. Chopped barley was subject to the following treatments: 1) control (C; sprayed with water) 2), T1 (inoculated with a mixture of esterase-producing *L. buchneri*, *L. plantarum* and *L. casei*), 3) T2 (inoculated with a mixture of non-esterase-producing *L. buchneri*, *L. plantarum*, and *E. faecium*) and T3 (inoculated with T2 plus exogenous enzymes (Rovabio Excel LC)). Forage was ensiled in PVC laboratory silos for 90 d at which point fermentation characteristics as well as in vitro and in situ digestibility were measured. Silages in T1 and T2 treatment had higher NDF concentration ($P < 0.01$), but lower water soluble carbohydrate content ($P < 0.01$) than C or T3 silage. Control silage had lower pH and concentrations of acetic acid, total VFA, total bacteria and lactic acid producing bacteria ($P < 0.01$), but higher levels of lactic acid and lactic acid: acetic acid ($P < 0.01$) than other silages. Gas production was lower in T3 silage than other treatments ($P < 0.01$) whereas C silage had a greater ($P < 0.01$) in vitro total gas production and rate of gas production. In situ NDF digestibility of T1 silage was greater ($P < 0.01$) than C silage whereas T3 silage had the lowest ($P < 0.01$) NDF digestibility. Esterase-producing *Lactobacillus buchneri* improved the ruminal NDF digestibility of barley silage, a response that was not observed if the inoculant lacked esterase activity or if fibrolytic enzymes were applied exogenously to the forage at the time of ensiling.

Key Words: *Lactobacillus,* barley silage, rumen digestion

1778 (T391) Effect of direct-fed microbials and monensin on in vitro fermentation of a high-froage substrate.

S. Wingard*, E. S. Vanzant, D. L. Harmon and K. R. McLeod, *University of Kentucky, Lexington, KY*

An in vitro experiment was conducted to determine effects of direct-fed microbials (DFM) on rumen fermentation of a forage-based diet in the presence and absence of monensin (MON). In vitro treatments were arranged in a 2 x 2 factorial and included 2 levels of DFM (0 and 50,000 cfu; consisting of primarily *Lactobacillus acidophilus* and *Enterococcus faecium*) and 2 levels of monensin (0 and 5 ppm). In vitro runs were conducted on 3 separate days, with each run consisting of 4 vessels/treatment ($n = 12$/treatment). Inoculum for in vitro experiments consisted of buffer plus a composite of strained rumen fluid obtained from 4 steers fed an 80:20 forage:concentrate (alfalfa/corn/SBM/urea) diet. Fermentation vessels were supplied with common substrate (400 mg of donor steer diet) and incubated in a water bath (39 C) for 30 h. Gas pressure was measured at 5-min intervals and samples were collected at termination for determination of methane production, pH, and concentrations of VFA and ammonia. Data were analyzed as a randomized complete block design with run as the blocking factor. An exponential model without lag was determined to be the best fit model for gas production data and was used to calculate rate and total production of gas. Interactions between DFM and MON were absent ($P > 0.10$) for gas production and fermentative end products, with the exception of a DFM x MON tendency ($P = 0.07$) for total VFA concentration. In the case of the latter, DFM increased total VFA concentration in the absence but not in the presence of MON. Addition of DFM did not affect ($P > 0.10$) gas production or fermentative end products except for a tendency ($P = 0.08$) for a slight increase in proportion of isovalerate. In contrast, MON decreased ($P < 0.001$) CH_4 production and rate and production of total gases. Similarly, MON decreased ($P < 0.001$) total VFA and NH_3 concentrations and molar proportions of acetate and butyrate and increased ($P < 0.001$) proportions of propionate, valerate, and isobutyrate and isovalerate. Independently, DFM and MON increased ($P < 0.001$) end point pH, resulting in an additive effect when the two treatments were combined. Addition of MON altered fermentation and was not influenced by DFM. In contrast, fermentation characteristics were largely unaffected by DFM with two exceptions: a slight increase in total VFA in the absence of MON and a small increase in pH that appeared to occur through a different mechanism than that for MON.

Key Words: direct-fed microbials, monensin, fermentation

RUMINANT NUTRITION III

1779 (W238) Prevalence of subclinical ketosis detected by near infra-red analysis of BHB in DHI milk samples. D. E. Santschi*, R. K. Moore and D. M. Lefebvre, *Valacta, Ste-Anne-de-Bellevue, QC, Canada*

Subclinical ketosis is a common early lactation disorder. Herd prevalence is often unknown because there are no specific clinical symptoms and because individual testing of dairy cows can be costly and time consuming. Since October 2011, Valacta (Dairy Centre of Expertise, Quebec and Atlantic Canada) offers routine infra-red testing of β-hydroxybutyrate (BHB) in DHI milk samples. Over 293,000 milk samples from fresh cows (DIM 5-35) from 4179 dairy herds have been analyzed for BHB concentration (199,003 multiparous and 94,036 primiparous cows). Based on a previously published trial comparing blood and milk BHB concentrations, thresholds were established as follows: cows with milk BHB concentrations $\geq$ 0.20 mM were declared ketotic (POS); cows with milk BHB concentrations below 0.15 mM were declared non-ketotic (NEG); and cows with intermediate BHB concentrations were classified as potentially ketotic (SUSPECT). Overall incidence of subclinical ketosis (POS and SUSPECT) was 24.7% over the first 5 weeks of lactation. Incidence for DIM 5 to 35 was 21.5% and 26.6% for primiparous and multiparous cows, respectively. Distribution of incidence in relation to DIM was different between primiparous and multiparous cows. Highest incidence for primiparous cows (33.7%) was in the first week postpartum but in the third week for multiparous cows (33.5%). By DIM 35, incidence declined to 13.1% and 17.9% for primiparous and multiparous cows, respectively. Among herds with at least 10 cows analyzed for BHB (n = 3560), within herd prevalence of ketosis for the 10th, 25th, 50th, 75th and 90th percentile were 11, 17, 24, 33 and 43% respectively. Ketosis prevalence was affected by month of calving ($P < 0.001$). Highest incidence was observed for cows calving in May-June and October-November whereas lowest incidence was observed for cows calving in August and September. Ketosis prevalence was also affected by breed ($P < 0.001$). Prevalence for Ayrshire (n = 12,443), Brown Swiss (n = 1814), Holstein (n = 271,367) and Jersey (n = 6554) cows was 24.4, 22.7, 24.7 and 34.6%, respectively. Milk BHB concentration was negatively correlated with milk Fat:Protein ratio (R = -0.39; $P < 0.001$) and the correlation was affected by breed. Correlations between milk BHB and Fat:Protein ratio were -0.34, -0.35, -0.39 and -0.32 for Ayrshire, Brown Swiss, Holstein and Jersey cows, respectively ($P < 0.001$). Results indicate subclinical ketosis incidence varies greatly among dairy herds and is influenced by breed and season. Monitoring of subclinical ketosis prevalence is important as a first step towards greater transition success.

Key Words: ketosis, dairy cow, DHI

1780 (W239) Role of treatment soybean meal with pistachio extract on total tract nutrients digestibility of Holstein bulls. A. Jolazadeh[1], M. Dehghan banadaky*[2], K. Rezayazdi[3] and N. Vahdani[4], *[1]University of Tehran, Karaj, Iran, [2]Department of Animal Science, Faculty of Agriculture, University of Tehran, karaj, Iran, [3]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran, [4]university of Tehran, karaj, Iran*

This experiment was conducted to study the effects of treatment soybean meal (SBM) with pistachio extract on total tract nutrients digestibility of Holstein bulls. The sun dried pistachio hulls were grounded through a 0.5 mm screen and soaked in water (1 pistachio: 10 water). Filtered extract was concentrated by heating at 95 ℃. SBM was treated with pistachio concentrated extract (PCE) containing 11.14% total phenol and 7.13% total tannin/DM of extract. Twenty-eight Holstein bulls (average initial weight 256 ± 63kg) were assigned randomly to one of four treatments with seven replicates in a completely randomized design for 94 days. Bulls were fed 70% concentrate diets and had free access to balanced total mixed ration (TMR) and fresh water. All bulls were individually fed and 10 d before the start of the experiment were adapted to the experimental diets. Treatments included: 1; control (SBM without PCE) 2; SBM with 5% PEC 3; SBM with 10% PEC and 4; SBM treated with 15% (kg PEC/100kg DM SBM). Total-tract apparent digestibility of DM, organic matter (OM), CP, NDF and EE were determined using acid-insoluble ash as a marker. There was no effect ($P <$ 0.05) of tannin supplementation on total tract nutrient digestibility such as: DM, OM, CP, EE and NDF. These results suggested that high levels of PCE can be used in diet without any adverse effects on total tract nutrient digestibility in bulls.

Key Words: nutrients digestibility, pistachios hulls, tannin

1781 (W240) Effect of polyherbal supplementation as feed additive on milk production and composition in lactating goats. K. Rezayazdi*[1], F. Mirzaei[2] and M. Hosseinabadi[3], *[1]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran, [2]Animal Science Research Institute, Karaj, Iran, [3]University of Tehran, Karaj, Iran*

The objective of this study was to evaluate the effect of adding a dried mixture of 7 herbal plants including thyme, mint, oregano, cumin, camel thorn, garlic and eucalyptus as a natural additive to the ration on milk production and composition in lactating goats. Because previously other researchers had studied about effects of these herbal plants on animals indivisually.Twenty goats (21 DIM, 2–3 years old, average BW 34.45 kg) were used in a completely randomized design with 2 treatments for a 40 day trial. Treatments were (1) control

ration (basal diet), (2) control ration + 250 mg kg^{-1} BW per d of a mixture of herbal plants. Animals were pen fed and all of data were analyzed with PROC MIXED procedure of SAS. Average milk production at the start of the experiment was similar in both groups (900 g/d). Milk production data and milk samples were collected every 10 day and milk composition was determined. The results showed that milk production (1073 and 1031 g/day for treatment 1 and 2, respectively) was not affected by addition of herbal plant mixture. Milk fat (2.76 and 2.79% for treatments 1 and 2, respectively), milk protein (2.76 and 2.79%) and milk lactose (5.44 and 5.40%) were not significantly different. It is concluded that herbal plant mixture were used in this study had no significant effect on milk production and composition in dairy goats.

Key Words: herbal plants, milk production and composition, dairy goats

---

1782 (W241) Changes of protozoal diversity in response to forage and protein of diets in the rumen of dairy cows. J. Zhang, D. Bu*, S. Zhao and J. Wang, *State Key Laboratory of Animal Science, Institute of Animal Science, Chinese Academy of Agricultural Science, Beijing, China*

The present study was conducted to investigate the changes of quantity and diversity of rumen protozoa in dairy cows fed with different forage and protein diets. Forty-eight healthy Chinese Holstein dairy cows were utilized in randomized block design, and the sixteen cows in every group had similar body conditions. The treatments were as follows: MF (forage sources: alfalfa hay and corn silage; protein sources: soybean meal and miscellaneous meals), CSA (forage sources: corn stover; protein sources: soybean meal and miscellaneous meals), CSB (forage sources: corn stover; protein sources: miscellaneous meals). Rumen fluid was collected via a stomach tube before and after morning feeding on 31, 61, and 91 d of experiment. Microbial DNA in rumen fluid sampled on 91 d was extracted by a CTAB plus bead beating method. The 18S rRNA gene sequences were trimmed and imported to MOTHUR for OTU analysis at 98% identity level. Results showed that the number of protozoa was not different among three groups based on microscopic counting and qPCR. Totally, 726 clones were obtained from three groups. There were 61 OTUs in three groups, 20 OTUs in CSA, 20 OTUs in CSB and 22 OTUs in MF. The three groups shared 10 OTUs, while CSA, CSB and MF had 6, 5 and 7 unique OTUs respectively. Compared with CSA (54.0), MF (46.2) and CSB (30.1) had lower species richness of protozoa based on ACE index. Compared with CSA (0.25), MF (0.11) and CSB (0.23) had higher diversity of protozoa based on Simpson index. Taxonomy analysis showed that *Dasytricha* (54.8%), *Entodinium* (16.4%), *Eudiplodinium* (14.2%), *Diplodinium* (7.7%) and *Isotricha* (3.3%) were the predominant genera in the rumen fluid. In different forage groups, *Diplodinium dentatum, Epidinium caudatum*, *Eudiplodinium maggii* were only found in CSA, while *Isotricha intestinalis, Ophryoscolex purkynjei* were only found in MF. But in different protein groups, there was no apparently changed protozoal species. In conclusion, different sources of forage and protein in diets had no significant effect on the number of rum. However, feeding corn stover can result in higher protozoal abundance, and feeding soybean meal can lead to lower protozoal diversity.

Key Words: protozoa; diversity; forages.

1783 (W242) Pyrosequencing-based profiling of bacterial 16S rRNA genes identifies the unique Proteobacteria attached to the rumen epithelium of bovines. S. Zhao, J. Wang* and D. Bu, *State Key Laboratory of Animal Science, Institute of Animal Science, Chinese Academy of Agricultural Science, Beijing, China*

The objective of this research is to characterize the unique bacterial community attached to the rumen epithelium in both dairy cows and beef cattle. The rumen content and rumen epithelium samples were collected from four Chinese Holstein dairy cows and five Australian beef cattle when the animals were slaughtered. The microbial DNA was extracted from rumen content and epithelium using CTAB plus bead beating method. Community compositions of bacterial 16S rRNA genes from content and wall were examined using a tag-encoded amplicon pyrosequencing assay with bacterial-targeting universal primers 8F and 533R. The sequencing was performed with Roche 454 GS FLX instrument. The platform QIIME was used for reads trimming and OTU analysis. The reads sharing more than 97% identity were clustered into OTUs. The results showed that 158 729 trimmed sequences with the length of 300-560 bp were kept. After OTU picking, 2735 OTUs were formed, and the average reads counts per sample was 7280. The bacterial species richness from epithelium was significantly lower ($P < 0.01$) than that from content according to Chao1 index, and bacterial α diversity from epithelium was also significantly lower ($P < 0.01$) than that from content according to Shannon index. The PCoA analysis revealed that epimural bacterial community was distinctly different from that in content, which implied some unique bacterial community attached to the epithelium of bovine. To further find out what the unique community was, taxonomy and significance test were carried out. While the *Fimicutes* (~42%) and *Bacteroidetes* (~20%) were the predominant abundant bacteria on epithelium, significant higher ($P < 0.01$) abundance of *Proteobacteria* (~26%) were present on epithelium than that in content (~3%). *Hylemonella*, *Desulfobulbus*, *Campylobacter* and unclassified *Neisseriaceae* were the predominant bacteria attached to epithelium compared to the content in both dairy cows and beef. These unique bacteria were microaerophilic (except for *Desulfobulbus*), and all of them were able to hydrolyze urea, which could further certify

the function of oxygen scavenging and urea hydrolysis for bacteria community attached to epithelium.

Key Words: rumen epithelium, bacterial community, pyrosequencing

1784 (W243) Genetic diversity of dipeptidyl peptidase IV from anaerobic bacterial cultivation in vitro **in dairy cow.**

J. W. Zhao[*1], J. Q. Wang[2], S. G. Zhao[2] and D. P. Bu[2], *[1]College of Animal Science and Technology of Inner Mongolia University for the Nationalities, Tongliao, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

The objective of this experiment was to reveal the genetic diversity of dipeptidyl peptidase IV (DPP-IV) gene from anaerobic bacterial cultivation in vitro and the influence of monensin to bacteria containing DPP-IV gene. There were two groups: one group substrate was casein (P), the other group substrate was casein with monensin added (M). Each group had three duplicated samples. Anaerobic culture was done after inoculating with rumen fluid. And then anaerobic bacterium was collected after 12 h culture and its DNA was extracted. DPP-IV gene library was established through PCR. Samples were detected by quantitative real-time PCR. Sixty-six sequence of DPP-IV gene were obtained from picking clones. The results of BLASTP analysis showed these sequences matched with *Prevotella ruminicola*, *Prevotella marshii* and *Paraprevotella xylaniphila*. Twenty-three operational taxonomic units (OTU) were found by Mothur software analysis, and OTU9 might be a DPP-IV gene of protein degradation bacteria sensitising to monensin. Quantitative analysis showed that the copy number of DPP-IV gene in P group was significantly higher than that of M group ($P < 0.01$). These results suggested that monensin affected the amount of bacteria containing DPP-IV gene.

Key Words: anaerobic bacterial cultivation in vitro, dipeptidyl peptidases IV, genetic diversity

1785 (W244) Effects of test weight, precision processing and processing index on in situ ruminal digestibility of barley grain in beef heifers.

Y. Zhao[1,2], S. Yan[2], Z. He[1,3], U. Anele[1], M. L. Swift[4], T. A. McAllister[5] and W. Yang[*1], *[1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada, [2]College of Animal Science, Inner Mongolia Agricultural University, Hohhot, China, [3]Key Laboratory for Agro-Ecological Processes in Subtropical Region, Institute of Subtropical Agriculture, The Chinese Academy of Sciences, Changsha, China, [4]Alberta Agriculture and Rural Development, Lethbridge, AB, Canada, [5]Agriculture and Agri-Food Canada, Lethbridge, AB, Canada*

The objective of this study was to evaluate the effects of test weight (TW; g/L), precision processing (PP) and processing index (PI) of barley grain on kinetics of in situ ruminal digestion. The study was designed as a 2×2×2 factorial arrangement with treatments: TW (low vs. high), PP (control vs. PP) and PI (75 vs. 85%). Ten barley samples with 5 low (574 g/L) and 5 high (632 g/L) TW were either dry-rolled with single roller setting (control) or sieved into small and large kernels, then dry-rolled based on kernel size of each fraction (i.e., PP). Each sample was dry-rolled moderately or coarsely with PI of 75 or 85%, which was calculated as TW after rolling/TW before rolling × 100%. Three beef heifers (650 ± 25 kg BW) fitted with rumen cannulas and fed diet consisting of 70% barley silage and 30% barley grain concentrate were used for in situ incubation. Kinetics of DM digestibility in situ after 0, 3, 6, 12, 24, and 48 h of incubation was estimated using the model: $y = a+b\ (1-e^{-ct})$. Effective ruminal degradability (ED) of DM was estimated using equation $ED = a + bc/(c + k)$ with k = 6%/h. There was no interaction between TW and PI on kinetic parameters, however, there was interaction between TW and PP on ED of DM ($P < 0.01$), and between PP and PI on potential degradable fraction, b ($P < 0.01$) and rate of degradation, c ($P < 0.04$). Overall, the TW of barley grain did not affect the kinetic parameters except that the ED was greater ($P < 0.01$) with high (43.4%) than low (41.8%) TW in control, but not in PP (low vs. high TW; 44.5 vs. 44.1%). Compared to control, PP reduced ($P < 0.01$) soluble fraction a (PP vs. control; 3.0 vs. 4.6%) and the b (73.6 vs. 75.4%), but increased ($P < 0.01$) the c (7.8 vs. 6.4%/h) and ED (44.3 vs. 42.6%). Decreasing PI from 85 to 75% considerably increased ($P < 0.01$) kinetics parameters, a (3.0 vs. 4.5%), b (71.7 vs. 77.3%), c (5.7 vs. 8.6%/h), and ED (37.2 vs. 49.7%). These results indicated that manipulating processing method such as PP and PI could effectively alter ruminal digestion kinetics of barley grain, whereas the effect of varying TW is limited.

Key Words: barley grain processing, in situ DM digestibility, beef heifers

1786 (W245) Longitudinal shifts in the rumen bacterial communities of dairy cows during the transition period. D. W. Pitta[1], S. Kumar[*1], B. Veiccharelli[1], B. Bhukya[1], K. Bittinger[2], D. Shirley[2] and J. Ferguson[2], *[1]University of Pennsylvania, Kennett Square, PA, [2]University of Pennsylvania, Philadelphia, PA*

The transition period in dairy cows refers to the period three weeks prior to calving to three weeks post-calving and is critical for sustained milk production and animal health. We evaluated the rumen microbial dynamics in primiparous and multiparous cows during their transition period. In the current study, ten animals from primiparous (n = 5) and multiparous groups (n = 5) were randomly selected based on the freshening date (expected date for parturition). Each animal was sampled for rumen contents by stomach tube, two hours after feeding, at four time points i.e., three weeks prior to the anticipated freshening date (S1), soon after the animal freshened (S2), four weeks (S3) and eight weeks (S4) into lactation. Both groups received the same dry cow ration (CP-14.65%; NDF-43.66%; Starch-21.9%) prior to calving and the same lactating cow ration (CP-17.21%; NDF-33.14%; Starch-27.19%) post calving. The genomic DNA form rumen samples was extracted and amplified using the primers BSF8 (27F) and BSR357 annealing to the V1-V2 region of the 16S rDNA bacterial gene. The amplicon libraries were sequenced on a 454 Jr Roche platform and analyzed for bacterial diversity using QIIME. A total of forty bacterial communities were analyzed that involved annotations of 100,000 reads, which were assigned to 15,861 operational taxonomic units (OTU). Bacterial community comparisons were based on the Uni-Frac distance metric which revealed that both study group and study day had an independent effect on the community compositions ($P < 0.05$; Permanova test). The most abundant phyla observed were *Bacteroidetes* and *Firmicutes* across all communities. As the cows transitioned into lactation, the ratio of *Bacteroidetes* to *Firmicutes* increased from 6:1 to 12:1 ($P < 0.05$; Mann-Whitney U test) and this ratio was higher in primiparous than in multiparous animals ($P < 0.05$). This study elucidated distinct shifts in the rumen microbiome confounded by dietary and physiological changes in both primiparous and multiparous dairy cows in their transition period. However, validating these results using more animals per lactation group is warranted.

Key Words: dairy cows, transition period, rumen bacteria, pyrosequencing, 16S pyrotags

1787 (W246) Effects of assumptions on estimating energetic efficiencies in lactating dairy cows. K. M. Kennedy* and C. C. Calvert, *University of California- Davis, Davis*

Theoretical estimates of efficiencies of metabolic and physiological processes have proven useful in teaching undergraduate and graduate courses in animal metabolism and bioenergetics. To maintain accurate numbers, new understandings have been applied to various biochemical pathways in ruminants. Further understanding of the mammalian ATP synthase, costs of membrane transport, electron transport, and oxidative phosphorylation have improved the accuracy of estimated theoretical efficiencies of energy metabolism. Advances include identifying the costs of: 1) the malate-aspartate shuttle for transporting protons and electrons into the mitochondria, 2) pyruvate transport into the mitochondria, and 3) counter transport of ATP and GTP out of the mitochondria with the concomitant cost of transporting ADP, GDP, and inorganic phosphorous into the mitochondria. As currently accepted, electron transport results in 10 and 6 protons pumped from the matrix to the intermitochondrial space when the electrons are derived from NADH + H^+ and $FADH_2$, respectively. The discovery that bovine heart ATP synthase requires the flow of 8 protons from the intermitochondrial membrane space into the mitochondrial matrix through the ATP synthase to produce 3 ATP is critical to estimating energetic efficiency in mammalians. Consequently, 2.7 ATP are produced from each NADH + H^+ formed in the mitochondria, 2.5 ATP from each NADH + H^+ formed in the cytosol, and 1.6 ATP from each mitochondrial $FADH_2$ when each is coupled to oxidative phosphorylation. Mitochondrial GTP formed in the TCA cycle is equivalent to 0.7 ATP when GTP is transported out of the mitochondria. Energy available from ATP hydrolysis varies from 32 to 52 kJ/mole of ATP with an average of 42 kJ/mol. Using these data, theoretical efficiencies and net ATP production/cost were calculated and compared to those of Baldwin [*Journal of dairy science* **51**(1): 104-111. (1968)] (Table 1787). These values demonstrate the importance of applying current research and ideas to create accurate values of theoretically estimated metabolic and physiological pathways.

Key Words: energy, metabolism, ATP

Table 1787. Theoretically estimated efficiencies and net ATP production/cost for various biochemical pathways

	Current		Baldwin, 1968	
Pathway	ATP Produced	Efficiency	ATP Produced	Efficiency
Propionate to glucose	-4.7	-	-4	-
Glucose to CO_2 and H_2O	32.9	49%	38	56%
2 Propionate to CO_2 and H_2O	28.2	38%	34	46%
Fat turnover	45.7	36%	-17	-
Milk lactose synthesis	-	76%	-	78%
Milk protein synthesis (100 g)	-	77%	-	82%
Milk fat synthesis	-	71%	-	72%
Total milk synthesis	-	75%	-	76%

1788 (W247) Nutrient supply estimations errors when using free ruminal bacteria as reference sample.

F. Díaz-Royón*, J. M. Arroyo and J. Gonzalez, *Departamento de Producción Animal, Escuela Técnica Superior de Ingenieros Agrónomos, Universidad Politécnica de Madrid, Madrid, Spain*

The chemical composition of bacteria associated with solid (SAB) and liquid (LAB) rumen-digesta phases was studied to confirm errors when LAB is used as reference sample to estimate nutrient supply from SAB (González et al., 2012). Three rumen and duodenum cannulated wethers were fed three isoproteic diets for three successive periods. Diets included protein concentrates (sunflower meal and spring pea) untreated or treated with malic or ortophosphoric acid and heat supplied in this order. Diets were formulated with 45% oat (avena sativa) hay and 55% concentrate (fresh matter basis; 30% corn grain, 30% barley grain, 15% sunflower meal, 22% spring pea, 3% minerals and vitamins) and offered daily at 45 g/kg BW0.75 in six identical meals. Bacterial samples (SAB and LAB) were isolated after 12 d of continuous intraruminal infusion of (15NH4)2SO4 (25 mg 15N/d). Results were compared by variance analysis considering wethers (as blocks) and diets in the model. Compared with SAB, LAB showed consistently lower contents (g/kg DM) of OM (780 vs. 693; $P < 0.001$), starch- glucose (33.4 vs. 19.9; $P = 0.013$), and total lipids (221 vs. 113; $P < 0.001$), but greater CP content (402 vs. 429; $P = 0.007$) and 15N enrichment (atoms %: 0.0585 vs. 0.0817; $P = 0.005$). Present data fitted well with the relationship predicting SAB 15N enrichment from the same LAB value reported in the previously cited study (variation coefficient of the mean prediction error = 13.0%). The mean ratio 15N-SAB/15N-LAB allows establishing CP supply from synthesized SAB is under evaluated by 25.6% when LAB is used as reference. This under evaluation was even greater for starch-glucose (44.2%) and lipids (61.9%) supply. These under evaluations were close to those previously reported by González et al., 2012. Taking into consideration that SAB is the main microbial source of nutrient supply, these errors should be factored in when attempting to improve ruminant nutrition. Predictions using 15N as marker are useful for correcting errors associated with the traditional use of LAB as reference sample, and therefore to obtain a more accurate estimate of microbial nutrient supply to the ruminant.

Key Words: rumen bacteria, chemical composition, 15N enrichment

1789 (W248) Evaluation of the Nordic dairy cow model Karoline in predicting methane emissions.

M. Ramin[*1] and P. Huhtanen[2], [1]*Swedish University of Agricultural Sciences (SLU), Umeå, Sweden,* [2]*Swedish University of Agricultural Sciences (SLU), Umea, Sweden*

Models are widely used to predict methane (CH_4) emissions, and are used to develop mitigation options and policies. In the current study, the performance of the Nordic dairy cow model Karoline was evaluated in predicting CH_4 emissions. Karoline is a dynamic, deterministic and mechanistic simulation model describing the digestion and metabolism of nutrients, and production in a dairy cow. The model was evaluated against observed data from studies reporting CH_4 emissions from respiration chamber studies. The dataset included a total of 184 treatment means from 31 published papers. The dietary and animal characteristics used for the model evaluation represent the typical range of diets fed to dairy cattle. When analyzed with a fixed regression analysis, there was a good relationship between predicted and observed CH_4 emissions measured from respiration chamber studies ($R^2 = 0.93$) with a small root mean square error of prediction (RMSPE = 10.1% of the observed mean). The mean bias was small but statistically significant, and there was no slope bias. Most of the error was due to random bias (96.4%), whereas the contributions of mean and slope bias were small (3.4 and 0.2%, respectively). By considering study as the random effect in the model (mixed model regression analysis), the fit improved to $R^2 = 0.98$ and RMSPE decreased to 6.1% of the observed mean. The influence of some input variables such as total DM intake, dietary concentrations of CP, NDF and ether extract, and OM digestibility (OMD) on the residuals (observed– predicted) of CH_4 emissions were not significant. The residuals of both CH_4 emissions and OMD were significantly related to each other, indicating the Karoline model requires accurate estimates of digestion kinetic parameters as input variables. It is concluded that the Nordic dairy cow model Karoline is a useful tool in predicting CH_4 emissions and understanding the system behavior. The model can also be used in developing mitigation strategies for the national inventories of CH_4emissions.

Key Words: Karoline model; methane emissions; mechanistic model

1790 (W249) Effects of different feeding frequencies on rumen tissue histology and cell proliferation of feedlot cattle. T. V. Carrara[*1], J. Silva[2], M. C. Pereira[2], I. C. Batista Júnior[2], C. A. Oliveira[2], A. C. J. Pinto[2], D. D. Estevam[1], M. D. Arrigoni[1], F. T. Pereira[2] and D. D. Millen[2,3], *[1]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [2]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [3]Supported by São Paulo State Foundation (FAPESP), São Paulo, Brazil*

This study, conducted at the São Paulo State University feedlot, Dracena Campus, Brazil, was designed to determine the effects of different feeding frequencies on rumen tissue histology and cell proliferation of rumen papillae of feedlot cattle. The experiment was designed as a completely randomized block, replicated 12 times, in which 48 18-mo-old yearling Nellore bulls (358.2 ± 19.4 kg) were fed in individual pens for 94-d according to the following treatments: 1) feeding one time daily (1x; 0800), 2) feeding two times daily (2x; 0800 and 1400), 3) feeding three times daily (3x; 0800, 1100 and 1400), and 4) feeding four times daily (4x; 0800, 1100, 1400 and 1700). The adaptation program consisted of ad libitum feeding of two adaptation diets over period of 14-d with concentrate level increasing from 60% to 86% of diet DM. The finishing diet contained: 67.0% cracked corn grain, 14.0% sugarcane bagasse, 9.0% soybean hulls, 5.5% soybean meal, 4.0% supplement containing 30% of urea, and 0.5% limestone (DM basis). At harvest, a 1-cm^2 fragment of each rumen was collected from ventral sac for histological assessment. Histological sections were stained with hematoxylin and eosin, embedded in paraffin wax, and sectioned. Morphometric measurements, such as papillae surface area, papillae height, papillae width, keratinized layer thickness, and mitotic index, were determined in four papillae per animal using computer-aided light microscope image analysis. In addition, cell proliferation was determined by immunohistochemistry technique using the monoclonal mouse anti-proliferating cell nuclear antigen. Orthogonal contrasts were used to assess linear, quadratic, and cubic relationship between feeding frequency and the dependent variable. Feeding frequency did not affect ($P > 0.10$) papillae width, keratinized layer thickness, and cell proliferation. However, as feeding frequency increased, papillae surface area in cm^2 (1x = 1.11; 2x = 1.11; 3x = 1.29; 4x = 1.22), papillae height in mm (1x = 2.85; 2x = 2.79; 3x = 3.29; 4x = 3.14), and mitotic index, as % of basal cells (1x = 9:12; 2x = 10.60; 3x = 12.85; 4x = 12.63) linearly increased ($P < 0.05$). Papillae surface area and papillae height were also affected ($P = 0.01$) cubically as feeding frequency increased. Thus, increasing feeding frequencies affected rumen tissue histology variables. In a practical way, feeding yearling Nellore bulls three times daily seems to be the most feasible option.

Key Words: mitosis, Nellore, papillae

1791 (W250) Survey of nutritional recommendations used by dairy cattle nutritionists in Brazil in 2013. D. P. Silva[*1], A. M. Pedroso[2], T. V. Carrara[3] and D. D. Millen[1,4], *[1]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [2]EMBRAPA, São Carlos, Brazil, [3]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [4]Supported by São Paulo State Foundation (FAPESP), São Paulo, Brazil*

This survey was designed to describe the nutritional recommendations and management practices adopted by Brazilian dairy cattle nutritionists in 2013. Forty-three nutritionists responsible for about 960 dairy farms, completed the survey within 1-mo, which was available online (www.surveymonkey.com) and consisted of 77 questions. The level of grains included in lactation diets recommended by 22 (55.0%) participants ranged from 31% to 50%, but 8 (20.0%) nutritionists recommended diets with 51% to 60%, and 10 (25.0%) used less than 31% grains. Likewise, the level of concentrate included in lactation diets recommended by 18 (43.9%) participants ranged from 41% to 50%, but 11 (26.8%) nutritionists recommended diets with 51% to 60%, and 12 (29.3%) used less than 31% concentrate. Corn was the primary source of grain used in lactation diets ($n = 37$; 97.4%). With respect to the energy unit used to formulate lactation diets, 40.5% ($n = 15$) nutritionists used TDN, followed by the NFC (29.7%; $n = 11$). The main source of information for feed energy values was the NRC (73.2%, $n = 30$), followed by CPM-Dairy (17.1%, $n = 7$). The typical range of roughage inclusion in finishing diets was 50.5%, and corn silage was the primary roughage source, being used by 30 nutritionists (79.0%). Moreover, the average recommended concentrations of NDF were 35.4%. Also, NDF was the fiber analysis method of choice by 29 of the nutritionists (76.3%), whereas physically effective NDF was cited by 7 (18.4%) of the respondents. Regarding coproduct use in lactation diets, citrus pulp pellets was the primary coproduct included in lactation diets, being used by 20 (51.3%) of the nutritionists. Use of whole cottonseed was reported by 8 (20.5%) nutritionists, whereas soybean hulls was reported by 7 (17.9%) of the respondents. When asked about feeding frequency, most of the clients served by the nutritionists surveyed typically feed twice daily (70.7%; $n = 29$), whereas 10 participants (24.4%) reported that their clients feed cows three times daily. This study presents a part of an overview of the practices and management recommendations currently applied by dairy cattle nutritionists from all regions in Brazil. Also, this survey may help to identify and solve problems in Brazilian dairy cattle operations, and moreover, these data may facilitate the design of industry-oriented research.

Key Words: Brazil, dairy, survey

1792 (W251) Effects of type of base forage on the Beta-carotene content of milk and blood plasma in lactating Holstein cows. H. C. Leicester[*1,2] and L. J. Erasmus[2], *[1]UC Davis, Davis, [2]University of Pretoria, Pretoria, South Africa*

It is well established that β-carotene has a positive effect on fertility of dairy cattle (Arechiga et al., 1998; J. Dairy Sci. 81, 390-402). The aim of this project was to determine the β-carotene content and variability of the main forage fed, blood plasma and milk of lactating Holstein cows managed in three typical South African production systems which differ in the base forage. These were pasture based systems (S1), predominantly corn silage based total mixed ration (TMR) systems (S2), and predominantly hay and alfalfa based TMR systems (S3). Within each system, 10 farms were selected based on their management and diet similarity within system and, from each farm, 20 cows where selected which had > 60 days in milk and were in lactation 2 or higher. The 20 cows/farm were chosen randomly from cows meeting these criteria. From each farm, a representative sample of the main forage, plasma samples from the 20 cows and a 2 liter bulk tank milk sample were collected. All samples were analyzed for β-carotene. The β-Carotene analyses of the predominant forages in each system revealed values of; S1; 20.9 ± 6.78 mg/Kg, S2; 3.1 ± 2.59 mg/Kg and S3; 22.4± 15.05 mg/Kg. Mean plasma β-Carotene of S1 cows was 5.5 ± 2.39 mg/L and this differed ($P < 0.05$) from S3 with values of 3.0 ± 0.66 mg/L, which tended ($P < 0.10$) to differ from S2 at 1.7 ± 0.06 mg/L. Bulk milk tank samples had β-Carotene levels of S1 (15.4 ± 7.40 mg/L), S2 (2.3 ± 0.43 mg/L) and S3 (4.1 ± 2.30 mg/L). While no guidelines exist for adequacy of β-Carotene levels in milk, plasma β-Carotene levels of < 1.5 mg/L is defined as 'deficient', 1.5 to 3.5 is 'marginal' and levels > 3.5 are 'optimal' (Schweigert and Immig, 2007; Int. Dairy Topics, 6,4). On this basis, S1 cows had 'optimal' plasma β-Carotene levels whereas S2 and S3 cows had 'marginal' β-Carotene levels, which suggests that dietary β-Carotene supplementation is required. However the wide variation in the β-Carotene levels of the base forages, both among and within systems, suggests that dietary β-Carotene supplementation should not be based solely on system, but should include β-Carotene analysis of the base forage.

Key Words: fertility production ICheck

1793 (W252) Effect of acute exposure to ergot alkaloids on short-chain fatty acid absorption and barrier function of isolated bovine ruminal epithelium. A. P. Foote[*1], G. B. Penner[2], M. E. Walpole[2], J. L. Klotz[3], L. P. Bush[4] and D. L. Harmon[4], *[1]USDA, ARS, US Meat Animal Research Center, Clay Center, NE, [2]University of Saskatchewan, Saskatoon, SK, Canada, [3]USDA-ARS, FAPRU, Lexington, KY, [4]University of Kentucky, Lexington*

Ergot alkaloids present in endophyte-infected tall fescue are the causative agents for fescue toxicosis in cattle. Ergot alkaloids have been shown to cause a reduction in blood flow to the rumen epithelium as well as a decrease in short-chain fatty acid (SCFA) absorption from the washed rumen of steers. It is possible that ergot alkaloids could negatively impact SCFA transport pathways and the barrier function of the rumen epithelium. An experiment was conducted to determine if acute exposure to an endophyte-infected tall fescue seed extract (EXT) would affect total, passive, or facilitated acetate and butyrate flux across the isolated bovine rumen epithelium as well as the barrier function measured by inulin flux and tissue conductance (G_t). Flux of ergovaline across the ruminal epithelium was also evaluated. Ruminal tissue from the caudal dorsal sac of Holstein steers ($n = 6$), fed a common diet, was collected and isolated shortly after slaughter and mounted between two halves of Ussing chambers under voltage clamp conditions. In vitro treatments included vehicle control (0.4% methanol), Low EXT (50 ng ergovaline/mL), and High EXT (250 ng ergovaline/mL). Results indicate that there was no effect of an acute exposure to ergot alkaloids on total, passive, or facilitated flux of acetate or butyrate across the isolate bovine rumen epithelium ($P > 0.51$). Inulin flux ($P = 0.16$) and G_t ($P > 0.17$) also were not affected by EXT treatment, indicating no alteration in barrier function due to acute ergot alkaloid exposure. Based on ergovaline concentrations measured in the serosal buffer of the High EXT treatment, the flux rate is approximately 0.25– 0.44 ng/(cm^2 · h). These data indicate that specific pathways for SCFA absorption and barrier function of the ruminal epithelium are not affected by acute exposure to an extract of tall fescue seed at the concentrations tested. Ergovaline has the potential to cross the rumen epithelium of cattle which could contribute to the reduced foregut blood flow seen in previous experiments and lead to reduced growth rates of cattle.

Key Words: ergot alkaloids, ergovaline absorption, fescue toxicosis

1794 (W253) Evaluation of the CNCPS v6.5 for predicting metabolizable energy and protein allowable milk in sugarcane based diets.

E. A. Collao-Saenz*[1], A. Foskolos[2], R. J. Higgs[2], M. N. Pereira[3] and M. E. Van Amburgh[2], *[1]Universidade Federal de Goiás, Jatai-GO, Brazil, [2]Cornell University, Ithaca, NY, [3]Universidade Federal de Lavras, Lavras, Brazil*

Sugarcane is a high energy yielding crop, and is an alternative feed for dairy cows in tropical regions. This experiment evaluated the sensitivity of CNCPSv6.5 for predicting milk yield in sugarcane based diets. Data for evaluation were obtained from 13 published experiments, representing 50 treatments. Metabolizable energy (ME) and protein (MP) allowable milk were predicted based on reported DMI and diet composition. An algorithm was used to adjust the nutrient composition of individual ingredients from commercial laboratory databases when feed chemistry data were incomplete. The correlation coefficients between observed and predicted milk yield were based on BLUP (R^2_{BLUP}) and model predictions using the mean study effect (R^2_{MP}). When milk yield was predicted based on the first limiting nutrient, either ME or MP, the correlation coefficient generated with R^2_{BLUP} was 0.985 and with R^2_{MP} was 0.81. With ME predicted milk yield, the R^2_{BLUP} correlation coefficient was 0.989 and for R^2_{MP}it was 0.81, and when the predictor was MP they were 0.92 and 0.67, respectively. The Bayesian Information Criterion was 219 for MP or ME, 110 for ME, and 127 for MP. The Mean Square Prediction Error (MSPE) using MP to predict milk yield was 5.4, and it was 10.8 when ME or MP or ME were predictors. When the MSPE was partitioned, 0.22%, 0.01% and 3.6% of the error was due to mean bias for the MP or ME, ME, or MP predicted milk yield, respectively, 35.41%, 32.94% and 30.72% was due to systematic bias, and 64.37%, 67.05% and 65.68% was due to random variation. Concordance Correlation Coefficients were computed to account for the accuracy and precision of the predictions, values were: 0.79 for MP or ME, 0.83 for ME, and 0.75 for MP. Using CNCPSv.6.5 to predict milk yield responses in sugarcane based diets was reliable. In the available data sets, the prediction of ME allowable milk yield was better than MP and this most likely reflects differences in actual rates of digestion and library values along with ingredient bias.

Key Words: dairy cattle, model evaluation, tropical feed

1795 (W254) Effects of different feeding frequencies on DMI variation and selective consumption by feedlot cattle.

J. Silva*[1], T. V. Carrara[2], M. C. Pereira[1], D. V. Vicari[1], I. C. Batista Júnior[1], L. A. Tomaz[1], D. H. Watanabe[1], A. L. Rigueiro[1], M. D. Arrigoni[2] and D. D. Millen[1,3], *[1]São Paulo State University (UNESP), Dracena campus, Dracena, Brazil, [2]São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil, [3]São Paulo State Foundation (FAPESP), São Paulo, Brazil*

This study, conducted at the São Paulo State University feedlot, Dracena Campus, Brazil, was designed to determine the effects of different feeding frequencies on DMI variation and selective consumption (sorting) of diets by Nellore cattle. The experiment was designed as a completely randomized block, replicated 12 times, in which 48 18-mo-old yearling Nellore bulls (358.2 ± 19.4 kg) were fed in individual pens for 94-d according to the following treatments: 1) feeding one time daily (1x; 0800), 2) feeding two times daily (2x; 0800 and 1400), 3) feeding three times daily (3x; 0800, 1100 and 1400), and 4) feeding four times daily (4x; 0800, 1100, 1400 and 1700). The adaptation program consisted of ad libitum feeding of two adaptation diets over period of 14-d with concentrate level increasing from 60% to 86% of diet DM. The finishing diet contained: 67.0% cracked corn grain, 14.0% sugarcane bagasse, 9.0% soybean hulls, 5.5% soybean meal, 4.0% supplement containing 30% of urea, and 0.5% limestone (DM basis). The DMI variation was calculated for each individual yearling bull as the difference in intake, expressed as % of variation, between consecutive days throughout the study. Samples of orts and diets were collected on days 12 and 51 of the study for particle size distribution determination, which was performed by sieving using the Penn State Particle Size Separator and reported on as-fed basis. Values equal to 1.0 indicate no sorting, < 1.0 show selective refusals, and > 1.0 indicate preferential consumption. Orthogonal contrasts were used to assess linear, quadratic, and cubic relationship between feeding frequency and the dependent variable. During the period of adaptation, DMI variation was affected ($P < 0.01$) cubically as feeding frequency increased (1x = 16.1%; 2x = 23.2%; 3x = 14.4%; 4x = 15.9%), however, feeding frequency did not affect ($P > 0.10$) DMI variation during the finishing period. Feeding frequency only affected particle sorting during the adaptation period, in which as feeding frequency increased, sorting for screen 3 (diagonal opening = 1.18 mm) was affected ($P < 0.01$) quadratically (1x = 0.993; 2x = 0.995; 3x = 0.999; 4x = 0.985). Thus, based on the results of this study, feeding frequency affects DMI variation and diet sorting only during the adaptation period. Cattle fed three times daily presented lower DMI variation and lesser extent of sorting.

Key Words: fluctuation, Nellore, sorting

1796 (W255) Evaluation of mineral excretion of lactating Holstein dairy cows supplemented with copper, manganese and zinc in organic and inorganic forms. G. Acetoze*[1], A. M. Gehman[2], K. A. Dawson[3] and H. A. Rossow[4], [1]*University of California- Davis, Tulare,* [2]*Alltech, Inc., Nicholasville, KY,* [3]*Center for Animal Nutrigenomics and Applied Animal Nutrition, Alltech, Nicholasville, KY,* [4]*VMTRC, University of California, Tulare, CA*

Forms of minerals, organic and inorganic, impact the amount of mineral available for intestinal absorption. However, in the ruminant, when inorganic minerals dissociate they can associate with feed components decreasing their availability for intestinal absorption. The objective of this study was to evaluate the impact of level of feeding organic and inorganic forms of Cu, Mn and Zn (Bioplex Cu, Mn, and Zn; Alltech, Inc.) on mineral fecal excretion of lactating dairy cows on a commercial dairy. Fifty lactating Holstein dairy cows (70 DIM) were randomly assigned to five treatments: Control, Organic75, Organic100, Organic125, and Inorganics ($CuSO_4 \cdot 5H_2O$, $MnSO_4 \cdot H_2O$ and ZnSO4 $\cdot$ H_2O) (Table 1796). Therefore control cows received only the levels of minerals present in the TMR based on NRC. Minerals were given by daily dosing individual cows with an oral solution of the mineral treatment for 28 d (24 d for adaptation, and 4 d of sample collection). Fecal samples were collected rectally twice a day (am and pm), combined for a 24h sample and sent for analysis of mineral content and composition. For 11 d, Cr was supplemented (10g/d) with minerals to estimate total fecal output. Statistical analysis was performed in R (version 2.15.1) using ANOVA. No differences were observed for fecal output (kg/d) ($P = 0.35$) and manganese excretion (g/d) ($P = 0.23$) among treatments. Copper and zinc excretion levels did differ among treatments ($P < 0.001$). Averages (g/d) for copper excretion were 0.48, 0.66, 0.68, 0.76 and 0.58 for Control, Organic75, Organic100, Organic125 and Inorganic, respectively; and averages for zinc excretion were 2.70, 3.21, 3.04, 3.42, 2.78 for Control, Organic75, Organic100, Organic125 and Inorganic, respectively. Greatest concentrations of mineral excretion were observed in cows supplemented with 25% above NRC requirement levels of Bioplex Cu and Zn while lowest levels of mineral excretion were observed in cows dosed with control and Inorganics. In conclusion, this study shows that mineral form only affects copper and zinc excretion. However, treatment comparisons are not corrected for contributions of minerals from other dietary components (DMI), so conclusions on levels of mineral fecal excretion may change when considering apparent absorption.

Key Words: minerals, fecal excretion, dairy cattle

Table 1796. Levels of minerals supplemented on top of TMR (control diet) for each treatment

	Control	Organic75	Organic100	Organic125	Inorganics
	(mg/d)				
Mn	354.00	125.07	166.76	208.45	166.76
Cu	472.00	215.07	286.76	358.45	286.76
Zn	1409.00	375.88	501.18	626.48	501.18

1797 (W256) Evaluation of milk yield and composition of F1 Holstein x Gir lactating cows supplemented with rumen-protected choline during the transition period. R. C. D. Souza*[1], R. C. Souza[1], A. B. D. Pereira[2], R. F. Cota[1], T. A. Torres[1], I. B. Fortes[1] and G. V. Fonseca[3], [1]*PUC Minas, Betim, Brazil,* [2]*University of New Hampshire, Durham,* [3]*PUC, Betim, Brazil*

The use of rumen-protected choline (RPC) is a strategy to improve fat metabolism in the liver and reduce the prejudicial effects of negative energy balance in dairy cows during the peripartum. The objective of this study was to evaluate milk yield and composition of cows supplemented with RPC during the transition period (from 21 d pre-partum until 21 d post-partum). Thirty two lactating F1 Holstein x Gir cows (16 multiparous and 16 primiparous) were blocked by parity and randomly assigned to one of two dietary treatments: no addition of RPC (NC) and addition of 60 g of RPC (AC; Toplac Transition, Nutrifarma, Taió, PR, Brazil). Diets contained 60% forage as corn silage and were isonitrogenous and isocaloric according to the NRC (2001) model. Supplementation of RPC was done from 21 d before expected parturition until 21 d post-partum. The experiment was analyzed as a randomized complete block design using the MIXED procedure for SAS and least square means were reported according to the tukey post-hoc test. Milk production was lower for multiparous cows in the NC diet (32.2 kg/d) compared to the AC diet (34.4 kg/d, $P < 0.05$), but no effect was observed for primiparous animals. A difference between treatments was observed for milk fat yield for multiparous cows (0.88 kg/d and 1.17 kg/d for NC and AC, respectively, $P < 0.05$) and primiparous cows (1.02 kg/d and 1.17 kg/d for NC and AC, respectively, $P < 0.05$) and somatic cells count for multiparous cows (401 x 10^3 cells and 258 x 10^3 cells for NC and AC, respectively, $P < 0.05$) but not for primiparous cows (143 cells/mL and 93.8 cells/mL for NC and AC, respectively, $P > 0.05$). Also, no difference was found between treatments and parity level for milk fat percentage, milk protein or milk solids non-fat. Rumen protected choline supplementation to F1 Holstein x Gir multiparous cows improved milk production and milk fat yield. Effect on primiparous cows was observed only on milk fat yield.

Key Words: rumen protected choline, milk yield, milk composition.

1798 (W257) Effects of supplemental bupleurum extract on blood material metabolism in heat-stressed dairy cows. X. Sun*, *Ministry of Agriculture-Laboratory of Quality* and *Safety Risk Assessment for Dairy Products (Beijing), Beijing, China*

This study investigated the effect of bupleurum extract (BE) on blood material metabolism of lactating dairy cows under heat stress. Forty lactating Chinese Holstein cows (75 ± 15 DIM, 37.5 ± 1.8 kg of milk/d, and 1.7 ± 0.4 parity) were randomly assigned to four groups and were individually fed a basal diet with 0, 0.25, 0.5, or 1.0 g BE/kg DM. The experiment lasted 10 weeks. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Blood samples were collected from all of animals via tail vein before the morning feeding on days 0, 21, 42, and 63. Data were analyzed by MIXED model procedure of SAS 9.2. Supplementation of BE decreased urea nitrogen (BUN) contents (5.65, 5.58, 5.81 vs 5.95 mmol/L, $P < 0.05$), but increased blood total protein (80.97, 81.08, 81.00 vs 77.22 g/L, $P < 0.05$) level. Cows fed 0.25 or 0.5 g/kg BE increased albumin content (38.61, 37.53 vs 36.18 g/L, $P < 0.05$) compared with control cows, but BE supplementation had no effects ($P > 0.05$) on blood glucose (GLU), nonesterified fatty (NEFA), total triglyceride (TG), low density liporotein cholesterin (LDL-C) and high density liporotein cholesterin (HDL-C). Sodium (Na) (136.63, 134.72, 136.05 vs 137.90 mmol/L; $P < 0.01$) and phosphorus (P) (1.94, 1.96, 1.81 vs 2.13 mmol/L; $P = 0.05$) concentrations in serum were decreased by BE supplementation, while potassium (K) (3.80, 3.83, 3.90 vs 3.48 mmol/L; $P < 0.01$) and calcium (Ca) (2.56, 2.59, 2.66 mmol/L; $P < 0.01$) concentrations were decerased than in controls, but BE supplementation had no effect ($P > 0.05$) on serum magnesium (Mg) concentration. Serum chlorine (Cl) concentration was increased in cows fed 0.5 g/kg BE (148.01 vs 140.79 mmol/L; $P < 0.05$) compared with control cows, and tended to be higher (144.08 vs 140.79 mmol/L; $P < 0.1$) in cows fed 0.25 g/kg BE, but was not affected in cows fed 1.0 g/kg BE. These findings suggest that BE supplementation could improved the protein metabolism and maintain the balance of electrolyte concentration.

Key Words: bupleurum extract; heat stress; blood material metabolism

1799 (W258) Evaluation of the updated version of CNCPS (v6.5). A. Foskolos*[1], E. A. Collao-Saenz[2], D. A. Ross[1], R. J. Higgs[1] and M. E. Van Amburgh[1], *[1]Cornell University, Ithaca, NY, [2]Universidade Federal de Goiás, Jatai-GO, Brazil*

The first version of The Cornell Net Carbohydrate and Protein System (CNCPS) was released in 1991, and since then it has been continuously under evolution. Our objectives are to describe the latest updates of the model resulting in version 6.5 and to evaluate model predictions against both literature and on-farm data. Degradation rates of protein and carbohydrate fractions were modified to meet new fractionation schemes, updated amino acid (AA) profiles on a whole feed basis were made and a combined efficiency of essential AA use was adopted representing an improved understanding of AA metabolism. Three different datasets were developed to evaluate lysine (Lys) and methionine (Met) requirements (AA dataset), rumen N balance (rumen dataset) and metabolizable energy (ME) and protein (MP) allowable (lactation dataset). In total 96 peer-reviewed studies with 367 treatments and 15 regional farms with 50 different diets were included. The AA dataset was used to estimate the concentration of Lys and Met that maximizes milk protein yield and content according to the broken line model with plateau: results suggested concentrations of 7.00 and 2.60%MP for Lys and Met, respectively for maximal protein yield and 6.77 and 2.85%MP for Lys and Met, respectively for maximal protein content. Proposed concentrations are slightly higher for Lys and 11-18% higher for Met compared with CNCPSv6.0 which can be attributed to changes in the AA profile of feeds. The ability of the model to predict post-ruminal flows of N and milk yield was assessed using the correlation coefficient based on the BLUP (R^2_{BLUP}) or model predictions using a mean study effect (R^2_{MP}) and the concordance correlation coefficients (CCC) to simultaneously account for accuracy and precision. The model predicted accurate and precise post-ruminal flows of rumen degraded and undegraded N (RDN and RUN, respectively; $R^2_{BLUP=}$ 0.98 and 0.92 and CCC = 0.88 and 0.80 for RDN and RUN, respectively), bacterial N ($R^2_{BLUP=}$ 0.97; CCC = 0.84) and provided a uniform offset of non-ammonia N that is robust with little bias ($R^2_{BLUP=}$ 0.98; CCC = 0.92). For the lactation dataset, the model predicted accurate and precise milk yield according to the first limiting nutrient (MP or ME) with a $R^2_{BLUP=}$ 0.95, $R^2_{MP=}$ 0.78 and CCC = 0.83. Results suggest a significant improvement of the model due to current updates.

Key Words: CNCPS, evaluation, dairy cattle

1800 (W259) Effects of bupleurum extract on performance and health status in heat-stressed late lactation dairy cows. B. Shi[1,2], N. Zheng[1], J. Cheng[1,2], L. Min[1], C. Yin[1] and J. Wang*[1,3], *[1]Ministry of Agriculture- Laboratory of Quality* and *Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

This study was conducted to investigate the effects of bupleurum extract (BE) on performance and health status in heat-stressed Chinese Holstein dairy cows. Forty lactating cows (days in milk = 207.98 ± 12.2; average milk yield = 30.96 ±

3.96 kg/d; parity = 1.96 ± 1.07) were randomly assigned to 1 of 4 treatments according to a completely randomized block design. Cows were individually housed in pens and fed ad libitum three times daily. Treatments consisted of 0, 0.5, 2.5 or 5% BE of dry matter (CG, LG, MG or HG).The experiment lasted for 11 weeks in hot summer. Ambient temperature and relative humidity were recorded daily (0600, 1400, and 2200). Milk yields, dry matter intake (DMI), respiration rates (RR) and rectal temperatures (RT) were recorded twice a week and milk samples were collected twice a week. Blood was collected in evacuated tubes via caudal venipuncture at 0, 3, 6, 9, 11 week. Data were analyzed by repeated measures using Proc Mixed procedure of SAS 9.2. During the experiment, average temperature-humidity index were 76.8 ± 6.3, 82 ± 6.54 and 78.3 ± 6.1 respectively at 0600h, 1400h and 2200h. There was no treatment effect on RR, RT, DMI and milk yield, while the values of DMI (19.41, 19.04, 18.61 vs. 19.19 kg/d) tended to decrease with increasing dose. Milk urea nitrogen in MG was lower (12.06 vs. 12.92 mg/dL, $P < 0.05$) than that in CG, while contents of milk fat, milk protein, lactose, total solids and somatic cell counts were not significantly affected ($P > 0.05$). The mean corpuscular hemoglobin in HG was lower than that in CG (16.56 vs. 16.98 pg, $P < 0.05$). The Mean corpuscular hemoglobin concentration (346.35, 347.81, 344.87 vs. 351.28 g/L, $P < 0.05$) was decreased due to BE supplementation. No significant difference in the number of leukocytes, red blood cell count, hematocrit, lymphocytes, mean corpuscular volume, mean platelet volume and red blood cell distribution width were detected among groups. There was no treatment effect on glutamic-pyruvic transaminase, glutamic oxalacetic transaminase, globulin, albumin, total protein and alkaline phosphatase. These results indicate that BE supplemented with high dose of 5% had no negative effect on the performance and health status in heat stressed late lactation dairy cows, and 5% is safety dose.

Key Words: bupleurum extract, performance, health status

1801 (W260) Estimation of NDF pool in the rumen of cattle using fecal excretion and diet characteristics.

H. C. Bonfa*[1], E. Detmann[2], S. Krizsan[3], S. C. Valadares Filho[2] and P. Huhtanen[3], *[1]UFV, Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [2]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [3]Swedish University of Agricultural Sciences (SLU), Umea, Sweden*

The objective of this work was to estimate ruminal pool of NDF in cattle from the fecal excretion of fiber and diet characteristics using a meta-analytical approach. The dataset was compiled from 60 experiments with lactating cows and growing cattle carried out in Europe and Brazil, totaling 227 treatment means. The dataset was analyzed using linear mixed models according to meta-analysis techniques. The variation among experiments was considered as a random effect in the models. An unstructured (co)variance matrix was used. The evaluation of the effect of animal category was accomplished on intercept and slopes through a "dummy" variable D (i.e. binary variable),where D = 0 for lactating dairy cows and D = 1 for growing cattle. All analyses were performed using the MIXED procedure of SAS 9.2.Different models were adjusted considering two different units for NDF pool (pNDF): kg and g/kg BW. The independent variables were selected based on biological relevance and also on estimates of partial Pearson's correlation with the dependent variable. In this way, the independent variables were: fecal excretion of NDF (fNDF), representing the undigested fiber pool; dietary NDF content (dNDF), representing the dietary input of fiber; and the ratio between dietary iNDF (indigestible NDF) and dNDF (iNDF/dNDF), representing the quality of dietary fiber.The adjusted models were: pNDF (kg) = 2.95 -2.75 × D + 1.217 ×fNDF(kg)– 0.08034 × $fNDF^2$ (kg) + 0.003×dNDF(g/kg DM)– 1.606 × (iNDF/dNDF), $R^2 = 0.95$, $s_{XY} = 0.54$, where D = 0 for lactating cows and D = 1 for growing cattle; and pNDF (g/kg BW) = 5.20– 3.62 × D + 1.067 × fNDF (g/kg BW)– 0.03324 × $fNDF^2$ (g/kg BW) + 0.005 × dNDF (g/kg DM)– 2.809 × (iNDF/dNDF), $R^2 = 0.93$, $s_{XY} = 0.94$. All terms were found significant ($P < 0.05$) and there was no lack of fit for both models ($P > 0.63$). The meta-analysis results brought into evidence that NDF rumen pool can be estimated from fecal and diet characteristics avoiding the utilization of invasive techniques.

Key Words: meta-analysis, mixed models, ruminal evacuation

1802 (W261) Performance and carcass traits of immunocastrated Nellore cattle fed to β-agonists.

D. Silva Antonelo[1], M. Rezende Mazon[1], K. Eduardo Zanoni Nubiato[1], D. Juliana Brigida[1], J. Fernando Morales Gomes[2], B. Luis Nery Garcia[1], M. Zanata[1], P. R. Leme[1] and S. Luz e Silva*[3], *[1]University of Sao Paulo, Pirassununga, Brazil, [2]University of Cundinamarca, Fusagasugá, Colombia, [3]University of Sao Paulo/FZEA, Pirassununga, Brazil*

Beta-adrenergic agonists (βAA) have been used to improve performance and carcass traits of feedlot cattle. The use of non-castrated males for meat production is a common practice because they grow fast, use energy more efficiently and produce leaner and high-yielding carcasses. This work was developed to evaluate the effect of βAA and immunocastration on the performance of feedlot finished Nellore cattle. Ninety-six males (409 ± 50 kg LW; 20 mo old) were divided in two groups and half of them received two doses of immunocastration vaccine (Bopriva) within 30 days interval. Animals were fed for 70 days a common diet containing 76% concentrate and 24% roughage (corn silage). Following they were split in 3 groups ($n = 32$) and fed 30 more days one of the follow-

ing treatments: control diet without βAA (CON); control diet plus 80mg/d zilpaterol hydrochloride (Zilmax) (ZIL); control diet plus 300mg/d of ractopamine hydrochloride (Optaflexx) (RAC). Individual DMI, ADG and F:G were recorded. Data was analyzed as complete block randomized design in a 2x3 factorial arrangement. No interaction was observed between sex condition and treatments. There was no difference in DMI (9.1 kg/d) but non-castrated males were heavier (551 vs 520 kg; $P = 0.0004$), tended to have a greater ADG (1.21 vs 1.06 kg/d; $P = 0.1084$) and F:G ratio (132 vs 115 g of DMI/kg ADG; $P = 0.1102$) than immunocastrated, respectively. Immunocastrated animals had smaller hot carcass weight (HCW; 304 vs 323 kg; $P = 0.0006$) without difference in dressing percentage (DP; 58.5%). Animals fed ZIL showed highest ADG and F:G ratio (1.39 kg/d and 156 g of DMI/kg ADG, respectively; $P < 0.05$). CON treatment showed the smallest ADG and F:G ratio (0.89 kg/d and 94 g of DMI/kg ADG, respectively; $P < 0.05$). Treatment RAC showed intermediate results (ADG 1.1 kg/d and F:G 122 g of DMI/kg ADG, respectively; $P < 0.0001$) compared to ZIL and CON. There was no effect of treatment on final BW, DMI and HCW. Animals fed βAA showed heavier carcasses (313 kg RAC; 320 kg ZIL) than CON (308 kg) resulting in a higher DP for ZIL (59.1%) when compared to RAC (58.3%; $P = 0.0351$) and CON (58%; $P = 0.0048$), respectively. Non-castrated animals have better feedlot performance and βAA improves animal efficiency in feedlot.

Key Words: feedlot, growth, ruminant nutrition

1803 (W262) Effects of nicotinamide on hormone levels, antioxidant status and immune function of cows in heat stressed dairy cows. J. Cheng[1,2,3], N. Zheng[1,3,4], X. Sun[1,2,3], D. P. Bu[3], L. Pan[3] and J. Wang[*1,3,4], *[1]Ministry of Agriculture- Laboratory of Quality* and *Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [4]Ministry of Agriculture- Milk and Dairy Product Inspection Center (Beijing), Beijing, China*

The experiment was conducted to investigate the effects of nicotinamide on the blood hormone levels, antioxidant status and immune function of heat-stressed dairy cows. Twenty healthy early lactation Holstein cows (78.8 ± 11.0 DIM, 37.7 ± 1.8 kg of milk/d, 1.7 ± 0.4 parity) were randomly arranged to control and nicotinamide supplementation group. Cows were fed basic diet in control group and basic diet plus 8 g/d nicotinamide in nicotinamide group for 10 weeks. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Blood samples were collected from all of animals via tail vein before the morning feeding on days 0, 21, 42, and 56. Data were analyzed by MIXED model procedure of SAS 9.2. Compared with control cows, cows fed nicotinamide had higher contents of insulin (0.37 vs 0.34 ng/mL; $P = 0.03$), triiodotyronine (1.43 vs 1.27 ng/mL; $P = 0.03$) and leptin (2.74 vs 2.25 ng/mL; $P = 0.02$). Nicotinamide supplementation had the tendency to increase the thyroxine (29.02 vs 27.57 ng/mL; $P = 0.08$) and heat shock protein 70 (3.06 vs 2.29 ng/mL; $P = 0.10$), but had no effect ($P > 0.05$) on the contents of glucagon, insulin-like growth factor-1, growth hormone, prolactin and neuropeptide in blood. Cows fed nicotinamide had the tendency to elevate the activity of superoxide dismutase (10.29 vs 9.63 U/mL; $P = 0.07$), but had no effects ($P > 0.05$) on the activity of glutathione peroxidase, the levels of total antioxidant capacity and malondialdehyde. The contents of immunoglobulin (Ig) A (238.83 vs 160.38 μg/mL; $P = 0.01$), IgG (34.90 vs 21.54 μg/mL; $P = 0.03$), interleukin-4 (IL-4) (91.23 vs 77.19 pg/mL; $P = 0.04$) and IL-6 (138.81 vs 97.79 μg/mL; $P = 0.01$) were increased, and the ratio of $CD4^+/CD8^+$ were higher tendency (1.47 vs 1.16; $P = 0.10$) in cows fed 8g/d nicotinamide than in controls, while the levels of IgM, tumor necrosis factor-α, lymphocytes and the proportion of $CD4^+$ and $CD8^+$ T lymphocytes had no difference ($P > 0.05$) compared with the control. These results indicate that nicotinamide supplementation helps to alleviate the hormone metabolism disorder, improve antioxidant activity, and enhance the immune function in heat-stressed dairy cows.

Key Words: nicotinamide, dairy cows, blood metabolism

1804 (W263) Effects of supplemental bupleurum extract on blood material metabolism in heat-stressed dairy cows. X. Sun[1,2,3], N. Zheng[1,3,4], J. Cheng[1,2,3], D. P. Bu[3], L. Pan[3] and J. Wang[*1,3,4], *[1]Ministry of Agriculture- Laboratory of Quality* and *Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [4]Ministry of Agriculture- Milk and Dairy Product Inspection Center (Beijing), Beijing, China*

This study investigated the effect of bupleurum chinense DC. extract (BE) on blood metabolism of lactating dairy cows under heat stress. Forty lactating Chinese Holstein cows (75 ± 15 DIM, 37.5 ± 1.8 kg of milk/d, and 1.7 ± 0.4 parity) were randomly assigned to four groups and were individually fed a basic diet(CP = 17.2%, NDF = 53.4%) with 0, 0.25, 0.5, or 1.0 g BE/kg DM, respectively. The experiment lasted 10 weeks. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Dry matter intake was recorded twice a week. Blood samples were collected from all of animals via tail vein before the morning feeding on days 0, 21, 42, and 63. Data were analyzed by MIXED model

procedure of SAS 9.2. Supplementation of BE increased dry matter intake (20.80, 21.61, 22.13 vs 20.91 kg/d, $P = 0.02$) and blood total protein (80.97, 81.08, 81.00 vs 77.22 g/L, $P = 0.03$) level, but decreased urea nitrogen (BUN) contents (5.65, 5.58, 5.81 vs 5.95 mmol/L, $P = 0.04$). Cows fed 0.25 or 0.5 g/kg BE increased albumin content (38.61, 37.53 vs 36.18 g/L, $P = 0.01$) compared with control cows, but BE supplementation had no effects ($P > 0.05$) on blood glucose (GLU), nonesterified fatty (NEFA), total triglyceride (TG), low density liporotein cholesterin (LDL-C) and high density liporotein cholesterin (HDL-C). Sodium (Na) (136.63, 134.72, 136.05 vs 137.90 mmol/L, $P < 0.01$) and phosphorus (P) (1.94, 1.96, 1.81 vs 2.13 mmol/L, $P = 0.05$) concentrations in serum were decreased by BE supplementation, while potassium (K) (3.80, 3.83, 3.90 vs 3.48 mmol/L, $P < 0.01$) and calcium (Ca) (2.56, 2.59, 2.66 vs 2.46 mmol/L, $P < 0.01$) concentrations were decerased than in controls, but BE supplementation had no effect ($P > 0.05$) on serum magnesium (Mg) concentration. Serum chlorine (Cl) concentration was increased in cows fed 0.5 g/kg BE (148.01 vs 140.79 mmol/L, $P = 0.04$) compared with control cows, and tended to be higher (144.08 vs 140.79 mmol/L, $P = 0.08$) in cows fed 0.25 g/kg BE, but was not affected in cows fed 1.0 g/kg BE. These findings suggest that BE supplementation could improved the protein metabolism and maintain the balance of electrolyte concentration.

Key Words: bupleurum extract; dairy cows; blood metabolism

1805 (W264) Effects of nicotinamide on blood material metabolism of dairy cows under heat stress. X. Sun[1,2,3], N. Zheng[2,3,4], D. P. Bu[3], L. Pan[3] and J. Cheng[*1,2,3], *[1]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [2]Ministry of Agriculture- Laboratory of Quality and Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [4]Ministry of Agriculture- Milk and Dairy Product Inspection Center (Beijing), Beijing, China*

The experiment was conducted to determine the effects of nicotinamide on the metabolism of carbohydrate, lipid, protein and the mineral of serum in heat-stressed cows under hot environment. Twenty healthy early lactation holstein cows (78.8 ± 11 DIM, 37.7 ± 1.8 kg of milk/d, 1.7 ± 0.4 parity) were randomly assigned to control and nicotinamide supplementation group. Cows were individually fed basic diet (*CP* = 17.2%,NDF = 53.4%) in control group and fed basic diet plus 8 g/d nicotinamide in nicotinamide group. The trial lasted 10 weeks. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Feed intake was recorded twice a week. Blood samples were collected from all of animals via tail vein before the morning feeding on days 0, 21, 42, and 63. Data were analyzed by MIXED model procedure of SAS 9.2. There was no significant difference in dry matter intake between treatments (20.60 vs 20.71 kg/d; $P > 0.05$). The concentrations of nonestesterifiedfattyacid (221.25 vs 250.08 uEq/L; $P = 0.03$), total triglyceride (0.13 vs 0.15 mmol/L; $P = 0.03$), total cholesterol (5.79 vs 6.57 mmol/L; $P = 0.04$), and low density lipoprotein cholesterol (1.43 vs 1.76 mmol/L; $P = 0.04$) were decreased significantly by nicotinamide supplementation. Nicotinamide supplementation had the tendency to decrease β-hydroxybutyricacid level (0.66 vs 0.76 mmol/L; $P = 0.10$), but had no effect ($P > 0.05$) on the levels of serum glucose, total protein, albumin and urea nitrogen. Compared with control group, the levels of sodion (139.59 vs 137.90 mmol/L; $P = 0.03$) and chloridion ion (148.72 vs 139.75 mmol/L; $P = 0.05$) in serum were increased significantly by nicotinamide supplementation, but there was no difference ($P > 0.05$) in the levels of serum kalium, magnesium, phosphonium between the two groups. These findings suggest that nicotinamide supplementation can improved the lipid metabolism and maintain electrolyte balance of cows under heat stress.

Key Words: nicotinamide; dairy cow; blood metabolism

1806 (W265) Supplementation of selenium plus vitamin E vs. canola oil in the diet of feedlot cattle: which one can improve nutritional quality of meat modifying gene expression? G. F. Greghi[*1], A. Saran Neto[2], H. Fukumasu[1], J. C. D. C. Balieiro[3], A. O. Latorre[4], L. B. Correa[1] and M. A. Zanetti[1], *[1]University of São Paulo- USP/FZEA, Pirassununga, Brazil, [2]University of São Paulo, Pirassununga, Brazil, [3]University of São Paulo- USP/FMVZ, Pirassununga, Brazil, [4]Adolfo Lutz Institute, São Paulo, Brazil*

The metabolic conversion of dietary components is a control mechanism for gene expression, so the present study aimed to evaluate the effects of selenium (Se), vitamin E and canola oil on the expression of antioxidant and lipogenic genes. Forty-eight Nellore bulls at calan gate allocated in the Department of Animal Science USP-FZEA-Brazil were divided into four groups: Control(C): basal diet (30% forage- corn silage- and 70% concentrate, dry matter according to the nutrient requirements recommended by NRC,1996); Se+Vit E: addition of 2.5mg Se+500 IU vitamin E; Canola: addition of 3% canola oil; Se+Vit E+Canola: addition of 3% canola oil+2.5mg Se+500 IU of vitamin E(/kg DM, always). After 12 weeks, the animals were slaughtered at the Abattoir-School Campus and liver samples collected. Total RNA was extracted using RNeasy Tissue Kit (Qiagen), measured at 260 and 280nm, analyzed by agarose gel. RNA was converted into cDNA using DNase I and High Capacity RNA-to-cDNA kit and it was used for determination of gene expression by RT-qPCR using Taqman probes, 18S as endogenous control (Applied Biosys-

Table 1806. Gene expression

GENE	C	Se+Vit E	Canola	Se+Vit E +Canola	Pr > F	C1	C2	C3
NRF2	1.1661	1.8295	0.8032	1.121	0.0525	0.7904	0.5756	0.0079
GPX-1	1.1209	1.6099	0.8125	1.1594	0.08	0.783	0.8467	0.0109
GPX-4	1.3153	2.6565	1.1741	1.0114	0.0265	0.553	0.1032	0.0118
SCD	1.4732	2.3247	1.0792	2.674	0.0568	0.289	0.0751	0.0572
HMG-CoA-R	1.1911	1.4905	0.2459	0.9522	0.0633	0.4948	0.811	0.0096

tems) and calculated by Pfaffl's equation. The data were analyzed by Mixed SAS 2009 and contrasts used were: control vs. other (C1); Se+Vit E and Canola vs. Se+Vit E+Canola (C2); Se+Vit E vs. Canola (C3). The results are in Table 1806. The supplementation with Se+Vit E and Canola didn't show effects when compared to the control (C1), but differences were observed between Se+Vit E and Canola (C3), which had opposite effects. Se+Vit E induced expression of cytoprotectives genes (NRF2, GPXs, GSS) and increased the expression of responsible gene for the synthesis of CLAs (SCD) encouraging studies to improve nutritional quality of meat, but caution is needed because it can induce the synthesis of cholesterol through the expression of the gene HMG-CoA-R. Although Canola didn't increase the expression SCD gene, canola oil reduced the expression of HMG-CoA-R gene.

Key Words: antioxidants, bovine, cholesterol.

1807 (W266) Effects of feeding a corn straw or mixed forage diet on immune function in dairy cows.

P. Sun[1], C. Qin[1,2], D. P. Bu[1], J. Q. Wang[*1] and P. Zhang[2], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Hunan Provincial Key Laboratory for Genetic Improvement of Domestic Animal, College of Animal Science and Technology, Hunan Agricultural University, Changsha, China*

It has been demonstrated in previous researches that dietary nutrients affect immune function through their regulations on producing and activating immune factors. This study was conducted to evaluate the effects of feeding a corn straw or mixed forage diet on immunity of lactating cows by analysing compositions of serum immunoglobulins (Igs), cytokines, inflammation factors and plasma lymphocyte subsets. Twenty primiparous, lactating and ruminally fistulated Holstein cows were used in this study. Cows were randomly assigned to high forage diet (HF, forage: concentrate = 60: 40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diet (LF, forage: concentrate = 40: 60) with corn straw as the forage source. This experiment lasted for 2 months, and blood samples were obtained via jugular vein before morning feeding at the last day of the trial period. Plasma lymphocyte subsets were determined by flow cytometry and other indexes were measured with ELISA kits. Data were analyzed using the PROC MIXED procedure of SAS 9.1. The results showed that levels of serum IgA (37.81 and 39.77 ng/mL), secretory IgA (sIgA) (1.55 and 1.59 ng/mL), interleukin-2 (IL-2) (132.55 and 137.96 ng/L), IL-4 (33.53 and 35.22 ng/L), IL-6 (8.27 and 8.53 ng/L), IL-10 (37.65 and 39.47 ng/L), IL-12 (31.57 and 33.66 ng/L), interferon-α (IFN-α) (16.71 and 16.94 ng/L), IFN-γ (865.44 and 851.58 ng/L), tumor necrosis factor-α (TNF-α) (199.49 and 206.46 ng/L), prostaglandin E_2 (PGE_2) (152.86 and 160.95 ng/L) and plasma $CD4^+$ lymphocyte subset (27.88 and 30.54%), $CD8^+$ lymphocyte subset (21.02 and 22.25%) and $CD4^+/CD8^+$ ratio (1.57 and 1.57) were not affected by experimental treatments ($P > 0.05$), and cows in LF group tended to have higher serum IgE (498.55 and 469.64 ng/mL, $P = 0.09$), IgM (195.01 and 182.75 ng/mL, $P = 0.09$) and insulin-like growth factors-1 (IGF-1) (15.14 and 13.78 μg/L, $P = 0.06$) concentrations than those in HF group, while serum IgG (16.57 and 17.46 μg/mL, $P = 0.09$) level tended to be higher in HF group ($P < 0.10$). The results of this study indicated that different dietary systems had no effect on immunity in lactating cows.

Key Words: diet system, dairy cow, immunity

1808 (W267) Fatty acid composition of milk from cows supplemented with canola oil.

K. C. Welter, C. M. de Magalhães Rodrigues Martins, M. M. Martins, B. Roqueto dos Reis, J. G. Rebelato Forti, A. Soligo Vizeu de Palma, B. L. Unglaube Schmidt and A. Saran Netto*, *University of São Paulo, Pirassununga, Brazil*

The objective of this study was to evaluate the inclusion of canola oil in the diet of dairy cows on the fatty acid (FA) composition of milk. Eighteen lactating Holstein cows were distributed in 6 contemporary 3 x 3 Latin Square, 3 periods and 3 treatments: T1 = control diet (without oil), T2 = inclusion of 3% canola oil and T3 = 6% inclusion of canola oil in the diet (dry matter). The cows were individually fed. The experiment was conducted during three periods of 21 days, with 14 days for adaptation and seven days to collections. The milk samples were collected to determine the fatty acid composition on the last day of each experimental period. Identification and quantification of fatty acid were done by gas chromatograph (column of 100 meters using hydrogen carrier gas). The results were analyzed using the MIXED procedure of SAS (2001). The effects of treatments were analyzed using two orthogonal polynomial contrasts: linear (L) and quadratic (Q), the significance

Table 1808. Fatty acid composition (g/100g total FA) of milk from cows fed canola oil

Fatty acid composition	Inclusion of canola oil (%)				*P*	
	0	3	6	*SEM*	*L*	*Q*
Saturated	64.91	55.29	51.42	1.25	< 0.0001	= 0.033
Y = 63.97(1.11)– 2.1958(0.1677)X						
Unsaturated	34.48	43.53	47.52	0.98	< 0.0001	= 0.0049
Y = 35.4756(1.1284) + 2.1664(0.1748)X						
Omega-3	0.20	0.39	0.43	0.02	< 0.0001	= 0.0008
Y = 0.2286(0.0268) + 0.03369(0.005927)X						
Omega-6	1.98	2.08	2.11	0.05	0.273ns*	0.728ns
Omega-6/Omega-3	11.51	5.52	5.33	0.06	< 0.0001	= 0.0002
Y = 10.49(0.6779)– 1.055(0.1728)X						
Thrombogenicity	2.92	1.99	1.74	0.09	< 0.0001	= 0.001
Y = 2.78(0.10)– 0.1948(0.02030)X						
Atherogenicity	2.43	1.52	1.25	0.09	< 0.0001	= 0.0002
Y = 2.32(0.096)– 0.1952(0.01845)X						

ns = not significant.

declared at $P \leq 0.05$. The inclusion of 6% of canola oil in the diet increased 53.49% of milk omega-3 concentration and reduced 53.69% of omega-6/omega-3 ratio, in compare with the control treatment. The thrombogenicity (capacity to promote heart attacks and strokes) and atherogenicity (capacity to promote atherosclerosis) decreased linearly ($P < 0.0001$) with the inclusion of canola oil in the diet (Table 1808). In conclusion, canola oil alters the fatty acid composition of milk, resulting in healthier milk with nutraceutical properties.

Key Words: omega-3, dairy, nutraceutical, health

1809 (W268) Effects of a corn straw or mixed forage diet on bovine milk fatty acid biosynthesis. M. Zhao[1], D. P. Bu[1], J. Q. Wang[*1], X. Q. Zhou[1,2], Y. Zhang[1] and P. Sun[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Northeast Agricultural University, Harbin, China*

The study was designed to investigate the effects of different forage types on milk fatty acid (FA) profile. Thirty two dairy cows were divided into group MF (alfalfa and corn silage as forage source) and group CS (corn stover as forage source). The whole experiment lasted for 15 wk (2-wk adaptation and 13-wk experimental period) following 2-wk covariate period (a total of 17-wk). Milk fat content and fatty acid profile were measured. Statistical analysis was performed using the PROC MIXED procedure of SAS 9.0. The results showed that milk fat content in group MF was higher than group CS, but no difference was observed (4.46 vs 4.38%, $P > 0.05$). The proportion of milk saturated fatty acid (SFA) was significantly higher in group MF (74.77 vs 69.93%). However, unsaturated fatty acid (UFA) in group CS was higher than group MF (25.23 vs 30.07%). Unlike polysaturated fatty acid (PUFA), proportion of monounsaturated fatty acid (MUFA) in group CS exhibited significantly higher level mainly due to the large proportion of *cis*-9 C18:1 (MUFA, 21.62 vs 26.51%). Feeding the MF diet significantly increased short- and medium-chain fatty acid (SMCFA) proportion but decreased long-chain fatty acid proportion in group MF (SMCFA, 47.38 vs 41.02%; LCFA, 52.62 vs 58.98%). Therefore, corn stover as forage source in the diet could increase the proportion of UFA but decrease the proportion of SMCFA in milk.

Key Words: alfalfa, corn silage, corn stover

1810 (W269) Influence of forage level and corn processing method on feeding behavior of Nellore bulls. M. Caetano[1,2], A. R. Cabral[3], G. B. Feltrin[1], R. S. Goulart[4], S. Luz e Silva[3], P. R. Leme[3] and D. P. D. Lanna[*1], *[1]University of Sao Paulo/ESALQ, Piracicaba, Brazil, [2]University of Adelaide, Roseworthy, Australia, [3]University of Sao Paulo/FZEA, Pirassununga, Brazil, [4]MSD Saúde Animal, Sao Paulo, Brazil*

The objective of this study was to investigate the influence of neutral detergent fiber from forage (NDFf) levels and corn processing methods (CPM) on feeding behavior of finishing *Bos indicus* cattle fed high-concentrate corn-based diets. Forty Nellore bulls (388.1 ± 25.8 kg) were used in a randomized complete block design in a 4 x 2 factorial arrangement. Four levels of NDFf (3, 8, 13, and 18% sugarcane silage DM basis) were evaluated for two CPM: high moisture corn (HMC) and finely ground dry corn (FGC). Animals were fed ad libitum for 81 d, with diets delivered twice daily in individual pens. Sugarcane silage contained 64.0% NDF and 10.8 mm of mean particle size, all diets had 8% of whole linted cottonseed and the geometric particle sizes were 1.30 and 5.84 mm for FGC and HMC, respectively. Feeding behavior was evaluated twice (24 h each period) with fixed intervals of five min. Activities evaluated were eating, drinking, ruminating (R), chewing (C) and idling (min/d). Intake (IN), rumination (RU) and total chewing rate (TCR) were calculated (min/kg of DM). Number of meals (NM), interval between meals (IR) and meal duration

(MD) were estimated (min). The first derivative was solved of a 2nd order polynomial to determine optimal NDFf level. Animals fed HMC had 12.6% lower DMI ($P < 0.01$) and 6.1% lower ME intake (MEI; $P = 0.04$) compared to those fed FGC, but the IN was 21.6% greater for HMC than FGC ($P < 0.01$). There was a quadratic effect of NDFf on DMI ($P < 0.01$), MEI ($P < 0.01$) and IN ($P < 0.01$), with 10.8, 11.4 and 10.0% NDFf yielding the highest intakes, respectively. These NDFf levels to achieve maximum DMI and MEI are greater than recommendations in literature. Interactions between CPM and NDFf were observed for R ($P < 0.01$) and C ($P < 0.01$), however, when the RU and TCR were calculated, linear effects of NDFf were found for both. Increasing NDFf level increases the RU ($P < 0.01$) and TCR ($P < 0.01$). The HMC increases NM ($P < 0.01$) and decreases IR ($P < 0.01$) and MD ($P < 0.01$) when compared to FGC. Increasing NDFf level increased linearly the MD ($P < 0.01$). In conclusion, zebu cattle required around 11% NDFf to maximize DMI and MEI. The HMC increased the NM (min) and the IN (min/kg of DM).

Key Words: behavior, feedlot, zebu

1811 (W270) Evaluation of a hand-held meter to detect subclinical ketosis in dairy cows. Z. J. Cao*, S. S. Xu and S. L. Li, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China*

TNN is a new hand-held meter for detecting subclinical ketosis of dairy cows by determining blood β-hydroxybutyrate (BHBA). The objective of this study was to evaluate the performance of this new cowside test by comparing BHBA results obtained using the hand-held meter with those results made with a laboratory method and comparing the accuracy between diagnostic performance using blood and using milk and urine. 275 blood samples and 97 urine samples and 85 milk samples from clinically healthy Holstein cows between 1 and 58 days post-calving were analysed. The correlation coefficients for BHBA with TNN versus laboratory methods were 0.92. Based on Bland-Altman plot, agreement between two methods was good for BHBA. In this study, the TNN test had sensitivities of 75 and 88% at 1.2 and 1.4 mmol of BHBA/L of whole blood, respectively. Specificities were 97 and 99%, respectively. Compared with TNN the sensitivities and specificities of urine test and milk test were lower. The sensitivities and specificities were 57 and 80% for milk tests, respectively, and 71 and 94% for urine tests, respectively, when 1.2mmol/L of blood was defined as the threshold. Raising the threshold of laboratory method to 1.4mmol/L, The sensitivities and specificities were 75 and 79% for milk tests, respectively, and 75 and 93% for urine tests, respectively. We conclude that TNN is a useful tool to diagnose subclinical ketosis and blood tests are better methods than urine tests and milk tests due to higher sensitivity and specificity.

Key Words: subclinical ketosis, β- hydroxybutyrate, diagnostic

---

1812 (W271) Effects of rumen protected choline supplementation on milk yield and plasma metabolites in dairy cows fed hay based diets. L. Pinotti*, M. Ottoboni, V. Caprarulo, A. Pilotto, A. Agazzi, G. Invernizzi, A. Baldi and G. Savoini, *Università degli Studi di Milano, Dep. VESPA, Milan, Italy*

Most of studies on the effect of rumen protected choline (RPC) supplementation in dairy cows have been done using silage based diets. Accordingly, the aim of the study was to evaluate the effect of RPC supplementation in early lactating dairy cow receiving hay-based diet. For this purpose 12 Italian Holstein multiparous cows, in the first month of lactation (28 DIM), were divided into two experimental groups: control group (CTR) receiving no choline, and RPC group receiving 20 g/day of choline in rumen protected form (Balchem Inc., New Hampton, NY). Diets contained 50% hay (alfalfa and Meadow Hay), and 50% concentrates. Cows were housed at the Animal Production and Research of the Università degli Studi di Milano, fed in a Roughage Intake Control feeding system, and milked twice a day. The experiment lasted 9 weeks. Dry matter intake and milk yield were measured daily. Plasma was collected on week 1, 2, 3, 5, and 9 of the experimental period and analyzed for glucose, cholesterol, triglycerides, nonesterified fatty acids, betaidrossibutirrate and urea N. Before statistical analysis, daily measurements for DMI and milk yield were condensed to weekly means. Data were analysed as a completely randomized design by Proc MIXED procedure of SAS using treatment and time as fixed factors and cow within treatment as a random factor. The REPEATED statement was used for variables measured over time. Through the 9 weeks, treatment did not affect DMI (22.7 vs. 23.5 kg/d in CTR and RPC respectively) and milk yield (28.2 vs. 29.4 kg/d). Dietary treatment did not affect the metabolic profile of experimental cows, except for plasma glucose concentrations that tended ($P = .010$) to be higher in RPC cows than those of CRT (61.08 vs. 56.75 mg/dL). In this study RPC supplementation did not reveal any alterations in milk yield and serum metabolites in dairy cow receiving a hay-based diet, even though an exhaustive comparison with silage-based diet, merit further investigations.

Key Words: choline, hay based diet, milk yield

1813 (W272) Liver metabolism of Holstein cows is altered by nutrient supply but not by lipopolysaccharide in vitro. M. Garcia*, B. J. Bequette and K. M. Moyes, *Department of Animal and Avian Sciences, University of Maryland, College Park*

Recent work suggests liver function is reduced during inflammation. To our knowledge, no studies have examined whether increased amino acid or propionate supply improves hepatic function during inflammation and how this is altered by stage of lactation. The objective of the current study was to characterize the effect of nutrient supply and lipopolysaccharide (LPS) challenge on hepatic intermediate metabolism for cows in early and mid-lactation by employing gas chromatography–mass spectrometry (GC-MS) and stable isotope tracer ([$^{13}C_3$] pyruvate). Liver samples were collected via biopsy from healthy early (n = 6, < 21 DIM) and mid-lactation (n = 6, < 110 DIM) Holstein cows. Liver slices were incubated for 2 h at 37°C in 3 mL of Krebs-Ringer bicarbonate buffer containing 2 mM of a 50:50 mix of labeled and unlabeled [$^{13}C_3$]pyruvate with addition of either phosphate buffered saline (control), 2 mM propionate, or 2 mM amino acids, with or without addition of LPS (200 ng/mL). Krebs cycle intermediates were determined by GC-MS by monitoring alanine, aspartate, and glutamate, which are in metabolic equilibrium with Krebs cycle intermediates. Data were analyzed as a randomized block design in a 3×2×2 factorial arrangement. Significance was declared at $P < 0.05$. Overall, LPS challenge had minimal effects on intermediary metabolism. Regardless of nutrient supply, the ^{13}C kinetics demonstrated that the liver of early lactation cows exhibits higher relative activity of phosphoenolpyruvate carboxykinase (PEPCK), a tendency for greater flux of pyruvate to oxaloacetate ($P = 0.07$, 82 vs. 74%), and a lower relative activity of pyruvate dehydrogenase (PDH) compared to pyruvate carboxylase (PC) when compared to cows in mid-lactation. Regardless of stage of lactation, propionate and amino acids increased the proportion of acetyl-CoA derived from pyruvate (13 and 10%, respectively) compared to control (7%), with no difference in the flux of oxaloacetate that derived from pyruvate. Moreover, propionate increased the relative activity of PDH compared to PC. In conclusion, results suggest that the LPS endotoxin exposure in vitro does not impair liver metabolic function and that cows in early lactation had a greater gluconeogenic capacity than cows in mid-lactation.

Key Words: cows, liver, nutrient flux

1814 (W273) Effect of postruminal infusion of fructose on hepatic steatosis. K. E. Boesche*, J. E. Sibray, S. L. Koser and S. S. Donkin, *Purdue University, West Lafayette, IN*

Periparturient dairy cattle are prone to metabolic disease and frequently experience hepatic steatosis. A more complete understanding of the development and impact of hepatic steatosis has been hampered by the lack of a predictable and convenient steatosis induction model. Intensive fructose consumption in both rats and humans rapidly results in hepatic steatosis and insulin resistance, but the impacts of fructose on hepatic steatosis in dairy cattle are unknown. The objective of this study was to examine the effects of postruminal fructose supply on accumulation of liver triglycerides (TG) and other parameters of fatty liver disease in lactating dairy cattle. Eighteen multiparous late-lactation (241.7 ± 28.5 d in milk) Holstein cattle were assigned to either control (CON), postruminal fructose infusion (INF), or a pair-fed (PAIR) group. INF cows were previously fitted with rumen cannulae and received 1000 g/d D-fructose for 7 d as a 16.67% w/v fructose solution delivered postruminally. Fructose dose averaged 1.47 g ± 0.11/kg body weight (BW) and was delivered over a 23 h period. Amount of feed offered to PAIR group was matched to the previous 24 h intake of INF cows to account for any potential impact of fructose infusion on voluntary feed intake. CON group was fed ad libitum. There were no differences ($P > 0.1$) between groups in BW or body condition score before or after the infusion period. Milk production decreased (26.2, 23.1, 23.3 ± 0.79 kg for CON, INF, PAIR, respectively; $P < 0.05$) in both INF and PAIR groups during infusion period and was accompanied by decreased feed intake (23.5, 20.1, 19.4 ± 1.21 kg/d dry matter intake; $P < 0.05$). Plasma TG levels were not significantly different ($P > 0.1$) before, during, or after fructose infusion, but were numerically lower in INF, compared to PAIR, after infusion. Liver TG levels did not differ ($P > 0.1$) by group before or after infusion. Plasma fructose levels tended to remain high (602.9, 485.8 ± 44.60 μM for INF, PAIR, respectively; $P < 0.1$) in INF group after infusion period. Plasma glucose levels did not differ ($P > 0.1$) by group, nor did serum nonesterified fatty acid levels ($P > 0.1$). Data do not support the use of 7 d postruminal infusion of D-fructose at 1000 g/d as a model to study hepatic steatosis in lactating dairy cattle.

Key Words: fructose, hepatic steatosis, postruminal infusion

1815 (W274) Effects of rare earth-chitosan chelate on liver and kidney parameters in lactating dairy cows. J. Li[1,2], J. Q. Wang[1], P. Sun[1], F. D. Li[2] and D. P. Bu*[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]College of Animal Science and Technology, Gansu Agricultural University, Lanzhou, China*

Rare earth-chitosan chelate (RECC) formed by β-NH_2 and rare earth ions with glucosamine molecule (1,4)-OH on the glycosidic bond, have been used as a new chelating ligand feed additives to promote efficient feed utilization in ruminants and improve animal productivity while reducing the need for

antibiotics and chemical additives. Numerous reports have indicated that suitable amount of RECC mixtures in the diet increase not only the liveweight gain of livestock and poultry but also milk and egg production. The objective of this study was to determine the effect of different proportion of rare earth-chitosan chelate (RECC) on hepatic and renal function of lactating dairy cows. Forty-eight lactating Holstein dairy cows (DIM = 130 ± 5, average milk yield = 33.2 ± 5.1 kg/d) were randomly assigned to 4 treatments (n = 12) with addition of RECC (0 (control), 0.15%, 0.75%, and 1.5%, respectively) in diets. The experiment lasted for 9wk with the first week for adaptation. Blood was collected in evacuated tubes via caudal venipuncture at 0, 2, 4, 6, 8 week and the tubes with blood samples were centrifuged at 3500 × g for 15 min to obtain serum, which was separated into several aliquots and stored at −80°C in an ultra-low-temperature freezer until further analysis. Data were analyzed by mixed or GLM procedure of SAS software. No significant differences (P > 0.05) were found for the activity of glutamic-pyruvic transaminase (ALT) and glutamic oxalacetic transaminase (AST), total protein (TP), albumin (ALB), globulin (GLB), Uric Acid (UA) and urea nitrogen(UREA) in all the dietary treatments. Compared with control, there were no difference (P > 0.05) in total bile acid (TBA) and creatinine (CRE) between 0.15% RECC and 0.75% RECC treatments, while increased (P < 0.05) when the RECC adding dose up to 1.5%. Feeding 0.15% or 1.5% RECC resulted in higher total bilirubin(TBIL)(5.77, 6.05 umol/L vs. 4.89, 4.89 umol/L) and indirect bilirubin (DBIL) (2.30, 2.54 umol/L vs. 2.00, 1.93 umol/L) vs. control and 0.75% RECC group (P < 0.01). These results suggested that the adding doses of RECC in dietary did not affect the activity of ALT and AST, while TBA, CRE, TBIL and DBIL were significantly increased in 0.15% RECC. So it was concluded that adding 1.5% RECC in dietary has a negative effect on the function of liver and kidney in dairy cows.

Key Words: dairy cows, liver and kidney parameters, rare earth-chitosan chelate

---

1816 (W275) Supplementation of *Aspergillus oryzae* α-amylase on ruminal volatile fatty acid distribution and digestive tract gene expression in beef steers fed a steam-flaked corn based finishing diet.

B. N. Gordon[1], S. W. Hahm[*1], J. J. Wagner[1], J. S. Jennings[2], H. Han[1] and T. E. Engle[1], [1]*Colorado State University, Fort Collins,* [2]*Texas A&M AgriLife Research, Amarillo*

The objective of this study was to investigate the impact of *Aspergillus oryzae* α-amylase (AAM) supplementation on rumen VFA profile and relative abundance of mRNA associated with nutrient absorption in ruminal and duodenal tissue from beef steers. Nine crossbred steers (average BW 622 ± 50 kg), with rumen and duodenal fistulas were housed in individual stations and fed a high concentrate finishing diet twice daily for 8 d. Treatments included CON (corn meal; n = 5) and AAM (750 fungal α-amylase units/g; n = 4). Dietary treatment supplements were applied as a top dress (3 g of α-amylase or corn meal into 150 g of dried distiller's grains (DDG) for the AM feeding and 2 g of α-amylase or corn meal into 100 g of DDG for PM feeding). On d 5, rumen fluid samples were obtained every 4 h for 24 h and analyzed for VFA concentration. On d 9, rumen papillae and duodenal mucosal tissue samples were collected. Total tissue RNA was extracted for real-time PCR analysis. Sodium/potassium ATPase pump α1, glucose transporter 2 and 5, putative anion transporter, isoform1, sodium/hydrogen antiporter isoforms1, 2 and 3, 3-hydroxy 3-methylglutaryl coenzyme A synthase isoform2, down regulated in adenoma, monocarboxylate co-transporter isoform1, and glyceraldehyde-3-phosphate dehydrogenase mRNA were tested. Relative expression (fold change) of mRNA in ruminal and duodenal tissues were analyzed using PROC GLM and VFA distribution was analyzed as a randomized block design with repeated measures using the MIXED procedure of SAS. Concentrations of VFA and the acetate to propionate ratio were similar across treatments. However, acetate:propionate ratio and butyrate molar percentage were numerically greater (P = 0.17) in AAM steers compared to controls. Genes tested were not significantly changed by AAM supplementation in the rumen or duodenum. However, genes involved in nutrient absorption were numerically decreased in the rumen and increased in the duodenum in the AAM supplemented steers compared to the controls.

Key Words: duodenum, fungal α-amylase, gene, rumen, steer, volatile fatty acids

---

1817 (W276) Effects of rumen-protected choline during the transition period on nonesterified fatty acids and β-hydroxybutyrate concentrations in periparturient dairy cattle.

I. M. Lima[1], R. A. Silva[1], C. H. Ramires[1], S. L. Viechnieski[2] and R. D. Almeida[*1], [1]*Universidade Federal do Paraná, Curitiba- Paraná, Brazil,* [2]*StarMilk Farm, Céu Azul- Paraná, Brazil*

The effects of rumen-protected choline (RPC) on nonesterified fatty acids (NEFA) and β-hydroxybutyrate (BHBA) concentrations, body condition score (BCS), and milk fat to protein ratio (FPR) were evaluated in periparturient dairy cows. Pregnant Holstein cows (n = 106) and heifers (n = 52) in a commercial farm in Southern Brazil were blocked by parity and expected day of calving and randomly assigned to 2 treatments. Cows in the first treatment were supplemented with rumen-protected choline (RPC; Reashure, Balchem Corp.), whereas cows in the second treatment were not supplemented (CON). All animals were housed together in transition pens, and RPC cows were individually top-dressed 60 g/d RPC to provide 17.3 g of choline while restrained in feedline headlocks from 21 d before to 28 d after calving. The CON diets

were top-dressed with 60 g/d of corn meal. Four blood samples were collected from each animal (7 d before calving, at calving, 7 and 14 d after calving). Data was analyzed using MIXED procedure of SAS with a model containing the effects of block, treatment, time, and treatment*time interaction as fixed effects, prepartum BCS as a covariable, and cow within treatment as a random effect. Body condition score did not differ ($P > 0.05$) between RPC and CON cows in all three observations (21 d before calving, at calving, and 28 d after calving). Multiparous cows showed greater ($P < 0.01$) NEFA and BHBA concentrations than primiparous ones; 0.361 ± 0.017 mmo/L vs. 0.294 ± 0.023 mmol/L; and 0.646 ± 0.019 mmo/L vs. 0.562 ± 0.024 mmol/L, respectively. Concentrations of NEFA peaked ($P < 0.01$) at calving; 0.473 ± 0.021 mmo/L, whereas BHBA concentrations peaked ($P < 0.01$) at 14 d after calving; 0.724 ± 0.044 mmol/L. Nonesterified fatty acids concentrations did not differ ($P > 0.05$) between RPC and CON cows; 0.355 ± 0.017 mmol/L vs. 0.324 ± 0.017 mmol/L. Similarly, BHBA concentrations did not differ ($P > 0.05$) between treatments; 0.633 ± 0.020 mmol/L vs. 0.606 ± 0.020 mmol/L, respectively for RPC and CON cows. Finally no milk FPR differences ($P > 0.05$) were observed between RPC and CON cows in the first test-day after calving; 1.30 vs. 1.34. In the particular conditions of this on-farm trial with very modest lipid mobilization (3.35 BCS at 21 d before calving and 3.10 BCS at 28 d after calving) no benefits on RPC supplementation were detected.

Key Words: choline, dairy cows, ketosis

1818 (W277) Effects of replacing alfalfa hay and corn silage with corn straw in diets on main hormones in blood of dairy cows.

X. Q. Zhou[1,2], D. P. Bu[2], Y. D. Zhang[2], M. Zhao[2], P. Sun[2] and J. Q. Wang[*1,2], *[1]Heilongjiang Bayi Agricultural University, Daqing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

To study the effects of replacing alfalfa hay and corn silage with corn straw in diets on main hormones related to metabolism in blood of Holstein cows, Twenty-four firstborn and healthy Holstein lactating dairy cows with similar DIM (55 ± 27 d) and body weight (520 ± 25 kg) were randomly divided into 2 groups. Diets contained similar concentrate mixtures with the same forage-to-concentrate ratio of 36:64 (dry matter basis). Different forage sources were then added: 17.30% alfalfa hay and 18.77% corn silage (MF); 36.07% corn straw (CS). The preliminary experiment lasted for 2 wks followed by a 60-day former experiment. The blood samples on d 61 were collected and evaluated the concentrations of insulin (INS), growth hormone (GH), leptin (LEP),cortisol (COR), insulin-like growth factor-1(IGF-1) and prolactin (PRL) in serum. Compared with the MF group, the concentrations of IGF-1 (384.31 vs 311.73%, $P < 0.01$) and LEP (3.67 vs 3.12%, $P < 0.05$) in CS group were significanly increased, but the concentrations of PRL (175.51 vs 230.37%, $P < 0.05$) was decreased. No difference was observed in other hormones ($P > 0.05$). Results showed that under the condition of the same concentrate, different forages can greatly affect concentrations of some hormones in the blood which closely relate to the changes of body's immune and production performance.

Key Words: corn straw, dairy cows, hormones

1819 (W278) Body condition score at calving alters the hepatic transcriptome in grazing dairy cattle.

H. Akbar[1], Z. Zhou[*1], K. Macdonald[2], K. E. Schütz[3], G. Verkerk[2], J. R. Webster[3], S. L. Rodriguez Zas[1], J. R. Roche[2] and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]DairyNZ, Hamilton, New Zealand, [3]AgResearch, Hamilton, New Zealand*

The objective of this study was to use transcriptomics and bioinformatics to evaluate changes in hepatic gene expression profiles in cows managed to achieve a high (H, 5.5 BCS), medium (M, 4.5 BCS), or low (L, 3.5 BCS) BCS (10-point scale). Target BCS at calving were achieved by managing feed allowance before dry off. Post-calving cows were allocated pasture and pasture silage. Liver from 10 cows per BCS group was biopsied on wk 1, 3, and 5 relative to parturition. A whole-transcriptome bovine microarray (Agilent) was used. An ANOVA with repeated measures using PROC MIXED resulted in 5888 DEG due to the main effect of BCS and 327 differentially expressed genes (DEG; False Discovery Rate < 0.05) due to BCS × wk. Bioinformatics analysis was performed with the Dynamic Impact Approach (DIA), focusing on pathways from the KEGG database. The BCS × wk DEG, analysis of most-impacted pathways revealed marked differences on wk 1 for H vs. L and M vs. L; 'fatty acid biosynthesis', 'biosynthesis of unsaturated fatty acids', 'ascorbate and aldarate metabolism', and 'steroid biosynthesis' were among the top 5 highly-impacted pathways when comparing H vs. L and L vs. M. All were highly-inhibited in H vs. L, but highly-activated in L vs. M. The degree of impact on pathways was quite low when comparing H vs. M on wk 1 and there were few differences in pathway flux (i.e. little change in activation/inhibition). Remarkably, on wk 3, pathways in L vs. M remained activated but signaling pathways such as NOD-like receptor, p53 signaling, and RIG-I-like receptor were among the most-impacted. The most-impacted pathways in H vs. L on wk 3 were, for the most part, the same as those observed on wk 1. 'Fatty acid biosynthesis' on wk 3 was the most-impacted pathway and markedly inhibited in H vs. M. Data from wk 5 indicate a lesser effect of BCS at calving on the transcriptome because impact values, regardless of BCS, were substantially lower than those in wk 1 and 3. However, it is noteworthy that the 'sulfur relay system' pathway, key for post-transcriptional RNA modifications in mammals, was the most impacted and inhibited pathway in H vs. M. Preliminary bioinformatics anal-

yses underscored the role of BCS at calving on liver function through alterations of the molecular phenotype and indicate a likely optimum BCS between 4.5 and 5.5.

Key Words: bioinformatics, nutrition, lactation

1820 (W279) Short term feed restriction increases afternoon but not morning milk fat concentration in lactating dairy cows. A. M. Abdelatty[*1,2], M. E. Iwaniuk[2], A. E. Weidman[2], B. B. Teter[2], M. A. Tony[1], F. F. Mohammad[1] and R. A. Erdman[2], *[1]Cairo University, Cairo, Egypt, [2]University of Maryland, College Park*

The elevated milk fat concentration exhibited by cows during the early periparturient period is related to the degree of body tissue mobilization. We hypothesized that feed restriction could be used as tool to study temporal changes in milk composition. Our objective was to test the effect of short-term feed restriction on milk fat concentration. Ten multiparous Holstein cows (100 + 17 DIM) were used in the 21 d study. During d 1 to 14, all cows were allowed ad libitum access to a total mixed ration that was formulated to meet 2001 NRC nutrient requirements for 40 kg/d milk production and this period was used as covariate in the ANOVA. Treatments (Trt) consisted of either ad libitum (AL) or restricted (RES) feeding during d 15 to 18 where RES cows were fed 60% of their d 1 to 14 ad libitum intakes. All cows returned to ad libitum feeding on d 19 to 21. Cows were milked twice daily at 0630 and 1630 h and fed once daily at 0900 h. Milk production and composition were measured at each milking on d 13 to 21. As expected, milking time influenced milk production and composition ($P < 0.001$) for fat and protein. While feed restriction decreased ($P < 0.001$) milk production, but not milk protein and fat percent. There were treatment by milking time interactions for milk fat ($P < 0.001$) and protein ($P = 0.008$) percent which were increased at the 1630 h but not the 0630 h milking. A day by treatment by milking time interaction ($P < 0.02$) was observed for milk fat which showed the greatest elevation at the 1630 h milking on d 16. These results demonstrate that feed restriction can be used to study temporal changes in milk composition.

Key Words: feed restriction, milk composition, dairy cows

1821 (W280) The mRNA expression of the classical genes of enzymes involved in milk fatty acid synthesis does not explain milk fat depression in dairy cows. A. Siurana*, D. Gallardo and S. Calsamiglia, *Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain*

Feeding polyunsaturated fatty acids (PUFA) to dairy cows results in milk fat depression (MFD) in some, but not all cows. The objective of this research was to compare the mRNA expression of enzymes involved in fatty acid (FA) synthesis in the mammary gland of cows resistant or sensitive to MFD resulting from feeding PUFA. Four cows were selected from a dairy farm after a switch from a control diet to a linseed-rich diet: two were resistant to MFD and had high milk fat content before and after the change (R-MFD); and two were sensitive to MFD and milk fat content decreased after the change into the linseed diet (S-MFD). Fresh milk samples were collected from each cow the week before and two weeks after the diet change, and analyzed for milk fat content, milk FA profile and transcriptional profiling of mRNA by Illumina RNA-sequencing technology. The study focused on the enzymes reported to be involved in MFD: acetyl-CoA carboxylase (ACACA), fatty acid synthase (FASN), glycerol-3-phosphate acyltransferase (GPAT), acylglycerol-3-phosphate acyltransferase (AGPAT), stearoyl-CoA desaturase (SCD1), fatty acid binding protein (FABP), lipoprotein lipase (LPL), sterol regulatory element binding protein (SREBP1) and spot 14 (S14). When S-MFD cows were fed linseed, milk fat decreased from 3.56 to 2.54%, the unsaturated:saturated FA ratio increased from 41/59 to 45/55 and short- and medium-chain FA proportion (C4 to C14 and 50% C16; SMFA) decreased from 33.9 to 32.8%, as expected, but there were no significant changes in the mRNA expression of the genes tested. When R-MFD cows were fed linseed, milk fat unexpectedly increased from 4.06 to 4.36%, the unsaturated:saturated FA ratio increased from 35/65 to 39/61,

Table 1820.

Milking:	0630 h		1600 h			*P* =		
Treatment	AL	RES	AL	RES	SEM	Time	Trt	Trt*Time
Milk, kg	21.6	19.2	18.8	15.2	0.72	0.007	0.001	0.014
Milk protein, %	2.88	2.87	2.73	2.87	0.058	0.001	0.392	0.001
Milk other solids, %	5.66	5.54	5.54	5.54	0.028	0.073	0.065	0.008
Milk Fat %								
Day 15	2.98	2.69	4.32	4.10	0.24	0.001	0.274	0.001
Day 16	2.96	2.89	4.30	5.86				
Day 17	2.96	2.87	4.20	4.94				
Day 18	3.00	2.89	4.16	5.10				
Days 19 to 21	3.03	2.86	4.12	3.89	0.13	0.001	0.232	0.742

SMFA proportion did not change (average of 31.4%) and only the expression of ACACA decreased and that of AGPAT6 and FABP3 increased. The unexpected over expression of AGPAT6 and FABP3 transcripts in R-MFD cows may be potential candidate genes involved in the MFD-resistance. Other genes that may also be involved need to be identified.

Key Words: milk fat depression, mRNA expression, extruded linseed.

1822 (W281) Effects of niacin supplementation and forage type on milk, digestibility, blood parameters and body temperature in lactating dairy cows.

R. B. Standish*, P. S. Erickson, N. L. Whitehouse, B. J. Isenberg, E. M. Barron, J. Y. Buckley and A. M. Pike, *University of New Hampshire, Durham*

This experiment evaluated the effect of niacin combined with either corn silage (CS) or grass silage (GS) based diets on apparent total tract nutrient digestibility, milk yield and composition, body temperature, and blood parameters. Four ruminally-cannulated Holstein cows were used in a 4 x 4 Latin square design with a 2 x 2 factorial arrangement of treatments with 28-d periods. Treatments were CS or GS based diets without or with 12 g niacin/d. One primiparous and three multiparous late lactation cows (225 ± 12 d in milk) were used. One cow was removed during the third period due to unrelated causes. Each period, dry matter intake (DMI) and milk production were recorded (d 19-28), and samples of blood (1300h, d 28), milk (0630 and 1730 h for 2 d), feeds (0545 and 1745 h on d 19-28), feces, and body temperature (both at 2-h intervals on d 26-28) were taken. Serum was analyzed for glucose and non-esterified fatty acids. Feed and feces were analyzed for acid insoluble ash, and digestibility was determined for dry matter (DM), organic matter (OM), crude protein (CP), neutral detergent fiber (NDF), acid detergent fiber (ADF), starch, fat, and hemicellulose (NDF-ADF). Data were analyzed using the mixed procedure of SAS. Orthogonal comparisons were used to evaluate main effects and interactions. Repeated measures were used to analyze body temperature and means were separated using Tukey's test. Intake of DM was greater (P = 0.01) for cows fed CS than for cows fed GS (29.01 and 24.09 kg/d, respectively). Digestibility of NDF was greater (P = 0.002) for cows fed GS than for cows fed CS (63.7 and 45.8%, respectively). Digestibilities of DM, OM, ADF, CP, and starch were similar among treatments. Hemicellulose digestibility was greater (P = 0.002) for cows fed GS versus cows fed CS (82.2 and 53.1%, respectively) because cows fed GS had lower DMI. Fat digestibility was greater (P = 0.02) for cows fed CS versus cows fed GS (93.0 and 82.4%, respectively). Milk yield was less for cows fed GS versus CS (20.0 and 29.9 kg/d, respectively). Fat (0.77 and 1.07 kg) and protein yields (0.61 and 0.96 kg) were less for cows fed GS versus CS (P = 0.02 and 0.04, respectively). Body temperature tended (P = 0.08) to be lower for cows fed GS and niacin (37.7°C) versus cows fed only CS (38°C). Niacin did not improve any parameter except for lowered body temperature.

Key Words: niacin corn silage grass silage

1823 (W282) Differences in hepatic transcriptional regulatory networks due to body condition score at calving in grazing dairy cattle.

H. Akbar[1], Z. Zhou*[1], K. Macdonald[2], K. E. Schütz[3], G. Verkerk[2], J. R. Webster[3], S. L. Rodriguez Zas[1], J. R. Roche[2] and J. J. Loor[1], *[1]University of Illinois, Urbana, [2]DairyNZ, Hamilton, New Zealand, [3]AgResearch, Hamilton, New Zealand*

Despite recent progress in nutrigenomics of peripartal dairy cattle, many components of transcriptional regulation in hepatic networks remain unknown. The objective of this study was to use gene network analysis on hepatic microarray data to identify transcription regulators (TR) and their target genes. Holstein-Friesian cows managed to achieve a high (H, 5.5 BCS), medium (M, 4.5 BCS), or low (L, 3.5 BCS) BCS (10-point scale) were used. Target BCS at calving were achieved by managing feed allowance before dry off. Post-calving, cows were allocated pasture and pasture silage (predominantly perennial ryegrass). Liver from 10 cows per BCS group was biopsied on wk 1, 3, and 5 postpartum. A whole-transcriptome bovine microarray (Agilent) was used. An ANOVA with repeated measures using PROC MIXED resulted in 5888 differentially-expressed genes (DEG) due to main effect of BCS (False Discovery Rate < 0.05) and 327 differentially expressed genes due to BCS × wk. TF network analysis was performed with Ingenuity Pathway Analysis (IPA). The network analysis uncovered TP53 as a central hub regulating a large spectrum of genes altered by BCS. Expression of TP53 was overall greater in H vs. M and L vs. M, but lower in H vs L. Other important TR altered by BCS were CTNNB1, SREBF1, RXRA, STAT1, NFKBIA and YWHAH. Among DEG with a BCS × wk effect due to H vs. M or L vs. M on wk 1, HNF4A was among 10 TR uncovered to have the greatest number of targets. Unlike wk 1, out of 9 TR identified in wk 3, the expression of MYC was downregulated in H vs. L but this TR had the greatest number of targets. Similarly, MYC had the greatest number of targets in L vs. M on wk 3 but was upregulated. Contrary to wk 1, on wk 5 the expression of MYC was upregulated in H vs. L and FOXP3 was identified as an important TR. Expression of FOXP3 on wk 5 was downregulated in H vs. M but among 16 TR identified it had the greatest number of targets. It is noteworthy that TP53, MYC, and FOXP3 are key controllers of cell proliferation/apoptosis in non-ruminant tissues/cells. Although HNF4A also is related with liver development, it has broader functions in terms of controlling expression of metabolic genes. Preliminary interpretation suggests an important role of a few TR in the control of liver function.

Key Words: gene networks, bioinformatics, systems biology

1824 (W283) Effects of a corn straw or mixed forage diet on mammary gland function and its endocrine regulation in early lactation dairy cows. T. Qin[1], H. Y. Wang[1], D. P. Bu[*2] and H. B. Zhu[1], *[1]Embryo Biotechnology and Reproduction Laboratory, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

The forage system is critical to lactation performance in dairy cows. The objective of this study was to evaluate the effects of two different forage patterns on the mammary gland and the endocrine regulation of its functions. Twelve multiparous, early-lactation Holstein cows were randomly assigned to high forage diet (MF, forage: concentrate = 60: 40) with Chinese wildrye, alfalfa hay and corn silage as the forage source or low forage diet (CS, forage: concentrate = 40: 60) with corn straw as the forage source. Body weight (BW), body condition score (BCS) and dry matter intake (DMI) of each cow were recorded. Milk yield were recorded daily,and milk compositions and somatic cell count (SCC) were detected. Blood samples were collected weekly, and mammary biopsies were taken on 16 days postpartum. Data were analyzed using the PROC MIXED procedure of SAS 9.1. From the 6-wk of lactation, cows fed MF diet produced more milk (23.05 and 18.24 kg/d; $P < 0.05$), and tended to produce more milk fat (1.08 and 0.81kg/d; $P = 0.07$) and protein (0.69 and 0.59kg/d; $P = 0.10$) compared with cows fed CS diet. In CS group, the milk SCC were greater than those in MF group (Somatic cell score: −5.25 and −6.88; $P = 0.02$). There were no differences in BW, BCS and DMI ($P > 0.05$). Compared to MF cows, insulin like growth factor-I (IGF-1) in blood (70.21 and 50.49 ng/mL; $P < 0.05$) and *IGF-1R* expression in mammary (1.86 ± 0.15 and 1.45 ± 0.11; $P = 0.02$) were lesser in CS group. Mean concentrations of serum BHBA (1.64 vs 0.51 mmol/L; $P < 0.0001$) and NEFA (832.3 vs 309.0 μEq/L; $P < 0.01$) in MF cows peaked in week 2 after calving, and greater than CS group. The secretory activity of mammary epithelial cells (MEC) and the rate of mammary cell proliferation in both groups had no significant difference ($P > 0.05$),but the rate of cell apoptosis in CS group were greater relative to the MF group (1429 ± 103 and 679 ± 128 counts/mm^2; $P = 0.003$). The results indicated that lactation performance of dairy cows were affected by forage patterns, which was closely related to their endocrine regulation in dairy cows.

Key Words: forage sources,mammary gland function,endocrine regulation

1825 (W284) Milk fatty acid profile of dairy cows grazing a tropical pasture supplemented with sources of rumen protected fat. J. D. Souza[*1], F. Batistel[2], C. Sitta[1] and F. A. P. Santos[2], *[1]University of Sao Paulo, Piracicaba, Brazil, [2]University of São Paulo, Piracicaba, Brazil*

The objective of this experiment was to investigate the effects of supplementation of early lactation dairy cows grazing a tropical pasture with diets containing calcium salts of palm oil (CSPO) or calcium salts of soybean oil (CSSO) on milk fatty acid profile. Twenty-seven cows (15 ± 3 DIM) were used in a randomized block design and subjected to the following treatments: a) control (no fat); b) 400 g CSSO cow^{-1} d^{-1}; c) 400 g CSPO cow^{-1} d^{-1}. Cows grazed paddocks of *Pennisetum purpureum* and received 8 kg cow^{-1} d^{-1} (DM) of concentrate twice daily. Treatment periods were 90 d in length and milk samples were taken at 30, 60 and 90 d of experimental period for milk fatty acid analysis by gas chromatography. Data were analyzed as repeated measures using a mixed model with block as random effect and means were compared by Tukey test. The CSSO increased C18:2 cis-9 trans-12, CLA cis-9 trans-11 and CLA trans-10 cis-12 in the milk fat compared with control and CSPO. Both fat sources increased C18:3 cis-9 cis-12 cis-15 in the milk fat. The *de novo* synthesis was reduced by both fat sources and the CSPO increased mixed fatty acids (C16 + C16:1), due to greater incorporation of C16 from the diet. The preformed fatty acids were increased by CSSO supplementation. The CSSO decreased total saturated fatty acids, and increased MUFA and PUFA compared to control and CSPO. Overall, both sources of fat changed the milk fatty acid profile, and CSSO increased unsaturated fatty acid whereas CSPO increased saturated fatty acids.

Key Words: palm oil, soybean oil, tropical pasture

Table 1825. Milk fatty acid profile of grazing dairy cows supplemented with fat

g/100g of fat	Control	CSSO	CSPO	SEM	*P*-value
C18:2 cis-9 trans-12	1.66^{c}	2.07^{a}	1.92^{b}	0.09	0.002
C18:3 cis-9 cis-12 cis-15	0.33^{b}	0.43^{a}	0.39^{a}	0.02	0.07
CLA cis-9 trans-11	0.66^{b}	0.86^{a}	0.69^{b}	0.05	0.005
CLA trans-10 cis-12	0.02^{b}	0.09^{a}	0.019^{b}	0.003	0.0001
De novo	25.6^{a}	20.8^{b}	21.4^{b}	0.99	0.005
Mixed	30.7^{b}	30.2^{b}	33.9^{a}	1.4	0.04
Preformed	43.7^{b}	49.0^{a}	44.7^{b}	2.2	0.04
Total of saturated	66.9^{a}	61.5^{b}	64.1^{a}	1.76	0.01
Total of MUFA	28.9^{b}	33.6^{a}	31.6^{ab}	1.3	0.04
Total of PUFA	4.2^{b}	4.9^{a}	4.3^{b}	0.24	0.02

1826 (W285) Evaluating daily variation in body weight, milk production, and rumination activity on a commercial dairy with robotic milking.
R. W. Bender*, D. E. Cook, T. L. Chandler, H. M. White and D. K. Combs, *Department of Dairy Science University of Wisconsin, Madison*

Emerging technologies allow commercial dairy producers to collect a wide array of individual cow data on a daily basis, with the potential to profoundly influence managerial and nutritional decision-making on a pen basis. The objective of this study was to utilize daily body weights, rumination activity, and milk production data from lactating dairy cows to evaluate random variation that exists on a commercial dairy. Data were obtained from a commercial robotic dairy farm in Melrose, WI via the Lely T4C herd management system for either a whole year (daily body weights and daily milk production) or one week (rumination). Data from approximately 500 cows in seven pens (1 pen per robot, approximately 70 cows per pen) was utilized. Cows were assigned to a pen post-calving and remained there until dry off. All data is presented as mean ± standard deviation. On this dairy, milk production averaged 37.4 kg, with a standard deviation of 1.0 kg among days within a pen, 14.4 kg among individual cows within a pen, and 21.2 kg among days within individual cows. Body weight averaged 689.2 kg, with a standard deviation of 4.5 kg among days within a pen, 75.6 kg among individual cows within a pen, and 34.6 kg among days within individual cows. Rumination (min per day) averaged 461.1 min, with a standard deviation of 6.1 min among days within a pen, 128.0 min among individual cows within a pen, and 43.6 min among days within individual cows. A statistical power calculation would suggest that with 7 pens and 95% confidence, a difference of 1.5 kg mean milk production, 6.5 kg mean body weight, or 8.0 min mean rumination time could be deemed statistically significant from day to day within this herd. Understanding the magnitude of the variability among these parameters could be a powerful tool to monitor pen level changes over a short period of time and implement immediate managerial modifications.

Key Words: body weight, milk production, rumination

1827 (W286) Peroxisome proliferator activated receptor-γ controls lipogenic gene networks in goat mammary epithelial cells.
W. Zhao[*1,2], J. Luo[1] and J. J. Loor[2], [1]*Northwest A&F University, Yangling, China,* [2]*University of Illinois, Urbana*

In non-ruminants, peroxisome proliferator-activated receptor-γ (*PPARG*) plays a crucial role in fatty acid (FA) metabolism through the regulation of lipogenic gene expression. However, whether or how *PPARG* regulates the activity of mammary lipogenic genes in ruminant mammary cells remains largely unknown. This study explored the potential role of *PPARG* in regulating mRNA expression of lipogenic genes in lactating goat primary mammary epithelial cells (GMEC). Adenoviral transfection of the *PPARG* response element into GMEC was used in this study. The *PPARG* agonist rosiglitazone (ROSI) was used to study gene expression changes in response to PPARG activation. Expression of 39 genes involved in milk fat synthesis plus 3 internal control genes was measured using qPCR. Data from triplicate cultures were log-transformed and statistically analyzed using the GLM of SAS. The multiple comparisons were corrected using Tukey's test and significance set at $P < 0.05$. Over-expression of *PPARG* without (Ad-PPARG+DMSO) or with (Ad-PPARG+ROSI) ROSI markedly upregulated ($P = 0.0001$) the expression of *PPARG* compared with the control (Ad-GFP (Green fluorescent protein)+DMSO) and ROSI (Ad-GFP+ROSI) treatments. Over-expression of *PPARG* without ROSI up-regulated ($P < 0.05$) the expression of some lipogenic enzymes (*ACSS2, ACSL1, SCD, DGAT1, FADS1, GPAM, LPIN1*), transcription regulators (*LXRα, MLXIPL, PPARG, PPARGC1B),* and components of the circadian CLOCK network (*CRY1, CRY2*). After ROSI treatment of PPARG-overexpressing GMEC there was a further and marked increase ($P < 0.05$) in the mRNA expression of lipogenic enzymes (*FASN, ACSS2, GPAM, LPIN1, ACSL1, SCD*), transcription regulators (*LXRα, PPARG, SREBF1, PPARGC1B*), and components of the circadian CLOCK network (*CLOCK, CRY1, CRY2*). It was noteworthy that expression of *RXRα*, a partner of *PPARG*, was down-regulated in PPARG-overexpressing GMEC with or without ROSI treatment. These results provide direct evidence that *PPARG* plays a crucial role in regulating fatty acid metabolism in goat mammary cells and underscore the importance of *PPARG* in the mammary gland during lactation.

Key Words: PPAR, nutrigenomics, milk fa synthesis

1828 (W287) Effects of ergot alkaloid exposure on serotonin receptor mRNA in the smooth muscle of the bovine gastrointestinal tract.
J. L. Klotz[*1], D. Kim[2], A. P. Foote[2] and D. L. Harmon[2], [1]*USDA-ARS, FAPRU, Lexington, KY,* [2]*University of Kentucky, Lexington*

Various serotonin (5HT) receptor subtypes have been located in the gastrointestinal tract and some are associated with gut motility. Cattle exposed to ergot alkaloids through consumption of contaminated feedstuffs have demonstrated signs (e.g.- increased rumen DM content and total content) that suggest a reduction in gut motility. Ergot alkaloids have been shown to interact with biogenic amine receptors and specifically serotonin receptors. Therefore, the objective of this study was to evaluate the effect of dietary exposure to ergot alkaloids has on the expression of 5HT receptor subtypes 5HTR2A (NM_001001157.1) and 5HTR4 (NM_001010485.1) in the smooth muscle of the reticulum, rumen, omasum, abomasum, duodenum, jejunum, ileum, cecum and colon of cattle. Ruminally cannulated Angus steers ($n = 12$; BW = 547 ± 31 kg)

were paired by weight and randomly assigned to 6 blocks. Steers were fed alfalfa cubes at 1.5 × NE_m and were ruminally dosed daily with 1 kg of either endophyte-infected (E+; 4.45 ppm ergovaline) or endophyte-free (E-) tall fescue seed for 21 d prior to slaughter. On d 22 steers were slaughtered and samples of smooth muscle from the different sites of the gastrointestinal tract were sampled, rinsed, homogenized in Tri-reagent, and total RNA was isolated. Semi-quantitative real-time PCR was conducted using SYBR green and glyceraldehyde 3-phosphate dehydrogenase (NM_001034034.2) as a reference gene. Resultant data were analyzed using mixed models of SAS. There was no interaction of sampling location by seed treatment for either gene evaluated. For 5HTR4 only the main effect of sampling location was significant ($P < 0.001$) with ileum and jejunum having the greatest amount of transcript ($P < 0.05$) followed by the colon and duodenum ($P < 0.05$). The remaining tissue sites did not differ. Expression of 5HTR2A in E- steers was greater ($P = 0.04$) than E+ steers with lower relative quantities of 5HTR2A in E+ steers for all tissue sampling locations except the abomasum ($P = 0.054$). The enteric 5HTR2A receptor is associated with smooth muscle contraction and the observed decrease in expression in E+ treated steers suggests that ergot alkaloids may play a role in negatively affecting gut motility. Future work will explore the effects alkaloids might have on genes that encode for the G proteins and other downstream signal transduction proteins associated with these 5HT receptors.

Key Words: bovine, ergot alkaloids, serotonin receptor

1829 (W288) Effect of mineral supplementation on lactational performance in early-lactating dairy cows fed a high-concentrate diet.

A. R. Alfonso-Avila[*1], E. Charbonneau[1], P. Y. Chouinard[1], G. Tremblay[2] and R. Gervais[1], *[1]Université Laval, Québec, QC, Canada, [2]Agriculture and Agri-Food Canada, Soils and Crops Research and Development Centre, Quebec, QC, Canada*

Previous studies reported an increase in milk fat synthesis when lactating dairy cows were fed diets with higher dietary cation-anion difference (DCAD) or K, supplied as K_2CO_3. This study investigated the effects of DCAD, cation source, and buffering capacity of the mineral supplement on lactational performance of early-lactating dairy cows fed a high concentrate diet. Ten primiparous and 25 multiparous Holstein cows averaging 38 ± 13 DIM were distributed according to a randomized block design (7 blocks) for 5 wk, including a 1-wk pretreatment collection period, used as a covariate. Treatments consisted of C) a basal diet formulated to contain 40% forage (60% corn silage) and 60% concentrate (16% CP, 47% non-fibrous carbohydrates, 29% NDF, DCAD +65 mEq/kg) as control; K1) C + 1.8% K_2CO_3 (DCAD: +326); K2) C + 2.6% $KHCO_3$ (DCAD: +324); K3) C + 1.9% KCl (DCAD +64); and Na) C + 1.4% Na_2CO_3 (+322). Orthogonal contrasts were used to assess the effects of K_2CO_3 (C vs. K1), buffering capacity (K1 vs. K2), DCAD (K1 vs. K3), and cation type (K1 vs. Na). Treatment period was 28 d with the last 5 d used for data and sample collection. The selected comparisons detected no effect of treatments on DMI (24.1 ± 1.2 kg/d; $P > 0.14$) and milk yield (36.8 ± 1.8 kg/d; $P > 0.12$). Blood K^+ concentration was higher in cows fed K1 (3.99 mmol/L) as compared with C (3.75; $P < 0.01$), K2 (3.79; $P = 0.02$), and Na (3.68; $P < 0.01$), whereas no difference was observed with cows fed K3 (3.89; $P = 0.20$). Blood Cl^- concentration was lower in cows fed K1 (106.1 mmol/L) as compared with Na (108.3; $P = 0.01$). However, no difference was observed in blood Na^+ concentration of cows fed K1 and Na (139.9 ± 0.4 mmol/L; $P = 0.18$). As compared with Na, cows fed K1 had a higher milk protein content (3.12 vs 2.93%; $P = 0.04$) but a similar milk protein yield (1087 ± 67 g/d; $P = 0.56$). Milk fat percentage was higher in cows fed K1 compared with C (4.03 vs 3.26%; $P = 0.02$), whereas milk fat yield (1305 ± 134 g/d; $P = 0.21$) or 4% fat corrected milk (34.0 ± 2.6 kg/d; $P = 0.61$) were not affected. As opposed to previously published results, under conditions of the current experiment, increasing DCAD or K^+ concentration in a high concentrate diet did not improve milk fat yield in early lactating cows.

Key Words: DCAD, potassium carbonate, milk fat synthesis

1830 (W289) Mineral profile, inmunoglobulins and antioxidant activity in culls cows fed DDGS.

A. Flores-Mariñelarena[*1], E. Acosta Sánchez[1], G. Corral-Flores[1], C. Rodríguez-Muela[1], J. A. Ramírez-Godínez[1], J. Dominguez-Viveros[1], A. Anchondo-Garay[1] and H. Ramírez-Garduño[2], *[1]Universidad Autónoma de Chihuahua, Chihuahua, Mexico, [2]INIFAP, Chihuahua, Mexico*

The objective was to evaluate the effect of four levels of Distillery Dry Grains (DDGS) in the diet of cull beef cows on body weight (BW) and average daily gain (ADG) every 15 d and the mineral profile (Zn, Mn and Cu) and immunoglobulins in blood serum, and the antioxidant activity (AA) in blood plasma (d 0 and d60). Thirty five mature cows of different genotypes with an average live weight of 350 ± 40 kg were randomly divided into four treatments with different levels of DDGS: T1 (Control, 0%, $n = 9$), T2 (5.7%, $n = 9$), T3 (11,23%, $n = 8$) and T4 (16.45%, $n = 9$). A completely randomized design with treatment and time of sampling as fixed effects was used. Data was analyzed with the GLM of SAS. For the multiple comparisons of means a Tukey's test was used. The BW and ADG were similar ($P > 0.05$) between treatments. Serum levels of Zn, Cu, and Mn between treatments did not differ ($P > 0.05$). During the feeding period the serum levels of Zn and Cu were similar ($P > 0.05$). However, levels of Mn were higher ($P < 0.05$) at d 0 than at d 60 (1.69 ± 0.11 μmol/L vs 1.36 ± 0.11 μmol/L, respectively). The AA

and immunoglobulins were similar ($P > 0.05$) between treatments at d 60, but were different ($P < 0.05$) at d 0 (5.74 ± 0.32 g *100 mL ^{1}) vs d 60 (8.12 ± 0.33 g *100 mL ^{1}) of the feeding period. It was concluded that the inclusion of DDG's in the diet of cull beef cows did not affect the ADG, the mineral profile and the AA. However, Mn concentration was reduced and immunoglobulin increased during the 60 d feeding period.

Key Words: cull cows, antioxidant activity, mineral profile, immunoglobulin

1831 (W290) Metabolic characteristics and truly metabolizable protein supply to dairy cattle from new cool-season forage corn varieties in western Canada. S. Abeysekara, D. A. Christensen, N. A. Khan, X. Huang* and P. Yu, *University of Saskatchewan, Saskatoon, SK, Canada*

The objectives of the present study were to quantitatively evaluate the metabolic characteristics of protein in the rumen and intestine of dairy cattle and to estimate the content of truly metabolizable protein (MP) in newly developed cool-season forage corn varieties. Six new corn cultivars, including 3 Pioneer (PNR) and 3 Hyland (HL), coded as PNR-7443R, PNR-P7213R, PNR-7535R, HL-SR06, HL-SR22, HL-BAX-XOS-RR, were evaluated in the present study. The metabolic characteristics, MP supply to dairy cattle, and energy synchronization properties were modeled by the DVE/OEB system and the NRC-2001 model. The parameters evaluated were (1) potential microbial protein (MCP) synthesis in the rumen from available degraded protein and energy (2) truly absorbable rumen synthesized microbial protein (AMCP) (3) truly absorbable rumen undegraded feed protein (ARUP) (4) truly absorbed rumen endogenous protein and (5) total truly MP (6) the degraded protein balance (DPB). Both models estimated significant ($P < 0.05$) differences in contents of MCP synthesized from rumen degraded protein (RDP) and ARUP among the cultivars. The NRC-2001 model estimated significant ($P < 0.05$) differences in total truly MP and DPB among the cultivars. According to NRC-2001 model, the contents AMCP, ARUP and total truly MP contents were higher ($P < 0.05$) for cultivar HL-SR06, resulting in the lowest ($P < 0.05$) DPB. Cultivar, HL-SR06 also had the highest rumen available N/kg of organic matter (OM) and high hourly effective degradability ratios among the corn cultivars. However, none of the cultivars reached the optimal target hourly effective degradability ratio (25 g N g/kg OM), demonstrating N deficiency in the rumen. Hyland-SR06 had the highest contents of MCP synthesized from RDP, ARUP and total truly MP. However, regardless of the differences among cultivars, forage corn based rations of dairy cows needs to be balanced with a high protein containing concentrate to improve the rumen degradable protein deficit.

Key Words: corn, protein metabolic characteristics, protein evaluation system

1832 (W291) Hepatic expression of genes associated with glutathione and fatty acid metabolism during the peripartal period reveal beneficial effects of MetaSmart and Smartamine M supplementation on health status in dairy cows. J. S. Osorio[1], P. Ji[2], J. K. Drackley[3], D. N. Luchini[4] and J. J. Loor*[3], *[1]University of Illinois, Champaign, [2]William H. Miner Agricultural Research Institute, Chazy, NY, [3]University of Illinois, Urbana, [4]Adisseo S.A.S., Alpharetta, GA.*

Fifty-seven multiparous Holstein cows were fed a control diet (CON, $n = 24$; 1.49 Mcal/kg DM prepartum and 1.75 Mcal/kg DM postpartum), CON plus MetaSmart (MS, $n = 15$; Adisseo France S.A.S.), or CON plus Smartamine M (SM, $n = 18$; Adisseo France S.A.S.). Treatments began on -21 days in milk (DIM) and continued through 30 DIM. MetaSmart (0.19% of DM) and SM (0.07% of DM) were top-dressed on the CON diet. Liver samples (n = 8-9/treatment) collected at -10, 7, and 21 DIM were used for real-time qPCR of genes associated with metabolism of Met, glutathione, fatty acid, and gluconeogenesis as well as inflammation, oxidative stress, hepatokines, growth hormone signaling, and DNA methylation. Data were analyzed using the MIXED procedure of SAS with the preplanned contrast CON vs. MS+SM. Expression of Met adenosyltransferase 1A (*MAT1A*) increased ($P = 0.001$) over time (-10 vs 21 d) in Met-supplemented cows while it decreased ($P = 0.002$) in CON cows. Glutathione metabolism-related genes such as glutathione reductase (*GSR*; $P = 0.02$) and glutathione synthase (*GSS*; $P = 0.004$) had lower expression at 21 DIM in Met-supplemented cows, while glutamate-cysteine ligase catalytic tended (*GCLC*; $P = 0.07$) to have a similar pattern as *GSR* and *GSS*. Expression of 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (*HMGCS2*) was lower ($P = 0.02$) in Met-supplemented cows at 21 DIM. *HMGCS2* is highly corelated with ketogenesis. Expression of peroxisome proliferator-activated receptor α (*PPARA*; $P = 0.04$) and phosphoenolpyruvate carboxykinase 1 (*PCK1*; $P = 0.03$) was greater in Met-supplemented cows, while a trend ($P = 0.06$) was observed for the hepatokine fibroblast growth factor 21 (*FGF21*). Increased expression of *MAT1A* over time in Met-supplemented cows coupled with greater *PPARA* expression is suggestive that Met, a methyl donor, might have promoted the activation of *PPARA* via S-adenosylmethionine by reducing DNA methylation of the PPARA promoter region. The role of the *PPARA-FGF21* axis as an activator of gluconeogenesis was underscored by the concomitant upregulation of *PCK1* in Met-supplemented cows. Postpartal down-regulation of *HMGCS2* in Met-supplemented cows could be related with a lower production of ketones bodies, which agrees with the trend ($P = 0.15$) observed in the overall group ($n = 57$) suggesting a lower predisposition to developing ketosis. The parallel down-regulation of *GSR*, *GSS*, and *GCLC*at 21 d might indicate a lower requirement for the antioxidant activity of glutathione in Met-supplemented cows.

Key Words: transition cows, gene expression, methionine

1833 (W292) Feed intake and feeding behavior of lactating dairy cows were affected by dietary fatty acid profile. H. Khalilvandi-Behroozyar[1], M. Dehghan Banadaky[*2], M. Ghaffarzadeh[3] and K. Rezayazdi[2], *[1]Department of Animal Science, Urmia University, Urmia, Iran, [2]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran, [3]Chemistry and Chemical Engineering Research Center of Iran, Tehran, Iran*

There are quite rare data regarding effects of dietary fatty acid profile on feeding and chewing behavior. The aim of this study was to evaluate the milk fatty acid profile in early lactating dairy cows supplemented with protected unsaturated fatty acids sources and prilled source of palm fatty acids. Twenty four multiparous Iranian Holstein cows individually were assigned to diets with different fatty acid profiles and supplemented through 30 days before expect calving date to 50 days in milk. Dietary treatments consisted of (1) Prilled Pam fatty acids (PO) [Energizer RP10 , 2 & 2.25% DM in pre- and postpartum, respectively]; (2) Ca-salts of sunflower oil (SO) [Persia Fat- SO]; (3) Ca-salts of fish oil (FO) [Persia Fat- FO] and (4) equal amounts of Persia Fat- FO & Persia Fat- SO. Calcium salts were supplemented as 2.2 and 2.5% of dietary DM in pre- and postpartum period, respectively. All rations contained identical forage and concentrate components. Feeding behavior was continuously monitored for 5 consecutive days in 15, 30 and 45 days in milk using video recordings. Data were analyzed using PROC MIXED of SAS 9.1 with repeated measures in time function. Dry matter intake for PO was less than Persia Fat with different FA profiles (20.17 vs. 23.56, 22.25 and 2.53, for treatments 1 to 4, respectively, $P < 0.05$). Supplementation of palm fatty acids decreased meal number, meal length and time to consume 1 kg of DM or NDF, but amount of feed intake in each meal was not affected. Time interval between meals was numerically increased ($P > 0.05$) by supplementation of PO (2.74 vs. 2.28, 2.51 and 2.53, for treatments 1 to 4, respectively).The PO treatment increased time spent ruminating in each bout, but increased rumination bout intervals. Total number of rumination bouts was not affected by fat supplement type. Total rumination time (660.48 min vs. 587.86, 584.8 and 73.75, for treatments 1 to 4, respectively) and rumination per kg of DM (32.74 min vs. 24.95, 26.28 and 25.47, for treatments 1 to 4, respectively) and NDF (102.39 min vs. 78.02, 82.21 and 79.62, for treatments 1 to 4, respectively) were increased for PO than PUFA supplemented cows. We conclude that saturated fat supplement suppress DMI via increase time spend to consume or rumination feed.

Key Words: palm oil, PUFA, rumination

1834 (W293) Whole cottonseed and vitamin E in diets for Nellore cattle finished in feedlot: Performance traits and Feed conversion. A. M. Ferrinho[*1], F. Baldi[2], B. M. Toda[1], F. B. Mendonça[1], B. L. Utembergue[1], R. R. Germano[1], A. S. C. Pereira[1], P. R. Leme[1] and S. L. Silva[1], *[1]Universidade de São Paulo, Pirassununga, Brazil, [2]Universidade Estadual Paulista "Júlio de Mesquita Filho"- UNESP, Faculdade de Ciências Agrárias e Veterinárias, Jaboticabal, Brazil*

This study aimed to evaluate the daily live weight gain, live weight evolution, feed efficiency (ratio live weight gain/dry matter intake), hot and cold carcass weight and carcass yield of bulls finished in feedlot feeding. A total of 54 bulls were confined, with approximately 350 kg initial weight, average age of 24 months, in a randomized blocks design with factorial arrangement of treatments (3 x 3), totaling 9 treatments with 6 animals in each treatment. The animals were fed three diets: 1) control without cottonseed (CTL), 2) containing cottonseed at 30% of DM (CAR) and 3) diet containing cottonseed at 30% of DM and 500 IU vitamin E/kg of DM (VITE). The diets used were composed of different concentrates, including dry corn grain, citrus pulp, sugarcane bagasse raw and soybean meal with forage concentrate ratio of 86:14 and an average of 55% CP in the three diets The animals were kept in pens, three to three, and fed once a day, for 83, 104 and 111 days and slaughtered. For feed conversion and carcass weight, the the fixed effects of treatment, slaughter period and the interaction between them, and the block random effect were included in the model. For repeated measured traits, the fixed effects of treatment, weighing period and the interaction between them, and the block random effect were included in the model. The data were submitted to an analysis of variance using the proc mixed command (SAS statistical program) applying a significance level of 5%. The interaction between treatment x slaughter period was significant ($P < 0.05$) for feed conversion where animals fed the VITE and CAR diets and slaughtered at 111 days showed better feed conversion efficiency with averages of 4.68 kg DM and 4.94 kg DM respectively. The interaction treatment x slaughter period was also significant ($P < 0.05$) for live weight evolution ($P < 0.01$). The mean daily live weight gains were 4.10 kg, 3.74 kg and 0.6 kg for CAR, VITE and CTL respectively. There was a significant effect of diets containing whole cottonseed (CAR and VITE) on hot and cold carcass weight compared to the diet without whole cottonseed ($P < 0.01$), while for carcass yield, animals slaughtered at 111 days showed higher (56,33%) than animals slaughtered before ($P < 0.05$). The animals fed diets with cottonseed have better performance for live weight gain, feed conversion and carcass weight.

Key Words: cottonseed, feed efficiency, daily live gain

1835 (W294) Effect of chitosan and lipid source combination on energy intake and milk yield and composition of dairy cows. T. A. Del Valle*[1], V. C. Galvão[1], F. C. R. D. Santos[1], E. F. Jesus[2], A. G. B. V. B. Costa[1], C. E. C. Consentini[1], G. F. D. Almeida[1], G. F. Cabral[3], F. Zanferari[1] and F. P. Rennó[1], *[1]School of Veterinary Medicine and Animal Science, University of São Paulo, Pirassununga, Brazil, [2]School of Agricultural and Veterinary Sciences of UNESP, Jaboticabal, Brazil, [3]School of Animal Science and Food Engineering of University of São Paulo, Pirassunga, Brazil*

The aim of this study was to evaluate the effects of chitosan and soybean oil in the dairy cow's diets, on energy intake and milk yield. Twenty-four Holstein averaging 174.7 ± 53.1 DIM, were randomly assigned in six Latin Square design with a two by two factorial arrangement of treatments. The diets contained chitosan (150 mg.kg^{-1} of body weight) and/or soybean oil (3.3% of the diet DM). Each experiment period had a 14 d adaptation period and an seven for collection data. Sampling of milk was done on days 16, 17 and 18 of each period to evaluate the composition. The net energy intake (NEI), energy requirement for maintenance (NE_m) and lactation (NE_L) were obtained from the equations of NRC (2001). NEI was decrease with the use of chitosan in the diets without supplementation of soybean oil, but has no difference between diets containing soybean oil as well as the dry matter intake. The NE_L was decrease by addition of soybean oil in the diet, regardless of the addition of chitosan. This occurred due to the reduction of on average 5.0 g.kg^{-1} the synthesis of fat in milk of animals fed soybean oil. Although the animals receiving chitosan and soybean oil had less milk yield (31.26 kg) compared with animals receiving only the soybean oil (32.86 kg) and in this diet decrease fat concentration was only 3.7g. kg^{-1}, making fat corrected milk unchanged. Milk yield did not differ between cows fed chitosan diet (33.87 kg) and control diet (32.85 kg).The net energy balance was decrease on chitosan diet (2.97 Mcal) compared with control diet (5.33 Mcal) and was not influenced by the addition of chitosan on diets containing soybean oil (5.0 Mcal). The efficiency of use of energy, measured by the ration between the NE_L and digestibility energy intake, was decrease by the addition of chitosan in diets with soybean oil and increased in diets without oil. Chitosan increases energy efficiency in dairy cows, provided that the diet has a low level of ether extract.

Key Words: fat, feed additive, milk energy

1836 (W295) Plasma urea concentration of beef heifers fed with different lipid sources and frequency supplementation. M. C. A. Santana*[1], V. C. Modesto[2], G. T. Pereira[2], R. A. Reis[2], G. M. P. Melo[2], H. J. U. Costa[2], T. T. Berchielli[2] and L. P. L. Moreira[2], *[1]Emater, Goiânia, Brazil, [2]UNESP, Jaboticabal, Brazil*

This research aims to evaluate urea plasma responses under different lipid sources and supplementation frequencies. The experiment was conducted throughout a 4-mo period during the dry season. The experiment was completely random, using a 3 × 2 factorial arrangement (3 supplements and 2 supplementation frequencies). The supplements were derived from 3 different sources, soybean grains, soybean oil and protected fat (Megalac-E), the 2 supplement frequencies were (D) daily or 3 days of week (Monday, Wednesday and Friday) called "alternate" (A). In the 4-mo experimental period, August–November, blood samples were taken from the jugular vein four hour after the morning feeding. Subsequently, these samples were centrifuged and stored until the urea blood level was evaluated. In all treatments, no urea levels differences were observed in August and September ($P > 0.05$). The Megalac–E that was supplied daily presented a higher urea plasma level in comparison to the alternate supplement of soybean oil in October ($P < 0.05$).The animals that were given soybean oil supplements daily showed lower urea plasma concentration values ($P < 0.05$) in November by treatments and periods. Overall, this data indicated that the urea blood level can be influenced according to the feeding strategy during the dry season.

Key Words: soybean grains, soybean oil, protect fat

Table 1836. Plasma urea concentration of heifers supplemented with different lipid sources at two different frequencies (mg/dL)

	D-SG	A-SG	D-SO	A-SO	D-ML	A-ML
August	27.5^{Aa}	26.8^{Aa}	27.6^{Aa}	26.7^{Aa}	27.8^{Aa}	26.2^{Aa}
September	21.1^{Aa}	21.1^{Aa}	29.9^{Aa}	21.6^{Aa}	26.1^{Aa}	28.6^{Aa}
October	24.8^{ABa}	23.0^{ABa}	28.9^{ABa}	17.9^{Ba}	32.3^{Aa}	25.0^{ABa}
November	24.4^{ABa}	28.0^{Aa}	13.5^{Bb}	23.5^{ABa}	21.9^{ABa}	22.3^{ABa}

Lowercase in columns and capital letters in rows differ ($P < 0.05$).
D = daily; A = alternately; SG = Soybean grain; SO = Soybean oil; ML = Megalac-E

1837 (W296) Effects of selenium supply, maternal plane of nutrition, and physiological stage on nitrogen flow, microbial efficiency, and metabolizable protein in primiparous ewes. K. J. McLean[*1], A. M. Meyer[2], L. R. Coupe[1], G. P. Lardy[1], K. A. Vonnahme[1] and J. S. Caton[1], *[1]North Dakota State University, Fargo, [2]Division of Animal Sciences, University of Missouri, Columbia*

Primiparous Rambouillet ewes (n = 84, age = 240 ± 17 d, BW = 52.1 ± 6.2 kg) were allocated to 2 × 3 × 2 factorial arrangement to evaluate dietary Se (adequate Se [11.5 µg/kg BW] or high Se [77.0 µg/kg BW]), nutritional plane (60% [restricted], 100% [control], or 140% [high]), and physiological stage at necropsy (parturition or d 20 of lactation) effects on nitrogen digestion and microbial CP production. At parturition, lambs were removed from all ewes and 42 ewes (n = 7 per treatment) were necropsied. Remaining ewes were transitioned to a common lactation diet to meet NRC requirements and machine milked for 20 d. Differences between treatments were determined by the GLM procedure in SAS. No three way interactions were present (P > 0.10), but many 2-way interactions were found (P < 0.05). Selenium did not influence N intake (P = 0.23). Nitrogen intake increased with plane of nutrition during gestation and lactation (P < 0.001; 13.3 vs. 20.2 vs. 31.4 ± 0.6 g during pregnancy and 40.4 vs. 41.6 vs. 42.2 ± 0.5 g during lactation for restricted, control, and high ewes, respectively). Microbial efficiency of ewes on restricted diets (7.0 ± 1.04 g microbial nitrogen/kg truly fermented) was decreased compared with control and high ewes (13.4 and 14.9 ± 1.04 g microbial nitrogen/kg truly fermented) but these differences were gone after 20 d of lactation (P > 0.15). Supranutritional Se supply and restricted and adequate nutrient planes increased microbial efficiency regardless of physiological stage (P = 0.04). Selenium supplementation increased (P = 0.04) total tract N digestion during gestation (69.3 and 71.4 ± 1.0%, respectively) but decreased N digestion during lactation (74.7 and 72.9 ± 0.9%, respectively). Ruminal N digestion was greater (P = 0.01) during gestation in restricted ewes compared with control or high ewes (59.1 vs. 44.9 and 39.9 ± 2.8%, respectively); however, post-ruminal N digestion was less (P = 0.02) in restricted ewes compared with control and high nutritional planes (13.1 vs. 26.1 and 28.1 ± 2.8%, respectively). Metabolizable protein increased (P < 0.001) during gestation with increasing nutritional intake but did not differ during lactation. Nutritional plane and Se supplementation had different effects on nitrogen digestion and microbial efficiency but those effects were dependent on physiologic stage.

Key Words: ewes, microbial efficiency, selenium

1838 (W297) Effect of prototype sequestering agents on performance and milk aflatoxin M1 concentrations of dairy cows fed aflatoxin B1-contaminated diets. I. M. Ogunade[*1], K. G. Arriola[1], R. M. Martins[1], B. Y. Coy[1], C. L. Curry[2], D. K. Terkoski[1], A. Rubright[1], M. G. Zenobi[2], Z. Ma[2], C. R. Staples[2] and A. T. Adesogan[2], *[1]University of Florida, Department of Animal Sciences, Gainesville, [2]Dep. of Animal Sciences, University of Florida, Gainesville*

This study examined if 3 in-feed mycotoxin-sequestering agents could reduce milk aflatoxin M_1 (AFM_1) concentration and improve the performance and immunological responses of dairy cattle fed diets contaminated with aflatoxin B_1 (AFB_1). Fifteen lactating cows were used in a 5 × 5 Latin square design with four 28-d periods and 3 replicate squares. Treatments included a Control diet (C), a toxin (T) diet containing 75 ug of AFB_1/kg of TMR DM and 3 diets containing T and one of three prototype sequestering agents (S1, S2, and S3). The AFB_1 was mixed with corn and molasses and dosed in gelatin capsules orally to cows before the TMR was fed on d 21 to 25. Milk was sampled twice daily on d 20 to 28 and plasma was sampled on d 20 and 25. The statistical model contained effects of diet, period, square, appropriate interactions and cow nested within square. Feeding T increased the milk AFM_1 concentration beyond the FDA safety threshold (0.5 ug/kg) and values were greater (P < 0.001) than those in cows fed C. Sequestering agents (S1, S2 and S3) did not reduce the transfer of AFB_1 to AFM_1. Feeding T reduced (P = 0.03) milk fat (0.93 vs. 1.05 kg/d) and protein (0.78 vs. 0.89 kg/d) yield and tended (P = 0.09) to reduce milk fat (3.74 vs. 3.84%) and protein (3.12 vs. 3.24%) concentrations compared to C. Feeding sequestering agents prevented these reductions in yields and concentrations of milk components except that S3 reduced milk fat yield. Cows fed S3 had lower (P = 0.01) DMI and greater (P = 0.01) feed efficiency (FCM/DMI; 1.34 vs. 1.12) than those fed C. Feeding T instead of C reduced (P < 0.05) red blood cell counts and hemoglobin concentration. Plasma acid-soluble protein concentration and monocyte counts were lower (P < 0.05) in cows fed S1, S2 and S3 compared to those fed T reflecting attenuation of the immunological challenge posed by feeding AFB_1. Sequestering agents had no effect on milk AFM_1 concentration but prevented adverse effects of AFB_1 on milk component yields and concentrations and immunological response indices

Key Words: milk, mycotoxin, sequestering agents

1839 (W298) Blood glucose concentrations and deposition of muscular and subcutaneous fat tissues of Nellore young bulls finished in pasture supplemented with crude glycerin. E. San Vito*, J. F. Lage, L. Maneck Delevatti, E. E. Dalanttonia, L. R. Simonetti, M. B. Abra and T. T. Berchielli, *Universidade Estadual Paulista Júlio de Mesquita Filho- UNESP, Jaboticabal, Brazil*

This trial aimed to evaluate the effects of feeding crude glycerin (CG)- 80% of glycerol- included as a substitute to corn grain in supplements of young bulls finished in pasture on rainy season on deposition of muscular and subcutaneous fat tissues and blood glucose concentration. The longissimus muscle area (LMA), rib fat thickness between the 12 and 13 ribs (RFT) and subcutaneous fat thickness in the region P8 (P8) were evaluated. Fifty Nellore young bulls with initial shrunk body weight of 427 ± 15.76 kg were randomly assigned to five treatments consisted of increasing crude glycerin concentration in the supplement: 0, 7, 14, 21, and 28% of dry matter. The CG used was derived from soybean biodiesel production. Animals were distributed in 10 paddocks of *Brachiaria brizantha* cv. Xaraés, with 1.8 ha each (2 paddocks per treatment). The animals were supplemented daily in a proportion of 300 g/100kg of BW. The supplement control was constituted of corn grain, soybean meal, urea, gluten meal and mineralized salt, containing 370 g/kg DM of CG. The measurements were done in the beginning of the experiment and in each 28 d, by ultrasound (Model Aloka 500, linear carcass probe with 17.2 cm and frequency of 3.5 MHz), to evaluate the deposition of muscular and subcutaneous fat tissues. Blood was collected in vacutainer tubes from the tail vein after 16 h withdrawal period from feed and water. Data was analyzed using the GLM procedure of SAS program and the effects of treatments (linear and quadratic) were considered significant at P>0.05. There was no statistical significance (P>0.05) among the treatments, and the final average values observed were: 71.5 cm < su*P* > 2 < /su*P* > to LMA, 4.4 mm to P8 and 3.7 mm to RFT. The gain observed in the variables (initial value– final value) LMA, P8 and RFT were 13.3 cm < su*P* > 2 < /su*P* > 1.7 mm and 1.3 mm, respectively. CG inclusion did not affect the blood glucose concentrations (P>0.05), however the values showed a quadratic effect (*P* = 0.020), with the highest concentration (81.8 mg/dL) in the level of 14% inclusion of crude glycerin. Addition of crude glycerin in supplement (28% of DM) does not affect the deposition of muscular and subcutaneous fat tissues or blood glucose concentrations of Nellore young bulls finished in pasture on rainy season.

Key Words: beef cattle, glycerol, pasture

1840 (W299) Effect of propolis on plasma metabolites and hematocrit of Holstein calves. P. Peravian*[1], K. Rezayazdi[2] and G. Nehzati[3], [1]*University of Tehran, Tehran, Iran,* [2]*Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran,* [3]*University of Tehran, Karaj, Iran*

The object of this study was to investigate the effect of propolis powder on the plasma metabolites and hematocrit of suckling calves. Propolis in this experiment was come from Taleghan vicinity (near Tehran). 40 Holstein female calves with 41 ± 1 kg of body weight from 14 to 65 d of old were used in a completely randomized design with 4 treatments and 10 replicates in each treatment. Treatments were 1) Control (without Monensin in starter and without propolis in milk), 2) Starter without Monensin and 500ppm soluble propolis powder in milk, 3) Starter without Monensin and 1000ppm soluble propolis powder in milk and 4) Monensin in starter and without propolis in milk. Starter was formulated according to NRC 2001 (21.6% CP and 2.89 ME (mcal/kg)). Calves received 6 L/d of milk replacer (milk protein based, 22% CP, 19% EE) for the 6 wk. Blood sample were collected every 14 d (3hours after feeding), then transferred to laboratory and hematocrit (platelets, hemoglobin, red blood cell, white blood cell, lymphocyte) were measured. Blood samples centrifuged and plasma separated from blood to measure metabolites (total protein, albumin, Immunoglobulin G). Results showed that mean concentration of Platelets (3.06, 4.95, 3.18, 5.63 *10^5/ml) and Lymphocytes (69.50, 72.25, 75.25, 71.75%) were not affected by treatments. Hemoglobin (11.12, 8.8, 10.15, 9.6 g/dl) red blood cell (11.28, 8.07, 10.19, 10.28 *$10^{6/}$ml) for treatments 1–4 respectively were not affected by treatments. For white blood cell (50.75, 60.75, 71.50, 52.25 *10^3/ml for treatment 1–4 respectively) there was a tendency to be affected by treatments (P = 0.06). Mean concentration of Total Protein (10.94, 11.31, 11.68, 11.54 g/dl) had a trend to significance (P = 0.09). Albumin (6.13, 5.63, 6.13, 5.66 g/dl) and Immunoglobulin G (1.91, 1.73, 2.00, 1.47(g/dl) for treatment 1–4 respectively) significantly affected by treatments (P < 0.05). It is concluded that 1000 ppm propolis in compare of Monensin has potential to improve immune responses through its effect on the WBC, Albumin and IgG of Holstein female calves.

Key Words: propolis, Holstein female calves, immune responses

1841 (W300) Effects of maternal plane of nutrition, selenium supply, and physiological stage on digestibility and ruminal fermentation in ewes.

K. J. McLean*[1], A. M. Meyer[2], L. R. Coupe[1], G. P. Lardy[1], K. A. Vonnahme[1] and J. S. Caton[1], *[1]North Dakota State University, Fargo, [2]Division of Animal Sciences, University of Missouri, Columbia*

Objectives were to investigate effects of nutritional plane and Se supply during gestation on digestibility and ruminal fermentation at parturition and early lactation. Primiparous Rambouillet ewes (n = 84, age = 240 ± 17 d, BW = 52.1 ± 6.2 kg) were allocated to 2 × 3 × 2 factorial arrangement of treatments. Factors included dietary Se (adequate Se [11.5 µg/kg BW] or high Se [77.0 µg/kg BW]), nutritional plane (60% [restricted], 100% [control], or 140% [high]), and physiological stage at necropsy (parturition or d 20 of lactation). At parturition, lambs were removed from all ewes and 42 ewes (n = 7 per treatment) were necropsied. Remaining ewes were transitioned to a common diet, which met lactation requirements, and mechanically milked for 20 d. Three way interactions were not present ($P > 0.10$). As expected, DMI was altered by both nutritional plane and physiological stage. In pregnancy and lactation, DMI increased with plane of nutrition ($P < 0.001$; 500 vs. 755 vs. 1183 and 1173 vs. 1237 vs. 1295 ± 19 g for restricted, control, and high ewes during pregnancy and lactation, respectively). Neither DMI nor total OM digestion were altered by Se supply. Total OM digestion was greater ($P = 0.03$) in restricted compared with high ewes during both gestation (75.8 and 67.0 ± 1.2%, respectively) and lactation (68.4 and 64.8 ± 1.2%, respectively). Both apparent ($P < 0.01$) and true ($P = 0.04$) ruminal OM digestion was greater in restricted (60.7 ± 1.42%) vs. control and high ewes (56.4 and 54.4 ± 1.42%, respectively). Ewes fed high Se during gestation had greater ($P = 0.03$) apparent and true ruminal OM digestion during gestation but were not different at d 20 of lactation. Ruminal acetate proportions were lower ($P = 0.03$) and the ratio of acetate + butyrate over propionate tended ($P = 0.09$) to be greater in high Se vs. adequate Se fed ewes. Ewes fed restricted diets had greater acetate ($P < 0.001$), lower propionate proportions ($P < 0.001$), and lower total VFA concentrations ($P < 0.01$). Ewes at parturition had greater total VFA ($P < 0.001$) than ewes during lactation. These data indicate that maternal plane of nutrition, Se supply, and physiological stage all impact digestion and ruminal fermentation which will influence circulating nutrients available for fetal growth and milk production.

Key Words: digestibility, ewes, selenium

1842 (W301) Effect of reduced energy density of close-up diet on dry matter intake, milk yield and energy balance in multiparous Holstein cows.

W. M. Huang*, A. Simayi, A. Yasheng, Z. H. Wu, S. L. Li and Z. J. Cao, *State Key Laboratory of Animal Nutrition, College of Animal Science and Technology, China Agricultural University, Beijing, China*

The objective of this study was to determine the effect of reduced energy density of close-up diet on DMI, milk yield and energy balance (EB) in multiparous Holstein cows which were fed for ad libitum intake. Thirty-nine dry cows were blocked and assigned randomly into 1 of 3 energy concentrations (6.8, 6.2, 5.4 MJ of NE_L/kg; 14.0% CP) diets to meet 100% (100NRC; n = 13), 90% (90NRC; n = 13), 80% (80NRC; n = 13) of the NRC (2001) dietary NE_L recommendation, respectively, from 21 d before expected day of calving. After parturition, all cows were fed the same lactation diet to 70 d in milk (DIM). Data were analyzed by SPSS with repeated measures procedure or One-Way ANOVA procedure. The DMI (14.3, 13.6, 12.6 kg/d; $P = 0.009$) and NE_L intake (NEI, 97.1, 83.3, 68.6 MJ/d; $P < 0.001$) prepartum were significantly different for 100NRC, 90NRC and 80NRC groups. In the last 24 h before calving, the 80NRC group consumed 1.3 kg and 0.7 kg more diet (DM) than the 100NRC and 90NRC groups ($P > 0.05$), respectively, but the NEI was very similar among the 3 treatments. During the first 4 wk postpartum, the DMI and NEI for the 80NRC group were numerically greater than those for the 100NRC ($P > 0.05$). The milk yields of 90NRC and 80NRC groups were numerically greater than 100NRC from 1 to 10 wk (36.6, 38.6, 38.7 kg/d; $P > 0.05$), but the 4% fat-corrected milk yields (45.4, 45.7, 45.4 kg/d; $P > 0.05$) were very similar due to the significantly higher milk fat content for 100NRC. The energy consumption for 100NRC, 90NRC and 80NRC were 149.8%, 126.2% and 101.1% of their calculated energy requirements prepartum, and 72.7%, 73.1% and 75.2% during the first 4 wk postpartum, respectively. In conclusion, the low energy density prepartum diet was effective in controlling NEI prepartum, and was beneficial in increasing DMI, whilst alleviating negative EB postpartum.

Key Words: dietary energy density, dry matter intake, milk yield

1843 (W302) Effects of lysolecithin on milk fat synthesis and milk fatty acid profile of cows fed diets differing in fiber and unsaturated fatty acid concentration.

D. E. Rico*, J. Y. Ying and K. J. Harvatine, *Penn State University, University Park*

Thirteen multiparous Holstein cows (> 70 DIM) were used in a crossover design that tested the effect of lysolecithin under diets differing in fermentability and polyunsaturated fatty acid (FA) concentration. Experimental periods were 20 d and

included two 10 d phases. During phase 1, a standard fiber and low fat diet was fed (32% NDF, no added oil) and during phase 2 a lower NDF higher oil diet was fed (30.5% NDF and 2% oil from whole soybeans and soybean oil). A 14 d washout period between experimental periods allowed milk fat recovery. Treatments were control and lysolecithin (10 g/d/cow of LYSOFORTE$_{brand}$, Kemin Industries, Des Moines, IA) extended in a ground corn carrier. Milk was sampled on d 0, 5, and 10 of each phase for determination of fat and protein concentration and FA profile. There was no effect of treatment or treatment by time interaction for DMI or milk yield, however on d 5 of phase 2 lysolecithin tended to decrease DMI ($P < 0.10$). There was a treatment by time interaction for milk fat concentration and yield ($P < 0.05$). Milk fat concentration was higher in lysolecithin on d 5 of phase 1, but decreased progressively in both treatments during phase 2. Milk fat yield was not different among treatments during phase 1, but was lower in lysolecithin on d 5 and tended to be lower on d 10 of phase 2 ($P < 0.10$). There was no effect of treatment or treatment by time interactions for milk protein concentration or yield. No treatment by time interactions were detected for the concentrations of milk de novo (< 16 C) or preformed (> 16 C) FA. Concentrations of de novo FA decreased, but preformed FA increased during phase 2 ($P < 0.001$) and no treatment differences were detected at any time point. There was an effect of time, but no treatment by time interactions for milk *trans* FA isomers ($P < 0.05$). Briefly, *trans* 11 C18:1 and *cis*-9, *trans*-11 conjugated linoleic acid (CLA) decreased progressively during phase 2 as *trans* 10 C18:1 and *trans*-10, *cis*-12 CLA increased progressively. Lysolecithin increased milk fat concentration when feeding a higher fiber and lower fat diet, but decreased milk fat yield when feeding a lower fiber and higher fat diet, although biohydrogenation pathways were not modified.

Key Words: dairy cows, lysolecithin, milk fat depression

1844 (W303) Effects of fescue toxicosis induced by endophyte-infected tall fescue seed on forestomach epithelial gene expression in Angus steers.

D. Kim[*1,2], J. L. Klotz[3] and D. L. Harmon[1], *[1]University of Kentucky, Lexington, [2]National Institute of Animal Science, Rural Development Administration, Suwon, South Korea, [3]USDA-ARS, FAPRU, Lexington, KY*

A previous report demonstrated that steers exposed to an endophyte-infected tall fescue seed extract had altered rumen epithelial blood flow and decreased ruminal flux of VFA. Thus, this study was conducted to determine whether there are differences in gene expression related to VFA absorption between steers dosed with endophyte-infected (E+; 4.45 mg ergovaline/kg) or endophyte-free (E-) tall fescue seed. Twelve ruminally cannulated Angus steers (BW = 547 ± 9 kg) were stratified based on BW and randomly allocated to 6 blocks. The steers were fed alfalfa cubes at 1.5 x NE$_m$ and dosed (1 kg/d) with ground tall fescue seed via rumen cannula once daily for 21 d. On d 22, the steers were slaughtered and tissue samples were immediately collected from rumen, reticulum, omasum, and abomasum. Samples were rinsed extensively with ice-cold physiological saline to remove residual feed and contents before separating epithelia from the underlying tissue. Thereafter, samples of epithelial tissue (1 g) were immediately homogenized with TRI-reagent. The expression levels of monocarboxylate transporter 1, 2, and 4 (MCT1, MCT2, and MCT4, respectively), sodium hydrogen exchanger 1, 2, and 3 (NHE1, NHE2, and NHE3, respectively), putative anion transporter 1 (PAT1), downregulated in adenoma (DRA), anion exchanger 2 (AE2), sodium bicarbonate cotransporter 1 (NBC1), 3-hydroxy 3-methylglutaryl coenzyme A synthase 2 (HMGCS2), and sodium potassium ATPase pump 1 (ATP1) were measured using SYBR-Green and abundances were quantified by qPCR using glyceraldehyde-3-phosphate dehydrogenase as the control gene. The levels of MCT1 and MCT4 expression were lower ($P < 0.05$) in the rumen tissue of steers dosed with E+ seed, whereas MCT2 was not different. The expression of NHE2 was lower ($P < 0.05$) for E+ steers, whereas NHE1 and NHE3 were not affected by seed in the rumen epithelium. The levels of DRA and AE2 expression were lower ($P < 0.05$) for E+ steers in the rumen epithelium, whereas PAT1, NBC1, HMGCS2 and ATP1 were not affected by seed treatment. Expression of these genes in reticulum, omasum, and abomasum epithelia, were not affected ($P > 0.05$) by seed treatment. These data indicate that endophyte-infected tall fescue seed may contribute to depression of ruminal VFA absorption in a dissociated state (pH > 5.8) by the depression of MCT1 and MCT4 in the rumen associated with NHE2, DRA and AE2. Consequently, this may contribute to decreased gain associated with fescue toxicosis in cattle.

Key Words: VFA transporter, gene expression, tall fescue

1845 (W304) Replacement of soybean meal by high energy cottonseed meal in diets of dairy cows: milk production and ovarian follicular dynamics.

F. M. Wingert, L. K. Hatamoto-Zervoudakis*, P. N. Cosentino, J. T. Zervoudakis and A. L. Cândida de Resende Fraga, *Federal University of Mato Grosso, Cuiaba, Brazil*

Supply of high biological value protein is key to reproductive and productive performance, however the cost is high. The aim of this study was to evaluate replacement of soybean meal by high energy cottonseed meal like protein source in dairy cows diets on productive and reproductive parameters. Five Girolanda cows with average body weight of 530 kg, distributed in 5x5 Latin square were used (5 levels of substitution of soybean meal by high energy cottonseed meal: 0% (FA0), 15% (FA15), 30% (FA30), 45% (FA40) and 60% (FA60) and 5 periods). Each period lasted 18 d. Milk production (MP) and

Table 1845. Milk production (MP, kg/day), body score condition (BSC, 1–5), number of recruited follicles (NRF), dominant follicle diameter (DFD, mm), and corpus luteum diameter (CLD, mm) of Girolanda cows feeding with diets with substitution of soybean meal by high energy cottonseed meal

Treatment	MP	BSC	NFR	FMD	CLD
FA0	14.4 ± 0.2[a]	2.9 ± 0.03	25.69 ± 1.22	15.10 ± 0.39	20.60 ± 0.7
FA15	12.4 ± 04[c]	2.9 ± 0.07	26.08 ± 1.31	17.90 ± 0.64	21.15 ± 0.7
FA30	14.6 ± 03[a]	2.9 ± 0.05	26.83 ± 1.12	16.90 ± 0.33	21.85 ± 0.6
FA40	14.5 ± 0.2[a]	2.9 ± 0.03	25.89 ± 1.28	14.90 ± 0.34	21.10 ± 0.9
FA60	13.7 ± 04[b]	2.9 ± 0.07	26.08 ± 1.01	18.30 ± 0.32	20.40 ± 1.0
P	< 0.0001	0.3002	0.8133	0.1039	0.6781

FA: diet without substitution; FA15 replacement 15% of soybean meal by high energy cottonseed meal; FA30 replacement 30% of soybean meal by high energy cottonseed meal; FA40 replacement 40% of soybean meal by high energy cottonseed meal; FA60: replacement 60% of soybean meal by high energy cottonseed meal; *P*: significance level
A, b, c…different letters in same column indicate differences by Tukey test

body score condition (BSC) were evaluated on the 18th day and ovarian evaluations (number of recruited follicles (NRF), dominant follicle diameter (DFD), and corpus luteum diameter (CLD)) were conducted from 7 to 18th day of supplementation by trans-rectal ultrasonography. Data were analyzed by Tukey test with 5%of significance level. Replacement of protein source (replacement of soybean meal by high energy cottonseed meal) do not influenced ($P > 0.05$) body score condition, number of recruited follicles, dominant follicle diameter, and corpus luteum diameter. However, could reduce milk production in higher and lower replacements levels (Table 1845). The replacement of soybean meal by high energy cottonseed meal as protein source at level of 30 or 40% is feasible because not alters reproductive and productive performance, and promotes reduced diet cost.

Key Words: protein sources, follicles, girolando

1846 (W305) Supplements with chelated mineral for cows Nellore: Growth performance, oocyte quality and oxidative stress. T. D. P. Trindade, L. K. Hatamoto-Zervoudakis*, C. Pasa, J. T. Zervoudakis, P. P. Tsuneda, F. M. Wingert and A. L. Cândida de Resende Fraga, *Federal University of Mato Grosso, Cuiaba, Brazil*

Nutrition has a major influence on reproductive performance (expression of estrus, follicular development, quality of gametes, ovulation rate, uterine environment, embryo development, maintenance of pregnancy, etc.). Chelated minerals may provided potential benefits to reproduction, enhancing mineral absorption and retention in animal tissues, improved functioning of dependent enzyme systems of minerals (antioxidant systems), best performance (higher daily weight gain, feed conversion, lower mortality, greater production of meat, eggs and milk). The objective of this study was to evaluated oocyte quality and production traits in Nelore cows grazing supplemented with copper, zinc and selenium in chelated form. 24 multiparous Nelore cows were used, with 36 mo of average age, 395 kg of body weight and body condition score of 4.8. Animals were divided into 2 groups: control group (CG, animals supplemented with inorganic mineral) and Supplemented Group (SG, animals supplemented with zinc, copper and selenium in chelated form). Each group was raised in a paddock of *Brachiaria brizantha* cv. Marandu, receiving 1 kg of supplement/animal/day. Every 2 wk the animals were weighed and body condition score (BCS) was evaluated. During experimental period (99 d), two aspirations (59 and 99 d of supplementation) were performed. Oocytes were assessed as viable and non-viable and follicular fluid levels of oxidative stress was measured by TBARS concentration. The experiment was a completely randomized design and data analyzed by ANOVA with a significance level of 5%. Chelated minerals supplementation did not affect ($P > 0.05$) total number of oocytes retrieved ($P = 0.5028$), numbers of viable oocytes ($P = 0.1449$), and body weight ($P = 0.3587$). The use of chelated minerals provided greater BCS at the end of experiment ($P = 0.0500$, 5.27 ± 0.14 versus 4.83 ± 0.17) and higher gain in body condition score ($P = 0.0178$, 0.82 ± 0.18 versus. 0.25 ± 0.13). Animals supplemented with chelated minerals showed less oxidative stress in follicular fluid (0.05 ± 0.01 versus 0.09 ± 0.02, $P = 0.047$). Oral supplementation with minerals zinc, copper and selenium in chelated form at used levels, improved body condition score and reduced oxidative stress in follicular fluid of Nelore cows at pasture during dry- water transition.

Key Words: Body score condition, chelate, oxidative stress

1847 (W306) Contribution of a chelated trace mineral supplement as a methionine source for dairy cows. M. O. Caldeira*[1], R. O. Rodrigues[1], M. R. Waldron[1,2] and G. I. Zanton[3], *[1]University of Missouri, Columbia, [2]Nutrition Professionals, Inc., Chilton, WI, [3]Novus International, Inc., St. Charles, MO*

This experiment sought to determine whether the methionine contained in a trace mineral supplement made a meaningful contribution toward meeting the methionine requirement of the dairy cow. Four multiparous ruminally-cannulated lactating Holstein dairy cows were used in 4 × 4 Latin square design with 7-d periods. Treatments were administered at a rate of 0.08 g of 2-hydroxy-4-methylthio-butanoic acid (HMTBa)/kg of BW on d 0 of each experimental period: 1) HMTBa chelated to Zn, 80% HMTBa, dosed ruminally (MIN; Minitrex Zn, Novus International, St. Charles, MO, USA), 2) Ca-salt of HMTBa,

84% HMTBa, dosed ruminally (MHA; MHA feed supplement, Novus International), 3) HMTBa free acid, 88% HMTBa, dosed ruminally (ALR; Alimet, Novus International), and 4) HMTBa free acid, 88% HMTBa, dosed post-ruminally (APR; Alimet Novus International). Approximately 5 kg of rumen mat contents from each animal were removed through the cannula, mixed with the appropriate treatment dose, and replaced in the rumen. For post-ruminal treatment, a 50cc syringe was placed in the omasal canal, and contents were expelled into the abomasum; all other animals received a post-ruminal infusion of water. Blood samples were collected regularly through each experimental period. Feed was restricted for 30 min before treatment administration, following which, animals were fed for ad libitum consumption. Data were analyzed using MIXED procedure of SAS, using averaged pre-infusion measurements as covariates. Plasma concentrations of methionine did not differ between MIN, MHA, and ALR treatments; however, APR resulted in a greater ($P < 0.001$) concentration of plasma methionine compared with other treatments. A treatment x time interaction ($P < 0.001$) was observed for plasma methionine, in which APR increased at 1.5 h after infusion, reaching peak at 3 h ($P < 0.001$), and leveling with other treatments at 12 h ($P > 0.10$). Greater plasma concentrations of HMTBa ($P < 0.001$) were found in APR than in MIN, MHA and ALR; however, these did not differ between each other ($P > 0.10$). There was a treatment x time interaction ($P < 0.001$) for HMTBa; APR peaked at 1.5 h after infusion ($P < 0.001$), declined sharply until 9 h when lower concentrations of HMTBa were observed compared with other treatments ($P \leq 0.05$). After 12 h, HMTBa treatments no longer differed ($P > 0.10$). In conclusion, the availability of methionine in plasma did not differ between treatments administered ruminally; however, significant increases were observed when treatments were administered post-ruminally. These results suggest that MIN may be used to contribute toward the methionine requirement for dairy cows.

Key Words: HMTBa, rumen, supplementation

1848 (W307) Effect of the supplementation of plant extracts, vitamins and their associations on feedlot performance and carcass traits of Nellore cattle.

M. B. Silva*[1], A. M. Jorge[2], F. D. Resende[3], G. R. Siqueira[4], G. F. Berti[5], C. L. Francisco[1] and A. M. Castilhos[1], *[1]Universidade Estadual Paulista- FMVZ, Botucatu, Brazil, [2]Faculdade de Medicina Veterinária e Zootecnia, Universidade Estadual Paulista, Botucatu-SP, Brazil, [3]Agência Paulista de Tecnologia dos Agronegócios- APTA, Colina, Brazil, [4]APTA-Polo Regional Alta Mogiana, Colina, Brazil, [5]Centro Universitário da Fundação Educacional de Barretos- Unifeb, Barretos, Brazil*

Fifty-six Nellore (*Bos indicus*) young bulls of +360 kg initial weight and +20 mo of age were used to evaluate the effect of the supplementation of vegetable extract, A, D and E vitamins and their associations on the feedlot performance (finishing phase) and carcass characteristics. Animals were maintained in individual pens for 105 d (21 and 84 d, for adaptation and trial period, respectively). Animals were individually weighed, and blocked by initial body weight. Pens within a block were randomly assigned to one of four treatments: (C) Control diet including A, D and E vitamin; (V) Control diet plus 50% A, D and E vitamin; (E) Diet including 0.14% (DM basis) of plant extracts; (A) Diet with association of these two additives (50% A, D and E vitamin + 0.14% (DM basis) of plant extract). The treatments provided the same diet for all animals (85 and 15%, for concentrate and forage, respectively), varying only the inclusion of the different additives. Further, all treatments received monensin (30 mg/kg of concentrate). Feed offered was monitored daily as well as feed refusals were collected and weighed to determine daily dry matter intake (DMI) and feed efficiency (F:G). Animals were weighed every 28 d after 16 h feed withdrawal for calculating average daily gain (ADG). No effects of treatments ($P > 0.10$) were observed for DMI (9.69, 10.28, 10.03, 9.98 kg/day for diets C, V, E, A, respectively), ADG (1.60, 1.66, 1.64, 1.64 kg/day for diets C, V, E, A, respectively), and F:G (0.17, 0.16, 0.16, 0.16 for diets C, V, E, A, respectively). Back fat thickness, LM area, hot carcass weight, cold carcass weight, and cooling losses were not affected by treatments ($P > 0.10$). In conclusion, supplementation of plant extracts, vitamins and their association did not produces additional benefits on the feedlot performance or carcass traits of Nellore cattle. Supported by CAPES/NUTRON.

Key Words: plant extract, feedlot performance, carcass, Nellore

---

1849 (W308) Body condition score assessment in a grazing Jersey herd in Costa Rica.

A. Saborío-Montero* and J. M. Sánchez, *Centro de Investigaciones en Nutrición Animal y Escuela de Zootecnia, Universidad de Costa Rica, San José, Costa Rica*

The aim of this research was to carry out a body condition score (BCS) observational study in a commercial grazing Jersey herd in Costa Rica (9°55′ N, 83°51′ W, 2350 m of altitude). The study comprised 5864 BCS records from 122 cows (29 primiparous and 93 multiparous) over a 16 mo period. Cows were scored weekly by the same person from ninth wk prepartum to 43th wk postpartum. The 1 to 5 points scale was used (1 = emaciated, 5 = obese). Animals feeding practices were based on intensive grazing of 30 d regrowth kikuyu (*Kikuyuocloa clandestina*) (14.8% DM, 23.4% CP, 54.0% NDF, 25.7% ADF, 1.4 Mcal/kg NE_L (3x), 2.2% Lignin) and supplementation of a balanced concentrate according to physiological stage. During the close up period animals were fed 4 kg of concentrate daily (14% CP, 1.7 Mcal/kg NE_L(1x), 35% Starch, 0.2% Ca), and during lactation 1 kg of concentrate (18.6% CP, 1.9 Mcal/kg

NE_L, 48% Starch, 1.0% Ca)/2.5 to 3 kg of milk. Primiparous and multiparous cows BCS at calving was 4 points (95% CI: 3.80–4.22 points) and 3.8 points (95% CI: 3.71–3.94 points), respectively. BCS nadir after calving differed ($P < 0.05$) between primiparous (3.1 points, 95% CI: 2.97–3.23 points) and multiparous cows (2.9 points, 95% CI: 2.76–2.96 points). When stratifying BCS at calving into values $\leq$ 3.25, 3.50 to 4.00 and $\geq$ 4.25 points, differences ($P < 0.01$) were found in nadir extreme values within primiparous or multiparous groups of cows. Values were 2.63, 2.94 and 3.29 points for primiparous and 2.27, 2.78 and 3.20 points for multiparous, respectively. Likewise, the average BCS change differed ($P < 0.01$) between extreme values in the same group, showing -0.25, -0.81 and -1.19 points for primiparous and -0.71, -0.93 and -1.21 points for multiparous cows in the same order. BCS at calving in primiparous cows was correlated with nadir ($r = 0.65$, $P < 0.001$) and BCS change ($r = -0.76$, $P < 0.001$). Similarly, BCS at calving in multiparous cows was correlated with nadir ($r = 0.62$, $P < 0.001$) and BCS change ($r = -0.55$, $P < 0.001$). Cows that calved with higher BCS, lost more BCS postcalving, but remained at a greater BCS at nadir and the whole lactation. Results suggest that BCS at calving could be used as a partial indicator of BCS nadir and BCS change from calving to nadir; which has important implications on production and fertility of cows. However more research should be done to extend these findings to wider populations.

Key Words: BCS, Body condition score, grazing Jersey cows

1850 (W309) Intake and nutrient digestibility of growing Nellore heifers and steers fed two levels of calcium and phosphorus.

L. F. Costa e Silva[*1], T. E. Engle[1], P. P. Rotta[1], S. C. Valadares Filho[2], R. D. Valadares[3], F. A. S. Silva[3] and E. C. Martins[3], *[1]Colorado State University, Fort Collins, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal De Vicosa, Vicosa, Brazil.*

An experiment was conducted to evaluate intake and nutrient digestibility of Nellore heifers and steers fed two levels of calcium and phosphorus. Thirty two Nellore heifers and eighteen Nellore steers were used. Four animals from each gender were used as baseline reference animals and slaughtered at the beginning of the experiment. Four animals from each gender were fed at maintenance (MAIN) and 10 steers and 24 heifers were assigned to the ad libitum (ADLIB) group. The ADLIB heifers were further divided into four groups. Treatments were: 1) Ca and P fed at requirements (CaPR) with a 50:50 of roughage:concentrate (R:C) diet; 2) CaPR with at 70:30 R:C diet; 3) 43% of the Ca and 80% of the P requirement (CaPL) with a 50:50 R:C diet; and 4) CaPL with a 70:30 R:C diet. The ADLIB steers in this experiment were fed CaPR. Half of the steers and the heifers were slaughtered at d 50 and the other animals were slaughtered a d 100 of the feeding period while all MAIN animals were slaughtered at d 100. Total feces and urine were collected from all animals 72 h before slaughter. Dry matter digestibility and apparent absorption and retention of Ca and P were similar across Ca and P treatments. Final body weight and, consequently, average daily gain was higher ($P < 0.05$) in heifers receiving the high concentrate diet compared to the low concentrate diet while the levels of Ca and P did not affected ($P > 0.05$) the performance. Under the conditions of this experiment, the level of dietary Ca and P can be reduced in the diet and not impact intake, digestibility or performance of growing Nellore heifers and steers.

Key Words: minerals, sugarcane, performance

1851 (W310) Ration composition in Wisconsin dairy herds: Factors affecting fertility.

A. H. Souza[*1], P. D. Carvalho[2], C. M. Drake[3], R. D. Shaver[2] and M. C. Wiltbank[2], *[1]University of California Cooperative Extension, Tulare, [2]University of Wisconsin, Madison, [3]University of California, Davis*

The aim of this study was to determine whether composition of total mixed ration (TMR) diets influence reproductive efficiency of dairy farms in Wisconsin. Dairy producers and nutrition consultants from all herds agreed to provide a single snapshot of their complete TMR-ration information used in the post-fresh and high-milk production pens. The nutritional information included all ingredients and nutrient composition of all mixes used, as well as a herd backup that contained accurate production, health and reproductive records with archive files with previous 12 mo. The final database included data from 49 free-stall Holstein-dairy herds in WI (DC305 $n = 44$ and PCDart $n = 5$). Size of herds enrolled in the data collection varied from 143 to 2717 lactating cows (average 719.6 ± 77.2), were milked 2 ($n = 6$) or 3 ($n = 43$) times per day, with average production per cow of 39.0 ± 1.3 Kg/day, and average DMI of 25.1 ± 0.5 Kg/day. Records from PCDart herds were absorbed into DC305 and calculations of reproductive parameters such as conception rate at first AI (CR1AI), overall conception rate (CR), and interval from calving to conception (ICC) were performed with the same standardized command in DC305 to summarize performance records from the previous 12 mo. Statistical analyses were performed with the proc MEANS, proc CORR, and proc MIXED of SAS (version 9.3). There was a great variation in diet composition, with CP varying from 16.0 to 18.7%, RDP from 9.1 to 12.3%, NDF from 24.9 to 35.1%, NFC from 31.7 to 46.6%, Starch 20.1 to 30.8%, and Fat from 3.1 to 6.7%. Milk production level was not associated with CR1AI, CR, or ICC ($P > 0.10$). However, greater DMI tended to be associated with lower CR1AI ($r = -0.25$, $P = 0.10$) and lower CR ($r = -0.25$, $P = 0.11$). Diet CP and RDP did not seem to affect CR1AI, CR, or ICC ($P > 0.10$). Similarly, Fat content did not influenced fertility parameters ($P > 0.10$). Interestingly,

percentage of NDF was positively associated with CR1AI (r = 0.36, P = 0.01). In addition, greater energy content in the diet measured as NFC, NFC-intake, or Starch were all detrimental to CR1AI (NFC: r = -0.54, P < 0.01; NFCi: r = -0.42, P < 0.01; Starch: r = -0.37, P = 0.03), and CR (NFC: r = -0.51, P < 0.01; NFCi: r = -0.44, P < 0.01;Starch: r = -0.21, P = 0.20). In conclusion, although diets should be balanced to meet milk production requirements, maximizing digestible fiber and lowering highly fermentable energy contents should improve fertility of high producing cows.

Key Words: dairy cows, diet composition, fertility

1852 (W311) Milk quality from dairy farms divided in five levels of production. L. L. Cardoso, M. I. Marcondes*, G. A. T. Ferreira, V. L. N. Brandao, A. S. Trece and A. S. Trece, *Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil*

This study aimed to characterize the physicochemical properties of milk from different production scales. A databank with 21,917 analyses, from January 2005 to December 2012, of 409 producers was used. Milk samples were collected twice a month and placed directly into milk cooling tanks. The properties were divided according to monthly average of daily milk yield in the following levels: 10 to 100 L of milk per day (N = 7858); 100 to 200 L (N = 6494), 200 to 500 L (N = 5085), 500 to 1000 L (N = 1725), 1000 to 5000 L (N = 755). Years and months were analyzed in a completely randomized split-plot design repeated in a time scheme, with years as plots and months as sub-plots. Within the reported period, 11.32% of the samples were from producers who account for 44.25% of production. Moreover, the great majority of the samples (88.68%) are from producers representing 55.75% of the supplied milk. An urgent need of improvement in management of total bacterial count (TBC) was observed throughout the year, and only August and September presented results below 100,000 CFU/mL. Somatic cell count (SCC), decreases in dry period, where June is the month with the lowest rate, and there is an increase in this SCC in the rainy season. This characterization is important so the industry can establish a protocol for mastitis control and mammary gland health throughout the year. No significant difference was found when correlating levels of production and SCC. However, TBC was affected by levels of production (P < 0.05), which mean that greater producers, in general, have a better management of this item. Protein was not affected by production levels (P > 0.05), and it increases in early dry period, with a subsequent decrease until the beginning of the rainy season. For small producers (up to 500 L, including the first three levels) June had the highest fat production. The data obtained in the study shows that dairy farming in the region is predominantly developed in small properties. However, higher volumes are produced by fewer producers. The quality of milk produced deserves attention from the entire production chain of milk, and it still presents problems as high TBC, high SCC and low total solids, requiring more efficient management techniques.

Key Words: fat, milk, protein

1853 (W312) MasterGraze silage for growing Holstein heifers. D. L. Gadeken*[1], K. Koone[2], S. harris[2], M. kirk[3] and D. Casper[1], *[1]South Dakota State University, Brookings, [2]Masters Choice, Anna, IL, [3]masters Choice, Anna, IL*

MasterGraze (MG) is a new corn silage hybrid that is a grazing corn. The MasterGraze hybrid will develop grain, but harvest is recommended before grain development which results in a plant that is high in sugar and crude protein (CP). Thus, the unique nutritional attributes of MG makes it an attractive forage source for dairy heifers. Twelve growing Holstein heifers weighing 220.1 ± 28.8 kg were assigned to 1 of 2 treatments varying in type of corn silage. The Control (C) ration consisted of conventional corn silage (Dekalb) and the MG ration consisted of MG corn silage. Corn silages were fed at 38.6% (DM basis) with 19.6% alfalfa hay and 41.8% grain mix. The experimental grain mixes consisted of ground shelled corn, soybean meal, urea, minerals and vitamins that were formulated for each corn silage's nutritional profile. The rations were formulated to be 16% CP (DM basis) and meet or exceed all nutrient requirements for a growing Holstein heifer. Due to a limited amount of MG silage, the experiment was conducted for 5 wk. Animals were trained and fed using the Calan feeding door system to determine daily DM intake. All heifers were fed the C corn silage during the training period and measurements were taken for 1 wk to be used as a covariate. Covariate adjusted average body weights (251.5 and 242.7 kg for C and MG, respectively) were similar (P < 0.24) for heifers fed both corn silages. Average dairy gains (1.22 and 1.16 kg/d) were similar for heifers fed both corn silages. Dry matter intakes were similar but, numerically lower for heifers fed MG (6.49 and 4.99 kg/d). Feed conversions were similar (0.23 and 0.34 kg gain/kg feed), but numerically greater for heifers fed MG. The limited animal numbers in this study prevented finding significant differences between treatments, however, the feed costs savings are approximately $0.09/heifer/d feeding growing dairy heifers MG corn silage given the same performance based on ration formulation. Given the numerical differences in DM intakes and feed conversions, the cost advantages are greater than $0.09/heifer/d with MG.

Key Words: vorn dilage, fairy heifers, MasterGraze

1854 (W313) Transcriptome profiling of milk in dairy cows fed linseed. A. Siurana*, D. Gallardo and S. Calsamiglia, *Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra 08193, Spain*

Feeding linseed to dairy cows results in milk fat depression (MFD), but there is a wide range of sensitivity, with some cows not showing any reduction in milk fat, while others having a strong MFD. The objective of this study was to compare the mRNA expression of transcripts expressed in pelleted milk cells in cows resistant or sensitive to MFD. Four cows were selected from a dairy farm after a switch from a control diet to a linseed-rich diet: two were resistant to MFD and had high milk fat content before (4.06%) and after the change (4.36%) (R-MFD); and two were sensitive to MFD and milk fat content decreased after the change into the linseed diet (3.56 to 2.54%, S-MFD). Fresh milk samples were collected from each cow the week before and 2 wk after the diet change, and transcriptional profiling of mRNA was analyzed by Illumina RNA-sequencing technology. A total of 24,880 transcripts were tested. When S-MFD were fed linseed, 54 transcripts increased mRNA expression by 3 to 23 fold, and 9 transcripts decreased mRNA expression by 3 to fivefold compared with the same cows fed the control diet. When R-MFD cows were fed linseed, 306 transcripts increased mRNA expression by 2 to 12 fold and 544 transcripts decreased mRNA expression by 2 to ninefold compared with the same cows fed the control diet. The largest differences were observed between R-MFD and S-MFD cows when fed linseed, where the R-MFD cows increased mRNA expression of 668 transcripts by 2 to 20 fold and decreased mRNA expression of 1161 transcripts by 2 to 81 fold compared with S-MFD cows. When cows were fed the control diet, the R-MFD cows increased mRNA expression of 156 transcripts by 2 to 23 fold and decreased mRNA expression of 740 transcripts by 2 to 42 fold compared with S-MFD cows. When R-MFD cows were compared with S-MFD cows regardless of the diet fed, 91 mRNA transcripts were expressed more, and 460 transcripts were expressed less in R-MFD compared with S-MFD cows. As an example, the gene of the fatty acid binding protein 7 increased mRNA expression by 19 (in the linseed diet) and 20 (in the control) fold in R-MFD compared with S-MFD cows. This preliminary study show the potential of Illumina RNA-sequencing technique to find new candidate genes implicated in MFD.

Key Words: RNA-sequencing, milk fat depression, linseed

1855 (W314) Feeding diets inducing milk fat depression to heat-stressed dairy cows on performance, energy partitioning, and antioxidant status. S. Kargar[1], M. Khorvash[1], G. R. Ghorbani[1] and D. J. Schingoethe[*2], *[1]Isfahan University of Technology, Isfahan, Iran, [2]South Dakota State University, Brookings, SD*

Effects of grain source and dietary oil supplement on production performance, energy balance, metabolic heat production, and markers of liver function of heat-stressed lactating dairy cows were evaluated using eight multiparous Holstein cows (77.0 d in milk) in a duplicated 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments. Experimental diets contained either ground barley or ground corn supplemented with either fish oil or soybean oil at 2% of dietary dry matter. Rectal temperature showed no change (averaging 38.9°C) regardless of diet but respiration rate tended ($P = 0.08$) to be decrease in cows fed fish oil as compared to cows fed soybean oil (58.4 vs. 62.5 breath/min). Dry matter intake tended ($P = 0.09$) to be greater for barley- vs. corn-based diets (23.2 vs. 22.3 kg/d), but was reduced for the fish oil compared to soybean oil supplemented diets (21.1 vs. 24.3 kg/d; $P < 0.001$) which was negatively correlated with plasma concentrations of alkaline phosphatase ($r = -0.45$; $P \leq 0.01$) and malondialdehyde ($r = -0.26$; $P < 0.15$). Actual milk yield and energy-corrected milk yield were not affected by grain source whereas feeding fish oil decreased milk yield as compared to soybean oil. Due to lesser dry matter intake, metabolic heat production was decreased in cows fed fish oil relative to cows fed soybean oil. Although feeding fish oil vs. soybean oil reduced net energy for both maintenance and lactation, net energy balance remained unchanged across treatments. However, back fat thickness positively changed (+4.0 mm) in cows fed corn- but not barley-based diets that were supplemented with fish oil vs. soybean oil ($P = 0.10$). There was an interaction between dietary grain source and oil supplement on in vitro indicators of plasma lipoperoxidation including basal and maximum conjugated dienes and calculated area under the curve which were greater in corn-based diets supplemented with fish oil vs. soybean oil. In vivo plasma lipoperoxidation estimated by the plasma level of the major lipoperoxidation product (malondialdehyde) was greater in cows fed fish oil vs. soybean oil which substantiated increased susceptibility of plasma lipoperoxidation in respective cows. Overall, results from current experiment suggest that in cows fed diets supplemented with soybean- vs. fish-oil biosynthesis in the mammary gland was prioritized over anabolism and oxidation in peripheral adipose and muscle tissues regardless of type of grain used.

Key Words: Milk fat depression, Heat stress, Dairy cow

1856 (W315) Altering ewe nutrition in late gestation; the impact on lamb performance. F. McGovern*[1], F. Campion[1], T. Sweeney[2], S. Fair[3], S. Lott[2] and T. M. Boland[1], [1]*School of Agriculture and Food Science, University College Dublin, Dublin, Ireland,* [2]*College of Agriculture, Food Science and Veterinary Medicine, University College Dublin, Belfield, Dublin, Ireland,* [3]*Department of Life Sciences, University of Limerick, Limerick, Ireland*

Exposing the fetus to adverse conditions in-utero may result in developmental adaptations to the postnatal, structural and physiological growth of the animal. Maternal nutritional status is one of the primary extrinsic factors, contributing to the programming of fetal nutrient availability and nutrient partitioning throughout gestation. Altering the level of nutrition received by the ewe has been shown to affect fetal growth, influencing birth weight, postnatal growth and metabolism, and reproductive function. The objective of this study was to examine the effects of offering ewes 80% (*R*), 100% (M), or 120% (E) of recommended metabolisable energy (ME) requirements from d 105 of gestation to parturition on subsequent ewe and lamb performance. In a randomized complete block design study, sixty twin bearing ewes were allocated to one of three dietary treatments (n = 20). Energy requirements were calculated individually for each ewe and amended according to specific treatment allocation. Ewe liveweight and body condition score (BCS) were recorded throughout the study. Within 1 h of birth, the birth weight, lambing difficulty and skeletal measurements were recorded from all lambs. Ewes were hand milked at 1, 10, and 18 h post-partum and lamb colostrum intake recorded. Lamb live weight was recorded intermittently from birth to slaughter and subsequent average daily gain (ADG) calculated. Restricting the metabolisable energy offered (*R*) to the ewe in late gestation resulted in a decline in ewe body weight ($P < 0.05$) and BCS ($P < 0.01$) at 24 h post-partum when compared to ewes offered the excess energy diet (E). Combined litter weight, colostrum yield at 1 h post-partum and total yield up to 18 h post-partum were greater for ewes offered the E diet than either of the other treatment groups ($P < 0.01$). While there was no difference in individual lamb birth weight ($P > 0.05$), lambs born to ewes offered the R diet had a lower ADG ($P < 0.01$) up to 21 d of age and remained lighter ($P < 0.05$) than those born to ewes offered the E diet up to weaning (d 98 post-partum). In conclusion, offering ewes a restricted level of ME for the final 6 wk of gestation negatively impacted ewe performance to parturition and compromised lamb growth to weaning.

Key Words: fetal programming, late pregnancy nutrition, lamb performance

1857 (W316) A sensory additive alters the eating behavior of dry dairy cows. C. Iglesias[1], F. Bargo*[2], A. Mereu[2], I. Ipharraguerre[2] and A. Bach[1,3], [1]*IRTA, Barcelona, Spain,* [2]*Lucta S.A., Barcelona, Spain,* [3]*ICREA, Barcelona, Spain*

Six Holstein dry cows were used to evaluate the effect of a sensory additive (ProEfficient, Lucta S.A.) on eating behavior in a complete randomized design. Cows divided into 2 pens were randomly assigned to 2 treatments: control TMR or the same TMR supplemented with ProEfficient (PE) at a dose of 15 g/cow/d. The TMR (73:27 concentrate: forage; 14.8% CP, 47.0% NDF, 1.32 Mcal NE_L/kg) was formulated to provide the nutrient requirements of dry cows following NRC (2001) recommendations. Cows were fed ad libitum through 4 automatic feeders mounted on scales within each pen. Feed consumption and feeding bouts were recorded automatically. Data were analyzed with a mixed-effects model with repeated measures using the PROC MIXED procedure of SAS (1999) with cow as a random effect and treatment, time, and their 2-way interaction as fixed effects. Although DM intake was not affected ($P > 0.05$) by treatments (11.4 kg/d ± 0.33 SE), cows receiving PE reduced ($P < 0.05$) the time dedicated to eat (119 vs. 149 min/d ± SE 7.60) whereas increased ($P < 0.05$) the eating rate (106.4 vs. 85.3 g/min ± 5.52 SE) compared with the control cows. Neither number of meals (4.3 ± 0.75 SE) nor meal size (2.66 kg/meal ± 0.19 SE) differed ($P > 0.05$) between treatments. Feeding a sensory additive increased eating rate without affecting total dry matter intake of dry cows.

Key Words: sensory additive, eating time, eating rate

1858 (W317) Effects of restricted versus conventional dietary adaptation over periods of 6, 9, and 14 d on blood lipopolysaccharide binding-protein concentration of feedlot cattle. D. V. Vicari*[1], A. Perdigao[2], L. L. Cursino[1], R. S. Barducci[2], M. D. Arrigoni[2] and D. D. Millen[3], [1]*São Paulo State University (UNESP), Dracena campus, Dracena, Brazil,* [2]*São Paulo State University (UNESP), Botucatu campus, Botucatu, Brazil,* [3]*São Paulo State Foundation (FAPESP), São Paulo, Brazil*

Two studies were conducted to determine the effects of restricting intake of the final finishing diet (REST) as a means of dietary adaptation compared with diets increasing in concentrate (STEP) over periods of six, nine and 14 d on blood lipopolysaccharide binding-protein (LBP) concentration of Nellore cattle. The first study was designed as a completely randomized block with a 2x2 factorial arrangement, replicated six times, in which 120 26-months old yearling Nellore bulls (361.3 ± 30.2 kg) were fed in 24 pens for 84 d according to the treatments: STEP for 9-d or 14-d and REST for 9-d or 14-d. The second study had the same design and characteristics just described, in which 120 22-months old yearling Nellore bulls

(352.03 ± 19.61 kg) were fed according to the treatments: STEP for 6-d or 9-d and REST for 6-d or 9-d. In each study, 48 animals (two per pen) were randomly chosen for blood collection, which was performed at end of the adaptation period and on Day 21 of the studies. Blood samples were collected from the jugular vein, and blood LBP concentration, expressed as $ng \cdot mL^{-1}$, was determined by using a commercial ELISA kit. For the first study, a significant ($P = 0.01$) period main effect was observed, in which animals on Day 21 presented greater concentrations of LBP than those at end of the adaptation period (128.1 vs. 56.7). A significant ($P = 0.01$) interaction was observed between protocols and duration of adaptation, where animals in REST protocol of 14-d had greater blood LBP concentration (157.2) than cattle in STEP protocol of 9-d (91.0), which had greater blood LBP concentrations than animals in REST protocol of 9-d (67.3) and STEP protocol of 14-d (54.2). In the second study, no significant ($P > 0.10$) protocols and duration of adaptation main effects were observed. However, a significant ($P = 0.01$) period main effect was observed, in which animals on Day 21 of the study present greater concentrations of blood LBP when compared to those at the end of the adaptation period (615.3 vs. 136.6). As the normal cattle blood LBP range varies from 50 to 500 $ng \cdot mL^{-1}$, adapting feedlot Nellore cattle in 14-d, regardless of the protocol, seems to be the most feasible option.

Key Words: acidosis, endotoxin, Nellore

1859 (W318) The effects of OmniGen-AF on serum metabolites, calcium concentrations and hormones of the adrenal axis during heat stress in lactating Holstein cows.

L. W. Hall*[1], F. A. Villar[1], J. D. Allen[2], J. D. Chapman[3], N. M. Long[4] and R. J. Collier[1], *[1]The University of Arizona, Tucson, [2]Northwest Missouri State, Maryville, [3]Prince Agri Products, Inc., Quincy, IL, [4]Clemson University, Clemson, SC*

The objective was to evaluate physiological, behavioral and hormonal changes in lactating cows supplemented with OmniGen-AF (Prince Agri Products, Inc.) subjected to heat stress. Thirty lactating Holstein cows from an Arizona were assigned to a control diet (CON, $n = 15$h) or control diet plus OmniGen-AF (OG, $n = 15$h). Cows within diet were balanced by DIM, milk production and parity (91 ± 5.9 DIM, 36.2 ± 2.5 kg/d, and 3.1 ± 1.4). The cows were fed OG at 56 g/h/d for 52 d on the dairy, added to the TMR. On d 52, six cows were randomly selected from each of the diet groups, transported to the Agricultural Research Center (ARC), University of Arizona and housed in environmentally controlled modules (EM). Original diet assignments were continued. The OG was top-dressed 2x/d (28 g/feeding) with molasses as the carrier and the CON cows received the molasses carrier 2x/d. Both were mixed into the top one-third of the TMR. In the EM, all cows were subjected to 7 d of thermal neutral (TN), 10 d of heat stress (HS), and 4 d of TN. Feed intake, milk production, and milk composition were measured daily. Rectal temperatures and respiration rates were recorded 3x/d (0600, 1400, and 1800 h). Blood samples were taken on Days 7 (TN), 8 (HS), 10 (HS), 17 (HS) and 18 (TN) during the ARC phase and analyzed for selected blood metabolites, hormones and immune biomarkers. Serum cortisol levels were highest on d 8 for both the CON and OG fed cows however OG cows had significantly lower cortisol ($P < 0.05$) on Day 8 (CO*N* = 0.8372 ug/dL; OG = 0.4838 ug/dL). No differences were detected at the other time points. Serum insulin and plasma glucose levels were not different between CON and OG cows. The OG cows maintained lower SCC compared to CON ($P < 0.01$). Serum calcium were not different, however, serum NEFA ($P = 0.10$) tended to be greater in OG cows throughout the 21 d ARC phase. Although serum cortisol were lower in OG cows, serum ACTH levels at each sampling point were higher ($P < 0.0001$). Results suggest that feeding OG to lactating cows reduced many of the effects associated with HS by reducing cortisol. However, ACTH increased in OG cows suggesting that OG may alter adrenal response to ACTH. Additional research is needed to determine the cause of reduced serum cortisol and elevated serum ACTH in cows fed OG.

Key Words: heat stress, lactating cows, OmniGen-AF

1860 (W319) Assessment of the effect of plant tannins on rumen fermentation and gut microbial diversity in goats using 16S rDNA amplicon pyrosequencing.

B. R. Min*[1], C. Wright[1], P. Ho[2], J. S. Eun[3], N. Gurung[1] and R. Shang[1], *[1]Tuskegee University, Tuskegee, AL, [2]Montgomery Blair High School, Silver Spring, MD, [3]Utah State University, Logan*

Two grazing experiments were performed to 1) investigate the effects of supplementing condensed tannins (CT)-containing pine bark (PB) powder on ADG, ruminal fermentation, and gut microbial diversity dynamics, and 2) to quantify the influence of different sources of tannins supplementations on ruminal fermentation and gut microbial diversity changes of goats grazing winter pea and ryegrass dominant forages. In Exp. 1, 20 Kiko cross male goats (*Capra hircus*; initial BW = 39.7 ± 2.55 kg) were randomly assigned to 2 experimental diets (alfalfa pellet vs. PB powder). Alfalfa pellet (no CT as a control) or PB (11% CT) was supplemented at 0.8% BW for targeted total DMI of 1.2% BW. The remainder DMI of each diet was obtained from grazing for 60 d. In Exp. 2, 12 Kiko cross goats were used to measure ADG, ruminal fermentation, and gut microbial population in the rumen of goats grazing bermudagrass. The animals were randomly assigned to 3 experimental diets: 1) no tannins (control), 2) chestnut extract at 100 g/d (CTE), and 3) quebracho CT extract at 100 g/d (QCTE). In Exp. 1, ADG was greater ($P < 0.05$) in PB (209 g/d) than the control (188 g/d). However, goats grazing winter pea and ryegrass forages with PB supplementation decreased ($P < 0.05$) concentrations of acetate (14.4 vs. 15.1 mM), propionate (3.34 vs. 3.83 mM),

butyrate (1.82 vs. 2.00 mM), and total VFA (22.5 vs. 23.7 mM) compared to those in the control, respectively. Bacterial population in PB-supplemented group was greater for *Bacteroides* (20.5 vs. 33.2%), *Firmicutes* (67.2 vs. 57.3%), and Proteobacteria (1.15 vs. 1.44%) phylum compared with control group, respectively. In Exp. 2, ADG was greatest for CTE (275 g/d) than QCTE (148 g/d) and the control (79.4 g/d). Goats grazing bermudagrass pasture with CTE had greater ($P < 0.05$) concentrations of acetate, propionate, butyrate, and total VFA compared to those in QCTE and control. Bacterial population in CTE-supplemented group was greatest for *Bacteroides* (51.5, 52.9, and 35.3%), *Firmicutes* (40.2, 36.7, and 55.9%), and Proteobacteria (2.28, 2.18, and 1.49%) phylum compared with QCTE and control group, respectively. Rumen archaeal population, however, was greatest in control group (0.70%) compared with CTE (0.23%) and QCTE (0.22%) group. Supplementing tannins in goat diets such as CTE, QCTE, or PB powder has the potential to improve ADG and modify rumen bacterial and archael population.

Key Words: goats, gut microbial diversity, tannins

1861 (W320) Effect of supplemental chelated Cu, Zn, and Mn on antioxidant status and hoof health of lactating cows.

X. J. Zhao[1], J. H. Wang[2], Y. M. Wang[*3] and L. Wang[1], *[1]College of Animal Science and Veterinary Medicine, Shandong Agriculture University, Taian, China, [2]College of Animal Science, Zhejiang University, Hangzhou, China, [3]Novus International Trading (Shanghai) Co., Ltd, Shanghai, China*

The objective of the study was to evaluate effect of supplemental Cu, Zn, and Mn as chelated trace mineral (CTM) on antioxidant status and hoof health of dairy cows. Forty eight Holstein cows in early lactation (DIM = 65) were randomly assigned into 1 of 2 treatments: 1) basal diet contains 17.2 mg Cu, 70.1 mg Zn, and 63.7 mg Mn/kg dry matter (CON); 2) basal diet supplemented with 150 mg Cu, 320 mg Zn and 130 mg Mn/head/d as CTM (Minitrex). Cows were gait scored using a 5-point Numerical Rating System where 1 and 2 are considered healthy, and $\geq$ 3 lame. Cows in each treatment were blocked as lame cows (n = 12) or healthy cows (n = 12) when data was analyzed. Over the 180 d experiment, DMI, milk yield and milk composition was tested every 10 d. Blood samples and hoof samples were taken at Day 0, 90, and 180 to test the blood antioxidant variables and hoof hardness, respectively. There was no difference in DMI, milk yield and milk composition between healthy and lame cows ($P > 0.05$). Cows receiving CTM had less milk fat concentrations ($P < 0.05$) than CON, but no difference was observed on milk fat yield or other milk components ($P > 0.05$). No differences were detected in blood superoxide dismutase (SOD), reduced glutathione (GSH), oxidized glutathione (GSSG), glutathione peroxidase (GSH-Px), catalase (CAT), and malondialdehyde (MDA) between healthy and lame cows ($P > 0.05$). Compared with CON, blood SOD, GSH, and GSH-Px in CTM cows were significantly increased while MDA and GSSG were significantly decreased ($P < 0.05$), and blood CAT was not affected by treatments ($P > 0.05$). Cows receiving CTM did not have hoof hardness that differed from the CON at Day 0 and 90, but had significant greater values than CON at Day 180 ($P < 0.05$). There was no interaction between CTM and cows health status. It was concluded that supplemental chelated Cu, Zn, and Mn could improve antioxidant status and hoof hardness regardless of lameness status.

Key Words: chelated trace mineral; antioxidant status; hoof health

---

1862 (W321) Effects of supplemental bupleurum extract on serum hormone and immune globulin levels in heat-stressed dairy cows.

X. Sun[1,2,3], J. Cheng[1,2,3], D. P. Bu[3], L. Pan[3], N. Zheng[1,3,4] and J. Wang[*1,3,4], *[1]Ministry of Agriculture- Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [4]Ministry of Agriculture- Milk and Dairy Product Inspection Center (Beijing), Beijing, China*

This experiment was conducted to evaluate the effects of bupleurum extract (BE) on serum hormone and immune globulin levels in dairy cows under heat stress. Forty lactating Holstein cows (75 ± 15 DIM, 37.5 ± 1.8 kg of milk/d, and 1.7 ± 0.4 parity) were randomly assigned to one of four treatments. Treatments consisted of 0 (control), 0.25, 0.5, or 1.0 g BE/kg DM. The experiment lasted 10 wk. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Blood samples were collected from all of animals via tail vein before the morning feeding on Days 0, 21, 42, and 63. Data were analyzed by MIXED model procedure of SAS 9.2. Compared with controls, cows fed 1.0 g/kg BE had higher thyroxine (T3) (1.43 vs. 1.16 ng/mL; $P < 0.05$) and prolactin (PRL) (230.50 vs. 188.19 uIU/mL; $P < 0.05$) levels, and 0.5 g/kg BE had the tendence to increase the T3 (1.27 vs. 1.16 ng/mL; $P < 0.10$) level, but 0.25 and 0.5 g/kg BE had no effect ($P > 0.05$) on PRL level. Serum growth hormone (GH) level was increased (2.17 vs. 1.21 ng/mL; $P < 0.05$) in cows fed 0.25 g/kg BE compared with control cows, and tended to be higher (1.76, 1.69 vs. 1.21 ng/mL; $P < 0.10$) in cows fed 0.5 and 1.0 g/kg BE. Supplementation of BE had decreased the cortisol (COR) levels (48.35, 49.43, 49.86 vs. 64.49 ng/mL; $P < 0.05$), but had no effect ($P > 0.05$) on the levels of thyroxine, Insulin, glucagon, neuropeptide Y, leptin, insulin-like growth factor, and heat shock protein 70. Cows fed 0.5 g/kg BE increased the immunoglobulin (Ig) A content (279.25 vs. 179.78 ìg/mL;

$P < 0.05$), and IgG level was increased (36.54, 36.14 vs. 27.13 mg/mL; $P < 0.05$) in cows supplemented with 0.25 or 0.5 g/kg BE, while the IgM and tumor necrosis factor-á (TNF-á) levels showed no difference ($P > 0.05$) when compared with the control cows. These findings suggest that BE supplementation could relieve metabolic disorders and enhance immune function in heat-stressed cows.

Key Words: bupleurum extract;serum hormone; immune globulin

1863 (W322) Dry matter intake, milk yield, and composition of Holstein cows fed organic minerals.

T. A. Del Valle*[1], E. F. Jesus[2], A. G. B. V. B. Costa[1], G. F. Cabral[3], V. C. Galvão[1], P. G. D. Paiva[2], T. S. Acedo[4], L. F. M. Tamassia[4] and F. P. Rennó[1], *[1]School of Veterinary Medicine and Animal Science, University of São Paulo, Pirassununga, Brazil, [2]School of Agricultural and Veterinary Sciences of UNESP, Jaboticabal, Brazil, [3]School of Animal Science and Food Engineering of University of São Paulo, Pirassunga, Brazil, [4]DSM Produtos Nutricionais, São Paulo, Brazil*

The aim of this study was to evaluate the effects of organic sources of minerals diet of dairy cows in mid-lactation on dry matter intake, milk yield and composition. Twenty Holstein cows with an average body weight of 625.30 ± 80.37 kg and DIM averaging 146.83 ± 67.34 were allocated to receive one of two diets: INO (inorganic): diet with addition of inorganic mineral sources; ORG (organic) diet with addition of organic mineral sources (zinc, cooper, selenium, chromium, manganese, cobalt, iron and sulfur; DSM Produtos Nutricionais, Brazil). The design was crossover. Each experimental period had 14 d adaptation and 7 d for sampling. Samples of milk were collected on 16th, 17th and 18th days of each period to evaluate the composition. The cows were allocated in individualy barns type free-stall, fed ad libitum and intake were estimated by bromatological analyzes of feeds and orts. Increases in fat-corrected milk ($P < 0.05$), fat yield ($P < 0.05$) and protein ($P < 0.10$) were observed in the animals receiving the diets containing organic mineral sources compared to those fed inorganic sources. This increasing in fat corrected milk shows an increased efficiency of energy use, most likely due to higher preparation of enzyme apparatus for metabolizing energy. Milk yield has not influenced by the treatments, showed a mean of 32.43 $kg.d^{-1}$ and difference of 0.63 $kg.d^{-1}$ of milk, which, together with the average increase of 1.4 $g.kg^{-1}$ fat led to increase in fat yield ($P < 0.05$). The protein content, although not statistically differ, was 0.8 $g.kg^{-1}$ higher in diet with organic sources and result in increase 0.05 kg the protein yield ($P < 0.10$). The dry matter intake average 21.27 $kg.d^{-1}$ and no effect of experimental diets was observed. Organic minerals increases energy efficiency in dairy cows, increasing the secretion of milk solids without change the intake.

Key Words: dairy cows, efficiency, milk fat

1864 (W323) Effects of sampling position on blood hormone concentration in dairy cattle.

M. Zhao, D. P. Bu, J. Q. Wang*, X. Q. Zhou, Y. Zhang, S. G. Zhao and P. Sun, *State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China*

To evaluate the effects of sampling position on blood hormone concentration in dairy cattle, ten dairy cows (Milk yield = 28.2 ± 2.1 kg/d, DIM = 121 ± 15 d) were selected. Blood samples from mammary vein, external pudic artery, coccygeal artery and vein were collected. Eight kinds of hormones were determined by radioimmunoassay method including insulin, growth hormone (GH), insulin-like growth factor-1 (IGF-1), leptin, adrenocorticotropic hormone (ACTH), estrogen, prolactin and progestin. Statistical analysis was performed using the PROC MIXED procedure of SAS 9.0. The results showed that no differences were observed in these hormones. Concentrations of hormones in mammary vein, external pudic artery, coccygeal artery and vein were averaged as followed: insulin (5.56 vs. 6.39 vs. 5.35 vs. 5.38 μIU/ml, $P > 0.05$), GH (2.29 vs. 2.34 vs. 2.34 vs. 2.40 ng/ml, $P > 0.05$), IGF-1 (290.57 vs. 260.63 vs. 283.64 vs. 266.99 ng/ml, $P > 0.05$), Leptin (3.04 vs. 3.10 vs. 3.17 vs. 2.97 ng/ml, $P > 0.05$), ACTH (11.35 vs. 11.43 vs. 11.50 vs. 12.15 pg/ml, $P > 0.05$), Estrogen(12.67 vs. 12.70 vs. 14.45 vs. 11.47 pg/ml, $P > 0.05$), Prolactin (315.88 vs. 312.47 vs. 290.28 vs. 302.24 μIU/ml, $P > 0.05$), Progestin(0.21 vs. 0.24 vs. 0.23 vs. 0.33 ng/ml, $P > 0.05$). It was implied that either of the four sampling positions could be representative for hormones measurement when estimating mammary gland metabolism.

Key Words: blood, hormone, mammary gland

1865 (W324) Effects of dietary protein composition on blood hormone levels in dairy cattle.

M. Zhao[1], D. P. Bu[1], J. Q. Wang*[1], X. Q. Zhou[1,2], Y. Zhang[1] and P. Sun[1], *[1]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [2]Northeast Agricultural University, Harbin, China*

The objective of this experiment was to investigate the effects of different protein sources on blood hormones profile. Thirty two dairy cows were pen fed with total mixed ration (TMR), which were divided into group soybean (corn stover 36.1%, soybean meal 11.3%, extruded soybean 2.1%, whole cottonseed 10.4%, rapeseed meal 4.2%, cottonseed meal 2.1%, beet pulp 4.2%, grind corn 25.6% and other supplements 4.1%) and group non-soybean (corn stover 36.1%, whole cottonseed 10.4%, rapeseed meal 9.6%, cottonseed meal 6.7%, beet pulp 7.5%, grind corn 25.6%, wheat bran 4.5% and other supplements 1.7%). Crude protein (CP) and neutral detergent fiber

(NDF) of TMR were 16.1% vs. 15.1% and 54.0% vs. 57.1% in group soybean and group non-soybean, respectively. The duration of this experiment was 15 wk (2-wk adaptation and 13-wk experimental period). Nine hormones were determined by radioimmunoassay method including insulin, growth hormone (GH), insulin-like growth factor-1 (IGF-1), Adrenocorticotropic hormone (ACTH), Leptin, Estrogen, Cortisol, Prolactin and Progestin. Statistical analysis was performed using the PROC MIXED procedure of SAS 9.0. Dry matter intake (DMI) and milk yield were 17.4 vs. 19.1 kg/d ($P < 0.01$) and 23.2 vs. 22.9 kg/d ($P > 0.05$) in group soybean and group non-soybean. Concentrations of hormones were averaged insulin (13.44 vs. 12.55 μIU/ml, $P > 0.05$), IGF-1 (384.31 vs. 286.33 ng/ml, $P < 0.01$), ACTH (9.67 vs. 6.00 pg/ml, $P < 0.05$), Estrogen (10.69 vs. 10.44 pg/ml, $P > 0.05$), GH (2.37 vs. 2.26, $P > 0.05$), Leptin (3.67 vs. 3.32 ng/ml, $P > 0.05$), Progestin (0.38 vs. 0.36 ng/ml, $P > 0.05$), Prolactin (175.51 vs. 174.00 μIU/ml, $P > 0.05$) and Cortisol (10.92 vs. 7.38, $P > 0.05$) in group soybean and group non-soybean, respectively. It demonstrated that protein sources could significantly influence DMI and have no effect on milk yield, which can also influence the function of hypothalamus pituitary adrenal axis and stimulate the cell proliferate.

Key Words: protein source, blood hormone, dairy nutrition

1866 (W325) The small ruminant nutrition system: Considering the ruminal fiber stratification for goats. J. G. L. Regadas Filho*[1], L. O. Tedeschi[2], A. Cannas[3], M. T. Rodrigues[4] and R. A. Vieira[5], *[1]Universidade Federal de Vicosa, Vicosa, Brazil, [2]Texas A&M University, College Station, [3]Universita Di Sassari, Sassari, Italy, [4]Universidade Federal de Viçosa, Vicosa, Brazil, [5]Norte Fluminense State University, Campos dos Goytacazes, Brazil*

The objective of this research was to assess the ability of a mechanistic model named Small Ruminant Nutrition System (SRNS) to predict the metabolizable energy intake (MEI) and milk yield (MY) by using a heterogeneous ruminal fiber pool scenario (GnG1; Regadas Filho et al., 2014) in comparison to a traditional homogeneous scenario (G1), The GnG1 scenario considers that the first ruminal fiber pool (raft) follows an age-dependent fractional rate for particle transference from a raft to an escapable pool (λ_r) and that the second ruminal fiber pool (escapable) follows an age-independent fractional rate of particle escape from the escapable pool (k_e); for G1, a scenario with only a single fractional rate passage (k_p) is adopted. All parameters were estimated individually by using equations published in the literature; however, for the G1 scenario, two rate passage equations were used, with one from sheep data (G1-S; Cannas et al., 2004) and another from goat data (G1-G; Tedeschi et al., 2012). The MEI, MY and DMI estimated by using these scenarios were compared with the results of an independent dataset ($n = 327$) that contained information regarding the DMI, MEI, MY, BW and milk and dietary compositions. The evaluation of the scenarios was performed using a coefficient of determination (r^2) between the observed and predicted values; mean bias (MB); bias correction factor (C_b) and concordance correlation coefficient (CCC). The MEI estimated by the GnG1 scenario yielded a precision and accuracy ($r^2 = 0.82$; MB = 0.21 Mcal.d^{-1}; $C_b = 0.98$) similar to that of the G1-S ($r^2 = 0.85$; MB = 0.10 Mcal.d^{-1}; $C_b = 0.99$) and G1-G ($r^2 = 0.84$; MB = 0.18 Mcal.d^{-1}; $C_b = 0.98$) scenarios. The results were also similar for the MY; however, a significant MB ($P < 0.01$) was found as follows: GnG1 ($r^2 = 0.74$; MB = 0.70 kg.d^{-1}; $C_b = 0.79$), G1-S ($r^2 = 0.71$; MB = 0.58 kg.d^{-1}; $C_b = 0.85$) and G1-G ($r^2 = 0.71$; MB = 0.65 kg.d^{-1}; $C_b = 0.82$). The GnG1 scenario can be assumed to maintain the theoretical basis of mechanistic models.

Key Words: fiber stratification, goat, heterogeneous fiber pool

---

1867 (W326) Effect of "COGU" technology on glucose uptake and mineral utilization and deposition in growing lambs. A. M. Temple*[1], G. A. Ayangbile[1], D. R. Vandermyde[1] and C. R. Vandermyde[2], *[1]Agri-King Inc., Fulton, IL, [2]Morrison Veterinary Clinic, Morrison, IL*

"COGU" is a proprietary combination of GRAS microbial fermentation extracts meant to diminish the negative impact of mineral interactions that may be responsible for inefficient digestibility, absorption and utilization of nutrients in livestock. The objective of this study was to observe the effect of COGU technology additive (COGU) on blood glucose uptake, mineral utilization and deposition in the ruminant. Twenty-four Katahdin wethers (average BW 15.8 ± 1.5 kg) approximately 55 d of age were fed ad libitum either a silage based control diet (CON), or CON plus 3.4 g/head/d of a supplement containing COGU. Lambs were penned in groups of six with two pens per treatment. ADG was calculated for each animal and DMI was measured for each pen throughout d 100 of the experiment. Jugular blood samples were analyzed for each animal during wk 0, 4, 8, 10, and 12. Eight CON and 9 COGU sheep were housed in crates 5 d for total collection of orts, fecal and urinary samples for digestibility and nutrient utilization. All lambs were euthanized at the end of the experiment, and tissues collected for biological analysis. Data were analyzed by ANOVA CRD. No differences ($P > 0.05$) were observed between dietary treatments for DMI, ADG, or digestibility of nutrients. However, COGU-supplemented lambs had numerically greater digestibility of Na, P, S and Cu. Blood glucose in COGU lambs was higher (CO*N* = 61.90 mg/dL, COGU = 72.98 mg/dL; $P = 0.0005$) throughout the trial. Previous unpublished research also showed higher blood glucose in COGU-supplemented lambs. Liver glycogen was numerically higher ($P > 0.05$) in COGU-supplemented lambs.

No differences were observed in blood NH3, BHBA, BUN, cholesterol, or NEFA. Rumen fluid contents showed COGU tended to increase ($P = 0.054$) the molar proportion of acetate, propionate, and butyrate. Duodenum mucosal cell scrapings in COGU treatment had decreased ($P = 0.019$) Mg. Copper, Mn, and Zn were numerically higher ($P > 0.05$) and Fe lower ($P > 0.05$) in duodenum mucosal cell scrapings of COGU-supplemented lambs. In conclusion, supplemental COGU seems to increase blood glucose uptake in the growing lamb. It also may affect mineral passage and utilization through the duodenum mucosal cell membrane.

Key Words: glucose, mineral, lambs

1868 (W327) Effect on plasma metabolites of Nellore bulls fed ractopamine hydrochloride and protein level.

N. R. B. Cônsolo*[1], F. Rodriguez[1], M. O. Frasseto[1], R. A. P. Maciel[2], V. Rizzi[3] and L. F. P. Silva[1], [1]*University of Sao Paulo, Pirassununga, Brazil,* [2]*University of Sao Paulo, São Paulo, Brazil,* [3]*Ouro Fino, Cravinhos, Brazil*

The aim of this study was to evaluate was to evaluate the effects of ractopamine hydrochloride (RH) and dietary crude protein (CP) on blood metabolites of Nellore young bulls. Forty eight Nellore bulls were grouped by BW, and randomly assigned to treatments in a 2x2 factorial arrangement of treatments. The factors were two levels of dietary CP (100 and 120% of MP requirement), and two levels of RH (0 and 300 mg/animal/d). Treated animal received RH for the final 35d before slaughter. Blood was collected at the beginning and at the end of RH supplementation by venipuncture and/or puncture of the coccygeal artery, before the morning feeding. Blood samples were collected into 10-mL BD Vacutainers, without anticoagulant, for the measurement of serum glucose, total protein, albumin, plasma urea nitrogen (PUN), aspartate aminotransferase (AST), γ-glutamyl transferase (GGT) and alkaline phosphatase (ALP). Blood parameters were analyzed using commercial kits (Laborlab, São Paulo, Brazil and CELM, São Paulo, Brazil) by endpoint or kinetic colorimetric methods in an ABS-200 Automatic Biochemistry Analyzer (CELM). The statistical analyses were conducted using SAS, version 9.1.2 for Windows (SAS Institute Inc., Cary, NC, USA). Data were analyzed as a randomized block design with a 2x2 factorial arrangement of treatments using the MIXED procedure of SAS. There was no effect of treatments, or of interaction, on plasma creatinine, AST or GGT ($P > 0.05$). Dietary CP level tended to increase blood urea (31.2 vs. 40.8 mg/dL, $P = 0.07$). RH supplementation altered glucose, ALP and total protein; however, the effect was dependent on the dietary CP level. RH supplementation decreased plasma glucose concentration at CP100 ($P = 0.05$), and had no effect at CP120 ($P = 0.87$). For ALP activity, RH supplementation increased its activity at CP120 ($P = 0.05$) and had no effect at CP100 ($P = 0.42$). RH supplementation increased plasma total protein at CP 120 ($P = 0.03$) and had no effect at CP100 ($P = 0.17$) In conclusion, RH supplementation and CP levels leads to slight changes on plasma metabolites.

Key Words: crude protein, β-agonist, plasma metabolites

1869 (W328) Impact of "COGU" technology on performance in lactating dairy cows.

A. M. Temple*, G. A. Ayangbile, D. F. Jones and D. A. Spangler, *Agri-King Inc., Fulton, IL*

"COGU" is a proprietary combination of GRAS microbial fermentation extracts meant to diminish the negative impact of mineral interactions that may be responsible for inefficient digestibility, absorption and utilization of nutrients in livestock. Two studies were initiated to investigate the effect of COGU on blood profiles and lactation performance of dairy cows. The first study was conducted on a commercial dairy farm in the Pacific Northwest. Water and forages in this region are known to have certain minerals in excess causing depressed milk production, high somatic cell counts and other metabolic issues. In a Washington herd of 1500 cows, three groups of 130 cows each were selected. Each group contained fresh cows, heifers, or high cows. Cows were fed a supplement containing COGU at a rate of 15 g/head/d in a corn silage based TMR diet for 41 d. Twenty cows averaging 75 DIM (± 3 d) from the high group were randomly selected for blood sampling and milk data collection. Blood samples were obtained 2 wk before feeding COGU (BCOGU), followed by wk 1, 2, and 4 fed COGU (COGU), and subsequently by sampling at wk 1, 3, and 5 after removing COGU (ACOGU) from the diet. On-farm milk production data was collected daily 2 wk before feeding COGU through 4 wk after removing COGU. Data were analyzed by ANOVA CRD. Blood glucose, BUN, and hemoglobin were increased ($P < 0.0002$) for cows fed COGU, and BHBA and NEFA were decreased ($P < 0.0001$). The 150 DIM adjusted production was higher ($P < 0.0001$) for cows fed COGU. In a second study, 180 commercial dairy farms across the United States representing 29,346 cows were randomly selected. COGU was blended into a supplement and fed at a rate of 15 g/head/d. Data for milk yield and components was collected for a minimum of 10 d to maximum of 120 d on these farms. Statistical analysis was performed with Kruskal–Wallis One-Way Nonparametric AOV and Dunn's All-Pairwise Comparison test. There were no differences in DMI intake ($P = 0.98$); however, milk yield, milk butterfat, milk protein, ECM, and ECM feed efficiency were all significantly higher ($P < 0.03$) at the end of the experimental period compared to the start of the experiment. COGU increased glucose uptake and nitrogen utilization as well as improved milk yield and components in dairy cows.

Key Words: glucose, milk yield, dairy cows

1870 (W329) A conceptual model of protein-precipitable polyphenols (condensed tannins) on protein binding and protein digestion in ruminants.

H. D. Naumann*[1], N. M. Cherry[2], L. O. Tedeschi[3], J. P. Muir[2,4] and B. D. Lambert[2,4], *[1]University of Missouri, Columbia, [2]Texas A&M AgriLife Research, Stephenville, [3]Texas A&M University, College Station, [4]Tarleton State University, Stephenville, TX*

There is a need to better understand the mechanisms by which biologically active protein-precipitable polyphenols (PPP) from forages bind to dietary protein in the rumen and how this impacts the ruminant animal's requirement for protein. The objective of this study was to model the effect of biologically active PPP on ruminal protein binding and the potential protection of rumen-bypass protein. Green live-leaf material from six species of warm-season perennial legumes was sampled during August of 2011 and 2012. The effect of biologically active PPP on protein-binding ability was evaluated by combining rhizoma peanut with experimental forages to create separate basal diets (by year) containing PPP ranging from 1–9%. Protein-binding ability was determined by an in vitro protein-precipitable phenolics assay and nitrogen analysis of the protein-phenolic precipitates. Data were analyzed in linear-segmented and quadratic-segmented regressions (PROC NLIN of SAS) to model the effects of biologically active PPP on protein-binding ability. The Model Evaluation System (MES; http://nutritionmodels.tamu.edu/mes.html) was used to compare the correctness of the linear- versus the quadratic-segmented regression. For the linear-segmented regression, β_0 is equal to α, β_1 is equal to β, and α, β, X_m and Y_m were equal to -3.2935, 6.3329, 6.4 and 37.24, respectively. For the quadratic-segmented regression, β_0 is equal to α, β_1 is equal to β, β_2 is equal to γ and α, β, γ, X_m and Y_m were equal to -10.7117, 11.4534, -0.6854, 8.32 and 37.14, respectively. The data pattern suggests that the relationship between PPP and protein bound is not linear in nature. Beyond a certain point, in this case a concentration of PPP occurring between 6.4 and 8.3%, the amount of protein bound does not increase as the concentration of PPP in the diet increases. While both segmented regressions were similar in terms of adequacy, the linear-segmented regression was slightly more precise than the quadratic-segmented regression (R^2 0.811 and 0.809, respectively) at accounting for variation that occurred in observed values. Overall, the regression comparison indicated that the linear-segmented regression is 1.2 times more likely to correctly predict observed values of protein binding by PPP than the quadratic-segmented regression. However, either model would be an acceptable tool for use in modeling the effect of forage PPP on rumen-protein binding and potential protection of rumen-bypass protein and in a decision support system.

Key Words: legume, protein, tannin

1871 (W330) Effect of sprouted barley grain supplementation of an herbage or haylage diet on ruminal fermentation and methane output in continuous culture.

A. N. Hafla*[1], K. J. Soder[1], A. F. Brito[2], M. D. Rubano[1] and C. J. Dell[1], *[1]USDA-Agricultural Research Service, University Park, PA, [2]University of New Hampshire, Durham*

A 4-unit dual-flow continuous culture fermentor system was used to assess the effect of supplementing 7-d sprouted barley (SB) or barley grain (BG), with a pasture (orchardgrass) or haylage diet, on nutrient digestibility, VFA production, bacterial protein synthesis, and methane production. Treatments were randomly assigned to fermentors in a 4 × 4 Latin square design with a 2 × 2 factorial arrangement of treatments using 7 d for diet adaptation and 3 d for sample collection. Treatments were: 1) pasture+SB, 2) pasture+BG, 3) haylage+SB, and 4) haylage+BG. Feedings (60 g of DM) occurred 4 times daily (0730, 1030, 1400, 1900 h) throughout four 10-d periods. Gas samples for methane analysis were collected 6 times daily (0725, 0830, 1000, 1355, 1530, 1630 h). Samples for pH, ammonia-N, and VFA analysis were taken on d 8, 9, and 10 and analyzed for DM, OM, CP, NDF, and ADF for determination of nutrient digestibilities, and estimation of bacterial protein synthesis. Data were analyzed using the MIXED procedure of SAS with period and treatment as fixed effects and fermentor as random. Orthogonal contrasts were tested using haylage vs. pasture and BG vs. SB treatments. Apparent and true DM digestibility was not affected by forage type. True DM digestibility was greater ($P = 0.05$) for diets supplemented with SB. Apparent and true digestibilities of OM and apparent CP were not affected by treatment (68, 83, and 89%, respectively). Apparent NDF and ADF digestibilities of pasture diets were greater ($P < 0.05$) compared to haylage diets (79 vs. 72% and 76 vs. 73%, respectively); however, supplement did not affect fiber digestibility. Diets supplemented with SB had greater ($P < 0.05$) mean and minimum pH than BG. Haylage diets produced greater ($P < 0.01$) concentrations of total VFA compared with pasture diets (72 vs. 61 mmol/L). Supplementation with BG produced a greater ($P = 0.03$) concentration of total VFA compared to diets supplemented with SB (68 vs. 64 mmol/L). Haylage diets produced greater ($P < 0.05$) concentrations of daily methane compared with pasture diets (35 vs. 27 mmol) but supplementation did not affect methane production. Bacterial efficiency was greater ($P < 0.05$) for pasture diets compared with haylage diets with no effect of supplementation. Supplementation with SB increased true DM digestibility of pasture and haylage diets, but did not impact fiber and CP digestibility, methane production, or microbial efficiency, compared to BG.

Key Words: sprouted barley, pasture, methane

1872 (W331) Effect of Lalsil bacterial inoculants on the pH of corn silage with low dry matter. M. Saberi*, K. Rezayazdi and M. Dehghan Banadaky, *Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran.*

To study the effect of commercial lactic acid bacteria inoculants (Lalsil) on the pH during the ensiling of corn silage with low dry matter,this experiment was conducted according to completely randomized design with 3 treatments and 4 replicates in each treatment. Treatments were: 1- control (no additives) 2- treated with Lalsil Mso1 (*Lactobacillus plantarum* and *Propionibacterium acidipropionici* applied at 1×10^5 cfu/g of the corn silage) 3- treated with Lalsil Fresh (*Lactobacillus buchneri* applied at 1×10^5cfu/g of the corn silage). pH of corn silage were measured at 1, 3, and 6 wk after ensiling. Statistical analysis of data was performed using PROC GLM and SAS statistical software. The results showed that DM (Dry matter), CP(Crude protein), NDF(Neutral Detergent Fiber) and ADF (Acid Detergent Fiber) composition of the corn silage were 18.87, 9.37, 61.75 and 25.50%, respectively. The difference between the first and sixth weeks of treatment was significant ($P < 0.05$). In the first and sixth weeks, treatment 1 had highest pH (3.92 and 3.80) and treatment contain Lalsil Fresh had lowest pH(3.83 and 3.70). There was no significant difference among treatments in the third week. It can be concluded that Lalsil bacterial inoculants could significantly reduced pH of corn silage, While Lalsil- Fresh was reduced pH of corn silage with low dry matter more effectively.

Key Words: corn silage, bacterial inoculants, pH

1873 (W332) The microbiome composition of the rumen is altered during the peripartal period in dairy cattle. H. Derakhshani[1], S. Alqarni[2], H. Khazanehei*[1], F. C. Cardoso[2], J. C. Plaizier[1], E. Khafipour[1,3] and J. J. Loor[2,3], *[1]Department of Animal Science, University of Manitoba, Winnipeg, MB, Canada, [2]University of Illinois, Urbana, [3]Department of Medical Microbiology and Infectious Diseases, Winnipeg, MB, Canada.*

Alterations in ruminal microbiota composition during the peripartal period were studied using eight multiparous fistulated Holstein dairy cows. Cows were fed a typical TMR to meet NRC (2001) requirements during the dry period and early lactation. Ruminal digesta samples were collected on days −14, −7, +10, +20 and +28 relative to calving. DNA was extracted after physical homogenization and utilized for PCR amplification of the V4 region of the 16S rRNA gene using barcoded universal primers to allow for multiplexing. Amplicons were purified, quantified and subjected to Illumina paired-end sequencing. The PANDAseq assembler was used to merge the paired-end sequences for further analyses using QIIME pipelines. After filtration and removing chimeric reads, assembled sequences were assigned to operational taxonomic units and aligned to Greengenes database. The Chao1 estimator of species richness and Unifrac distance matrices were used to calculate α-diversity and β-diversity of microbial communities, respectively. Differences in bacterial composition across time were tested using the PERMANOVA procedure in PRIMER v6 software. Partial least square discriminant analysis (PLS-DA) of SIMCA was performed to identify taxa that were most characteristic of each time point. A total of 1393,235 sequences were generated and an average of 35,990 high-quality sequences per sample were obtained after quality filtering steps, which resulted in identification of 16 phyla and 303 taxa of which 145 were classified at the genus level. The microbial profile of ruminal digesta differed across time points with highest differences observed when comparing day −14 to day +28 ($P = 0.03$), and day −7 to day +28 ($P = 0.05$). At the phylum level, the abundance of Actinobacteria increased while Armatimonadetes, Cloriflexi, Tenericutes, Verrucomicrobia, and WPS-2 decreased in the postpartum compared with prepartum. At the genus level, the abundance of *Atopobium, Clostridium, Coprococcus*, *Lactobacillus*, *Moryella*, *Olsenella, Pediococcus*, *Shuttleworthia Streptococcus,* and *Weissella* increased postpartum compared with prepartum. Variation in the ruminal microbiota among cows was smaller before calving but gradually increased after calving. This may have been associated with the normal decline in voluntary dry matter intake (DMI) before parturition. The greater dissimilarity postpartum in microbial communities among cows may be due to individual differences in physiological responses. Factors such as DMI, the degree of negative energy balance around parturition, and the occurrence of metabolic disorders during this period could affect the ruminal ecosystem and, thus, alter its microbial composition.

Key Words: dairy cows, rumen microbiota, transition period, illumina sequencing

1874 (W333) Evaluating rations offered to a group of cattle as a component of ration formulation software. J. Ferguson*, Z. Wu, D. T. Galligan, L. Baker and N. Thomsen, *University of Pennsylvania, Kennett Square.*

Rations are typically formulated for a target cow representing a group of cows. Lead factors may be used to select the target milk production for the group. Body weight, lactation number and milk composition are chosen based on mean values for the group of cows to be offered the ration. It is often not known how the offered ration impacts the ME and MP across all cows in the group. To provide an assessment of ME and MP balance for a ration fed to a group of cows, the UPenn Ration Analyzer incorporated a group model within its software program. Records from DHIA milk production (more than 1000,000) from 2000 farms and five breeds were used to construct production curves based on rolling herd averages

(RHA) for parities 1, 2, and 3+. The user inputs breed, lactation number, the mean BW for parities 1, 2, 3, 4+, the range in DIM for the group, and the herd RHA. The group model constructs a production profile of cows based on the user inputs and assigns stochastic variation to production and DIM for the group. Intake of DM for each cow in the group is predicted using the NRC. The ME and MP balance for each cow in the group is calculated based on the formulated diet and plotted by DIM. The user can view graphs of the predicted range in milk production, ME and MP balance by DIM and a table with mean DMI, milk volume, and fat, protein content for the group. The user can adjust the scale of the variance in milk production, the mean milk production, DMI, and fat and protein content if the actual values in the herd differ from predicted. A second model allows imported DHIA milk production records for the group to be fed the formulated diet to compare with the model predicted values. A third model allows the user to least cost the diet for the group within constraints on ME and MP balance for the group of cows. The user can reformulate the ration to better meet the ME and MP needs of the group. Preliminary validation from farms suggests that the group evaluator model provides a useful tool for regrouping cows and evaluating rations for improved ME and MP balances, particularly avoiding excesses in MP.

Key Words: ration formulation, production, cattle groups

1875 (W334) Epidemiological study about the effects of chelated minerals on milk, reproductive performance, and locomotion scores of dairy cattle.

A. Bach[*1,2], A. Pinto[3] and M. Blanch[4], *[1]Department of Ruminant Production, IRTA, Caldes de Montbui, Spain, [2]ICREA, Barcelona, Spain, [3]Department of Ruminant Production, IRTA, Barcelona, Spain, [4]Novus Int. Inc., St Charles, MO*

The objective of this experiment was to evaluate the effects of a partial replacement of chelated trace minerals (CTM) (Mintrex, Zn, Cu, and Mn; with methionine hydroxy-analogue as a ligand; Novus International, MO) compared with a ration containing only inorganic trace minerals (ITM) on locomotion score, milk production, and reproductive performance of dairy cows in different herds. Twenty-seven herds that were feeding the same TMR were enrolled in a 6-mo study. Fifteen herds continued to receive the same TMR (containing ITM), and the remaining 12 herds fed the same TMR with a partial replacement of ITM for CTM. The ITM premix provided 57 ppm of inorganic Zn, 9 ppm of inorganic Cu, and 27 ppm of inorganic Mn; whereas the CTM premix contained 32 ppm of inorganic Zn and 25 ppm of chelated Zn, 3 ppm of inorganic Cu and 6 ppm of chelated Cu, and 17 ppm of inorganic Mn and 10 ppm of chelated Mn. The first month of study was used as a basal line, and then herds were exposed to dietary treatments for 5 mo. Feed composition, feed intake, milk production, lameness score, and reproductive performance were monitored for each herd. All data, except conception rates, were analyzed using a mixed-effects model and conception rates were analyzed with a three-level mixed-effects logistic regression model with herd as experimental unit. There were no differences in feed intake (24.1 ± 0.20 kg/d) and milk production (31.4 ± 0.23 kg/d) between treatments. The overall proportion of cows with a lameness score $\geq$ 3 (considered lame cows) was not different between ITM and CTM herds. However, there was an interaction ($P < 0.001$) between treatment and month of experiment due to a greater incidence of lameness in CTM than in ITM herds during the first 2 mo of study (32.70 vs. 29.47%, respectively), and a lesser incidence in the last 3 mo of study (31.30 vs. 34.73%, respectively). Conception rate was not affected by treatment, but when cows that were serviced with less than 30 d of exposure to treatments were removed from the dataset, cows in the CTM herds had 2.9 greater ($P < 0.05$) odds of becoming pregnant than cows in the ITM herds. It is concluded that a partial replacement of inorganic Zn, Cu, and Mn for organic sources decreases lameness scores over time and improves conception rate after a minimum exposure of 30 d.

Key Words: lameness, reproduction, trace minerals

1876 (W335) Apparent synthesis of thiamin and vitamin B_{12} in rumen of lactating dairy cows fed alfalfa or orchardgrass silages at different maturity stages.

D. S. Castagnino[*1,2], K. Kammes[3], M. S. Allen[3], R. Gervais[1], P. Y. Chouinard[1], D. E. Santschi[4] and C. L. Girard[2], *[1]Université Laval, Québec, QC, Canada, [2]Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada, [3]Michigan State University, East Lansing, MI, [4]Valacta, Ste-Anne-de-Bellevue, QC, Canada*

Effects of maturity stage of forages on apparent ruminal synthesis and post-ruminal supply of thiamin and vitamin B_{12} were evaluated in two experiments. Alfalfa and orchardgrass were harvested and ensiled as a) early-cut, less mature (EC) and b) late-cut, more mature (LC). Diets containing alfalfa or orchardgrass silages of each maturity stage as the sole forage were offered to ruminally and duodenally cannulated lactating Holstein cows in crossover design experiments. Experiment 1 compared diets containing EC and LC alfalfa silage (~22% forage NDF and ~27% total NDF) offered to 16 cows in two 17-d treatment periods. Experiment 2 compared diets containing EC and LC orchardgrass silage (~25% forage NDF and ~30% total NDF) offered to 13 cows in two 18-d treatment periods. Intakes of thiamin increased with maturity stage of forages in Experiment 1 ($P < 0.01$; 79.3 vs. 46.5 ± 2.08 mg/d) and in Experiment 2 ($P < 0.01$; 76.0 vs. 60.9 ± 1.84 mg/d for LC and EC, respectively). In contrast, intakes of vitamin B_{12} were lower for LC than EC in Experiment 1 ($P < 0.01$; 191 vs. 329 ± 8.47 μg/d) and in Experiment 2 ($P < 0.01$; 53.1 vs.

Table 1877. Effects of DCAD concentration on production parameters

	DCAD, meq/kg					*P* <	
Item	250	375	500	625	SEM	Linear	Quadratic
DMI, kg/d	22.3	22.9	23.1	23.6	0.52	0.007	0.902
Milk, kg/d	38.9	39.5	39.5	38.8	1.52	0.937	0.228
Fat, %	3.28	3.50	3.50	3.62	0.146	0.001	0.418
Protein, %	2.95	2.99	2.95	2.92	0.056	0.167	0.152
3.5% FCM, kg/d	37.1	39.2	39.2	39.1	0.98	0.008	0.037
FE, 3.5%FCM/DMI	1.67	1.71	1.71	1.66	0.038	0.759	0.085

76.3 ± 1.71 μg/d). In Experiment 1, duodenal flows of thiamin were greater for LC than EC (P = 0.02; 156 vs. 130 ± 7.21 mg/d) but the duodenal flows of vitamin B_{12} were not affected by treatment (P = 0.21, 12182 ± 556.1 μg/d). In Experiment 2, duodenal flows of vitamins were not affected by treatment (thiamin, P = 0.20, 199 ± 8.47 mg/d; vitamin B_{12}, P = 0.28, 8518 ± 426.0 μg/d). The apparent ruminal synthesis of thiamin and vitamin B_{12} were not affected by treatment in either experiment (Experiment 1: thiamin, P = 0.45, 79.8 ± 6.56 mg/d; vitamin B_{12}, P = 0.28, 11924 ± 426.0 μg/d; Experiment 2: thiamin, P = 0.18, 130 ± 8.57 mg/d; vitamin B_{12}, P = 0.29, 8454 ± 426.0 μg/d). Delaying the harvest of alfalfa or grass resulted in a greater dietary supply of thiamin and a lower supply of vitamin B_{12}. Nevertheless, the stage of maturity did not affect apparent ruminal synthesis and had little or no effect on the post-ruminal supply of these vitamins.

Key Words: dairy cow, thiamin, vitamin B_{12}

1877 (W336) Potassium carbonate as a cation supplement to increase dietary cation anion difference and improve dairy feed efficiency in lactating dairy cows.

A. E. Weidman, M. E. Iwaniuk* and R. A. Erdman, *University of Maryland, College Park*

Supplementation with potassium carbonate (K_2CO_3) increases dietary cation anion difference (DCAD) which results in increased dairy feed efficiency. Our previous study with early lactating Holstein cows showed that increasing DCAD from approximately 250 to 400 meq/kg (Na-K-Cl Equation, DM basis) resulted in a linear increase in 3.5% FCM/DMI [feed efficiency (FE)]. However, the optimal DCAD for maximal FE could not be determined as the maximal FE response was achieved at a DCAD of 400 meq/kg. The objective of this study was to determine the optimal DCAD required for maximal DMI, milk production and FE using a broader range in dietary DCAD concentrations. Twenty Holstein cows (8 primiparous and 12 multiparous) averaging 95 (± 25) DIM were individually fed a basal diet containing 64% corn silage, 6% alfalfa hay, and 30% concentrate (DM basis). Dietary treatments consisted of 250 (basal), 375, 500, and 625 meq/kg DCAD where K_2CO_3 was added to the basal diet to obtain the desired DCAD concentrations. The treatments were applied in a 4 × 4 Latin square design with 3-wk experimental periods. Dietary treatments had no effect on milk production or milk protein concentration. Increasing DCAD from 250 to 625 meq/kg linearly increased DMI (P = 0.007) and milk fat percentage (P < 0.001), while 3.5% FCM increased curvilinearly (linear, P = 0.008; quadratic, P = 0.037) with increasing DCAD. There was a quadratic trend (P = 0.085) for dairy FE where maximal FE occurred at DCAD concentrations of 375 and 500 meq/kg. The optimal DCAD for DMI and fat percent could not be determined since maximums occurred at a DCAD of 625 meq/k. FE and 3.5% FCM were optimized at a DCAD concentration of 442 meq/kg. Results of this and other studies in our laboratory show that DCAD can be used to increased feed efficiency to help dairy producers reduce feed costs and improve profitability.

Key Words: DCAD, feed efficiency, dairy cows

1878 (W337) Degradation ruminal kinetics of organic matter, neutral detergent fiber and crude protein of sorghum wet distiller grain without solubles in comparison to the original sorghum grain.

A. I. Trujillo[*1], M. D. L. A. Bruni[2] and P. Chilibroste[3], *[1]Facultad de Agronomia, Universidad de la Republica, Montevideo, Uruguay, [2]Facultad de Agronomia Universidad de la Republica, Paysandu, Uruguay, [3]Facultad de Agronomia, Universidad de la Republica, Paysandu, Uruguay*

A study was conducted to characterize ruminal crude protein (CP) and energy supply of sorghum wet distillers grains (SWDG; 31.4 ± 0.7% CP and 70.2 ± 2.2% neutral detergent fiber–NDF, 11.0 ± 0.7% fat, dry basis) from an ethanol plant in Uruguay in comparison to the original sorghum grain (SG). In situ technique was conducted to determine ruminal organic matter (OM),NDF and CP degradation kinetics, their respective effective degradability (considering passage rate of 2% h^{-1}, ED) and the relationship between rumen available Nitrogen (N) and fermentable OM (N:OM ratio) from 3 batches of SWDG and SG. Duplicate samples (5 g of 2–mm ground) of each feed were incubated in the rumen of 2 lactating dairy cows for 0, 2, 4, 8, 12, 24, 48, and 72 h. Data were fitted to the nonlinear model $D(t) = a+b(1-e^{-kd(t-t0)})$ with PROC NLIN of SAS program to determine degradation parameters, where D is percentage disappearance of OM, NDF or CP at the time t, (a) soluble fraction, (b) slowly degradable fraction, (c) deg-

radation rate, and t0 is lag time. Parameters were analyzed with PROC GLM in a completely randomized design and compared by Tukey test. There were not differences for any degradation parameters between batches, neither in SWDG nor in SG. Comparing degradation parameters of SWDG with SG the results were: fractions (a) and (b) of OM were lower (8.1 vs. 22.7%, 54.5 vs. 73.9%; $P < 0.05$) but (c) was greater (4.8 vs. 3.5% h^{-1}; $P < 0.05$); (t0) was only present in SWDG (3.1 h); (c) of NDF was greater (6.3 vs. 3.5% h^{-1}, $P < 0.05$) but (c) of CP was lower (1.1 vs. 1.9% h^{-1}; $P < 0.05$); fraction (b) of NDF was lower (69.5 vs. 79.3%, $P < 0.05$) and fraction (b) of CP did not differ (71 vs. 71.7%); fraction (a) of NDF and (t0) were only present in SWDG (5.6% and 2.7 h), and fraction (a) of CP was lower (0.0 vs. 18.2%). The ED of OM and CP were lower in SWDG compared to SG (44.3 vs. 69.8; 25.5 vs. 52.8%, respectively; $P < 0.05$) but the ED of NDF was greater (58.3 vs. 50.6%; $P < 0.05$). The N:OM ratio for microbial growth was better in SWDG than in SG (29.4 vs. 8.4 g of N effectively degraded/kg OM effectively degraded). The SWDG seems to be a good supply of ruminal PC and energy in ruminants' diets.

Key Words: sorghum, ethanol by-product, in situ

1879 (W338) Relative bioavailability of phosphorylated ascorbic acid in lactating dairy cows. C. K. Reynolds*[1], D. J. Humphries[1], C. E. S. Barratt[1], P. C. Aikman[1] and W. Steinberg[2], *[1]University of Reading, Reading, United Kingdom, [2]DSM Nutritional Products, Basel, Switzerland*

Rumen degradation limits ascorbic acid (AA) absorption from the small intestine. The objective of the present study was to determine the relative bioavailability of AA and phosphorylated AA (PAA) introduced into the abomasum of dairy cows. Four rumen fistulated lactating (207 DIM; 33.3 ± 1.8 kg/d milk) Holstein cows were fed a TMR once daily for ad libitum DMI (17.3 ± 0.7 kg/d). Cows initially received one of 4 treatments in a balanced 4 × 4 Latin Square design experiment with 1 wk periods. Treatments were control, 10 g AA in 250 mL saline injected rapidly into a jugular vein (JV) catheter, 10 g AA in 2 gelatine capsules placed into the abomasum via the rumen, or 10 g of AA as PAA (Rovimix Stay-C 35) in 2 gelatine capsules placed into the abomasum. After period 2, abomasal AA and PAA dose was increased to 100 g AA in 750 mL water. Controls were JV saline injection and abomasal gelatine capsules or water. Blood (JV) was sampled at intervals from 1 h before to 8 h after dosing. Urine was collected and sampled at intervals before and for 10 h after AA doses. Blood and urine were sampled at 24, 48, and 72 h after dosing. Samples were treated to convert dehydroascorbic acid to AA, stored at −80°C, and analyzed for total AA within 10 d. The area under the curve (AUC) for plasma AA concentration was calculated and the decrease in plasma AA concentration following the JV dose used to calculate AA kinetics. Data were analysed using mixed models for effects of cow, period, and treatment ($n = 6$). Comparison of the AUC for abomasal versus JV doses suggests the relative bioavailability of AA (7%) and PAA (5%) were similar but very low. The half-life of the JV dose averaged 66 ± 23 min, with an estimated pool size of 178 ± 42 L and a clearance rate of 2.07 ± 0.34 L/min. Urinary excretion accounted for only 7% of the JV dose, and plasma AA concentration remained elevated for 48 h. Estimates of the relative bioavailability of AA and PAA in lactating dairy cows suggest absorption from the small intestine is low. This may in part be due to a lack of previous exposure of small intestinal enterocytes to AA or differences in metabolism of intravenously injected versus absorbed AA.

Key Words: ascorbic acid, dairy cows, absorption

1880 (W339) Changes in serum IgG and total protein concentrations in calves fed differing amounts of colostrum replacer. J. D. Quigley, L. L. Deikun*, T. M. Hill, H. G. Bateman, II, J. M. Aldrich and R. L. Schlotterbeck, *Provimi North America, Brookville, OH*

It is unclear whether differences in serum IgG concentration of calves at 24 h (acquired passive immunity) influence the onset of active IgG production or the age at which serum IgG concentrations normalize. Our objective was to monitor changes in serum IgG and total protein (TP) concentrations in calves fed to achieve high (H) or low (L) passive immunity. Newborn Holstein calves (initial BW = 42.2 ± 4.7 kg) were individually fed a colostrum supplement ($n = 23$; 50 g of IgG/feeding) or a colostrum replacer ($n = 22$; 150 g of IgG/feeding) at 0.5 ± 0.22, 6.6 ± 0.46, and 12.9 ± 1.94 h of age. Blood was collected and serum analyzed for IgG using radial immunodiffusion and total protein using optical refractometer every 7 d from wk 0 (2–3 d of age) to wk 8. Calves were vaccinated with Inforce 3 (Zoetis) on arrival, Bovi-shield Gold 5 (Zoetis) at 2 and 6 wk and Presponse HM (Boehringer Ingelheim Vetmedica) at 5 and 8 wk, as prescribed by a veterinarian. Data were analyzed as a completely randomized design using repeated measures ANOVA. Serum IgG (g/L) and total protein (TP; g/dl) concentrations at 24 h of age were 19.4 ± 0.63 and 4.07 ± 0.076, respectively, in calves fed H, and 8.52 ± 0.62 and 3.32 ± 0.074, respectively, in calves fed L. Serum IgG and TP were affected by a week ´ treatment interaction ($P < 0.001$). Serum IgG concentration in calves fed H declined to 13.7 g/L at wk 3, then increased to 20.7 g/L at wk 8. Serum IgG in calves fed L declined to 6.3 g/L at wk 1, then increased to 20.6 g/L at wk 8. By wk 7, serum IgG concentration were similar ($P > 0.05$). Serum IgG was < 10 g/L for 0.3 and 4.9 wk in calves fed H and L, respectively. Total protein concentrations were lower in calves fed L from wk 0 to 6 ($P < 0.01$); thereafter, differences were not significant. Temporal changes in serum TP and IgG concentrations were independent. Active IgG synthesis was dependent on age of calf and acquisition of passive immunity.

Calves with lower serum IgG concentrations at wk 0 began producing IgG at an earlier age and produced more IgG, so that by wk 7, circulating IgG concentrations were similar to those in calves with successful passive immunity.

Key Words: colostrum, immunoglobulins, calves

1881 (W340) Apparent synthesis of thiamin, riboflavin, vitamin B_6 and vitamin B_{12} in rumen of lactating dairy cows fed 2 concentrations of nitrogen and 2 energy sources.

V. Beaudet[*1,2], R. Gervais[1], P. Y. Chouinard[1], P. Noziere[3], B. Graulet[3], M. Doreau[3] and C. L. Girard[2], *[1]Université Laval, Québec, QC, Canada, [2]Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada, [3]INRA-URH, Saint Genès Champanelle, France*

Effects of nitrogen supply and energy sources on apparent ruminal synthesis (ARS) and post-ruminal supply of thiamin, riboflavin, vitamin B_6, and vitamin B_{12} were evaluated using 4 lactating Holstein cows distributed in a 4 × 4 Latin square design with treatments arranged according to a 2 × 2 factorial. The cows were fitted with cannulas in proximal duodenum. The treatments were 2 concentrations of nitrogen: HIGH: 14% CP, i.e., 110% of the protein requirements and an adequate supply in rumen-degradable protein (RDP), vs. LOW: 11% CP, i.e., 80% of the protein requirements with a shortage in RDP; energy sources were STARCH from barley, corn, and wheat vs. FIBER from soybean hulls and dehydrated beet pulp. Diets were corn silage based, had the same forage: concentrate ratio (60:40, dry matter basis) and were isoenergetic. STARCH resulted in greater ($P < 0.01$) intakes of thiamin (51 vs. 34 ± 2.4 mg/d), riboflavin (1172 vs. 1050 ± 25.8 mg/d) and vitamin B_6 (202 vs. 161 ± 3.9 mg/d) as compared with FIBER, whereas nitrogen concentrations had no effect ($P \geq 0.76$). Vitamin B_{12} intake was not affected by treatments ($P \geq 0.43$) and averaged 86 ± 2.0 µg/d. Duodenal flow ($P = 0.34$; 35 ± 7.0 mg/d) or ARS ($P = 0.46$; −6 ± 7.6 mg/d) of thiamin were not significantly affected by treatments. STARCH increased duodenal flow of riboflavin ($P < 0.01$; 1546 vs. 1091 ± 92.4 mg/d) and vitamin B_6 ($P < 0.01$; 68 vs. 45 ± 4.9 mg/d) but decreased vitamin B_{12} flow ($P < 0.01$; 3127 vs. 9319 ± 731.1 µg/d) as compared with FIBER. HIGH nitrogen increased riboflavin and vitamin B_6 duodenal flows ($P = 0.02$; 1481 vs. 1156 ± 85.5 mg/d and $P = 0.01$; 67 vs. 47 ± 4.6 mg/d, respectively) and ARS ($P = 0.04$; 372 vs. 43 ± 95.2 mg/d and $P = 0.04$; -114 vs. -135 ± 6.3 mg/d, respectively). Nitrogen supply had no effect on vitamin B_{12} duodenal flows ($P = 0.64$) or the ARS ($P = 0.63$). Energy sources had no effect on ARS of vitamin B_6 ($P = 0.11$) but STARCH tended to increase the apparent production of riboflavin ($P = 0.06$; 374 vs. 41 ± 102.3 mg/d). Inversely, FIBER enhanced ARS of vitamin B_{12} ($P < 0.01$; 9234 vs. 3040 ± 730.3 µg/d, respectively). There was no interaction between treatments ($P \geq 0.09$). The apparent ruminal balance was affected by the nitrogen concentration for synthesis of riboflavin and degradation of vitamin B_6, and by the energy sources for synthesis of riboflavin and vitamin B_{12}.

Key Words: apparent ruminal synthesis, B vitamins, dairy cow

1882 (W341) Apparent synthesis of thiamin and vitamin B_{12} in rumen of lactating dairy cows fed alfalfa or orchardgrass silages of different particle lengths.

D. S. Castagnino[*1], K. Kammes[2], M. S. Allen[2], R. Gervais[3], P. Y. Chouinard[3], D. E. Santschi[4] and C. L. Girard[1], *[1]Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada, [2]Michigan State University, East Lansing, MI, [3]Université Laval, Québec, QC, Canada, [4]Valacta, Ste-Anne-de-Bellevue, QC, Canada*

Effects of forage particle length on apparent ruminal synthesis and post-ruminal supply of thiamin and vitamin B_{12} were evaluated in two experiments. Alfalfa and orchardgrass were harvested and ensiled at two theoretical lengths of cut: 19-mm (long cut, LC) or 10-mm (short cut, SC). Within a forage type, rations containing silages of each length of cut as the sole forage were offered to ruminally and duodenally cannulated lactating Holstein cows in crossover design experiments. Experiment 1 compared diets containing LC and SC alfalfa silage (~47% forage, ~20% forage NDF and ~25% total NDF) offered to 13 cows in two 19-d treatment periods. Experiment 2 compared diets containing LC and SC orchardgrass silage (~50% forage, ~23% forage NDF and ~28% total NDF) offered to 15 cows in two 18-d treatment periods. In Experiment 1, intakes of thiamin and vitamin B_{12} were greater ($P < 0.01$) for LC than SC (thiamin: 89.4 vs. 77.5 ± 2.13 mg/d; vitamin B_{12}: 118.6 vs. 67.1 ± 2.55 µg/d). Neither duodenal flows of thiamin ($P = 0.94$, 174.2 ± 18.87 mg/d) and vitamin B_{12} ($P = 0.17$, 8223 ± 713.0 µg/d) nor apparent ruminal synthesis of these vitamins (thiamin, $P = 0.15$, 90.9 ± 17.82 mg/d; vitamin B_{12}, $P = 0.16$, 8131 ± 711.0 µg/d) were affected by treatment in Experiment 1. In Experiment 2, there was no effect of treatment on the intake of vitamins (thiamin, $P = 0.79$, 71.9 ± 2.55 mg/d; vitamin B_{12}, $P = 0.85$, 111 ± 3.9 µg/d), duodenal flows (thiamin, $P = 0.80$, 156 ± 9.5 mg/d; vitamin B_{12}, $P = 0.88$, 6887 ± 476.0 µg/d), or their apparent ruminal synthesis (thiamin, $P = 0.82$, 84.1 ± 8.14 mg/d; vitamin B_{12}, $P = 0.88$, 6725 ± 473.0 µg/d). The reduction of legume particle length decreased the dietary supply of thiamin and vitamin B_{12}. However, forage particle length, in the studied range, did not affect apparent synthesis of thiamin and vitamin B_{12} in rumen or the supply of these vitamins to the sites of absorption.

Key Words: dairy cow, thiamin, vitamin B_{12}

1883 (W342) Concentration of vitamin B12 in colostrum and milk from dairy cows fed different energy levels during the dry period. M. Duplessis[*1,2], S. Mann[3], D. V. Nydam[3], C. L. Girard[2], D. Pellerin[1] and T. R. Overton[4], *[1]Université Laval, Département des sciences animales, Québec, QC, Canada, [2]Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada, [3]Cornell University, Department of Population Medicine and Diagnostic Sciences, Ithaca, NY, [4]Cornell University, Department of Animal Science, Ithaca, NY*

Bovine colostrum and milk are an excellent source of vitamin B_{12} for calves and humans, respectively, who rely on exogenous sources to meet their vitamin B_{12} requirements. The aim of the experiment was to evaluate vitamin B_{12} concentration in colostrum and milk from dairy cows fed different levels of energy during the dry period. A total of 84 Holstein cows were assigned to one of the following dietary treatments 60d before the expected calving date: 1) High energy one-group dry cow diet (HE; 1.35 Mcal NE_m/kg DM; 56% corn silage, 12% wheat straw, and 32% concentrate mix on a daily DM basis); 2) Low energy one-group dry cow diet (LE; 1.14 Mcal NE_m/kg DM; 28% corn silage, 36% wheat straw, and 36% concentrate mix on a daily DM basis); or 3) Intermediate step-up diet (IE; low energy diet from dry off until 30d before the expected calving and then switching to a diet representing a 50:50 blend of the low and high energy diets until parturition). After calving, all cows were fed the same diet using a TMR (44% corn silage, 13% grass silage, and 43% concentrate mix on a daily DM basis) until 42 d in milk (DIM). Colostrum samples were taken at the first milking after the parturition and milk samples were taken during the morning milking at 11 and 39 ± 2 DIM. Data were analyzed using treatment, time as well as treatment x time interaction as fixed effects. A significant treatment × sample interaction was observed ($P = 0.02$; Table 1883). Vitamin B_{12} concentration in colostrum differed among treatments ($P = 0.0002$) whereas no diet effect was observed on milk samples ($P > 0.97$). Colostrum from LE cows had a vitamin B_{12} concentration higher than IE cows ($P = 0.001$; Table 1883). In summary, results suggest that energy levels in diets during the dry period could change vitamin B_{12} concentration in colostrum but had no effect later on milk concentration of vitamin B_{12}.

Key Words: dairy cow, vitamin B_{12}, colostrum

Table 1883. Vitamin B_{12}concentration in colostrum and milk according to treatments

Vitamin B_{12} (pg/mL)[1]	HE	LE	IE
Colostrum	27,815[ab] ± 1353	31,677[b] ± 1353	23,502[a] ± 1378
Sample 1	3932[a] ± 1353	3701[a] ± 1378	3774[a] ± 1378
Sample 2	3339[a] ± 1353	3125[a] ± 1378	3000[a] ± 1378

[a,b] Means in the same row with different superscripts differ ($P < 0.05$)

1884 (W343) Ruminal bacterial community structure of dairy cows fed conventional and reduced-fat dried distillers grains with solubles. *H. A. Ramirez Ramirez, C. J. R. Jenkins*, S. C. Fernando, C. L. Anderson, N. D. Aluthge and P. J. Kononoff, University of Nebraska, Lincoln*

Four lactating, ruminally cannulated Holstein cows with (mean ± SD) 98 ± 11 DIM and 603 ± 52 kg BW were used in a Latin square design to test the effects of feeding regular dried distillers grains with solubles (DDGS) or reduced-fat DDGS (RF-DDGS) combined with rumen inert fat (RIF, as Ca-salts of long chain fatty acids) on ruminal bacterial community structure using a DNA pyrosequencing approach. Cows were housed in a tie-stall barn, fed once daily, and milked twice daily. In each 21-d period, cows were randomly assigned to 1 of 4 dietary treatments (values expressed on a DM basis): control diet (CON) was a conventional dairy ration (no corn ethanol by-products); a second diet (DG) contained 30% DDGS; a third diet (RF) contained 30% LF-DDGS and; a fourth diet (COMBO) contained 30% LF-DDGS supplemented with 1.9% RIF. Ruminal digesta was collected at 0, 8, and 23 h post-feeding on d 21 of each period and was immediately frozen (-20°C) for later analysis of the bacterial community. The rumen bacterial community was evaluated from frozen samples using the Roche 454 pyrosequencing platform. The sequences generated were analyzed using established MOTHUR and QIIME (Quantitative Insights Into Microbial Ecology) pipelines. Diet did not affect bacterial community composition at phylum level. The most abundant phyla were Firmicutes (46 ± 4.78%) and Bacteroidetes (51 ± 4.87%). The phylum TM7 accounted for 2.25 ± 0.41%. The Tenericutes, SR1, and Spirochaetes phyla were grouped as "Others" and accounted for 0.58 ± 0.10%. Time post-feeding had an effect ($P = 0.02$) on phyla distribution; the proportion of Firmicutes decreased from 52 to 39 ± 4% by 9 h post-feeding and increased to 46 ± 4% by 23 h; conversely Bacteroidetes increased from 45 to 58 ± 4% at 9 h post-feeding and decreased to 51 ± 4% by 23 h post-feeding. The results from this experiment demonstrate that phyla distribution is relatively stable across diets; nonetheless diurnal patterns in ruminal bacterial phyla relative to time post-feeding were observed. To our knowledge, this is the first study in dairy cattle that utilizes high throughput sequencing to analyze bacterial community structure to evaluate diurnal variation of the rumen bacterial community.

Key Words: microbial community, bacteria, sequencing

1885 (W344) Diet influences microbial community composition, and methane emission in growing and finishing beef cattle. S. C. Fernando*[1], A. L. Knoell[1], C. L. Anderson[1], A. C. Pesta[2], G. E. Erickson[2] and T. J. Klopfenstein[2], [1]*University of Nebraska, Lincoln,* [2]*University of Nebraska-Lincoln, Lincoln*

Methane production in ruminants via enteric fermentation is dependent on the microbial community within the ruminant animal. The microscale processes of this microbial community are greatly influenced by diet. However, the interactions between diet, microbial community composition, and methane emission are poorly understood. To better understand how diet influences microbial community structure and methane emission, methane/CO_2 ratio and microbial community composition were evaluated in animals on a common diet and under different dietary conditions (high and low quality forage, with and without monensin supplementation, and different levels of modified distillers grain plus solubles (MDGS) supplementation) in a 84-d growing trial, followed by a 125-d finishing trial that evaluated four different fat sources (corn oil, tallow, MGDS, corn-no oil) and monensin supplementation. Methane and CO_2 measurements were made during feeding using an individual feeding facility that contained 120 individual bunks equipped with the Calan gate system and an automated gas collection system. Gases were analyzed using a mobile GC unit. CO_2 was used as an internal standard and the methane/CO_2 ratio was used to determine the effects of diet on methane emission. Samples were collected for microbial community analysis via stomach tubing, and the microbial community structure was analyzed by sequencing the 16S rRNA gene. In growing cattle and finishing cattle, microbial community structure (both archaea and bacteria) and methane levels were similar in all animals on the common diet. In growing cattle, diet quality (high vs. low quality forage) significantly influenced ($P < 0.05$) the methane/CO_2ratio and the microbial community composition, where high quality forage produced higher levels of methane. However, the level of methane emitted did not change by level of supplementation, but the microbial community composition did change significantly. In finishing cattle, methane levels were highest in MDGS diets and significantly decreased ($P < 0.05$) in corn control diet and 3% tallow diets. The microbial community did not show significant changes in total microbial community structure during supplementation of different fat sources. These data suggest dietary intervention can be used in growing cattle to change microbial community structure, which in turn can affect methane emission levels. Identifying the members of the rumen microbial community from high and low methane emitting cattle and diets would help identify microbial community members that influence methane production in cattle, which may lead to dietary and other intervention strategies to change these microbial populations in the rumen.

Key Words: microbial community, methane, archaea

1886 (W345) Dietary fatty acid profile affects plasma metabolic profile of peripartum Holstein cows. H. Khalilvandi-Behroozyar[1], M. Dehghan Banadaky*[2], M. Ghaffarzadeh[3] and K. Rezayazdi[2], [1]*Department of Animal Science, Urmia University, Urmia, Iran,* [2]*Department of Animal Science, University of Tehran, Karaj, Tehran, Iran,* [3]*Chemistry and Chemical Engineering Research Center of Iran, Tehran, Iran*

Concentration of plasma NEFA usually increases around calving due to mobilization of adipose tissue as a result of the inability of high-producing cows to consume enough energy to meet requirements for milk production and maintenance. Elevated NEFA concentration in the periparturient period is the major factor influencing postpartum accumulation of lipid in hepatic tissue. Whereas postpartum fat supplementation is a common practice in the dairy industry, prepartum fat supplementation is less common. The objective of this study was to examine the effect of feeding diets containing fat supplements enriched in either saturated FA or PUFA on metabolic responses of periparturient Holstein cows. Twenty four multiparous Iranian Holstein cows were assigned to diets with different fatty acid profiles and supplemented through 30 d before expected calving date to 50 d in milk. Dietary treatments consisted of (1) Prilled Palm fatty acids (PO) [Energizer RP10 , 2 & 2.25% DM in pre- and postpartum, respectively]; (2) Ca-salts of sunflower oil (SO) [Persia Fat- SO]; (3) Ca-salts of fish oil (FO) [Persia Fat- FO] and (4) equal amounts of Persia Fat- FO & Persia Fat- SO. Calcium salts were supplemented as 2.2 and 2.5% of dietary DM in pre- and postpartum period, respectively. All rations contained identical forage and concentrate components. Metabolite analyses were performed on blood samples collected weekly pre and post-partum and daily from -10 to 10 d relative to expected calving from tail vein. Data were analyzed using PROC MIXED of SAS 9.1 according with repeated measures in time function. Prepartum plasma contents of glucose, triacyl glycerol, cholesterol, total protein, urea, NEFA, BHBA and glycerol were not affected by type of lipid supplement, but Insulin, LDL, HDL, albumin and TNF-α concentration significantly increased in PO supplemented group than those supplemented with Persia Fat. In postpartum period, plasma levels of triacyl glycerol, total protein and urea were not affected by dietary fatty acid profile. However, Feeding Persia Fat, greatly reduced plasma concentration of NEFA, BHBA and glycerol along with lowering effects for TNF-α, suggesting that feeding protected PUFA sources can manage mobilization of body reserves. Statistically significant lower glucose and higher Insulin concentration in PO fed cows, in line with higher TNF-α levels can be a hint to lower insulin sensitivity compared with Persia Fat fed animals. Different profiles of protected PUFA sources didn't have any significant difference.

Key Words: PUFA, palm oil, insulin resistance, NEFA

1887 (W346) Prediction of enteric methane emissions in Holstein dairy cows fed various forage sources.

D. E. Rico[*1], P. Y. Chouinard[1], F. Hassanat[2], C. Benchaar[2] and R. Gervais[1], *[1]Université Laval, Québec, QC, Canada, [2]Agriculture and Agri-Food Canada, Dairy and Swine Research and Development Centre, Sherbrooke, QC, Canada*

Milk fatty acid (FA) profile has been previously used as a predictor of enteric CH_4 output in dairy cows fed diets supplemented with plant oils. The objective of this study was to investigate the relationships between milk FA and enteric CH_4 emissions in lactating dairy cows fed different types of forage. A total of 81 observations from 3 separate 3 × 3 Latin square design (with 32-d periods) experiments using a total of 27 lactating cows (96 ± 27 DIM; Mean ± SD) were used. In all experiments, dietary forages were included at 60% of ration DM and were: 1) 100% corn silage 2) 100% alfalfa silage 3) 100% barley silage 4) 100% timothy silage 5) 50:50 mix of corn and alfalfa silages, 6) 50:50 mix of barley and corn silages, and 7) 50:50 mix of timothy and alfalfa silages. Enteric CH_4 was measured in individual air-flow controlled chambers during 3 consecutive days. Milk was sampled during the 6 d of each period and analyzed for components and FA profile. Test variables included DMI (kg/d), dietary NDF (%), dietary EE (%), milk yield (kg/d), milk components (%), and individual milk FA (% of total FA). Associations between test variables and CH_4 were analyzed using the CORR procedure of SAS. The GLMSELECT procedure was used to identify a set of candidate models using the LASSO and LARS methods. Data were then fitted into a random regression using the MIXED procedure including the random effects of cow and period. The VC and UN covariance structures provided best fit for the random and repeated statements, respectively. Denominator degrees of freedom were calculated by the Satterhwaite equation. A positive association was observed between CH_4 and DMI (r = 0.59, P < 0.001), whereas negative associations were observed between CH_4 and *c*9–17:1 (r = -0.58, P < 0.001), and *t*8, *c*13–18:2 (r = -0.51, P < 0.001). The selected model predicted observations with a coefficient of determination of 0.92 and was: CH_4 (g/d) = 357.1 + 15.2 × DMI– 56.9 × 15:0– 81.7 × *c*9–17:1– *t*10–18:1 × 41.0– *c*11–18:1 × 53.3– *t*8, *c*12–18:2 × 243.0– *t*8, *c*13–18:2 × 563.7.0– t11, c15–18:2 × 242.9. Milk FA profile and DMI can be used to predict CH_4 emissions in dairy cows across a range of dietary forage sources.

Key Words: dairy cows, methane emissions, milk fatty acids.

1888 (W347) RNA-Seq detection of differential gene expression in the rumen of beef steers associated with feed efficiency phenotypes.

R. J. Kern[*1], A. K. Lindholm-Perry[2], H. C. Freetly[2], W. M. Snelling[2], J. R. Miles[2], J. W. Kern[3] and P. A. Ludden[1], *[1]University of Wyoming, Laramie, [2]USDA, ARS, US MARC, Clay Center, NE, [3]Kern Statistical Services, Sauk Rapids, MN*

The efficient utilization of feedstuffs is an economically important trait in beef production. The rumen is important to the digestive process of steers interacting with feed, microbial populations, and volatile fatty acids indicating it may play a critical role in feed efficiency. To gain an understanding of the molecules and pathways involved in gain, intake and utilization and identify candidate genes associated with steer feed efficiency, RNA-Seq was performed on rumen papillae from steers with extreme feed efficiency phenotypes (n = 16). The study population was divided into four Cartesian quadrants for intake × gain and steers (n = 4) from each quadrant were sampled. Three statistical analyses were performed to identify differentially expressed genes among feed efficiency phenotype. Two analyses were performed on total gene expression, the Negative Binomial and the Kruskall-Wallis. A separate analysis was performed by Cofactor Genomics on exon cluster expression. The Negative Binomial analysis identified 27 genes differentially expressed among feed efficiency phenotypes based on false discovery rate (FDR < 0.05). The Kruskall-Wallis analysis identified 19 differentially expressed genes based on P-value (P < 0.05). Cofactor Genomics identified 187 differentially expressed genes based on P-value (P < 0.05) and fold change (FC > 2). All genes identified by the Negative Binomial and Kruskall-Wallis analyses were tested for validation using real-time PCR and a subset of genes (n = 23) identified by Cofactor Genomics were tested for validation. Several genes (*ACAT1, CYP1A2, KLK10, KLK12, MIF, PDEE1A,* and *MYL1)* were identified by at least one analysis in this study and are supported by other studies. Five genes were identified by more than one analysis in this study (*KLK7, KLK10, KLK12, ARHGAP27,* and *RGS5)*. Cell death and survival, immunological disease, and metabolic disease were the top gene networks identified in association with gain, intake, and efficiency, respectively. Genes expressed in rumen papillae of beef steers may play a role in the feed efficiency of the animal. USDA is an equal opportunity provider and employer.

Key Words: RNA-Seq, beef cattle, rumen papillae

1889 (W348) Bioassay activity of different tannin sources by gas production technique. N. Vahdani[1], M. Dehghan banadaky[*2], F. Khalighi-Sigaroudi[3] and K. Rezayazdi[4], *[1]University of Tehran, Karaj, Iran, [2]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran, [3]Institute of Medicinal Plants, Academic Center for Education, Culture and Research (ACECR), Karaj, Iran, [4]Department of Animal Science, University of Tehran, Karaj, Tehran, Iran*

Use of agricultural by-products, (such as pistachio hull, Pomegranate hull, Grape pomace, etc.), is often a useful way of overcoming shortage of animal feeds in many countries. These by-products contain tannins, causing reduction of protein utilization in ruminants. Tannin activity is affected by its source so this study was conducted to evaluate the effect of different sources of tannins on tannin biological effect by gas production technique. Each assay was repeated three times (runs). In all assays, 1 g of each sample was incubated in 120 mL serum bottles with or without 1 gr polyethylene glycol, PEG (MW. 4000), in triplicate. Rate and extent of gas production was determined by reading gas volumes at 2, 4, 6, 8, 12, and 24h of incubation time. Results showed that tea green leaves (1.44 in 2h after incubation) and grape pomace (1.45 in 2h after incubation) had more active tannins than others in all of incubation times ($P < 0.05$). In spite of same TP (180.18 and 182.5 gr/kgDM) and TT (115.35 and 108.38 gr/kgDm) content, pistachio hull and oak fruit tannins had different biological effect. Because there is no significant correlation between TP, TT and biological activity of tannins in all of incubation times. These results prove that independent of tannin content, different sources of tannins have different activities.

Key Words: tannin, bioassay, PEG

1890 (W349) Differences in formulation and bioavailability of commercial injectable fat-soluble vitamin products. D. B. Snider[*1], R. A. Zinn[2] and R. L. Stuart[3], *[1]Iowa State University, Ames, [2]University of California-Davis, El Centro, [3]Stuart Products Inc, Bedford, TX*

Injectable fat-soluble vitamins are utilized more quickly and efficiently than oral products. The major concern with injectables is chemical form and bioavailability of vitamins. A commercial product (VITAL EAD (V); Stuart Products, Inc.) contains retinyl palmitate, the storage form of vitamin A, and another commercial product (Natural EAD (N); Neogen Corp.) contains retinyl propionate. Otherwise, vitamin D and vitamin E sources and concentrations were the same. Two experiments were conducted to compare bioavailability of vitamins E and A. Exp 1 compared bioavailability in serum collected at 0, 24, 48, and 72 h. post-injection, and Exp 2 compared bioavailability at 0, 4, 8, 12, and 24 h post-injection. All serum samples were analyzed for α-tocopherol and total vitamin A. Exp 1 utilized ten animals (130 kg), and Exp 2 utilized eight animals (200 kg). In Exp 1, five animals were injected with 5 mL of either product to provide 500,000 I.U. A, 50,000 I.U. D and 1500 I.U.E per animal. In Exp 2, four animals were injected with 6 mL of either product to provide 600,000 I.U. A, 60,000 I.U. D and 1800 I.U. E per animal. In Exp one, serum α-tocopherol concentrations at 0, 24, 48, and 72 h for V-injected animals were 0.48, 20.02, 5.22, and 4.05 μg/mL, respectively. Total vitamin A concentrations were 0.13, 5.85, 3.39, and 4.18 μg/mL, respectively. For N, serum α-tocopherol concentrations were 0.57, 5.72, 3.74 and 4.00 μg/mL; and total serum vitamin A concentrations were 0.13, 0.17, 0.07, and 0.08 μg/mL for the four sampling times. At 24 and 48 h samplings, serum α-tocopherol concentrations were different between the two products ($P < 0.01$). For total vitamin A, all sampling periods were different ($P < 0.001$). In Exp 2, serum α-tocopherol concentrations at 0, 4, 8, 12, and 24 h were 1.13, 15.50, 28.30, 23.8 and 20.3 μg/mL, respectively and total vitamin A concentrations were 0.22, 3.05, 8.34. 8.49, and 11.87 μg/mL for the V-injected animals. For N, serum α-tocopherol concentrations were 1.15, 5.25, 7.18, 7.00, and 8.95 μg/mL; and serum total vitamin A concentrations were 0.25, 0.32, 0.31, 0.30 and 0.39 μg/mL for the five time periods. All post-injection times 24 h and below were significantly different ($P < 0.01$) in favor of V. The basis for differences in bioavailability of the injectable vitamin A forms, notwithstanding similar label concentrations is uncertain and warrants further consideration.

Key Words: vitamin E, vitamin A, injectable, bioavailability

1891 (W350) Individual and additive value of conventional and non-conventional technologies in beef steers housed and fed using a GrowSafe feeding system. A. R. Harding[*1], G. K. Jim[2], C. W. Booker[2], E. J. Behlke[2], S. L. Parr[2], S. J. Hannon[2], T. M. Greer[2], Z. D. Paddock[2], M. L. May[2], L. Burciaga-Robles[2] and C. R. Krehbiel[1], *[1]Oklahoma State University, Stillwater, [2]Feedlot Health Management Services, Ltd., Okotoks, AB, Canada*

This study evaluated the effects of conventional and non-conventional production technologies in cattle. Animals (384 steers, 1101 ± 63 lb.) were utilized in an RCBD. Non-conventional production (NCP) included non medicated supplement and; NCP1:DFM (Sage Biosciences Inc., Edmonton, Alberta); NCP2: enzyme (Sage Biosciences Inc., Edmonton, Alberta); NCP3: Oleobiotec Ruminant (Oleo; Laboratoires Phodé, Terssac, France); NCP4: DFM, enzyme and Oleo. Blended production (BP) systems included BP1: supplement with Rumensin and Tylan (Elanco Animal Health, Guelph, Ontario), DFM, enzyme, and Optaflexx (Elanco Animal

Health) for the last 28 d; BP2: supplement with Rumensin, Tylan, DFM, enzyme, Oleo, and Optaflexx (last 28 d). Controls included a negative control (NEG): non-medicated supplement; and conventional production (CP): supplement with Rumensin, Tylan, and Optaflexx for the last 28 d. Animals were randomized within each production system to receive an implant (Component TE-S with Tylan (Elanco Animal Health), parasiticide (Dectomax; Zoetis Canada, Kirkland, Québec), both, or neither. Cattle were fed an average of 91 d and individual DMI were measured using GrowSafe (GrowSafe Systems Ltd., Airdrie, Alberta). Data were analyzed using the GLIMMIX procedure (SAS Institute Inc, Cary, North Carolina). Carcass adjusted ADG was improved ($P < 0.05$) in the NCP3, BP1,BP2 and CP groups over the NEG cattle. Carcass adjusted G:F improved ($P < 0.05$) in the NCP3, NCP4, BP1, BP2, and CP treatments over the NEG cattle. No differences ($P < 0.05$) were detected in carcass characteristics or animal health variables. Live and carcass adjusted ADG and G:F were improved in implanted animals vs. non-implanted animals ($P < 0.001$). Carcasses of implanted animals were less likely ($P < 0.05$) to grade Canada AAA and more likely to grade Canada AA than non-implanted animals. No performance or carcass differences were noted ($P > 0.05$) for parisiticide treatments. No interactions ($P > 0.05$) were observed between dietary program,implant, or parisiticide and no differences ($P > 0.05$) in animal health were detected for any treatments. The results of this study indicate that Oleo has potential to improve the performance of beef steers but not to the same extent as conventional production practices.

Key Words: feedlot, cattle, technology

1892 (W351) Effects of supplemental bupleurum extract on serum hormone and immune globulin levels in heat-stressed dairy cows.

X. Sun[1,2,3], J. Cheng[1,2,3], N. Zheng[1,3,4], D. P. Bu[3], L. Pan[3] and J. Wang[*1,3,4], *[1]Ministry of Agriculture- Laboratory of Quality & Safety Risk Assessment for Dairy Products (Beijing), Beijing, China, [2]College of Animal Science and Technology, Anhui Agricultural University, Hefei, China, [3]State Key Laboratory of Animal Nutrition, Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China, [4]Ministry of Agriculture- Milk and Dairy Product Inspection Center (Beijing), Beijing, China*

This experiment was conducted to evaluate the effects of bupleurum extract (BE) on serum hormone and immune globulin levels in dairy cows under heat stress. Forty lactating Holstein cows (75 ± 15 DIM, 37.5 ± 1.8 kg of milk/d, and 1.7 ± 0.4 parity) were randomly assigned to one of four treatments. Treatments consisted of 0 (control), 0.25, 0.5, or 1.0 g BE/kg DM. The experiment lasted 10 wk. Average temperature–humidity index (THI) was more than 72 throughout the experimental period. Blood samples were collected from all of animals via tail vein before the morning feeding on Days 0, 21, 42, and 63. Data were analyzed by MIXED model procedure of SAS 9.2. Compared with controls, cows fed 1.0 g/kg BE had higher thyroxine (T_3) (1.43 vs. 1.16 ng/mL; $P < 0.05$) and prolactin (PRL) (230.50 vs. 188.19 uIU/mL; $P < 0.05$) levels, and 0.5 g/kg BE had the tendence to increase the T_3 (1.27 vs. 1.16 ng/mL; $P < 0.10$) level, but 0.25 and 0.5 g/kg BE had no effect ($P > 0.05$) on PRL level. Serum growth hormone (GH) level was increased (2.17 vs. 1.21 ng/mL; $P < 0.05$) in cows fed 0.25 g/kg BE compared with control cows, and tended to be higher (1.76, 1.69 vs. 1.21 ng/mL; $P < 0.10$) in cows fed 0.5 and 1.0 g/kg BE. Supplementation of BE had decreased the cortisol (COR) levels (48.35, 49.43, 49.86 vs. 64.49 ng/mL; $P < 0.05$), but had no effect ($P > 0.05$) on the levels of thyroxine, Insulin, glucagon, neuropeptide Y, leptin, insulin-like growth factor, and heat shock protein 70. Cows fed 0.5 g/kg BE increased the immunoglobulin (Ig) A content (279.25 vs. 179.78 μg/mL; $P < 0.05$), and IgG level was increased (36.54, 36.14 vs. 27.13 mg/mL; $P < 0.05$) in cows supplemented with 0.25 or 0.5 g/kg BE, while the IgM and tumor necrosis factor-α (TNF-α) levels showed no difference ($P > 0.05$) when compared with the control cows. These findings suggest that BE supplementation could relieve metabolic disorders and enhance immune function in heat-stressed cows.

Key Words: bupleurum extract;serum hormone; immune globulin

1893 (W352) Influence of additional tannins extract level on feedlot performance of finishing hair lambs.

R. Barajas*, E. B. Bonilla, L. R. Flores, J. J. Lomeli and J. A. Romo, *FMVZ-Universidad Autónoma de Sinaloa, Culiacan, Mexico*

Forty eight Pelibuey x Katahdin hair lambs weighing 21.3 ± SD 3.23 kg were used in a 70 d experiment to determine the influence of tannins extract level supplementation on feedlot performance of finishing hair lambs. Animals were blocked by initial weight and in groups of three, lambs were placed in 16 plastic floor elevated pens (1.5 × 1.6 m). In a complete randomized block design, within a block, pens were randomly assigned to four treatments as follows: 1) A 92% concentrate diet (14% CP; 2.07 Mcal of NEm/kg) formulated with corn grain and soybean meal without addition of tannins extract (CTRL); 2) CTRL and supplementation with 0.15% (DM basis) of tannins extract (TE15); 3) CTRL plus 0.3% (DM basis) of tannins extract (TE30); and 4) CTRL added with 0.45% (DM) of tannins extract (TE45). Lambs were fed twice a day. Tannins extract was supplied as a condensed and hydrolyzable tannins-blend obtained from quebracho and chestnut trees (Silvafeed-Bypro; SilvaTeam-Inudor, S.A., Argentina). Results were analyzed by ANOVA for a complete randomized block design, and the influence of TE level on performance variables was explored using polynomial contrasts. Pen was used as the experimental unit. Quadratic responses to TE level

supplementation on final weight and average daily gain were observed ($P = 0.05$), mean values of ADG were 0.214, 0.242, 0.236, and 0.220 kg/d for CTRL, TE15, TE30, and TE45 treatments, respectively. Dry matter intake was not affected by treatments ($P = 0.38$). Feed conversion (feed/gain ratio) responded in a quadratic form ($P < 0.01$) to tannin extract supplementation level, with mean values of 4.61, 4.06, 4.25, and 4.75 kg of DMI/kg of gain, for treatments containing 0, 0.15, 0.30, and 0.45% of tannin extract in dietary DM, respectively. It is concluded, that addition of tannin extract to the diet improves in a quadratic manner the feedlot performance of finishing hair lambs, and the better supplementation level could be between 0.15 and 0.3% of dietary dry matter.

Key Words: feedlot-performance, lambs, tannins

1894 (W353) Supplementation of dairy cows before calving with β-carotene. R. C. Oliveira[1], B. M. Guerreiro[2], N. N. Morais Junior[3], R. L. Araujo[1], R. A. N. Pereira[4,5] and M. N. Pereira[*1,5], *[1]Universidade Federal de Lavras, Lavras, Brazil, [2]Universidade de São Paulo, São Paulo, Brazil, [3]Instituto Federal de Educação, Ciência e Tecnologia do Espírito Santo, Colatina, Brazil, [4]Empresa de Pesquisa Agropecuaria de Minas Gerais, Lavras, Brazil, [5]Better Nature Research Center, Ijaci, Brazil*

The pre-calving supplementation of β-carotene was evaluated. The data set contained 283 Holsteins that received a treatment for > 14 d (29.1 ± 6.9 d). Cows were paired blocked by parity and expected calving date and assigned to a treatment: Beta-carotene (1.2 g/cow/d. Rovimix, DSM) or Control. The same TMR batch was offered to all cows and β-carotene was top dressed per cow once a day. Milk yield was recorded daily and sampled at 30.1 ± 8.3 d post-calving. Frequency distributions were analyzed with GENMOD of SAS using logistic regression for binomial data. Continuous variables were analyzed with MIXED. Within parity, nonparametric estimates of the survivor function for reproductive variables were computed using the product-limit method of the Kaplan-Meier method with LIFETEST. Plasma β-carotene content at the start of the experiment was similar (2.99 µg/mL, $P = 0.59$) and peaked at 3.26 µg/mL on day -15 pre-calving for supplemented cows (2.62 µg/mL for Control, $P < 0.01$). Colostrum density, milk yield, and milk solids content were similar ($P > 0.32$). Milk yield from d 20 to 109 of lactation was 3105 kg for primiparous and 3595 kg for multiparous ($P < 0.01$). Beta-carotene tended to increase milk protein content from 2.90 to 2.96% ($P = 0.09$) and to decrease the proportion of primiparous with a milk fat to protein ratio > 1.4 from 25.8 to 9.7% ($P = 0.10$). The proportion of primiparous with difficult calving, SCC > 200,000 cells/mL, metritis, progesterone > 1 ng/mL at 21 and 42 d, % conception at first service, and % pregnant at 90 and 150 d were similar ($P > 0.46$). There was a trend for decreased incidence of SCC > 200,000 cells/mL in multiparous supplemented with β-carotene (38.9% vs. 28.1%, $P = 0.12$), other variables were similar ($P > 0.21$). Beta-carotene reduced the proportion of multiparous with retained placenta 12 h post-calving from 29.9% to 21.7%, time of placenta release was 392 min (340 to 440) for β-carotene and 490 min (395 to 540) for Control (Median and 95% confidence interval. LogRank $P = 0.05$ and Wilcoxon $P = 0.04$). For primiparous, β-carotene did not determine placenta release (incidence was 15.4%). Responses in the intervals from calving to first estrous, to first service, and to conception were not detected. The pre-calving supplementation of β-carotene increased the plasma content around calving. There was no detectable response in milk yield or reproductive performance. β-Carotene reduced the incidence of retained placenta in multiparous cows.

Key Words: β-carotene, retained placenta, transition period

1895 (W354) Relationship between residual feed intake and mitochondrial function. M. M. Masiero*, M. S. Kerley and W. J. Sexten, *University of Missouri, Columbia*

Crossbred steers were used to determine if mitochondria complex I (C1) differed among residual feed intake phenotypes (RFI) and if C1 subunits (B-RFI) could account for additional differences in DMI. All experiments were analyzed as a completely randomized design. In Exp. 1 ($n = 26$) and 2 ($n = 24$) steers were fed no-roughage corn-based diets. Steers ($n = 13$) were fed an alfalfa haylage (30% diet DM) based diet during growing phase of experiment three and finished using no-roughage corn-based diets. We hypothesized calf DMI was influenced by metabolic efficiency (RFI) and subsequently C1 subunits could describe additional animal to animal DMI variation. Individual DMI was collected using GrowSafe feed intake system and used to calculate RFI and B-RFI. Band RFI was calculated similar to RFI with DMI as dependent and ADG, metabolic mid weight (MMWT) and C1 subunit (Band3) as independent variables. Blood samples were collected during growing phase of all experiments with an additional sampling during experiment three finishing phase to isolate mitochondria from lymphocytes. Complex I quantities were measured using immunocapture. Complex I subunits were separated into bands using gel electrophoresis and three bands were measured by densitometry. Dry matter intake was less and G:F was greater for–RFI compared to +RFI ($P < 0.05$) steers in all experiments. Band-RFI improved coefficient of determination by 17.04, 1.66, 12.65, 7.12, 12.89, and 2.68% compared to regressing intake on ADG and MMWT for experiment one, two, growing phase of three, finishing phase of three, and total period of experiment three using mitochondria measurements of growing and finishing phase of three, respectively. In experiment three, RFI was calculated for growing (d 0 to 70) and finishing (d 71 to 140) phases independently and for the total 140 d period. Residual feed intake correlation was 0.14 be-

tween growing and finishing phases ($P = 0.63$), 0.79 between growing phase and total period ($P = 0.001$) and 0.65 between finishing phase and total period ($P = 0.01$). Using band 3 in regression equations improved agreement of–RFI from 60 to 75% and +RFI from 57 to 83% between growing phase and total period of experiment three. Growing and finishing phases had 40 and 29% agreement of–RFI and +RFI steers, respectively. In conclusion, mitochondrial complexes accounted for additional variation in intake among steers. Adding band 3 to intake regression equations improved coefficient of determination of all experiments. Residual feed intake phenotype may be influenced by age or cattle growing phase.

Key Words: feed efficiency, mitochondria, residual feed intake

---

1896 (W355) Bioavailability of rumen protected choline sources when supplemented at different concentrations. K. J. Herrick*[1], J. A. Davidson[2], F. R. Valdez[1], M. J. Christofferson[1] and S. E. Schuling[3], *[1]Kemin Industries, Inc., Des Moines, IA, [2]Land O'Lakes Purina Feed, Gray Summit, MO, [3]Hubbard Feeds, Inc., Des Moines, IA*

Plasma choline is not an accurate measure of choline supplementation because of extensive liver metabolism. Our objective was to evaluate a method to estimate the bioavailability of rumen protected choline (RPC) products by comparing the response of plasma metabolites involved with choline metabolism. Choline chloride (0, 3, 6, or 9 g/d) was mixed in 2 L of isotonic solution and infused daily into the duodenum of 4 duodenally and ileal cannulated steers (337 ± 23.7 kg BW) to determine a response curve. An additional 6 steers and 2 heifers (322 ± 23.7 kg BW) were used in a replicated 4 × 4 Latin square experiment with 7 d periods to evaluate the RPC products. Both experiments were run concurrently and plasma was collected from all animals for 1 wk before the start of the experiment. Choline chloride was provided using 2 rumen protection technologies (SF and BT; Kemin Industries, Inc.). Treatments provided the following daily amounts of choline chloride: 1) 13 g by SF (LSF), 2) 36.0 g by SF (HSF), 3) 14.5 g by BT (LBT), and 4) 39.0 g by BT (HBT). All treatments were mixed with 0.45 kg of a concentrate mix and individually fed. In both experiments, plasma was collected at 0, 4, and 8 h after feeding on the last day of the baseline and each period. Plasma was analyzed for choline and amino acids. Response curves were determined by regressing plasma choline, methionine, homocysteine, and cysteine against infused dose using the Fit Model procedure in JMP (SAS Institute, 2010). These curves were used to calculate choline chloride delivered by RPC treatments. Plasma and calculated delivered choline chloride were analyzed using the Fit Model procedure in JMP with hour of sampling and treatment as fixed effects and cow as random effect. Plasma amino acids and choline did not differ ($P > 0.05$) between RPC treatments. Calculated delivered choline chloride (4.71, 3.81, 3.37, and 6.25 g/d) did not differ ($P > 0.05$) for the LSF, HSF, LBT, and HBT treatments, respectively. However, the calculated delivered choline chloride for the RPC products was greater ($P < 0.05$) than during the baseline period. This would suggest that the method was appropriate and both of the RPC products were effective in providing a source of choline chloride.

Key Words: rumen protection, choline chloride, bioavailability

---

1897 (W356) Effect of method of flaxseed processing and tannins on the growth performance and carcass fatty acid profile of lambs. E. Castillo-Lopez*, M. Edrosolam, P. J. Shand, D. A. Christensen and G. B. Penner, *University of Saskatchewan, Saskatoon, SK, Canada*

The objective of this study was to evaluate the effect of flax, method of processing, and tannin inclusion on the growth performance of feedlot lambs and the carcass fatty acid composition. Forty Suffolk × Arcott lambs (22 females and 18 males) with an initial BW of 37.7 ± 5.87 kg were assigned to 1 of 2 blocks and within block to 1 of 5 dietary treatments in a randomized complete block design. Treatments (DM basis) were 1) CONT, a diet containing 15% barley silage, 53.6% ground barley, 11.9% canola meal, 6.4% alfalfa dehydrated, 4.0% oat hulls, 3.7% beet pulp, 3.3% fat and 2.1% mineral supplement; 2) FLAX, inclusion of 8.6% flaxseed; 3) FLAX+T, inclusion of 8.6% flaxseed and 4% tannins; 4) EF, inclusion of 20.5% extruded flaxseed; 5) EF+T, inclusion of 20.5% extruded flaxseed and 4% tannins. At the end of the 60 d study, ruminal fluid, blood, longissimus dorsi (LM), and subcutaneous back fat samples were collected and analyzed for fatty acid composition. Fatty acids were expressed as percentage of total fatty acid methyl esters. Data were analyzed as a randomized complete block design using the MIXED procedure of SAS. Treatment did not affect final BW ($P = 0.60$) or ADG ($P = 0.36$) with averages of 55.3 ± 3.10 kg and 324.0 ± 29.75 g/d, respectively. The proportion of saturated fatty acids in ruminal fluid ($P < 0.01$) and plasma ($P < 0.05$) was greatest in lambs fed CONT and CONT had the lowest ($P < 0.01$) proportion of polyunsaturated and omega-3 fatty acids in plasma. The proportions of saturated ($P = 0.93$) and polyunsaturated ($P = 0.15$) fatty acids in LM were unaffected. However, lambs fed FLAX+T, EF or EF+T had the greatest ($P < 0.01$) proportion of omega-3 fatty acids, with a minimum of a 2.3-fold greater concentration ($P < 0.01$) than CONT. The proportion of polyunsaturated fatty acids in subcutaneous fat was greatest ($P < 0.01$) in lambs fed FLAX+T or EF+T. Lambs fed FLAX+T had the greatest ($P < 0.01$) concentration of omega-3 fatty acids in subcutaneous fat with an estimate of 3.13 ± 0.189%: a value 3.3-fold higher ($P < 0.01$) than CONT. Overall, the fatty acid profile of lamb was improved when flaxseed or extruded flaxseed was fed without

affecting growth performance. Tannins had minimal additional effects on carcass fatty acid profile.

Key Words: extrusion, flaxseed, omega-3 fatty acids

1898 (W357) Evaluating the energy and protein requirements for growing Nellore heifers and steers fed two levels of calcium and phosphorus.

L. F. Costa e Silva*[1], T. E. Engle[1], S. C. Valadares Filho[2], P. P. Rotta[1], M. I. Marcondes[3], B. C. Silva[4] and M. V. C. Pacheco[3], *[1]Colorado State University, Fort Collins, [2]Universidade Federal de Viçosa, Department of Animal Science, Viçosa, Minas Gerais, Brazil, [3]Universidade Federal de Vicosa, Vicosa, Brazil, [4]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil.*

An experiment was conducted to evaluate the energy and protein requirements for growing Nellore heifers and steers fed with two levels of calcium and phosphorus. Thirty two Nellore heifers and eighteen Nellore steers were used. Heifers were divided in four groups. Four animals served as baseline reference animals, four were fed at maintenance (MAIN) and twenty four received ad libitum (ADLIB) access to feed. The ADLIB animals were further divided into four groups and assigned to treatments. Treatments were: 1) Ca and P fed at requirements (CaPR) with a 50:50 of roughage:concentrate (R:C) diet; 2) CaPR with at 70:30 R:C diet; 3) 43% of the Ca and 80% of the P requirement (CaPL) with a 50:50 R:C diet; and 4) CaPL with a 70:30 R:C diet. All steers in this experiment were fed CaPR. Half of the heifers and steers were slaughtered at d 50 and the other animals were slaughtered a d 100 of the feeding period while all MAIN animals were slaughtered at d 100. Total feces and urine were collected from all animals 72 h before slaughter. The net energy (NEm) and metabolizable energy (MEm) requirement for maintenance were obtained by exponentially relating the heat production and the metabolizable energy intake, while the net energy requirements for gain (NEg) were obtained using empty body weight (EBW) and EBW gain (EBG). The net protein requirements for gain (NPg) were estimated according to EBG and retained energy (RE). NEm and MEm were 70.1 and 118 kcal/kg $EBW^{0.75}$, respectively. Net protein for maintenance was 1.28 g/kg $BW^{0.75}$and NEg and NPg were estimated using the following equations: $NEg = 0.053 \times EBW^{0.75} \times EBG^{0.6301}$ and $NPg = 137.85 \times EBG – 0.05 \times RE$, respectively. Under the conditions of this experiment, the energy and protein requirements for growth were: $NEg = 0.053 \times EBW^{0.75} \times EBG^{0.6301}$ and $NPg = 137.85 \times EBG – 0.05 \times RE$, respectively.

Key Words: energy, protein, sugarcane

SMALL RUMINANT I

1899 (M365) A simple method to estimate feed required for maintenance of small ruminants.

A. L. Goetsch*[1], R. Puchala[1], A. T. Dolebo[1], T. A. Gipson[1], Y. Tsukahara[1] and L. J. Dawson[1,2], *[1]American Institute for Goat Research, Langston University, Langston, OK, [2]Center of Veterinary Health Sciences, Oklahoma State University, Stillwater*

A simple means to estimate feed required for maintenance by Katahdin (K) sheep and Spanish (S) goats (initial BW = 30.6 ± 0.40 and 21.8 ± 0.27 kg, respectively; 8 mo old) by frequent BW measurement and adjustment of feed offered was evaluated. Ten K and S wethers in 1.05 × 0.55 m pens were fed grass hay (64.1% NDF, 10.4% CP, and 55.4% TDN; DM basis), initially at 58 and 55 g/kg $BW^{0.75}$ (air-dry basis; i.e., ME intake of 427 and 452 kJ/kg $BW^{0.75}$, respectively), at 0800 h for 5 wk. Three times weekly BW was measured at 1300 h in 50-g increments, and hay fed was varied thereafter by 0–5% (i.e., ≤ 40 g/d) to maintain BW. Breed (732 and 538 g for K and S, respectively; SE = 11.5) and wk (625, 653, 632, 623, and 641 g for wk 1, 2, 3, 4, and 5, respectively; SE = 9.4) affected daily air-dry intake (ADI; $P < 0.001$), although breed × wk did not ($P = 0.508$). Variation among days in ADI differed between breeds in wk 2 (SD = 4.68 and 14.5 g; $P = 0.002$) and 5 (SD = 64.6 and 31.1 g for K and S, respectively; $P = 0.044$). Body weights were smoothed using LOWESS and fitted by a segmented polynomial with the middle segment constrained to a flat line. Regression coefficients of the first and third segments and the two join points were estimated using nonlinear regression. The average of the first and second join points was 16 and 28 d, respectively, indicating BW stability between these times. Also, ADI of each wether was regressed against ADG in 2- and 3-d periods based on unsmoothed BW in wk 2–5, 3–5, 2–3, 2–4, 3–4, and 4–5. The only weeks without an intercept different from 0 ($P > 0.10$) were 2–5 and 2–4. Hence, the intercept of wk 2–4 regressions was used to determine feed required for maintenance, with values of 727 and 538 g ADI (SE = 11.6), corresponding to a ME requirement for maintenance of 447 and 426 kJ/kg $BW^{0.75}$ for K and S, respectively. Variability was homogenous between breeds ($P = 0.867$), although intercept SE averaged 6.0 and 12.9 g ADI for K and S, respectively. In conclusion, after 2 wk of adaptation, frequent weighing and change in offered feed for 2 wk may offer a relatively simple means of estimating maintenance feed needs of small ruminants.

Key Words: maintenance, goats, sheep

1900 (M366) Dermal application of PGF2a for estrus synchronization in goats: Preliminary feasibility.

C. E. Ferguson*[1], D. J. Kesler[2], H. Nordberg[1] and J. Veillon[1], *[1]McNeese State University, Lake Charles, LA, [2]University of Illinois, Urbana-Champiagn*

The administration of vaccines and other veterinary products can result in abscesses and scar tissue within the carcass of the animal. The use of PGF_{2a} for estrus synchronization purposes only increases the likelihood of these occurrences. The objective of this study was to test the efficacy of PGF_{2a} dissolved in DMSO, a needle-less, transdermal delivery, compared with intramuscular injections of PGF_{2a}. In this study a total of 16 small cross-bred Spanish breed-type goats were used. The injection group received two 15 mg injections (im) of PGF_{2a} while the transdermal group received two 15 mg administrations dissolved in 2 mL of DMSO (placed between shoulder blades) both 10 d apart. All does were paint marked and exposed to a mature buck for 4 d. Approximately 35 d from buck removal all does were evaluated for pregnancy via ultrasonography. Statistical comparisons were performed in SAS using a chi-square analysis. There were no significant differences between the mean ± SD BCS (1 to 5 scale) for does receiving the injection protocol (1.7 ± 0.7) and does receiving the transdermal protocol (2.0 ± 0.8). Also there were no significant differences in the number of transdermal does displaying estrus (within 4 d) (5/7, 71%) compared with injection does (4/9, 44%). The pregnancy rate was higher ($P > 0.05$) for transdermal does (4/7, 57%) compared with injection does (2/9, 22%), however there was no significant different ($P > 0.05$) in the number of pregnant does from those showing estrus in the transdermal (3/5, 60%) and injection group (2/4, 50%). There was no difference ($P < 0.05$) in the time from last PGF_{2a} to onset of estrus among transdermal (58 ± 13 h) and injection does (42 ± 12 h). A total of 9 out of 16 does (56%) displayed estrus within a 4 d time period where only 19% would be expected randomly. These results suggest that administration of PGF_{2a} via DMSO (transdermal) should produce similar results as im injection for purposes of estrus synchronization. This procedure may result in a method of estrus synchronization without increasing carcass damage to goats.

Key Words: goats, PGF_{2a}, DMSO, estrus synchronization

1901 (M367) *Longissimus* muscle fatty acid profile of crossbred Boer goat kids fed diets containing crude glycerin. M. O. M. Parente*[1], K. S. Rocha[1], H. N. Parente[1], E. M. Ferreira[2], R. D. C. R. E. Queiroga[3], A. S. M. Batista[4], R. M. S. Gomes[1], P. R. O. Silva[1] and J. S. Araújo[1], *[1]Universidade Federal do Maranhão, Chapadinha, Brazil, [2]Escola Superior de Agricultura Luiz de Queiroz- ESALQ/ USP, Piracicaba, Brazil, [3]Universidade Federal da Paraíba, João Pessoa, Brazil, [4]Universidade do Vale do Acaraú, Sobral, Brazil*

Crude glycerin is a co-product of biodiesel production with a high concentration of glycerol. Due to the high production of biodiesel, there is a wide availability of crude glycerin and it is becoming an interesting ingredient for animal nutrition. Most studies focus on the sheep as small ruminants, while limited research exists evaluating crude glycerin in the diet of goat kids. Twenty crossbred Boer goat kids (20.8 ± 2.9 kg of BW at slaughter) were used in a randomized complete block design to determine the effect of partial replacement of corn by crude glycerin on *Longissimus* muscle fatty acid profile. Kids were penned individually for 51 d and fed an isonitrogenous (14.0 ± 0.2% CP, DM basis) diet composed of 70% concentrate and 30% forage (Coastcross Bermudagrass hay). Increasing levels of crude glycerin (80.0% glycerol, DM basis) were 0, 4, 8 or 12% corresponding to the experimental diets G0, G4, G8 and G12, respectively. Total lipids of muscles were extracted, esterified and methylated. Methyl esters were separated by gas chromatography (VARIAN 430-GC, California, USA) using a 60 m capillary column. Orthogonal polynomials for treatment responses were determined by linear, quadratic, and cubic effects. Effects were declared significant at $P < 0.05$, and trends are discussed between $P > 0.05$ and $P < 0.10$. Linear decrease ($P < 0.05$) for linoleic acid (3.57, 2.84, 3.76 and 2.33) and w6:w3 ratio (10.61, 9.71, 7.26 and 7.18 for G0, G4, G8 and G12, respectively) were observed with crude glycerin inclusion. The proportion of capric and eicosanoic acids tended ($P = 0.06$) to increase linearly. Saturated, Monounsaturated and Polyunsaturated fatty acids were not affected by treatments. In conclusion, the partial replacement of corn by crude glycerin cause a little effect on meat fatty acid profile.

Key Words: co-product, meat, quality

1902 (M368) Performance and carcass characteristics of finishing goat kids fed diets containing crude glycerin. M. O. M. Parente*[1], K. S. Rocha[1], H. N. Parente[1], E. M. Ferreira[2], I. G. R. Araújo[1], R. C. Rodrigues[1], R. M. S. Gomes[1] and P. R. O. Silva[1], *[1]Universidade Federal do Maranhão, Chapadinha, Brazil, [2]Escola Superior de Agricultura Luiz de Queiroz- ESALQ/USP, Piracicaba, Brazil*

The crude glycerin (co-product of biodiesel) has the potential to partially replace corn, because glycerol (an 80% constituent of crude glycerin) is converted to propionate in the rumen and acts as a precursor for hepatic glucose synthesis. However, most studies focus on the sheep and beef cattle, while limited research exists evaluating crude glycerin in the diet of goat kids. Therefore, the objectives of this trial were to determine the effects of partial replacement of corn by crude glycerin on performance and carcass characteristics of goat kids. Twenty crossbred Boer goat kids (initial BW of 17.08 ± 2.1 kg and 110 d old) were used in a randomized complete block design according to initial BW and age. Kids were penned individually during 51 d and fed an isonitrogenous (14.0 ± 0.2 CP, DM basis) diet composed of 70% of concentrate and 30% of forage (coastcross hay). Increasing levels of crude glycerin (80.0% glycerol, DM basis) were 0, 4, 8, or 12% corresponding to the experimental diets G0, G4, G8 and G12, respectively. Orthogonal polynomials for treatment responses were determined by linear, quadratic, and cubic effects. Effects were declared significant at $P < 0.05$ and trends are discussed between $P > 0.05$ and $P < 0.10$. Body weight (BW), average daily gain (ADG), G:F, dry matter intake, protein intake and ether extract intake were not affected by glycerin as a replacement for ground corn. Dry matter intake was 0.58, 0.65, 0.54 and 0.59 kg/d while ADG was 106, 106, 90, and 94 g for G0, G4, G8 and G12, respectively. The NDF intake tended ($P = 0.08$) to decrease linearly. Carcass characteristics (hot carcass weight, hot carcass yield and subcutaneous fat thickness) were unaffected by crude glycerin addition. Adding up to 12% crude glycerin to finishing kids does not affect the performance and carcass characteristics.

Key Words: Boer, cost of production, growth

1903 (M369) Effect of reducing dietary cation-anion difference on acid-base balance, plasma minerals level and anti-oxidative stress of female goats. W. X. Wu* and Y. Yang, *College of Animal Science, Guizhou University, Guiyang, China*

Reducing dietary cation-anion difference (DCAD, Na^+K-Cl-S, mEq/kg DM) has been proved an effective way to prevent milk fever in dairy cows. Based on the similar physiological gastro-intestinal tract anatomy and metabolic process between female goats and dairy cows, this study was conducted to evaluate the effects of varying DCAD on fluid

acid-base status, plasma mineral concentration and anti-oxidative stress capacity of female goats. Urinary pH, plasma Ca, P and Mg; and anti-oxidative stress indices of total superoxide dismutase (T-SOD), hydrogen peroxide (H_2O_2), glutathione peroxidase (GSH-Px) and malondialdehyde (MDA) were determined to evaluate the effect. Forty-eight Guizhou black female goats (15 ± 1.9 mo old, 22.3 ± 3.75 kg live weight) were randomly allocated to 4 blocks of 12 goats each and fed 1 of 4 diets that differed in DCAD level. Levels of DCAD were preliminarily designed to be control (+150 mEq/kg DM, CON), high DCAD (+300 mEq/kg DM, HD), low DCAD (0 mEq/kg DM, LD) and negative DCAD (-150 mEq/kg DM, ND), respectively. A commercial anionic salts (Animate) and sodium bicarbonate ($NaHCO_3$) were supplemented to reduce and increase DCAD level, respectively. There was no difference in dry matter intake for 4 groups of goats. Urine pH was aggressively decreased ($P < 0.0001$) with reduced DCAD and there was a strong association between DCAD and urine pH ($R^2 = 0.793$, $P < 0.0001$). Compared with CON and HD, feeding of LD and ND resulted in greater ($P < 0.05$) plasma Ca concentration. Plasma P level was increased ($P < 0.05$) when anionic salts were supplemented. The DCAD alteration did not affect ($P > 0.05$) plasma Mg level. There was no significant ($P > 0.05$) difference in plasma GSH-Px activity and H_2O_2, but anionic salts supplementation in LD and ND significantly increased ($P < 0.05$) plasma T-SOD activity and tended to reduce MDA ($P < 0.1$) over HD and CON. Results from this study indicated that reducing DCAD could decrease urine pH and increase plasma Ca concentration of female goats. Specially, reducing DCAD was helpful to enhance oxidative stress tolerance capability of female goats.

Key Words: dietary cation-anion difference, urine pH, plasma calcium, anti-oxidative stress, female goats

---

1904 (M370) Effect of dietary linseed supplementation on milk fatty acid profile in dairy goats with different α^{S1}-casein (CSN1S1) genotype.

A. Nudda*, G. Battacone, N. P. P. Macciotta, A. Fenu and G. Pulina, *Dipartimento di Agraria, University of Sassari, Sassari, Italy*

In this study, the effects of dietary supplementation with extruded linseed on milk fatty acid profile of dairy goats with different α-^{s1} casein (CSN1S1) genotype are investigated. A flock of 68 Alpine goats were genotyped by IEF at the CSN1S1 locus. Ten were selected for the experiment: 5 homozygous for the weak *F* allele (*FF*) and 5 heterozygous for a strong allele (*AA or BE*). Goats of each genotype (weak and strong) were allocated into two groups: one was the control (CON) and one was supplemented with 150 g/d of extruded linseed (LIN). The trial lasted 8 wk. Data were analyzed using a mixed linear model that included the period, diet, genotype and diet × CSN1S1 genotype interaction as fixed factors, and the goat as random factor. Results confirmed the lower protein content (-11%) and higher milk yield (+26%) in weak genotype. A significant interaction diet x genotype was found for fat content: it was higher in LIN compared to CON only in the strong genotype (3.4 vs. 4.0%), whereas it did not change in weak genotype (3.3 vs. 3.2%). Goats fed LIN had greater proportions of vaccenic acid (18:1 trans11), CLA c9t11 and 18:3n-3 than goats fed CON. The genotype affected some FA: in particular the weak group showed a higher proportion ($P < 0.05$) of linoleic (2.5 vs. 2.1 g/100 g total FA), CLA c9t11 (0.8 vs. 0.6 g/100 g total FA), C16:1 and C22:4n6, and a lower proportion of stearic (7.4 vs. 8.6 g/100 g FA) compared to strong. Furthermore, the delta9 desaturation ratios were higher in weak CSN1S1 genotypes for C14 and trans11 C18:1. This study evidenced the impact of genetic variants of CSN1S1 on milk fat content and composition. *Acknowledgements: research funded by Fondazione Banco di Sardegna project*.

Key Words: goat milk, α_{S1}-casein, linseed diet by genotype interaction

---

1905 (M371) GIS hot-spot analysis of pasture utilization of two separate herds of goats over time.

T. A. Gipson*[1], S. P. Hart[1] and R. Heinemann[2], *[1]American Institute for Goat Research, Langston University, Langston, OK, [2]Kiamichi Forestry Research Station, Oklahoma State University, Idabel*

An understanding of pasture landscapes that promotes or hinders efficient utilization is essential for proper management. The objective of this study was to characterize pasture utilization of two separate herds of goats utilizing the same pasture in different years. The study area was a 14.1-ha pasture of predominantly fescue, bermudagrass, panicums, bahia grass, and broomsedge bluestem but was reverting to a wooded area containing predominately pecan, elm, and honey locust sapling-size trees. In year one (Y1), the study area was stocked with 36 Spanish goats, of which 10 were fitted with GPS collars and in year two (Y2), the study area was stocked with 58 Spanish goats, of which 19 goats were fitted with GPS collars. Different goats were used in Y1 and Y2. For the first 2 wk of pasture introduction, goats wore the collars, which recorded a fix every 5 min. An average nearest neighbor analysis yielded a z score of -150.2 ($P < 0.01$) for Y1 and -150.1 ($P < 0.01$) for Y2, indicating highly clustered events for both years. A GIS point-in-polygon (PiP) analysis was conducted for each year using the same grid (1792 10 × 10 m squares) for each year and with unique grid identifiers. Moran's I, a measure of spatial autocorrelation, indicated a peak at 30 m and that value was used in the hot-spot (Getis-Ord Gi* statistic) analysis conducted on the resulting PiP. Based on the resulting z-scores from the hot-spot analysis, each square was classified as very low (VL), low (L), moderate (M), high (H), and very high (VH) usage. Y1 had greater ($\chi^2 = 13.89$, $P < 0.01$) VL and lower VH squares (82% and 1%, respectively) compared with Y2 (80% and 3%, respectively). Hot-spot analysis revealed

two areas of H and VH usage for both years. One of the areas was a small grove of trees that had almost a 100% overlay for both years. The degree of similarity in pasture usage was high as indicated by a Spearman's rank correlation coefficient (0.76; $P < 0.01$) of the square z-scores for Y1 and Y2. Even though the two herds of goats never interacted and were separated by time, their pasture utilization was strikingly similar. Further work is needed to investigate the physical features of the pasture to understand the causes behind this similarity.

Key Words: GIS, GPS, goats

1906 (M372) Model evaluation of methane emission from goats.

M. H. M. R. F. Fernandes[*1], K. T. Resende[2], A. R. C. Lima[1], I. A. M. A. Teixeira[2], B. Biagioli[1] and T. F. V. Bompadre[1], *[1]UNESP, Univ Estadual Paulista, Department of Animal Science, Jaboticabal, Jaboticabal, Brazil, [2]UNESP, Univ Estadual Paulista, Department of Animal Science, Jaboticabal, SP, Brazil*

There have been several attempts to develop mathematical models to predict methane (CH_4) emissions because they can be easily applied in practical situations to estimate diet ME. Because studies evaluating the suitability of different mathematical models available for methane emission prediction in goats are lacking, this study was performed to evaluate 3 empirical models (Blaxter and Clapperton, Moe and Tyrrel, Pelchen and Peters) based on their ease of application, common use and their feasible input variables. The prediction ability of those models was evaluated using a database of two metabolism trials, in which 45 individual measurement of methane emission from goats (averaging 30 ± 2.93 kg BW) was taken using SF_6 technique. Models were evaluated by regressing residual (observed minus predicted) values on the predicted values centered on their mean values. The intercepts of the regression equations were used to estimate mean biases, whereas linear biases were assessed using the slopes of the regression equations. Also, using the same database, an empirical model was developed taking into account the coefficient of determination (R^2), forward selection, and Cp of Mallows. Observed DMI ranged from 280 to 1300 g/d. Observed methane emission ranged from 8 to 22 g/d, which represented methane losses ranging from 3.5 to 11% of dietary GE intake. Results showed a significant mean and linear biases ($P < 0.001$) for all models, showing that these models over predict methane emissions from goats. Moe and Tyrrell model presented the highest linear bias which was −65.5 g/d at the maximum predicted value (86.9 g CH_4/d). Pelchen and Peters model exhibited the lowest magnitude of the linear bias, which was less than 2 g/d at the minimum (11.5 CH_4/d) and -10 g/d at the maximum (27 g CH_4/d) predicted methane values. The linear bias of Blaxter and Clapperton model ranged from approximately 4 g/d (at the minimum predicted values) to -15 g/d (at the maximum predicted values). A simple regression equation was developed using same database. Accordingly, the best-fit linear model that represents goat methane emission was defined as follows ($R^2 = 0.51$, RMSE = 2.23, $P < 0.001$, CP = 11.4): CH_4(g/d) = 4.36 ± 2.07 + 0.17 ± 0.06 × BW (kg) + 0.006 ± 0.001 × DMI (g/d).

Key Words: bias, empirical model, CH_4

1907 (M373) The effect of some herbal plants on plasma metabolites of lactating goats.

K. Rezayazdi[*1], F. Mirzaei[2] and M. Hosseinabadi[3], *[1]Department of Animal Science, Faculty of Agriculture, University of Tehran, Karaj, Iran, [2]Animal Science Research Institute, Karaj, Iran, [3]University of Tehran, Karaj, Iran*

The objective of this study was to investigate the effects of a dried mixture of 7 herbal plants including thyme, mint, oregano, cumin, camel thorn, garlic, and eucalyptus as a natural dietary additive on plasma metabolites of lactating goats. Twenty lactating goats (3 wk after kidding, 2–3 yr old, average BW = 34.45 kg) were used in a completely randomized design with 2 treatments for a 40 d trial. Treatments included (1) a control ration, consisting of barley and alfalfa (50:50 DM basis) without herbal plant mixture, and (2) control ration + 250 mg kg^{-1} body weight per day herbal plant mixture. Amount of basal diet for the 2 groups was 0.5 kg/head/d. Animals had free access to water and green fodder. Blood samples were collected at the end of experiment after morning feeding for determination of plasma glucose, triglyceride (TG), urea nitrogen (BUN), total protein and cholesterol concentrations. Results showed that mean concentration of plasma glucose (60.5 and 57.5 mg/dL), total protein (10.0 and 9.6 g/dL), BUN (21.5 and 24.2 mg/dL) and TG (31.5 and 30.3 mg/dL) were not affected by herbal plants, but cholesterol concentration (73.7 and 59.7 mg/dL was significantly lower in treatment 2 ($P < 0.05$). It is concluded that herbal plant mixture were used in this study significantly decreased cholesterol concentration in plasma of lactating goats.

Key Words: blood metabolites, herbal plants, lactating goat

1908 (M374) Seasonal variation influences the semen characteristics and freezability in Xinong Saanen goat.

W. Wang[1], J. Luo[*2] and S. Sun[1], *[1]Northwest A&F University, Yangling, China, [2]Northwest A & F University, Yangling, China*

The aim of this study was to evaluate how season of ejaculate collection influences seminal quality parameters before and after freeze–thawing of Xinong Saanen buck semen. Ejaculates were collected from eight bucks and throughout the four seasons of 1 yr identified in the northern hemisphere (spring, summer, autumn and winter). During the study period, semen was collected at 10-d intervals during each season with an ar-

tificial vagina. Semen samples were evaluated by the combination of traditional and Computer-Assisted Sperm Analysis (CASA) semen assessment methods and sperm quality parameters (motility and morphology) were compared at fresh and after freeze–thawing, respectively. The results demonstrated that season of ejaculate collection influenced ($P < 0.05$) semen quality of Xinong Saanen bucks before freezing. During spring, summer and autumn, the ejaculate subjectively motility; volume; sperm concentration; sperm output and membrane integrity were higher ($P < 0.05$) than in the winter. The CASA also illustrated seasonal variation greatly affected semen motility kinetic parameters. An increase in the curvilinear velocity (CLV); straight line velocity (SLV); beat cross frequency (BCF) and amplitude of lateral head displacement (LHD) was observed during spring, summer and autumn, followed by a significant ($P < 0.05$) decrease during the winter. Furthermore, season of ejaculate collection influenced sperm freezability. Semen characters after freeze–thawing followed a phenomenon similar to that of the fresh ejaculate except in spring. In details, sperm quality was higher ($P < 0.01$) in summer and autumn than in spring and winter, in terms of total motile sperm (MS); rapidly progressive motile sperm (RPMS); CLV; SLV; average path velocity (APV); BCF and LHD base on the CASA. The membrane integrity and acrosome integrity were obtained from summer to autumn were higher ($P < 0.01$) than in spring and winter. Consequently, it can be said that Xinong Saanen bucks have distinct seasonal spermatogenic activity, with better semen quality characteristics being recorded during spring, summer and winter before freezing. Sperm from ejaculates collected during summer and autumn are more suitable for cryopreservation. Thus, it is possible to implement intensive goat breeding strategy with two kidding seasons in 1 yr to produce adequate quantities of goat milk and equalize the need for milk throughout the year, and moreover, the poor semen characteristics emphasize the need in avoiding making use of semen collection for cryopreservation purposes during spring and winter seasons of the year.

Key Words: Xinong Saanen goat, sensonality, semen characteristics, freezability, CASA

1909 (M375) Mean retention time of particulate matter through gastrointestinal tract of growing goat.

R. F. Leite[*1], F. O. M. Figueiredo[2], M. M. Freire[3], V. B. Carvalho[1] and I. A. M. A. Teixeira[1], *[1]UNESP, Univ Estadual Paulista, Department of Animal Science, Jaboticabal, SP, Brazil, [2]Sao Paulo State University, Jaboticabal/SP, Brazil, [3]UFAL, Maceio, AL, Brazil*

The objective of this study was to evaluate mean retention time (MRT) of particulate matter through gastrointestinal tract (GIT) of growing goat of different sex and body weight. A total of 58 Saanen goats (20 intact males, 20 castrated males and 18 females) were housed in individual pens with free access to water. Then, the goats of each sex were randomized in 3 different slaughter BW (around 15, 22, 30 kg). They were fed ad libitum with the same diet (45.4% corn plant hay and 54.6% concentrate comprised), and diet was offered twice daily at 0700 and 1600 h. The animals were slaughter when reached 16.5 ± 0.9; 22.8 ± 1.3; 31.6 ± 1.5 kg of BW. Then, GIT was removed and separated into reticulorumen, omasum, abomasum, small intestine, cecum and colon. The content of each GIT compartment was sampled. To determine the passage rate, we used the ruminal emptying technique of slaughtered animals. The indigestible NDF (iNDF) was used as internal marker. The concentration of iNDF was determined by incubating the samples in rumen-fistulated cattle per 288 h, using Ankom bags (F57). The experiment was analyzed as split plot designed (3 sex and 3 slaughter BW) using PROC MIXED of SAS. The effect of slaughter BW was decomposed into 2 orthogonal polynomial contrasts (linear and quadratic) and the effect of sex was compared by Tukey test. The significance was declared at $P \leq 0.05$. Sex did not influence the MRT for all compartments ($P > 0.05$). On average the reticulorumen retention time was 35.8 h (67% of retention in GIT) and it was similar between sex and BW. As BW increased the MRT in the omasum increased linearly and the MRT in the abomasum decreased linearly ($P \leq 0.05$). It was observed a significant interaction between sex and BW for MRT of omasum and colon ($P < 0.01$). Whereas, females with 22 kg of BW presented lower MRT compared to males (intact and castrated) in the same BW. In conclusion, the increase of BW mainly influenced MRT in the omasum and abomasum compartment. Females present different pattern of MRT for omasum and colon than males.

Key Words: body weight, iNDF, sex

1910 (M376) Goat kids of different genders change the proteic metabolism when subjected to feed restriction.

N. C. D. Silva[1], K. T. Resende[1], I. A. M. A. Teixeira[*1], H. C. Bonfa[2], C. J. Harter[1], F. O. M. Figueiredo[3], R. F. Leite[1] and M. M. Freire[4], *[1]UNESP, Univ Estadual Paulista, Department of Animal Science, Jaboticabal, SP, Brazil, [2]UFV, Universidade Federal de Viçosa, Department of Animal Science, Viçosa, MG, Brazil, [3]Sao Paulo State University, Jaboticabal/SP, Brazil, [4]UFAL, Maceio, AL, Brazil*

The objective of this study was to evaluate the effect of gender and feed restriction on proteic metabolism of 72 Saanen goat kids (24 intact males, 24 castrated males and 24 females) with initial BW of 15.8 ± 0.17 kg. At the beginning of the experiment 6 animals of each gender were slaughtered with 15 kg of BW to estimate their initial body composition, these animals were considered baseline for the comparative slaughter technique. The remaining animals of each gender were distributed into 6 groups of 3 animals subjected to different

levels of feed restriction (ad libitum, 25% and 50% feed restriction). A whole group was slaughtered when the kid fed ad libitum reached 30 kg BW. Protein retention was estimated by the difference between the final and initial body composition. Blood samples were collected from all animals every 10 d, in a total of 7 collections for blood metabolites and 5 collections for hormones profile. In these samples we evaluated total protein, albumin, urea, creatinine, γ glutamyltransferase (GGT), creatine kinase (CK), triiodothyronine (T3) and IGF-I. Data were analyzed as split plot design, using mixed model of SAS. The retention of body protein (kg) was not affected by gender, only showing a linear decrease with the increase of feed restriction ($P < 0.0001$). The total protein, creatinine and CK seric levels increased with the increase of experimental time ($P < 0.05$). When fed ad libitum, urea concentration was highest in females (58.1 mg/dl), followed by castrated males (54.3 mg/dl) and intact males (51.2 mg/dl; $P = 0.0154$). When the goats were subjected to 25% of feed restriction, the difference between genders was no longer observed, however, when subjected to 50% of feed restriction castrated males showed the highest serum urea level (54.02 mg/dl). The GGT activity in intact males was higher ($P < 0.0001$) when they were fed ad libitum (51.31 ± 1.58 U/L) and decreased with the increase of feed restriction. Whereas castrated males fed ad libitumpresented lower activities of GGT compared to those fed restricted and females remained constant at all levels of feed restriction. IGF-1 plasmatic were similar between castrated males and females (81.3 ng/ml), and lower than found in intact males (106.20 ng/ml; ($P < 0.0001$). Intact males showed lower concentrations of T3 compared to females ($P < 0.05$). Despite goats of different gender show similar protein accretion, they act physiologically different when subjected to feed restriction. Males changed their proteic metabolism to keep the protein synthesis.

Key Words: metabolism, sex

1911 (M377) Effects of dietary chromium supplementation on performance, liver and blood metabolites of kids. A. Emami[1], M. Ganjkhanlou[2], A. Zali[2], A. Akbari-Afjani[3] and M. Dehghan-Banadaky[*2], [1]*University of Birjand, Birjand, Iran,* [2]*University of Tehran, Tehran, Iran,* [3]*University of Zanjan, Zanjan, Iran*

This study was performed to determine the effects of supplementing chromium-methionine (Cr-Met) on fattening performance, liver and blood metabolites in Mahabadi goat kids. Thirty-two male kids (BW = 22 ± 2 kg, 4mo) were used in a completely randomized design to one of 4 treatments: control, 0.5, 1.0 and 1.5 mg Cr as Cr-Met/animal/d. The diet was formulated to meet the requirements recommended by NRC with 30% forage (alfalfa and corn silage): 70% concentrate ratio as TMR. The diets were the same, except for top-dress addition of Cr-Met fed in 2 equal meals (0700 and 1700 h) and orts were collected before morning meal. Animals were housed individually for 84 d. Animals were weighed in 21-d intervals. For measuring blood metabolites (glucose and cholesterol), blood samples were collected every 21 d before morning feeding. The end of trial following 16h fasting kids were slaughtered and some of the liver were immediately stored at -20C for assessing moisture, fat and crude protein content. Data considering dry matter intake(DMI), average daily gain (ADG) and blood metabolites were analyzed by Mixed Model procedure and liver metabolites with GLM MODEL procedure and adjust Tukey-Kramer (SAS 9.1). Intake (DMI), ADG, liver metabolites and blood plasma cholesterol were not significantly affected by dietary Cr-Met ($P > 0.05$). However supplementing diet with chromium significantly decreases plasma glucose relative to the control ($P < 0.05$). In conclusion, the results of this experiment indicated that dietary supplementation of Cr-Met failed to affect growth performance, plasma cholesterol and liver metabolites but decreased plasma glucose of Mahabadi goat kids.

Key Words: chromium methionine, blood metabolite, Mahabadi goat kid

---

1912 (M378) Effect of Tasco on fecal egg counts and packed cell volume in meat goats. N. C. Whitley*, S. H. Oh, K. Moulton, R. Franco, S. B. Routh and C. Kyle, *North Carolina A&T State University, Greensboro*

The effect of Tasco on goat gastrointestinal nematode parasite fecal egg counts (FEC) and packed cell volume (PCV) was investigated in two experiments (Exp) using Boer and Boer crossbred goat kids. In Exp 1, female goats at 264 ± 2.5 d of age and 31 ± 0.99 kg BW were artificially infected with 2000 L3 *Haemonchus contortus* every other day for 6 d. At 56 d post-infection, 20 goats were assigned to treatments of Control (Con) or Tasco (TA), $n = 10$/treatment. For Exp 2, 36 naturally-infected, 119 ± 2.4 d old female and castrated male goats at 22.5 ± 0.4 kg were assigned to Con and TA ($n = 18$/treatment). Pre-treatment FEC and BW means were similar. Goats were individually housed in 1.5 × 1.5 m pens with ad libitum water access. A commercially pelleted 17% CP meat goat feed was used. For Exp 1, goats were fed Tasco at 2% feed offered or a similar amount of their daily feed ration (2% BW with coccidiostat) mixed with 20 mL corn oil 2–3 h prefeeding for 14d. For Exp. 2, Tasco was added at 2% DM by the feed company before pelleting (no coccidiostat). Both TA and Con pre-weighed rations were fed daily to allow for 10% orts for 21d. Goats were weighed on d 0 and 21 (Exp 2) and fecal sampled at d 0, 7, and 14 (and d 21 for Exp 2) for FEC by modified McMaster's technique. Percentage PCV was measured in jugular blood samples on d 0, 7, 14, and 21 (d 0 and 14 only for Exp 1). Orts were weighed on d 7 (Exp 1 and 2), and d 14 and 21 (Exp 2). For Exp 1, half the goats regularly left unconsumed Tasco. However, analyzed separately (con-

sumed all vs. part) or together, FEC was not impacted by TA, while PCV was higher ($P < 0.01$) for TA (33.3 ± 0.56%) than Con (30.3 ± 0.58%). For Exp 2, FEC (1820 ± 156 epg), PCV (29.6% ± 0.4%), ADG (0.15 ± 0.02 kg) and FE (0.19 ± 0.02 kg gain/kg feed) were not impacted by TA. Pre-treatment fecal larval identification indicated 84.5% *H. contortus*. Intake was not influenced by TA. Overall, Tasco addition to the diet did not have consistent effects on PCV and FEC in goats and did not impact growth or feed efficiency.

Key Words: goat, parasites, Tasco

1913 (M379) Pharmacokinetic processes of lithium used for food aversion in sheep and goats.

C. L. Manuelian[1], E. Albanell[1], M. Rovai[1], A. Salama[*1,2], G. Caja[1] and R. Guitart[3], *[1]Group of Ruminant Research (G2R), Universitat Autonoma de Barcelona, Bellaterra, Barcelona, Spain, [2]Animal Production Research Institute, Dokki, Giza, Egypt, [3]Laboratory of Toxicology, Faculty of Veterinary, Universitat Autonoma de Barcelona, Bellaterra, Barcelona, Spain*

Conditioned taste aversion (CTA) is a useful management tool to control weeds in commercial crops. Lithium chloride (LiCl) is a safe product used in livestock CTA studies to induce aversion to palatable plants. Despite the use of LiCl in numerous studies, there is a lack of information on the pharmacokinetics that accompany different CTA doses in domestic livestock. This information is needed for using selective grazing in practice, and to avoid any possible soil contamination by excreted Li. With this aim, we studied the kinetics of Li elimination in 2 experiments: 1) Murciano-Grandina lactating goats ($n = 6$) after a single dose of 200 mg LiCl/kg BW; and 2) Manchega dairy sheep, open and dry, after a single dose of 225 mg LiCl/kg BW. For Exp.1, goats were penned in metabolic cages for measuring daily milk yield, water and feed intake. Samples of urine, feces, milk and blood were collected over a period of 168 h. In Exp.2, ewes were maintained as a group in a pen with head lockers, where they were restrained at every sampling time for feces (rectum) and blood (jugular) collection over 192 h. Concentration of Li was measured by graphite furnace Atomic Absorption Spectrometry and data corrected for its basal concentration. Withdrawal period (Wp) was calculated with a statistical tolerance limit of 95% (EMEA/CVMP/036/95). Individual biological half-life ($t_{1/2}$) was calculated using PK Solutions computer program (Farrier, 1997). Results showed that plasma Li concentration reached a maximum at 4 h in lactating goats (14.5 ± 0.8 mg Li/L plasma) and 12 h in dry sheep (17.7 ± 0.8 mg Li/L plasma). Values of $t_{1/2}$ were 30.9 ± 2.1 and 40.3 ± 3.8 h for sheep and goats, respectively ($t = 2.39$; DF = 10; $P < 0.03$). In goats, recovery rate of administered Li was 101.7% at 96 h (urine, 92.4 ± 4.4%; feces, 6.5 ± 1.3%; milk, 2.8 ± 0.4%); however the estimated Wp established in feces was 9 and 11 d for sheep and goats, respectively. In conclusion, Li was fully eliminated in sheep and goats, but needed longer time than reported in other species (i.e., rat and human). LiCl can be used safely to induce CTA for controlling weeds by grazing in organic crops after a waiting period of approximately 1 wk before moving the animals to the crop. *Funded by Plan Nacional I+D+I AGL 2010–22178-C02–01.*

Key Words: conditioned aversion; small ruminants; lithium chloride

---

1914 (M380) Influence of partial replacement of corn by crude glycerin on water consumption, feed intake and nutrient apparent digestibility.

D. M. Polizel[1], R. S. Gentil[1], E. M. Ferreira[1], R. A. Souza[1], A. P. A. Freire[1], J. A. Faleiro Neto[2], A. V. Pires[3] and I. Susin[*1], *[1]Escola Superior de Agricultura Luiz de Queiroz- ESALQ/USP, Piracicaba, Brazil, [2]Faculdade de Medicina Veterinária e Zootecnia- FMVZ/USP, São Paulo, Brazil, [3]University of São Paulo- ESALQ/USP, Piracicaba, Brazil*

Glycerin is a co-product from biodiesel production and it can improve energy efficiency when replaces corn. Five Dorper x Santa Inês ram lambs (BW 59.7 ± 1.3 kg), cannulated in the rumen, were used in a 5 × 5 Latin Square design to determine the effects of partial replacement of corn by crude glycerin (CG) on water consumption, feed intake and nutrient apparent digestibility. Animals were fed a total mix ration composed of 90% concentrate and 10% coastcross hay. The diets were isonitrogenous (15.9 ± 0.2 CP, DM basis) and the crude protein content was adjusted by increasing soybean meal. Crude glycerin (83.6% glycerol, DM basis) was included in the ration at 0, 5, 10, 15 or 20% (DM basis), corresponding to the experimental diets G0, G5, G10, G15 and G20, respectively. The diet was fed ad libitum, once daily. Every experimental period lasted 19 d. The first 15 d were used to adapt the lambs with the diets and the remaining 4 d were used to determine daily feed intake, water consumption and fecal output. For total collection of feces, harnesses with collection bags were used to avoid contamination of feces by urine. Data were analyzed using the MIXED procedure (SAS Inst. Inc.) and the LSMEANS option was used to generate individual means. Orthogonal polynomials for diet responses were determined by linear, quadratic or cubic effects. CG did not affect ($P > 0.05$) water consumption (4.77, 5.02, 5.01, 5.25, 4.56 L/d), dry matter (1.56, 1.51, 1.45, 1.43, 1.47 kg/d), crude protein (0.25, 0.25, 0.24, 0.22, 0.23 kg/d) and organic matter intakes (1.48, 1.43, 1.36, 1.33, 1.38 kg/d). Crude glycerin decreased ($P < 0.01$) NDF intake (0.29, 0.28, 0.24, 0.22, 0.24 kg/d) and increased ($P < 0.01$) mineral matter intake (0.08, 0.08, 0.09, 0.09, 0.10 kg/d). There was no effect on NDF (55.9, 54.5, 56.3, 56.7, 58.0%) and crude protein digestibilities (82.4, 81.7, 82.8, 81.5, 83.6%), However, DM (83.3, 82.5, 84.2, 85.4, 85.7%) and OM (84.8, 84.0, 85.9, 86.5, 86.8%) digest-

ibilities showed a linear increase ($P < 0.01$). Crude glycerin can replace corn up to 20% of dietary DM increasing DM and OM apparent digestibilities.

Key Words: glycerol, sheep, biodiesel

1915 (M381) Post-weaning performance by intact male F1 Kiko × Boer progeny from does selected based on parasite resistance: 1-yr summary.

L. S. Wilbers*, B. C. Shanks, J. D. Caldwell, K. L. Basinger, W. M. Haslag, J. D. Walker, K. M. Jones and A. L. Bax, *Department of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO*

Goats are popular with small landowners and fit into a variety of farming systems. High market prices and continuing parasite challenges have led some producers to consider confinement feeding as a system to improve performance and avoid parasite problems. Therefore, the objective of this study was to evaluate post-weaning performance by intact male F_1 Kiko × Boer progeny from does selected based on parasite resistance. Weaned, intact male F_1 Kiko × Boer progeny ($n = 16$; 10.7 ± 0.59 kg weaning weight; 94.4 ± 2.73 d of age) from two lines of does selected for high resistance to internal parasites (HL; $n = 11$) or for low resistance to internal parasites (LL; $n = 5$) were compared. Animals were confined in a small ruminant barn with full access to a high-concentrate feed ration, water, and mineral supplement. Kid weaning weight, 47-d post-weaning weight, and final weight did not differ ($P \geq 0.19$) across treatments. Weaning to 47 d post weaning ADG, 47 d post-weaning to final ADG, and total ADG did not differ ($P \geq 0.15$) across treatments. Weaning to 47 d post weaning gain, 47 d post-weaning to final gain, and total gain did not differ ($P \geq 0.20$) for HL compared with LL. Therefore, selecting does based on parasite resistance may not influence post-weaning performance of their crossbred male progeny when offered a high-concentrate diet.

Key Words: goats, high-concentrate, parasite resistance

1916 (M382) Effects of thyme oil (*Thymus vulgaris*) on in vitro ruminal fermentation kinetics.

A. D. B. Ribeiro*[1], A. V. Pires[2], I. Susin[3], M. V. Biehl[2], V. N. Gouvea[1], M. V. C. Ferraz Jr.[1], M. L. Day[4], L. H. Cruppe[4], J. A. Faleiro Neto[1] and J. P. C. Thieme[2], *[1]University of São Paulo- FMVZ/USP, Pirassununga, Brazil, [2]University of São Paulo- ESALQ/USP, Piracicaba, Brazil, [3]Escola Superior de Agricultura Luiz de Queiroz-ESALQ/USP, Piracicaba, Brazil, [4]The Ohio State University, Columbus*

The objective of the present study was to investigate the effects of dietary thyme oil (1.25, 2.50 and 3.75 mL/kg DM) or monensin (Rumensin; 20 mg/kg DM) on ruminal in vitro gas production kinetics. Diets were formulated using the Small Ruminant Nutrition System to meet the requirements of growing sheep and were 80% Tifton hay (*Cynodon sp.*) and 20% concentrate DM. Homogenized samples of each diet (1.0 g) were placed into 160 mL serum bottles with 10 mL of rumen inoculum and 90 mL of a buffer solution. Rumen inoculum was collected from 4 fistulated male lambs before the first feed of the day was offered. Each lamb was fed one of the four diets, ad libitum. Six bottles were used per treatment and two additional bottles containing buffered medium, rumen fluid and the feed additives were used as background control. The volume of gas produced was indirectly measured at 2, 4, 6, 8, 10, 12, 15, 18, 21, 24, 36, 48, 72, and 96 h of incubation using the pressure reading technique. To estimate kinetic parameters of gas production data were fitted to the model $Y = A \{1- \exp^{[-b(t-L)-c(\sqrt{t}-\sqrt{L})]}\}$, where Y = cumulative gas production (ml) at time t; A = the asymptotic gas production (ml); b and c = constant rates (h^{-1} and $h^{-1/2}$, respectively); t = incubation time (h) and L = lag time (h). Thyme oil additive at 3.75 mL/kg resulted in similar gas production compared to monensin (194.1 ± 3.3; 197.2 ± 1.1 mL, respectively) and in reduced ($P < 0.05$) gas production compared to either 1.25 mL/kg (209.8 ± 0.9 mL) or 2.50 mL/kg (211.0 ± 0.5 mL) of thyme oil. The fractional degradation rate (FDR) was reduced ($P < 0.05$) in the 2.5 and 3.75 mg/ml thyme oil treatments (0.045 ± 0.0007 h) compared to treatment with monensin (0.049 ± 0.0003 h), while the 1.25 mL/kg treatment (0.047 ± 0.0003 h) did not differ from any other treatment. Lag time was reduced ($P < 0.05$) in the monensin (1.16 ± 0.03 h) compared to the 3.75 mL/kg thyme oil treatment (2.26 ± 0.17 h), however no difference was detected among monensin, 1.25 mL/kg (1.66 ± 0.16 h) and 2.50 mL/kg (1.24 ± 0.17 h) of thyme oil. In conclusion, thyme oil may be an effective alternative to monensin for manipulation of rumen fermentation.

Key Words: thyme oil, rumen gases, sheep

SMALL RUMINANT II

1917 (W358) The effects of live yeast, glucan and mannan on performance, rumen and blood parameters of fattening lambs. O. Canbolat[1], I. Filya[1], V. Akay[*2] and A. Kamalak[3], *[1]University of Uludag, Faculty of Agriculture, Department of Animal Sciences, Bursa, Turkey, [2]Global Nutritech Biotechnology LLC, Richmond, VA, [3]University of Kahramanmaras Sutcu Imam, Faculty of Agriculture, Department of Animal Sciences, Kahramanmaras, Turkey*

The objective of this study was to evaluate the effects of a live yeast (*Saccharomyces cerevisiae* NCYC R618, $4x10^9$ CFU/g), glucan and mannan containing feed additive (Synerall (SYN), Global Nutritech Biotechnology LLC, Richmond, VA) on performance, and rumen and blood parameters of fattening ram lambs. Forty 4-mo old Kivircik ram lambs (29.58 ± 1.6 kg initial BW) were stratified and blocked by BW to 1 of 4 individually fed, isocaloric, isonitrogenous dietary treatments containing 0, 1, 2 or 4 kg SYN per ton of TMR on DM basis. Diets containing cracked barley, wheat and corn grains, sunflower meal, and premix were fed once daily for ad libitum consumption. Lambs were weighed on 21-d intervals, and the study continued 63 d. At the end of the study, rumen fluids and blood samples were collected. Dry matter intake and F:G ratio were similar among treatments ($P > 0.05$). Weight gain during the study was statistically significant among treatments ($P < 0.001$), and was highest in the 2 kg SYN per ton treatment. Daily weight gain was statistically significant among treatments ($P < 0.001$), and was highest in the 2 kg SYN per ton treatment. Rumen pH was statistically significant among treatments ($P < 0.001$), and was highest in the 2 kg SYN per ton treatment. Rumen ammonia N levels were statistically significant among treatments ($P < 0.001$), and was lowest in the 2 kg SYN per ton treatment. Total VFA, acetic acid and propionic acid percentages were also the highest in the 2 kg SYN per ton treatment. Rumen lactic acid levels were statistically significant among treatments ($P < 0.001$), and were lowest in the 2 and 4 kg SYN per ton treatments. Blood glucose levels were statistically significant among treatments ($P < 0.001$), and was highest in the 2 kg SYN per ton treatment. In conclusion, the addition of 2 kg Synerall per ton in fattening lamb diets increased weight gain and improved rumen and blood parameters.

Key Words: Synerall, yeast, glucan, mannan, weight gain, rumen parameters

1918 (W359) Effect of prostaglandin $F_{2\alpha}$ on fertility of ewes treated with a short-term progesterone-based estrous synchronization protocol. C. D. Paul*, *West Virginia University, Morgantown*

Previous studies have shown either no effect or a lower fertility in ewes treated with $PGF_{2\alpha}$ at the end of a short-term progesterone-based estrous synchronization (STPBES) protocol. The objective of this study was to further evaluate the effects of $PGF_{2\alpha}$ when used as a component of STPBES treatments in ewes. Ewes ($n = 423$) from 4 farms located in WV and PA were randomly assigned to receive controlled internal drug releasing devices (CIDR-g, 0.3 g progesterone) for 5 ($n = 243$) or 7 ($n = 180$) days. At insert removal, approximately half of the ewes in each treatment group were randomly assigned to received either 0 ($n = 203$) or 4 ($n = 220$) mL Lutalyse (20 mg dinoprost; $PGF_{2\alpha}$) and were joined with sexually mature rams. Data were analyzed using analysis of variance with the model consisting of the main effects of duration of treatment with CIDR devices, injection with $PGF_{2\alpha,}$ farms, and their interactions and additionally, least square means for treatment effects were determined. The mean estrous response was 82.2 ± 36.9% and was not affected by treatments. Conception rate ($P = 0.01$; 67.1 ± 4.0% vs. 52.9 ± 4.0%), pregnancy rate ($P < .01$; 58.1 ± 3.5% vs. 44.0 ± 3.3%) and proportion of ewes lambing to the first service ($P < .0001$, 45.8 ± 3.8% vs. 33.9 ± 3.9%) were higher in ewes that did not receive $PGF_{2\alpha}$ (CIDR devices alone) than in ewes treated with CIDR devices and $PGF_{2\alpha}$. Conception ($P = 0.01$; 67.1 ± 4.1% vs. 52.9 ± 3.9%) and pregnancy rates ($P < .0001$; 56.0 ± 3.1% vs. 46.2 ± 3.9%) were higher, and proportion of ewes lambing to the first service period ($P = 0.07$, 44.3 ± 3.9% vs. 35.4 ± 3.8%) tended to be higher in ewes treated with CIDR devices for 5 d compared to those treated for 7 d. In conclusion, injection of $PGF_{2\alpha}$ at insert removal in STPBES protocols did not increase estrous response and decreased fertility at the synchronized estrus.

Key Words: prostaglandin, ewes, fertility, progesterone

1919 (W360) Anthelmintic activity of selected aldehydes and ketones against sheep gastro-intestinal nematodes. E. Ortu[*1], G. Sanna[2], A. Scala[2], G. Pulina[1], P. Caboni[3] and G. Battacone[1], *[1]Dipartimento di Agraria, University of Sassari, Sassari, Italy, [2]Dipartimento di Medicina Veterinaria, University of Sassari, Sassari, Italy, [3]Dipartimento di Scienze della Vita e dell'Ambiente, University of Cagliari, Cagliari, Italy*

Ruminant gastrointestinal nematodes cause annually important economic losses to livestock production such as reduction of milk and meat yield. Because the resistance of parasites to conventional anthelmintic products is growing, studies evaluating the effectiveness of alternative products against gastrointestinal nematodes seem interesting. Compounds of botanical

origin are considered as an important source of secondary metabolites with anthelmintic activity. This study was performed to evaluate the nematicidal activity of aldehydes of plant origin such as furfural, 2-hydroxybenzaldehyde and (E,E)-2–4-decadienal and ketones such as 2-undecanone against gastrointestinal nematodes. Fecal samples were collected from the rectum of Sarda dairy ewes and worm eggs were identified by Mc Master technique, while the third stage larvae (L_3) of Strongyle type nematodes were obtained by coproculture after 10 d. Larvaes were identified as Haemonchus contortus (24,7%), Teladorsagia spp.(51,5%) and, Trichostrongylus spp. (23,8%). The larval development assay, by using Cellstar 96-well cell culture plates, was performed to evaluate the effects of the plant origin compounds against L_3 larvaes. For calculation of EC_{50} (mg/mL) inhibition effects, for the tested compounds on L_3 of gastrointestinal nematodes, the motility was assayed at concentration range of 0.28–5.99 mg/mL. Stock solutions were prepared in methanol whereas aqueous solution of tween (0.3% *v/v*) or 0.1 M phosphate- buffered saline solution (PBS) were used for further dilutions or as negative control. Each treatment consisted of 25 L_3 per well and was replicated six times. L_3 were analyzed after 1, 24, and 48 h with an inverted microscope 10x and were ranked into two categories: motile and immotile/paralyzed. The percentages of L_3 paralyzed were corrected by eliminating the natural death-paralysis in the negative control in according to the Schneider-Orelli formula. The 2-undecanone and (E,E)-2–4-decadienal showed the highest nematicidal activity with a $EC_{50/24h}$ = 0.88 and 1.03 mg/mL respectively, while for furfural and 2-hydroxybenzaldehyde this concentration reference was 1.83 and 2.19 mg/mL, respectively. The experimental data revealed in vitro dose- dependent anthelmintic activity. However, the in vitro promising effects against gastrointestinal nematodes have to be carefully evaluated under in vivo conditions.

Key Words: parasite infection, in vitro, sheep

1920 (W361) Ovine footrot gene marker screening in a Katahdin sheep flock. T. Wuliji*[1], J. G. Hickford[2], W. R. Lamberson[3], B. C. Shanks[1] and S. Azarpajouh[1], *[1]Department of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO, [2]Lincoln University, Lincoln, New Zealand, [3]University of Missouri, Columbia*

An extensive polymorphism at the DQA2 and DQA2-like loci located within the Major Histocompatibility Complex (MHC) in sheep have been identified and subsequently have been utilized to develop a gene marker testing procedures for footrot resistance. Although hair sheep breeds, such as Katahdin, are reputed to have better disease resistance, no genotypic markers have been reported for footrot resistance. The footrot gene-marker test reports five basic footrot scores (1, 2, 3, 4, and 5) corresponding to alleles of the MHC DQA2 and DQA2-like loci. This gives 15 possible score combinations (1,1; 1,2;... 4,5; 5,5), where 1,1 is claimed to have the highest resistance and 5,5 the lowest resistance to footrot infection. Blood samples were collected on FTA blood DNA collection paper cards from 600 Katahdin sheep and Katahdin crossbred ewes and rams from Lincoln University farms, Jefferson City, Missouri. DNA extraction and the gene marker test were performed at the Lincoln University Gene Marker Laboratory, Lincoln, NZ. Blood samples from 583 sheep with gene marker test results were analyzed. A chi-square test was used to test difference in variant alleles, animal genotypes, and score group distribution frequency. As footrot tolerance genes are assumed to exert a dominant effect, an expressed value for a pair of alleles was derived and animals were grouped into five categorical groups (1 to 5). Variant allelic distributions in 5 score groups were 10.0%, 21.2%, 45.3%, 17.6%, and 5.9%, respectively. Whereas, animals classed into five gene marker score groups were 18.5%, 33.3%, 42.0%, 5.8%, and 0.3%, respectively. Both allelic distribution and genotypic distributions were significantly ($P < 0.01$) different among the five gene marker score groups. The percentage of animals in the footrot tolerance score (1 and 2) was 52%, with a moderate score of 3 was 42%, and with scores of 4 and 5 were 6%. Therefore, by using footrot marker screening, the potential to select a high resistant flock is possible within three to five breeding seasons.

Key Words: Katahdin, footrot, DNA marker

1921 (W362) The effects of gonadotropic stimulation on fertility of progesterone-treated nulliparous ewes bred during seasonal anestrous. A. K. Redhead*, *West Virginia University, Morgantown*

Attempts to breed fall born ewe lambs and yearlings (nulliparous females) during seasonal anestrus have resulted in limited success. Low fertility in these nulliparous females may be related to a deficiency of ram induced gonadotropic release necessary to stimulate sufficient estrogen production to induce estrus. The objective of this study was to evaluate the effects of gonadotropic stimulation on fertility in nulliparous females bred out of season. Nulliparous females (N = 311) from 5 farms throughout WV and PA received progesterone using CIDR inserts (0.38 g progesterone) for 5 d before ram introduction between the months of April and July. At insert removal, females at each farm were randomly assigned to receive a single injection of gonadotropin containing 240 IU eCG and 120 IU hCG (GS: 3mL P.G. 600, Intervet, i.m) or to receive no further treatment (C). Pregnancy diagnosis was conducted using transrectal ultrasonography between Days 25–30 post ram introduction, at which time rams were removed, and a second pregnancy diagnosis was conducted 20–30 d later. Analysis of variance was conducted using the GLM procedures of SAS to evaluate the effects of gonadotropic stimulation, farm and their interaction, and the least square means were computed for reproductive performance variables. Gonadotropin treated females had higher estrous re-

sponse (P = 0.002, 72% ± 3.7 vs. 51% ± 4.0), conception rate (P = 0.0562, 68.3% ± 6.0 vs. 44.5% ± 11), pregnancy to the first service (P = 0.003, 66% ± 4.2 vs. 37% ± 4.4), proportion of females lambing to the first service period (P = 0.0051, 54.5% ± 4.4% vs. 34% ± 4.4%), proportion of females lambing (P = 0.0013, 54% ± 4.4 vs. 34% ± 4.4) and lambing rate (P = 0.0018, 77.6% ± 7.0 vs. 45.1% ± 7.0) than C females. The results of the current study indicate that inadequate gonadotropin stimulation or estrogen production might be limiting fertility in nulliparous ewes bred during seasonal anestrus. Further, supplementation with the gonadotropin combination, P.G. 600 at progesterone withdrawal significantly increased fertility of progesterone-primed nulliparous females when bred outside their normal breeding season.

Key Words: out of season, ewe lambs, yearlings, fertility, P.G. 600, gonadotropic stimulation

---

1922 (W363) Effects of hair sheep breed on performance response of ram lambs to artificial infection with *Haemonchus contortus*. Y. Tsukahara*, T. A. Gipson, S. P. Hart, L. J. Dawson, Z. Wang, R. Puchala, T. Sahlu and A. L. Goetsch, *American Institute for Goat Research, Langston University, Langston, OK*

Twelve Dorper (D; 4.5 ± 0.44 mo, 31.9 ± 1.75 kg), 18 Katahdin (K; 3.8 mo, 24.3 ± 0.76 kg), and 12 St. Croix (C; 4.5 ± 0.17 mo, 19.7 ± 0.99 kg) ram lambs were used to investigate among and within breed differences in the first year of a centralized test for growth performance and response to artificial infection with *Haemonchus contortus*. Rams were randomly selected from 3 commercial farms in Missouri and Oklahoma. The test at Langston University entailed an adjustment period of 2 wk followed by 8 wk of data collection. Breeds were housed separately in adjacent pens with automated feeders allowing free-choice access to a 15% CP (DM) and 50% concentrate pelletized diet. During adaptation, anthelmintic treatment resulted in low fecal egg count (FEC; < 550/g), after which 10,000 infective larvae were administrated orally. Packed cell volume (PCV) was measured weekly and FEC was determined 4 times in wk 6–8. For analysis, initial BW and FEC were covariates, and the logarithmic transformation ln(x + 2000) was used for mean FEC (MFEC). Variability in MFEC and mean PCV (MPCV) was homogenous among breeds. Breed affected ($P \leq 0.01$) DMI (2.5, 2.2, and 1.9 kg; SEM = 0.10), MFEC (3431, 1273, and 1241 eggs/g, original scale; SEM = 90.7), and MPCV (29.1, 29.7, and 32.9% for D, K, and C, respectively; SEM = 0.68). Residual feed intake (RFI), ADG, and ADG:DMI were similar ($P > 0.05$) among breeds. Rams were categorized into 3 groups within breeds based primarily on MFEC and MPCV (High, Medium, and Low resistance) using the cubic clustering criterion of SAS, which resulted in unbalanced numbers in the groups (5, 5, and 2 for D, 12, 5, and 1 for K, and 8, 1, and 3 for C, respectively). Group means were similar ($P > 0.05$) in ADG, DMI, and RFI but varied ($P < 0.05$) in MFEC (627, 2137, and 3302 egg/g; SEM = 109.7) and MPCV (32.3, 30.2, and 29.2% for High, Medium, and Low, respectively; SEM = 0.72). In conclusion, D appeared less resistant than C or K based on MFEC after an artificial challenge with *H. contortus* larvae in a standardized environment. However, variability in MFEC and MPCV within breed was sufficient to allow assignment to different classes for use in a breeding program to enhance flock resistance.

Key Words: internal parasitism, resistance, sheep

1923 (W364) Effect of sodium butyrate administered in the concentrate on rumen development and productive performance of lambs in intensive production system during the suckling and the fattening periods. S. Cavini[1], S. Iraira[1], A. Siurana*[2], A. Foskolos[1], A. Ferret[1], M. A. Gomez[3] and S. Calsamiglia[1], *[1]Animal Nutrition and Welfare Service, Universitat Autonoma de Barcelona, Bellaterra, Spain, [2]Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [3]Nutega/Novation, Madrid, Spain*

Sodium butyrate (SB) has been shown to improve growth rate, rumen development and health of calves. In intensive lamb production systems, the fattening period starts after a relative short suckling period, and lambs are fed a high concentrate diet. The aim of this experiment was to determine the effect of supplementing SB in the concentrate on rumen development and productive performance of lambs during the suckling and the fattening periods. During suckling, 66 Ripollesa-breed lambs were distributed with their mothers in 4 pens. Treatments were: control concentrate (CON), and concentrate supplemented with 3.6 g of SB (Butirex C4)/Kg of DM (SBC). At weaning, 9 lambs were slaughtered for sample collection and 10 were use for the herd replacement, and the remaining 47 lambs were distributed into 12 pens for the fattening period. Treatments were: 1) CON-CON for lambs fed CON in both periods; 2) CON-SBC for lambs fed CON in the suckling and SBC in the fattening period; 3) SBC-CON for lambs fed SBC in the suckling and CON in the fattening period, and 4) SBC-SBC for lambs fed SBC in both periods. At 88 d of age all lambs were slaughtered. In both periods, concentrate dry matter intake (DMI), average daily gain (ADG), body weight (BW), hot carcass weight (HCW), dressing percentage (DP), reticulum-rumen weight (RRW), rumen fluid pH, and density, length, width and keratinization of rumen papillae were measured. Feed conversion ratio (FCR) was calculated for the fattening period only. During the suckling period, SBC lambs had higher DMI (69.3 vs. 101.7 g ± 6.25), ADG (232.0 vs. 250.5 g ± 5.84), HCW (8.42 vs. 9.23kg ± 0.196) and DP (49.3 vs. 53.8% ± 1.04) ($P < 0.05$), and tended to have higher rumen papillae length (1.15 vs. 1.68 mm ± 0.168) and lower RRW (303.4 vs. 262.7 g ± 12.8; $P < 0.10$). During the fattening

period, no difference was found among treatments. Results indicate that the supplementation of SB in the concentrate improved rumen development and productive performance of lambs during the suckling period. However, at 3 mo of age, the administration of SB did not improve production in lambs reared in an intensive production system.

Key Words: sodium butyrate, lamb, rumen development, productive performance.

1924 (W365) Nutrients intake and performance of lambs fed diets with two levels of crude protein and concentrate.

R. S. Santos[1], K. G. Ribeiro[*2], O. G. Pereira[3], S. C. Valadares Filho[3], S. D. J. Villela[4], J. L. Silva[1] and P. G. F. Duarte[1], *[1]Federal University of Vicosa, Vicosa, Minas Gerais, Brazil, [2]Universidade Federal de Vicosa, Vicosa, Minas Gerais, Brazil, [3]Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil, [4]Federal University of Vales do Jequitinhonha e Mucuri (UFVJM), Diamantina, Brazil*

This study aimed to evaluate the dry matter (DMI), crude protein (CPI) and total digestible nutrients (TDNI) intake, the average daily gain (ADG), daily carcass gain in relation to body weight fasting (CG_{BWF}) and feed conversion (FC) of lambs fed diets containing two levels of concentrate (CONC) and two levels of crude protein (CP). Thirty-two intact Santa Ines x Texel lambs with an average body weight of 19 kg were used. They were distributed in a 2x2 factorial in a randomized block design with four treatments and eight replicates. The diets had 40 or 60% of CONC (plus corn silage as forage source) and 10.0 or 14.4% CP (high or low), in relation to the requirement of 12.5% CP according to the NRC (2007) for lambs with live weight of 20 kg and gains of 200 g/day. Feed was offered ad libitum to the animals at 8 h and 15 h. The offered and leftover feeds were weighed to estimate the daily DMI. The predetermined slaughter weight was 30 kg, when the animals were submitted to a solid fasting period of 16 h, and weighed again to determine the slaughter weight. The durations of the confinement varied from 50 (14.25% CP and 60% CONC) to 106 (10% CP and 40% CONC) days. The data were subjected to analyses of variance and F test at a 10% probability using the statistical program SAEG 9.1. There was no interaction effect on intake of nutrients, but there were independent effects of CP and CONC levels. Higher nutrients intake were recorded for lambs fed the higher CONC or CP levels, whose CP intakes of DM, CP and TDN were, respectively, 972.8 and 821.68, 79.46 and 142.56, and 603.56 and 711.63 g/day. Only ADW was affected by the interaction CP x CONC, with values of 0.090 (10% CP and 40% CONC) to 0.200 kg/day (14.25% CP and 60% CONC). The CP levels affected CG_{BWF} (0.059 vs. 0.106 kg) and FC (7.19 and 5.29) and CONC levels affected CG_{BWF} (0.066 and 0.098 kg) and FC (7.27 and 5.20). We concluded that diets with highest CP or concentrate levels resulted in greater nutrients intake and better animal performance.

Key Words: average daily gain, daily carcass gain, feed conversion

---

1925 (W366) Milk production, blood glucose, insulin and non-esterified fatty acids concentration in ewes fed diet containing crude glycerin.

D. M. Polizel[1], R. S. Gentil[1], E. M. Ferreira[1], R. A. Souza[1], M. V. C. Ferraz Jr.[2], M. C. A. Sucupira[3] and I. Susin[*1], *[1]Escola Superior de Agricultura Luiz de Queiroz- ESALQ/USP, Piracicaba, Brazil, [2]University of São Paulo- FMVZ/USP, Pirassununga, Brazil, [3]Faculdade de Medicina Veterinária e Zootecnia- FMVZ/USP, São Paulo, Brazil*

Crude glycerin is a glucogenic substrate in ruminants and can decrease symptoms of pregnancy toxemia. The objective in this trial was to determine the effects of partial replacement of corn by crude glycerin (CG) on dry matter intake (DMI), milk yield, milk composition and blood metabolites (glucose, insulin and non-esterified fatty acids) in periparturient ewes. One hundred and eighteen, 90 d pregnant, Santa Inês ewes were used. After lambing, 32 ewes (BW 62.8 ± 1.3 kg) were allotted in a randomized complete block design, defined by pre-lambing diet, sex and offspring number. Diets were isonitrogenous (13.0 ± 0.3% CP, DM basis), composed of 70% concentrate and 30% raw sugarcane bagasse and fed daily, "ad libitum". Crude glycerin (83.6% glycerol, DM basis) levels were zero or 10% (DM basis), corresponding to the experimental diets G0 and G10, respectively. From the second until the eight week of lactation dry matter intake was determined. In the same period, once a week, the ewes were separated from the lambs and mechanically milked after intravenous administration of 10 IU of synthetic oxytocin. Three hours after the first milking, the ewes were milked again and milk production and composition were determined. Glucose and NEFA were measured at -14, −7, 0, 7, 14, 28, and 56 d relative to lambing and insulin at -14, −7, 0, and 7 d. Data were analyzed as repeated measures over time using the MIXED procedure (SAS Inst. Inc.). The LSMEANS option was used to obtain the means. Crude glycerin did not affect ($P > 0.05$) DMI (2.2; 2.2 kg/d) and milk production (168.6; 164.7 g/3 h). However, there was a decrease ($P = 0.01$) in milk fat percentage (8.0 vs. 7.0%). Ewes fed diets with glycerin had decreased ($P < 0.01$) NEFA concentration (0.27 vs. 0.18 mEq/L). Glucose (61.8 vs. 67.6 mg/dL) and insulin (10.8 vs. 15.5 µIU) were not affected by treatments, but there was an interaction between treatment x week ($P < 0.05$). Crude glycerin increased glucose (101.2 vs. 133.7mg/dL) and insulin concentration (10.5 vs. 24.5 µIU) at parturition. Crude glycerin can partially replace corn without affecting DMI, milk yield and milk composition. Crude glycerin improves energy balance of periparturient ewes.

Key Words: glycerol, free fatty acids, NEFA

1926 (W367) Apparent digestibility, rumen metabolism and nitrogen balance in lambs fed high-concentrate diets containing increasing levels of ground cottonseed. R. A. Souza[1], R. S. Gentil[1], E. M. Ferreira[1], D. M. Polizel[1], A. P. A. Freire*[1], J. A. Faleiro Neto[2] and I. Susin[1], *[1]Escola Superior de Agricultura Luiz de Queiroz- ESALQ/USP, Piracicaba, Brazil, [2]Faculdade de Medicina Veterinária e Zootecnia- FMVZ/USP, São Paulo, Brazil*

The objective in this trial was to determine the effects of feeding ground cottonseed (GCS) on apparent digestibility, rumen metabolism and nitrogen balance. Five ram lambs, Dorper x Santa Inês (45.2 ± 0.8 kg), cannulated in the rumen, were allotted in a 5x5 Latin Square design. Each experimental period lasted 22 d, 17 d for adaptation and 5 d for sampling. Diets were isonitrogenous (15% CP, DM basis) and composed of 90% concentrate and 10% coastcross hay. Treatments were defined by the levels of GCS inclusion: 0, 7, 14, 21 or 28% (DM basis). Diets were fed ad libitum and total feces and urine were collected. On the last day of sampling, the rumen content was sampled every 2 h during 12 h, starting before feeding. The data were analyzed as repeated measures over time by using the MIXED procedure (SAS Inst. Inc.) The LSMEANS option was used to generate individual diet means. Orthogonal polynomials for diet responses were determined by linear, quadratic, and cubic effects. Apparent digestibilities of DM (80.7, 77.3, 79.2, 76.2 and 74.4%), OM (82.3, 78.8, 80.8, 77.7 and 76.2%), CP (81.4, 80.9, 81.8, 79.3 and 79.7%) and NFC (89.4, 82.6, 84.0, 78.8 and 80.7%) were linearly reduced ($P < 0.05$) and EE (89.7, 93.3, 94.4, 95.0 and 93.7%) was linearly increased ($P < 0.05$) while NDF was not affected. Total SCFA (90.5, 95.7, 96.5, 83.4 and 71.7 mM) and propionate (35.1, 34.5, 36.4, 31.4 and 24.7 mM) had quadratic response ($P < 0.05$) with higher values for the inclusion of 14%. Acetate (47.4, 50.4, 47.8, 43.3 and 38.4 mM) had a linear decrease ($P < 0.05$) and pH (5.4, 5.5, 5.4, 5.6 and 5.7) showed a linear increase ($P < 0.05$). Isobutyrate, butyrate, acetate:propionate ratio and ammonia were not affected ($P > 0.05$). Nitrogen intake and excretion were linearly reduced ($P < 0.05$) resulting in no effect on retained nitrogen ($P > 0.05$). The inclusion of GCS affected negatively DM, OM, CP and NFC apparent digestibilities. Propionate and SCFA were higher with the inclusion of 14% of GCS.

Key Words: co-product, SCFA, rumen ammonia nitrogen

1927 (W368) Intake and performance of finishing lambs fed diets with licuri nut (*Syagrus coronata*) cake. R. L. Oliveira*, J. B. Costa, T. M. Silva, M. S. Borja, M. D. C. Magalhães, A. D. S. Nunes, C. B. D. Pellegrini, W. F. D. Souza and N. G. D. N. Júnior, *Universidade Federal da Bahia, Salvador, Brazil*

The objective of this study was to determine the impact of including licuri nut (*Syagrus coronata*) cake in the diet of crossbred Santa Inês finishing lambs on their intake and performance. Forty-four vaccinated and vermifuge-treated non-castrated lambs aged on average 6 mo and with an average weight of 21.2 kg ± 2.7 were fed equal proportions of roughage (Tifton 85 grass hay) and a concentrate mix composed of corn meal, soybean meal, 1% urea, vitamin-mineral premix, and inclusion of licuri cake at the levels of 0, 8, 16, and 24% in substitution of the soybean meal and corn meal in isonitrogenous diets, these levels being the treatments. Animals were confined in individual stalls for 70 d, fed twice daily, and weighed at the beginning and end of the experiment to calculate weight gain and feed conversion. Samples of feed and orts were collected to determine the intakes of dry matter (DM), crude protein (CP), ether extract (EE), non-fibrous carbohydrates (NFC) and total digestible nutrients (TDN). The data were adjusted to regression analysis, using the SAS 9.1 (2004) statistical software. The increase in the inclusion level of licuri cake led to a linear decrease in DM intake ($\hat{Y} = -21.352\ X + 1312$; $P < 0.001$), with reduction of 39% between the level with 0 and 24% of cake, respectively. Probably this reduction may be was associated with the elevation in NDF content, thereby demonstrating a considerable elevation in ADF representing the accrual in the lignin fraction, linked to decrease in NFC. The decrease in the intakes of CP, NFC and TDN is a consequence of the drop in DM intake. On the other hand, EE intake was quadratically affected ($\hat{Y} = -0.0551\ X^2 + 1.4271\ X + 31.967$; $P < 0.05$), increasing until addition of 12.95% of licuri cake, and reducing from this point. The average daily gain decreased linearly ($\hat{Y} = -0.004x + 0.218$; $P < 0.0001$) as the licuri cake was added. This decrease is mainly related to the drop in CP and TDN intakes. Feed conversion was not affected by the proposed levels. Including licuri cake reduces the intake and performance of the animals and the decision of whether or not to use it in the feeding of lambs will depend on the cost and economic return.

Key Words: intake, sheep, weight gain

1928 (W369) Growth and carcass characteristics of lambs fed high-concentrate diets containing different sources of non-protein nitrogen.

A. P. A. Freire*[1], F. L. M. Silva[1], D. M. Polizel[1], R. A. Souza[1], R. S. Gentil[1], R. C. Araujo[2] and I. Susin[1], *[1]Escola Superior de Agricultura Luiz de Queiroz- ESALQ/USP, Piracicaba, Brazil, [2]GRASP Ind. & Com. LTDA, Curitiba, Brazil*

Nitrate supplements can be used as non-protein nitrogen (NPN) in ruminant diets. The interest in this NPN source is due to its capability of reducing methane emissions. Forty-four Dorper x Santa Inês lambs (initial BW 21.05 ± 2.65 kg and 79 ± 5 d old) were used in a randomized complete block design, according to initial BW and age, to determine the effects of supplementing urea or calcium nitrate on growth and carcass characteristics. Lambs were penned individually during 56 d and fed an isonitrogenous (16% CP, DM basis) total mixed ration composed of 80% concentrate and 20% coastcross hay. The experimental diets were: C (control, with soybean meal), U (1.1% urea), NEN (2.65% non-encapsulated calcium nitrate) and EN (3.0% encapsulated calcium nitrate). Diets containing nitrate were formulated to have the same content of NO^{3-} (DM basis). Urea was added to have the same crude protein equivalent as nitrate. In the first week of feeding a gradual adaptation period was used to avoid toxic effects of nitrate or urea. Data were evaluated using orthogonal contrasts. The first contrast was the C vs. non-protein nitrogen (NPN), the second contrast was U vs. calcium nitrate (U vs. CN) and the third was formed by NEN vs. EN. The control animals had greater ($P < 0.01$) ADG (389, 355, 345, and 346 g for C, U, NEN and EN, respectively) and feed efficiency (gain:feed = 0.286, 0.265, 0.269 and 0.264 for C, U, NEN and EN, respectively) compared with NPN. However, there was no difference ($P > 0.05$) between U vs. CN and NEN vs. EN. Dry matter intake (1.37, 1.35, 1.29 and 1.32 kg/d for C, U, NEN and EN, respectively) and carcass characteristics (dressing percentage, longissimus muscle area, back fat thickness and body wall thickness) were unaffected ($P > 0.05$) by the experimental diets. Lambs fed 2.65% non-encapsulated or 3% encapsulated calcium nitrate have similar performance and carcass characteristics of lambs fed 1.1% urea.

Key Words: calcium nitrate, urea, sheep

1929 (W370) Zilpaterol hydrochloride modify the fatty acids profile of intramuscular fat of feedlot lambs.

H. Dávila-Ramos* and J. C. Robles-Estrada, *Universidad Autonoma de Sinaloa, Culiacan, Mexico*

The objective of this study was to determine the effects of dietary zilpaterol hydrochloride supplementation on fatty acid profile of lambs´s intramuscular fat. Forty crossbred male lambs (37.7 ± 0.67 kg) were used in a 43-d feeding trial (5 pens per treatment in a randomized complete block design). Lambs were fed with finishing diet (2.57 Mcal/kg of ME) containing cracked corn 60%, sudangrass hay 16%, soybean meal 12%, molasses 9.5%, and mineral premix 2.5%, twice daily. Animals were randomly allotted to pens (6 m^2) with full shade and ad libitum water. Treatments were: 1) control, no zilpaterol supplementation (ZIL-0); 2) zilpaterol for 20 d (ZIL-20); 3) zilpaterol for 30 d (ZIL-30); and 4) zilpaterol for 40 d (ZIL-40). Zilpaterol was supplemented at a rate of 0.20 mg/kg of live weight d^{-1} (as zilpaterol hydrochloride, Zilmax, Intervet México, México City). Twenty *Longissimus dorsi* muscle samples (50 g, five per treatment) were collected from left side carcass of twenty crossbred male lambs (Pelibuey × Katahdin, 50.3 ± 3.83 kg final live weight). The muscle samples were frozen (-18°C) and transported to laboratory for fatty acids analysis. Samples were thawed (4°C) and ground to homogenize them. Modified method (Folch et al.,1956) was used for lipid extraction from the muscle samples. The fatty acid composition was determined with gas chromatography (Varian, USA) and column (SP TM-2560 Fused Silica Capilary Column) 100 × 0.25 mm × 0.2 mm filmthickness and flame ionization detector. The results were analyzed with a completely randomized design, comparing means of treatments with orthogonal contrasts and orthogonal polynomials. Zilpaterol hydrochloride supplementation decrease 3.2% ($P = 0.01$) estearic fatty acid, and increase ($P = 0.06$) 3.6% linoleic fatty acid of intramuscular fat. ZIL-30 improved fatty acids profile with respect ZIL-20, reducing the level of estearic fatty acid (4.6%; $P < 0.01$) and increased linoleic (5.2%; $P = 0.06$) and araquidonic fatty acids (1.8; % $P = 0.07$). The results indicated that zilpaterol hydrochloride supply until 40 d reduced ($P = 0.01$; linear component) estearic fatty acid proportion and increased ($P \leq 0.05$) linoleic and araquidonic fatty acids. However, the oleic fatty acid present in greater proportion was not modified by zilpaterol supplementation. Zilpaterol hydrochloride supplementation resulted in increasing the levels of polyunsaturated fatty acids and a reduction in the levels of saturated fatty acids.

Key Words: zilpaterol chlorhidrate, fatty acids, lambs

1930 (W371) Composition of cheeses made from milk of ewes fed with soybean seed or linseed concentrates.

C. F. A. M. Penna*[1], M. I. Simão[2], F. P. Paula[3], M. O. Leite[1], M. P. Cerqueira[1], L. M. Fonseca[3], M. R. Souza[1] and I. Borges[3], *[1]Universidade Federal de Minas Gerais (School of Veterinary Medicine), Belo Horizonte, Brazil, [2]Universidade Federal de Minas Gerais (Veterinary School/UFMG), Belo Horizonte, Brazil, [3]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil*

High solids, fat and protein contents of sheep's milk render it an attractive option for production of exclusive cheeses. However, this activity is still being structured in Brazil. The objective of the present work was to evaluate the composition and yield of cheeses produced with milk obtained from sheeps

fed diets containing soybean seed or linseed. Twenty-eight Lacaune, Santa Inês and crossbreeds sheep were allocated to two equal groups according to the diet. The milk obtained from each experimental group was used for cheese manufacture, and samples of this milk and whey were collected for laboratorial analyses and to complement cheese yield determination. The cheeses were aged for 30 d under low temperature storage (10–12°C), and analyzed for determinations of fat, protein, moisture and total solids contents. The data was evaluated using SNK test at 5% of significance. No influence of the diets on milk and whey composition was found ($P > 0.05$). Similarly, no difference was found for cheese yield and composition in both treatments and the general values observed were: yield of 26.9% (3.77 L/kg), moisture (42.6%), total solids (57.2%), fat (26.2%), protein (22/1%), and fat in dry matter (FDM) (45.8%). It is concluded that choice of the best concentrate to be used for sheep milk production should be based on diet cost, since the option of soybean seed or linseed did not affect cheese yield and composition.

Key Words: cheese composition, diet, cheese yield

1931 (W372) Pregnancy and lambing rates in anestrous ewes bred to a new synchronization protocol and laparoscopic timed artificial insemination (TAI).

S. B. Turner*[1], M. B. Gordon[1], T. Gowan[2], J. A. Small[2] and D. M. W. Barrett[1], *[1]Faculty of Agriculture, Dalhousie University, Truro, NS, Canada, [2]Agriculture and Agri-Food Canada, Truro, NS, Canada*

Reproductive performance in seasonally anestrous ewes is poor even after the application of conventional controlled breeding techniques. Estradiol-17β (E_2) has been shown to synchronize follicular wave emergence in anestrous ewes treated for 12 or 14 d with a medroxyprogesterone acetate sponge. The objective of this study was to determine the effects of an E_2 treatment administered 6 d after CIDR insertion on E_2 concentrations, estrus, pregnancy rates, and lambing rates in ewes bred out of season. Ewes from three farms (Farm A: $n = 22$; Farm B: $n = 48$; Farm C: $n = 28$) received CIDRs (Day −12) followed by an injection of eCG (500 IU; Day 0) at CIDR removal and an injection of sesame oil without (1 mL; Control) or with E_2 (350 µg; Day −6) 6 d before CIDR removal. Treatments were balanced for breed, age, parity, and BCS. Blood samples were taken from half of the ewes on Day −6 and 0 to determine E_2 concentrations. On Day 1 ewes were exposed to rams to observe estrus. Ewes were subjected to laparoscopic TAI on Day 2. Pregnancy was diagnosed by transabdominal ultrasonography on Day 50. Estrus, pregnancy rates, and lambing rates were analyzed using logistic regression. Day of lambing and E_2 concentrations were analyzed using ANOVA. The percent of ewes observed in estrus within 36 h of CIDR removal was similar between treatments (E_2: 24.5%; Control: 34.7%; $P > 0.05$). Pregnancy rates were similar between treatments (E_2: 40.8%; Control: 40.8%; $P > 0.05$) and were higher on Farm C than Farm B (Farm A: 45.5%; Farm B: 22.9%; Farm C: 67.9%; $P < 0.05$). Lambing rates were also similar between treatments (E_2: 34.7%; Control: 34.7%; $P > 0.05$) and were higher on Farm C than Farm B (Farm A: 40.9% Farm B: 16.7%; Farm C: 60.7%; $P < 0.05$). Relative to CIDR removal, ewes lambed earlier on Farm B (Farm A: 141.7 ± 1.3 d; Farm B: 136.6 ± 1.4 d; Farm C: 143.2 ± 0.9 d; $P < 0.05$) and ewes treated with E_2 lambed earlier (E_2: 138.9 ± 1.0 d; Control: 142.2 ± 1.0 d; $P < 0.05$). Concentrations of E_2 were similar between treatments on Day −6 (E_2: 1.5 ± 0.1 pg/mL; Control: 1.6 ± 0.1 pg/mL; $P > 0.05$) and Day 0 (E_2: 1.6 ± 0.1 pg/mL; Control: 1.3 ± 0.1 pg/mL; $P > 0.05$). Differences were mainly observed among farms potentially due to differences in breed, BCS, semen, or management practices. The addition of an E_2 treatment during a CIDR-eCG heat synchronization protocol does not clearly increase pregnancy and lambing rates in seasonally anestrous ewes.

Key Words: anestrus, ewes, controlled breeding

1932 (W373) Effect of supplementation with water-washed neem fruit and/or yeast on the performance and digestibility of west african dwarf sheep.

M. K. Adewumi* and T. O. Ososanya, *University of Ibadan, Ibadan, Nigeria*

This experiment was conducted to determine the performance of rams fed diets supplemented with water-washed neem (Azadirachta indica) fruits with or without yeast (*Saccharomyces cerevisiae*). Sixteen West African Dwarf (WAD) rams with an average weight of 14.41 (s.d = 2.54kg) were assigned to one of four diets with 4 animals per diet in a complete randomized design. The diets were: a total mixed ration (A); B (A plus 5.0 g of baker's yeast per animal per day); C (A plus 5.0% water-washed neem fruit inclusion in the diet); and D (A plus 5.0% water-washed neem fruit inclusion in the diet and 5.0 g of yeast per animal per day). The animals were fed at 5% body weight. At the end of the 56-d feeding trial, three animals per treatment were moved into individual metabolic cages. Average daily gain was higher ($P < 0.05$) in the D (120 g) compared to the other diets. Average daily dry matter intake (g) in C (929.58) and D (958.62) was similar ($P > 0.05$) but higher ($P < 0.05$) than B (839.32). The feed conversion ratio for A (10.05) was similar ($P > 0.05$) to B (11.99) and C (11.61) but higher ($P < 0.05$) than D (7.99). The digestibility of dry matter, crude protein and ash were similar ($P > 0.05$) for A, B and C. However, there was a significant difference between A and D. There was no significant ($P > 0.05$) difference in the digestibility of neutral detergent fibre, acid detergent fibre and cellulose of A and B. The metabolizable energy intake and the digestibility of organic matter was not different ($P > 0.05$) among B, C and D but were higher($P < 0.05$) than A. The nutrients digestibility of D was consistently higher ($P < 0.05$) than A except for ether extract and hemicelluloses components. Water-washed neem fruits significantly ($P <$

0.05) increased nitrogen intake (g) in C (14.02) and D (14.76). Nitrogen retention (g) was higher ($P < 0.05$) for D (11.32) than for A (5.47), B (6.49) and C (8.78), respectively. These results suggest a positive synergic effect of baker's yeast and water-washed neem fruit on the performance characteristics, digestibility and nitrogen retention of WAD rams.

Key Words: baker's yeast, water-washed neem fruit, nitrogen retention

---

1933 (W374) Effect of crude protein level and zilpaterol supplementation on growth performance and carcass dressing of finishing hairy lambs.

A. E. Angulo[*1], I. C. Perez[1], A. Plascencia[2], H. L. Lopez[1], P. M. Peraza[1], E. I. Gonzalez[1] and F. G. R. Rincon[1], *[1]Universidad Autonoma of Sinaloa, Culiacan Sinaloa, Mexico, [2]UABC, Mexicali, Mexico.*

Forty Pelibuey × Katahdin (37.66 ± 2.2 kg) crossbred intact male lambs were used to evaluate the interaction of two dietary protein levels (15 and 18% CP) and two dietary zilpaterol (ZH) levels (0 and 6 mg/kg of feed) on growth performance and carcass dressing. Lambs were equally grouped by weight into five uniform weight groups and assigned to 5-pen blocks (two lambs per pen). The experiment lasted 30 d. Low protein and high protein diets contained 2.92 and 2.89 Mcal ME/kg, respectively. Treatments were: 1) Low protein-no ZH (LP-0); 2) Low protein-ZH supplementation (LP-ZH); 3) High protein-no ZH (HP-0), and 4) high protein-ZH supplementation (HP-ZH). No interactions were detected between protein level and ZH supplementation. Protein level did not affect ($P > 0.05$) dry matter intake or ADG, but low-protein diets tended to increase ($P = 0.08$) feed efficiency and carcass dressing; however, the latter could be more by the slight difference on energy concentration between LP and HP diets (2.92 vs. 2.89) rather than protein level per se. ZH supplementation did not affect DM intake, but increased ADG (13.8%, $P < 0.05$) and feed efficiency (16.2%, $P < 0.05$) with no effects on carcass characteristics. The Increases on protein level of diet from 15 to 18% did not improve the response to ZH supplementation.

Key Words: zilpaterol clorhidrate, CP level, pelibuey sheep

1934 (W375) Performance of lambs fed with crude glycerin diets.

V. B. Carvalho[*1], J. M. Bertocco Ezequiel[2], R. F. Leite[1], S. F. F. Petrorossi[3], T. R. Delphino[3], H. L. Perez[3], J. R. Paschoaloto[3], M. T. C. Almeida[3], V. R. Favaro[4] and E. H. Fernandes[3], *[1]UNESP, Univ Estadual Paulista, Department of Animal Science, Jaboticabal, SP, Brazil, [2]UNESP, Jaboticabal, Brazil, [3]UNESP, Univ Estadual Paulista, Department of Animal Science, Jaboticabal, Brazil, [4]State University of Sao Paulo, Jaboticabal, Brazil*

The objective of this trial was to evaluate the effect of total corn replacement by crude glycerine (CG) on performance of feedlot lambs. Forty Santa Ines intact males lambs were used with initial BW of 22.9 ± 4.10 kg, assigned in a completely randomized block. Diets consisted of Tifton-85 hay, corn, crude glycerin (83% glycerol), corn gluten meal, corn oil, urea, sunflower meal, soybean hulls and mineral. The diets presented 18% of roughage and 82% of concentrate. Five treatments were used: 0% CG, 7.5% CG, 15% CG, 22.5% CG and 30% CG on dry matter basis. The animals were housed in individual pens with free access to water. The feed intake of animals were adjusted to ensuring 10% daily feed leftovers (ad libitum). The diets were offered twice daily at 0700 and 1600 h with 50% of total in each meal. Weekly before feeding, the animals were weighed to evaluate of BW gain. The DMI, days in feedlot, average daily gain (ADG) and feed efficiency (FE) were calculated at the end of the experiment. The data were analysed using the MIXED procedure of SAS and the treatments were compared using orthogonal contrasts (linear and quadratic) considering 5% significance level. There was no difference treatments among the variables measured ($P > 0.05$). On average, the animals presented 73 d in feedlot and 37.85 ± 1.42 kg final BW. The DMI in average was 1.35 kg d^{-1}, 0.21 kg d^{-1} of ADG and 0.15 kg of FE (kg of gain per kg of DMI). These results indicated that the use of the diets containing high concentrations of glycerin did not affect negatively the dry matter intake and animal performance.

Key Words: byproducts, feed efficiency, feedlot

1935 (W376) Sexual response of anovulatory Dorper X Pelibuey nullip arous and nulliparous and multiparous ewes exposed to males + estrogenized females. M. D. L. A. De Santiago*, *Universidad Autonoma Agraria Antonio Narro, Torreon, Mexico*

The aim of this study was to determine whether the stimulus exerted by the presence of males + estrogenized females, promotes both estrus (EA) and ovulatory activity (OA) in anestrous ewes in northern Mexico, (26°N). The study was conducted in April during the natural sheep anestrous season at this latitude. Sheep ewes (n = 104) were isolated from males 2 mo before the beginning of the experiment. All females were subjected to evaluation of ovulatory activity by transrectal ultrasonography (Aloka SSD- 500) on days -21, -14 and −7, and all of them were classified as anovulatory. To synchronize reproductive activity, each ewe was treated with an intravaginal sponge impregnated with fluorogestone acetate (FGA; Chronogest CR; Intervet) on days −9 to -2. Thereafter, on Day 0, 50 nulliparous and 54 multiparous females were randomly assigned to four experimental groups: two groups of nulliparous (Stimulated Nulliparous, SN; n = 25, and Non Stimulated Nulliparous NSN; n = 25) with similar body weight; 30 ± 1.1 Kg and body condition; 2.9 ± 0.1) and two groups of multiparous (Stimulated Multiparous, SM; n = 24, and non stimulated multiparous; NSM n = 30), with similar body weight; 42 ± 1.0 kg and body condition 3.2 ± 0.1. Males and females were fed with rolled corn, sorghum, wheat and sorghum silage. On March 19 (Day 0) each group of the stimulated females (SN and SM) was exposed to two inactive males (3.0 ± 0.1 BCS; scale 1–4) and 5 estrogenized females, (2 mg estradiol cypionate IM every third day). In the same way, each group of the non-stimulated females (NSN and NSM) was exposed to two inactive males and 5 non estrogenized females. Rams were alternated between groups, and remained in contact during 15 d. Experimental groups were placed at a distance of approximately 100 m from each other. EA was recorded twice daily (AM and PM) and OA by ultrasonographic scanning, observing the presence of corpora lutea, on d 16. EA and OA were compared using Chi^2 test (MYSTAT 12). The percentage of multiparous ewes depicting estrus [SM (63); NSM (60)] was greater ($P < 0.05$) regarding nulliparous [SN (0); NSN (16)]. The same was true with respect to ovulation, favoring ($P < 0.05$) to the multiparous group [SM (75); NSM (57)] with respect to nulliparous [SN (4) and NSN (25)]. Therefore, multiparous ewes depicted a greater ability to respond to male effect than nulliparous, regardless the presence or not of estrogenized females.

Key Words: Ewes, sexual activity, female effect

1936 (W377) Feeding behavior of feedlot lambs fed with high levels of crude glycerin. V. B. Carvalho*[1], J. M. Bertocco Ezequiel[2], R. F. Leite[1], S. F. F. Petrorossi[3], T. R. Delphino[3], M. T. C. Almeida[3], J. R. Paschoaloto[3], H. L. Perez[3], V. R. Favaro[4], E. M. Oliveira[3] and A. P. D`Aurea[3], *[1]UNESP, Univ Estadual Paulista, Department of Animal Science, Jaboticabal, SP, Brazil, [2]UNESP, Jaboticabal, Brazil, [3]UNESP, Univ Estadual Paulista, Department of Animal Science, Jaboticabal, Brazil, [4]State University of Sao Paulo, Jaboticabal, Brazil*

The objective of this trial was to evaluate the effect of crude glycerin (CG) inclusion on feeding behavior of feedlot lambs. Forty Santa Ines intact males lambs were used with initial BW of 22.9 ± 4.10 kg, assigned in a completely randomized block. Diets consisted of Tifton-85 hay (Cynodon dactylon), corn, crude glycerin (83% glycerol), corn gluten meal, corn oil, urea, sunflower meal, soybean hulls and mineral. The diets presented 18% of roughage and 82% of concentrate. The CG used is a byproduct from biodiesel originated from vegetable oils of soybean and sunflower. Five treatments were used: 0% CG, 7.5% CG, 15% CG, 22.5% CG and 30% inclusion of CG on dry matter basis, whereas, the diet with 30% of CG promoted a total replacement of corn. The animals were housed in individual pens with free access to water. The feed intake was adjusted to ensuring 10% of orts (ad libitum). The diets were offered twice daily at 0700 and 1600 h with 50% of total in each meal. Feeding behavior was performed during 48 h by 2 trained observers that made visual observations every 5 min of feeding, drinking, ruminating, resting and other activities. Further, the ruminating efficiency was determined. The means of 2 d were calculated expressed in 24 h. The data were analyzed using the MIXED procedure of SAS and the treatments were compared using orthogonal contrasts (linear and quadratic) considering 5% of significance level. There was no difference treatments among the variables measured ($P > 0.05$). The exception was drinking activity that showed a quadratic response ($P = 0.04$). On average, the animals presented 16.6 min drinking, 234.4 min eating, 428 min ruminating, 535 min resting and 226.8 in other activities. The ruminating efficiency was 325 (min of ruminating/kg DMI). In conclusion, crude glycerin in feedlot lambs influences only time spent drinking.

Key Words: animal nutrition, biodiesel, feed intake

SWINE SPECIES: SWINE SPECIES REPRODUCTION AND MANAGEMENT

1937 (M383) Dietary supplementation with organic or inorganic selenium and pyridoxine in gilts on gene expression in the porcine expanded blastocysts in vivo. D. Bueno Dalto[*1,2], S. Tsoi[3], I. Audet[1], M. Dyck[3] and J. J. Matte[1], *[1]Agriculture & Agri-Food Canada, Sherbrooke, QC, Canada, [2]Department of Animal Science, Universidade Estadual de Londrina, Londrina, Brazil, [3]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*

This study aimed to determine the effect of dietary selenium (Se) and pyridoxine supplementation, in gilts, on gene expression in the porcine expanded blastocyst (PEB). Eighteen gilts were randomly assigned to one of the 3 experimental diets: 1) basal diet (natural Se content of 0.2 mg/kg) without supplemental Se or pyridoxine (CONT, $n = 6$); 2) basal diet + 0.3 mg/kg of feed of sodium selenite, and 10 mg/kg of feed of hydrochloride pyridoxine ($MSeB_6$10, $n = 6$); and 3) basal diet + 0.3 mg/kg of feed of Se-enriched yeast, and 10 mg/kg of feed of hydrochloride pyridoxine ($OSeB_6$10, $n = 6$). All gilts were inseminated at their fifth estrus, and sacrificed 5 d after. Both uterine horns were flushed for embryo harvesting. Expanded blastocysts were selected for the porcine embryo-specific microarray: direct comparisons were done for $MSeB_6$10 vs. CONT and $OSeB_6$10 vs. CONT, whereas a reference design comparison were used for $OSeB_6$10 vs. $MSeB_6$10. Data were analyzed according to a randomized arrangement of treatments in blocks with the 3 dietary treatments as the main independent variables. Microarray data were analyzed using FlexArray, with threshold fold change $\geq$ 1.7 and P-value $\leq$ 0.05. CONT had lower blood Se concentration than Se-supplemented gilts ($P < 0.01$), but no differences were found between Se sources ($P = 0.38$). CONT had lower pyridoxine concentrations than $B_6$10 gilts ($P < 0.05$). Plasma glutathione peroxidase (GSH-Px) activity tended to increase during the experimental period ($P < 0.06$), but no treatment effect was detected ($P = 0.57$). $MSeB_6$10 vs. CONT and $OSeB_6$10 vs. CONT respectively showed 24 and 446 differentially expressed genes, whereas the corresponding number was 190 for $OSeB_6$10 vs. $MSeB_6$10. No specific biological processes were affected using Gorilla gene list analysis in $MSeB_6$10, however $OSeB_6$10 stimulated protein folding but not selenoprotein synthesis. Although all associated genes for GSH-Px and other selenoprotein synthesis were found, none of them were differentially expressed in any comparison. Antioxidant genes such as glutaredoxin-3 (GLRX3), peroxiredoxin-4 (PRDX4) and coenzyme Q6 monooxygenase (COQ6) were up-regulated in $OSeB_6$10 vs. CONT, and thioredoxin and thioredoxin domain containing 17 were downregulated in $OSeB_6$10 vs. CONT and $OSeB_6$10 vs. $MSeB_6$10, respectively. GLRX3, PRDX4 and COQ6 expression were validated by real-time PCR. In conclusion, $OSeB_6$10 affects PEB metabolism more markedly than $MSeB_6$10. Although supplements of both Se sources and pyridoxine did not influence GSH-Px -related genes expression in the PEB, they are involved with other antioxidant enzymes regulating antioxidant defense and cell proliferation, at this stage.

Key Words: porcine embryo, selenium, gene expression

1938 (M384) Comparing the growth curves of females and immuno castrated males in commercial conditions. S. López-Vergé[*1], G. Ibanez[2] and J. Gasa[1], *[1]Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Globosuinos Agropecuária S/A, Paraná, Brazil*

Concerning pigs, intact males grow faster than females; inversely, surgically castrated males perform worse than females. Immuno castration appears as an alternative to surgical castration in pigs, since it features less detrimental effects on growth and guarantees the full preservation of animal welfare conditions. The objective was to compare the growth curve parameters obtained from females and immuno castrated males, reared in commercial conditions. The experiment lasted 105 d and 168 piglets from 6 commercial white genetic lines (28 piglets each) were selected at the end of the nursery period (24.8 kg ± 5.10 kg BW). Animals were allocated to a growing-finishing facility and segregated by sex (males and females). Pigs were fed with up to 6 consecutive different corn-soybean diets in a controlled ad libitum way and ractopamine (10 ppm) was added as a feed additive 28 d before slaughtering. A total of 166 animals finished the experiment (124.4 kg ± 6.20 kg BW). Males were immuno castrated by giving them 2 doses of vaccine Vivax (Zoetis) around 56 and 28 d before slaughtering. Pigs were weighed weekly individually (up to 15 times) and data was adjusted using the double exponential Gompertz model (Live Weight = A*exp(-exp(b-(c*t))); the resulting growth parameters were statistically analyzed by ANOVA. Immuno castrated males had greater ADG (mean values of 1070 vs. 997 g/d, $P < 0.001$) and tended to have a better G:F (441 vs. 428 g of growth/kg feed, $P = 0.076$) than females. Immuno castrated males, compared with females, had greater values for mature live weight (A) (334.3 vs. 272.9 kg; $P < 0.001$), and also maximum growth rate ((A*c)/e) (1249 vs. 1099 g/d, $P < 0.001$), age ((b/c) (155 vs. 141 d, $P < 0.001$) and live weight (118.5 vs. 103.6 kg, $P < 0.001$) at the inflection point (which corresponds to the maximum growth rate with age). In contrast, specific growth rate (c) was higher for females (0.0111 vs. 0.0105, $P < 0.025$) compared to immuno castrated males. It is concluded that Gompertz model was a useful tool to

demonstrate that Immuno castrated male pigs grow faster and more efficiently than females.

Key Words: immuno castrated pigs, growth curve, Gompertz approach

---

1939 (M385) Growth performance of Sarda purebreed suckling piglets reared in smallholder farms.

C. Sulas[1], S. Fele[2], G. G. Fruttero[2], S. B. Gusai[2] and G. Battacone[*1], *[1]Dipartimento di Agraria, University of Sassari, Sassari, Italy, [2]Agenzia LAORE Sardegna, Cagliari, Italy*

The Sarda pig has been recently included in the Italian register of swine native breeds to preserve its genetic diversity and typical productions. Sarda piglets are usually raised on small farms. The most important product is the suckling piglet slaughtered at about 8–10 kg of body weight, used for the preparation of traditional dishes. In this study, a survey was performed to assess growth performances of purebred Sarda piglets during suckling period in smallholder farms. Twenty sows located in two farms, were housed in individual pens before farrowing. Stillbirths, born live, and birth weights for all litters were recorded. All piglets were ear-tagged and weekly weighed until weaning. Animals were grouped according to litter size: medium-small (5 to 8 pigs born alive), and medium-large (9 to 12 piglets). Effects of farm, litter size group and sex on individual average daily gain (ADG) were tested with an ANOVA model. A multiple linear regression model was used to evaluate the influence of age, litter size and sex on body weight. Birth weight of piglets did not differ between farm and litter size category, whereas, males were heavier ($P = 0.039$) than females (1556 vs. 1458 g, respectively). The ADG of the piglets during the suckling time did not differ for sex and farm. Piglets of medium-large litters had a slower growth than medium-small litters (ADG was 108 vs. 124 g, respectively). Results of regression analysis (R-Sq = 0.75) indicate a significant influence of age and litter size ($P < 0.01$) on body weight. Growth performances of suckling pigs were less than that of pigs of most conventional swine breeds. However, profitability of this breed seems strongly linked to the consumers preference for its meat as a key component of originally regional dishes.

Key Words: growth, suckling piglets, Sarda pig breed

1940 (M386) Piglet body weight at weaning: A key success factor for post-weaning performance?

D. Solà-Oriol, S. López-Vergé* and J. Gasa, *Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain*

The aim of the study was to evaluate the importance of piglet BW at weaning (WBW) on post-weaning performance and mortality. A total of 4320 male and female crossbreed piglets [Pietrain x (Landrace x Large White)] were used. All the animals were individually weighted at weaning (28 d-old). The selected animals (240 per batch without those corresponding to the percentile 10 and 90) were distributed into 3 BW categories: Low (L; BW < 6.5 kg, $n = 92$); Middle (M; 6.5 kg < BW < 8.5 kg, $n = 216$) and High (H; BW > 8.5 kg, $n = 94$) and allocated in groups of 10 piglets. The same commercial pre-starter diet formulated to contain 10.35 MJ/kg NE, 17.9% CP and 1.32% Lys was offered ad libitum. Feed intake (FI), BW and mortality rate (MR) were weekly monitored to calculate FI and ADG (0 to 14 d post-weaning). Performance data were analyzed with ANOVA by using the GLM procedure of SAS taking into account the WBW category. The initial differences between WBW categories were maintained along the pre-starter period ($P < 0.01$). Lower ADG ($P < 0.01$) but not FI ($P > 0.10$) was observed between WBW categories for the first week post-weaning (H = 99^{b} g/d; M = 115^{a} g/d and L = 122^{a} g/d; $P < 0.01$). For the second week post-weaning, higher ADG and FI was observed for H compared to M and L groups ($P < 0.01$). Overall, higher FI was observed for H than M and L (H = 325^{a} g/d; M = 293^{b} g/d and L = 265^{c} g/d; $P < 0.01$), however, no difference in ADG was achieved (H = 207 g/d; M = 203 g/d and L = 192 g/d; $P > 0.05$). Moreover, higher MR was observed for H than for M and L during the pre-starter period (1.98 vs. 0.2 and 0.3%; $P < 0.05$). The H animals failed to meet the energy requirements during the first week after weaning probably due to a longer anorexia period. After that, H animals start suddenly to eat high amounts of solid feed, following digestive and malabsorptive problems which may explain the higher MR, causing important losses. These results confirmed that in large suckling periods (28 d) the early contact with solid feed may optimize performance and reduce mortality after weaning in pigs with high BW.

Key Words: performance, mortality, weaning, piglet

1941 (M387) Comparison of fecal microbiota among healthy piglets during the weaning transition using barcoded 16S rDNA pyrosequencing.

J. P. Chae, E. A. Pajarillo and D. K. Kang*, *Dep. of Animal Resources Science, Dankook University, Cheonan, South Korea*

The objective of this study is to investigate change in the fecal microbiota of healthy piglets during the weaning transition using barcoded pyrosequencing of the prokaryotic 16S rRNA gene. It is believed that the gastrointestinal microbiome changes over time beginning from birth until adulthood in response to changes in diet, environmental stress and diseases. In particular, the weaning process results in reduced metabolic activity, malabsorption of nutrients, and susceptibility to enteric diseases as a consequence of abrupt separation from the sow before joining other litters in a different environment. Fifteen crossbred piglets weaned on the Day 28 were used in the study. Fecal samples were obtained immediately before

weaning (4 wk of age) and after weaning (6 wk of age), and were subjected to genomic DNA extraction for pyrosequencing analysis. As the piglets underwent the weaning transition a trend toward increased bacterial diversity was observed, based on species abundance as measured by the Shannon-Weaver index. *Firmicutes* (54.0%) and *Bacteroidetes* (59.6%) were the most dominant phyla during pre-weaning and post-weaning, respectively. During the weaning transition a distinct shift from *Bacteroides* sp. to *Prevotella* sp. as the most abundant genus was observed. Additionally, we detected a number of abundant species in the piglet gastrointestinal tract that have not been reported previously. *Clostridium rectum, C. clostridioforme, C. lactatifermentans* and *Butyricimonas virosa* were uniquely detected before weaning while *Roseburia cecicola and Blautia wexlerae*were detected during the post-weaning period only.

Key Words: bacterial diversity, piglets, weaning

1942 (M388) Piglets' early body weight and milk consumption partially explain post-weaning performance.

S. López-Vergé*, D. Solà-Oriol and J. Gasa, *Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain*

It's well known that piglets' BW at birth is an important factor determining their subsequent performance. Furthermore, equally important is trying to maximize milk intake during the suckling period. The objective was to assess the influence of the piglets' BW at birth and BW at weaning on pig performance over time. A total of 305 crossbreed piglets [Pietrain x (Landrace x Large White)] from 30 litters were used. All the animals were individually weighed at Day 2 (CF; cross fostering), 27 (weaning), 41 (14 d post-weaning), 62 (35 d post-weaning), 98 (growing) and 173 (slaughter). Piglets were fed ad libitum the same commercial pre-starter, starter, growing and finishing diets. The relationship between the BW at CF and BW at weaning with the BW at the different productive steps until slaughter was analyzed using the CORR procedure of SAS. BW at CF was related with BW at weaning ($P = 0.002$). Considering the Pearson correlation coefficient (r), showed that the BW at weaning was highly related to the BW at 14 d post-weaning [41 d-old ($r = 0.80$, $P < 0.001$)] but its influence was progressively reduced on Days 62 ($r = 0.51$, $P < 0.001$), 98 ($r = 0.19$, $P < 0.001$) and 173 ($r = 0.18$, $P < 0.001$), respectively. The strong relationship between BW at weaning and at 14 d post-weaning resulted in a huge BW difference between the 30% heavier and 30% lighter piglets (at weaning: 8.52 kg vs. 6.43 kg, $P < 0.001$; 14 d post-weaning: 12.17 kg vs. 10.63 kg, $P < 0.001$); difference which were reduced from 32.5% at weaning to 14.5% 2 wk later. The BW at CF also had an effect, but not as strong as BW at weaning, having the best correlation at 14 d post-weaning ($r = 0.40$, $P < 0.001$). Thus, we observed an attenuated effect on Day 27 ($r = 0.36$, $P < 0.001$), 62 ($r = 0.33$, $P < 0.001$), and 173 ($r = 0.27$, $P < 0.001$), respectively. It is concluded that both BW at CF and at weaning, play a significant role on pig BW performance and variability along the productive cycle. However these effects are gradually replaced over time, indicating that new factors become more important explaining BW variability. A higher effect of the BW at weaning was observed at the beginning of the nursing period, but it was diluted later on.

Key Words: performance, correlation, piglet

1943 (M389) Effects of parity and selection for uterine capacity on sow litter performance traits.

B. A. Freking* and J. L. Vallet, *USDA ARS USMARC, Clay Center, NE.*

Selection for 11 generations for uterine capacity (UC) was previously reported to increase litter size in gilts by 1.6 more fully formed pigs at birth compared to an unselected control line (CO) despite averaging 1 less ova shed. Our objective was to characterize litter performance traits in each line from subsequent sow parities following a shift in management scheme to a continuous flow farrowing system that more closely resembles industry conditions. Gilts entered into the system and were farrowed in contemporary groups of a maximum of 19 litters and maintained in this system through four parities if successfully mated in that contemporary group. A total of 203 litters (90 CO, 103 UC; 101 Parity 1, 49 Parity 2, 33 Parity 3; and 20 Parity 4) were analyzed. A mixed model analysis of variance was conducted. Fixed effects of farrowing group, line, parity (1–4), and two-way interactions involving line were fitted. The random effect of sire ($n = 75$) of the litter within farrowing group and line was included in the model. UC line averaged 1.3 ± 0.38 greater ($P < 0.01$) pigs born alive with 0.5 ± 0.14 fewer ($P < 0.01$) stillbirths than CO. Average pig birth weight was similar ($P = 0.99$) between lines, thus the UC line exceeded ($P < 0.05$) the CO line by 1.1 ± 0.38 kg in litter birth weight. UC line averaged 1.6 ± 0.32 greater ($P < 0.001$) pigs weaned than CO. Average pig wean weight was similar ($P = 0.64$) between lines, thus the UC line exceeded ($P < 0.05$) the CO line by 6.0 ± 2.07 kg in litter wean weight. Parity effects were observed as expected from first through fourth parities and no interactions of parity effects were observed with line. Improved reproductive performance of the UC line was maintained in sow litters similar to those previously measured in gilts. Selection for uterine capacity improved fetal survival resulting in increased number born alive with a similar average birth weight. This resulted in an increase in total weaning weight of sows through four parities. USDA is an equal opportunity provider and employer.

Key Words: pigs, selection, uterine capacity

1944 (M390) Gene expression profiles in muscle of black Iberian pigs supplemented with organic selenium compared with sodium selenite in finishing diets. D. E. Graugnard*, A. C. Smith, M. L. Spry, L. F. Spangler and K. M. Brennan, *Alltech Inc., Nicholasville, KY*

Supplementation with organic Se provides positive benefits through increased bioavailability and absorption compared with inorganic Se. The objective of this study was to evaluate the effect of different sources of Se on muscle gene expression in finishing black Iberian pigs. The finishing experimental period started when the animals reached 80 kg and ended at slaughter at approximately 120 kg. The treatments consisted of a standard finishing diet supplemented with organic Se (0.2 ppm Se as Sel-Plex; SP, Alltech Inc) or inorganic Se (0.2 ppm as sodium selenite; SS). Skeletal muscle samples were obtained at slaughter and stored in RNA later until analysis. Total RNA was isolated from samples (n = 5/trt) using standard methods and was hybridized to the Affymetrix Porcine Genome array. Expression data were statistically analyzed using the GeneSpring GX 10.0 software in which SP. was directly compared to SS using a t test. Statistical differences were declared at $P < 0.05$ without considering a fold change cut-off. Genes differentially expressed were imported into Ingenuity for biological function analysis. Results indicated that 1205 genes (757 up- and 448 downregulated) were differentially expressed ($P < 0.05$) in SP. relative to SS. The biological function analysis resulted in several enriched functions related to muscle development. Among these, positive activation of lipid metabolism, cellular and tissue development (Z score > 2) were the most relevant to the study. Further analysis of the biological functions identified specific genes associated with the regulation of β-oxidation and overall energy metabolism including *CPT1C, SCD5, MYO1B* and *CAST* among others. In addition, upstream molecule analysis indicated that more than 30 genes were controlled by *TGFB1* (Transforming growth factor β 1), which is closely related to Se in the regulation of oxidative stress. In conclusion, this study shows evidence of multiple molecular mechanisms affected by SP. in skeletal muscle of black Iberian pigs that relate to performance and meat quality.

Key Words: Se, swine, gene expression, microarray, muscle

1945 (M391) Neither photoperiod in the farrowing room nor time of weaning affect nursery performance. L. Eastwood, J. Shea and D. Beaulieu*, *Prairie Swine Centre, Inc., Saskatoon, SK, Canada*

Weaning may result in anorexia and reduced growth in pigs especially during the initial 24 to 48 h in the nursery. This study was designed to determine if altering the photoperiod in the farrowing room and/or if weaning at the end of the light or dark cycle would affect performance post-weaning. Twelve farrowing rooms, 13 sows/room, were assigned to one of four treatments approximately one wk before farrowing. Treatments, arranged as a 2 × 2 factorial included 2 farrowing room photoperiods; 16 h light:8 h dark (16L:8D) or 8L:16D, and 2 weaning times; end of the dark or end of the light cycle. Pigs were weaned at 25 (± 1) d of age into nurseries maintained on a 16L:8D regime at time 0 of the dark cycle. Pigs were fed standard commercial diets, in a 2 phase feeding program in the nursery. The phase 1 nursery diet was spiked with ferric oxide pellets for 24 h post-weaning and anal swabs taken at 48 h post-weaning allowed pigs to be designated as "eaters" or "non-eaters". Neither farrowing room photoperiod nor weaning time affected ADG ($P > 0.10$) in the farrowing room (236 g/d; birth to weaning) or nursery (437 g/d, weaning to 54 d of age). On d 0 to 7 post-weaning, there was a tendency for a photoperiod by weaning time interaction for ADFI ($P = 0.06$). The lowest intakes (123 g/d) were observed for pigs who had been on the 16L:8D lighting regime and weaned at the end of the dark cycle. ADFI was similar among the other treatments and averaged 157 g/d. Neither photoperiod nor time of weaning affected the percentage of pigs (34%) identified as "eaters" during the initial 24 h in the nursery ($P > 0.10$). Pigs identified as "eaters" were lighter at weaning (7.26 vs. 7.62 kg BW; $P < 0.01$), but showed improved ADG from d 0 to 7 post-weaning relative to "non-eaters" (187 vs. 141 g/d; $P < 0.01$). Nursery exit weights were similar between "eaters" (19.6 kg) and "non -eaters" (21.0 kg; $P > 0.10$). Farrowing room photoperiod and/or weaning at the end of the dark or light cycle did not affect nursery performance. Pigs exhibiting evidence of phase 1 feed consumption immediately post-weaning were lighter; however they had higher ADG immediately post-weaning than those identified as non-eaters.

Key Words: swine, weaning, photoperiod

1946 (M392) Behavior traits and growth characteristics of newly weaned piglets. M. R. Zukle*, J. E. Naginis and L. A. Pettey, *California State Polytechnic University, Pomona*

Four litters of newly weaned piglets (n = 37; 7.01 kg BW) were used to evaluate the potential correlations between weight of the piglet, behavioral traits, and growth rate in the first 7 d following weaning. Piglets were weaned at an average of 27 d-of-age and moved into an environmentally controlled nursery facility. Littermate piglets were penned together and allowed ad libitum access to feed and water. Room temperature was maintained between 26 and 32°C. Above each pen a video camera connected to a data storage unit recorded all piglet behaviors. Feed and water disappearance and piglet weight were recorded daily. Video files of piglet behavior were evaluated for frequency (FREQ) and amount of time (TIME) involved in the following behaviors: mobile/active, aggression, eating, and drinking. Piglet weaning weight in wk

1 was negatively correlated (r = -0.47) to weight change as heavier piglets tended to lose more or gain less weight than their lighter weight contemporaries. The daily correlation of weaning weight to weight change was numerically the least (r = -0.25) on d 1, and the greatest on d 4 (r = -0.48). Using pen averages, feed intake increased linearly ($P < 0.05$) from d 0 to 7, while water intake increased numerically each day. As expected, FREQ and TIME spent eating and drinking increased linearly ($P < 0.05$) during the first week post-weaning. On d 1, FREQ of eating behavior was not correlated (r = +0.15) to piglet weight change, while FREQ of drinking and aggression were negatively correlated (r = -0.58 and -0.73, respectively) to piglet weight change. On d 2, FREQ of eating and drinking were positively correlated (r = +0.44 and r = +0.72, respectively) to weight change and FREQ of aggression was not correlated (r = +0.25) to piglet weight change. These correlations seem to show that piglets that lost more weight tended to exhibit less inclination towards eating and exhibited more instances of drinking or fighting on d 1. By d 2 to 7, FREQ of eating behavior was positively correlated (r = +0.50) to FREQ of watering behavior and was positively correlated (r = +0.75) to weight change. Data from this study supports previous work where larger piglets tended to lose more weight than smaller piglets post-weaning, which may be due to increased frequency of aggression and water intake on the first day away from the sow.

Key Words: piglet, growth, behavior

1947 (M393) Oxidative stress is higher in replacement gilts than in multiparous sows. J. Lapointe*, C. Roy and M. Lavoie, *Agriculture and Agri-Food Canada, Sherbrooke, QC, Canada*

The recent success obtained in term of increasing the litter size of sows has not correlated with a reduction of replacement rate. There is thus an increased economic demand for gilts with optimal reproductive potential and longevity. Unfortunately, replacement gilts are known to be more susceptible to diseases and less productive than multiparous sows. While it is straightforward to identify the physiological failure which leads to the removal of a gilts from the herd, identification of the underlying molecular reasons for the occurrence of these events continues to be more challenging. Interestingly, reproductive performance, resistance to diseases and longevity could all be largely affected by oxidative stress. To investigate if oxidative stress conditions could account for the poor performance and longevity observed in replacement gilts in comparison to older multiparous sows. Three distinct groups of 15 F1 conventional Yorkshire x Landrace sows were formed based on their similar age and parity. These groups were primiparous gilts (group 1), third parity sows (group 2) and fifth parity sows (group 3). All animals were slaughtered during the post-ovulatory period of the estrous cycle and blood as well as tissues samples were collected and frozen at −80°C. Principal biomarkers of oxidative damage to proteins (Carbonyls) were analyzed in plasma and liver samples using ELISA procedures. Specific mRNA expressions of the major antioxidants glutathione peroxidases 1 and 4 (GPx1, GPx4) as well as superoxide dismutases 1 and 2 (Sod1, Sod2) were monitored in liver and kidney samples by quantitative RT-PCR. Specific enzymatic activities of glutathione peroxydases and superoxide dismutases were measured by spectrophotometric assays. The plasmatic concentrations of protein carbonyls were significantly different between the three groups with the higher concentrations being observed in gilts ($P \leq 0.001$). The mRNA expression levels of GPx1 and GPx4 were also significantly increased in the liver of primiparous gilts when compared to multiparous sows ($P \leq 0.05$) while no differences were observed in kidneys ($P > 0.10$). Sod2 enzymatic activity was found to be higher in the liver of primiparous gilts than fifth parity sows ($P \leq 0.05$). It is well established that the expression and activity of antioxidants increase in response to oxidative stress. Taken together, our results indicate that replacement gilts sustain significantly higher oxidative conditions than multiparous sows. Current findings may contribute to the design of nutritional regimens that will increase the productivity of gilts by counteracting oxidative stress.

Key Words: oxidative stress, gilts, longevity.

SWINE SPECIES NUTRITION

1948 [Withdrawn]

1949 (W379) Effect of porcine digestive peptides as sweet milk whey replacer for piglets diets: preferences, acceptance and performance during the nursery period. J. E. Figueroa[1,2], D. Solà-Oriol[3], R. Davin[*4], E. Borda[5], S. A. Guzmán-Pino[4] and J. F. Pérez[4], *[1]SNiBA, Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain, [2]Universidad de Chile, Santiago, Chile, [3]Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [4]Animal Nutrition and Welfare Service, Department of Animal and Food Sciences, Universitat Autònoma de Barcelona, Bellaterra, Spain, [5]Bioiberica, Barcelona, Spain*

The aim of the present work was to study the productive performance of nursery pigs when sweet milk whey (SMW) is replaced by porcine digestive peptides (PDP; 620 g/kg of CP, Bioibérica SA, Palafolls, Barcelona, Spain). A total of 240 pigs were randomly distributed after weaning into 2 groups (12 pens/group) depending on the presence of SMW or PDP on their diets. The SMW group was fed a pre-starter (0- 14 d) and starter (15- 33 d) diet with 142 g/kg and 49 g/kg SMW respectively; the PDP group was offered an iso-caloric and iso-proteic diet with 20 g/kg of PDP and 300 g/kg of wheat replacing dairy products. Feed intake and body weight were measured weekly to calculate average daily feed intake (ADFI), average daily gain (ADG) and gain: feed ratio (GFR). A choice test and one-feeder test of 30 min each were performed in another group of animals 3 wk after weaning (36 pen pairs) to evaluate the preference and acceptance for both diets, respectively. Feed intake was recorded by measuring the initial and final weight of the feeders. SMW and PDP diet positions were balance across pig's pairs. Data were analyzed with ANOVA using the GLM procedure (performance values) or the MIXED procedure (preference and acceptance values) of the statistical package SAS. Despite clear differences on feed preference (211 vs. 77 g; $P = 0.039$) and acceptance (287 vs. 192 g; $P = 0.001$) between diets with or without whey respectively, no effects were observed on performance at the end of the nursery period (20.92 vs. 21.13 kg for BW, 0.62 vs. 0.63 kg/d for ADFI and 0.52 vs. 0.53 kg/d for ADG). Despite the reduced preferences and acceptance observed, the use of dairy products appears to be unnecessary if a high valuable protein source is offered during nursery.

Key Words: familiarity, preferences, lactose

1950 (W380) High nutrient intake alters muscular growth and metabolic status of neonatal intra-uterine growth-retarded pigs. F. Han*, L. Chen, L. Che, B. Yu, X. Ding, Y. Luo, S. Bai, D. Chen, Y. Xuan and K. Zhang, *Institute of Animal Nutrition, Sichuan Agricultural University, Chengdu, China*

Intra-uterine growth-retarded (IUGR) neonates have shown an impairment of postnatal skeletal muscle morphology and function. We hypothesized that the growth and development of skeletal muscle of IUGR neonates might be affected by increased nutrient intake during the suckling period. Therefore, we investigated the effects of high nutrient intake (HNI) on the muscular growth and metabolic status of IUGR and normal-birth weight (NBW) piglets. Piglets with a birth weight near the mean litter birth weight (within 0.5 SD) were identified as NBW, whereas those at least 1.5 SD lower birth weight were defined as IUGR. A total of twelve pairs of IUGR and NBW piglets (7 d old) were randomly assigned to two different nutrient-level formula milk groups. After 21 d of rearing, muscle weight and morphology, activities of energy metabolism-related enzymes and muscle protein deposition-related genes involved in the insulin-like growth factor 1/Ak thymoma/mammalian target of rapamycin pathway were determined. The results indicated that semitendinosus and psoas major muscle weights were lighter (-31.7%~37.3%, $P < 0.001$) in IUGR piglets, whereas HNI significantly increased psoas major muscle weight (+31.3%, $P < 0.001$) and length (+17.6%, $P = 0.006$). Likewise, IUGR decreased the cross-sectional areas (-26.4%~40.0%, $P = 0.002$) and myofiber numbers (-20.8%~23.8%, $P = 0.004$) of semitendinosus and psoas major muscle. Furthermore, IUGR piglets with HNI exhibited more myofibers (+25.7%, $P < 0.001$) than those counterpart IUGR piglets, and these alterations in the muscle growth traits of IUGR piglets receiving HNI were accompanied by increasing muscular gene expressions of *insulin-like growth factor 1* (+49.0%, $P = 0.003$), *insulin-like growth factor 1 receptor* (+56.9%, $P < 0.001$), *Ak thymoma* (+60.8%, $P = 0.002$), *mammalian target of rapamycin* (+55.4%, $P < 0.001$), *ribosomal protein s6* (+78.6%, $P = 0.003$), *eukaryotic translation initiation factor 4E* (+75.0%, $P = 0.002$) that are related to muscle protein deposition. Otherwise, IUGR decreased lactate dehydrogenase activity (-13.1%, $P = 0.015$) and activity ratios (-23.0%~26.9%, $P < 0.001$) of lactate dehydrogenase: citrate synthase and lactate dehydrogenase: β-hydroxy-acyl-CoA dehydrogenase, but increased β-hydroxy-acyl-CoA dehydrogenase activity (+16.2%, $P = 0.023$) in longissimus dorsi muscle. Inversely, HNI increased lactate dehydrogenase activity (+14.1%, $P = 0.021$) and activity ratios (+21.8%~39.1%, $P = 0.004$) of lactate dehydrogenase: citrate synthase and lactate dehydrogenase: β-hydroxy-acyl-CoA dehydrogenase, but decreased β-hydroxy-acyl-CoA dehydrogenase activity (-17.1%, $P =$

0.006). In conclusion, the present findings suggest that increased nutrient intake during the suckling period altered muscular metabolic status and improved skeletal muscle growth possibly via regulation of insulin-like growth factor 1/Ak thymoma/mammalian target of rapamycin signaling pathway.

Key Words: intra-uterine growth-retarded pigs, nutrient intake, skeletal muscle

1951 (W381) The inclusion of yeast-derived protein in weanling diet improves growth performance, anti-oxidative capability and intestinal health of piglets. L. Hu, L. Che*, G. Su, Y. Xuan, G. Luo, F. Han, Z. Fang, Y. Lin, S. Xu and D. Wu, *Institute of Animal Nutrition, Sichuan Agricultural University, Chengdu, China*

This study aimed to investigate the effects of yeast-derived protein (YP) on growth performance, intestinal health and oxidative status of weaned piglets. A total of 80 weaned piglets (PIC 327 × 1050, 26 ± 2 d-old) were randomly allocated into 2 groups, 5 pens each group and 8 piglets each pen, receiving control diet and diet with inclusion of 4% YP at the expense of fish meal (YP diet) for a period of 28 d. Piglets had free access to pelleted feed and water. Feed intake was recorded daily and piglets were weighed weekly for calculating ADG, ADFI and G:F. At d 28, blood samples were collected from the cervical vein and centrifuged (3000 ×g, 4°C, 15 min) to separate serum for biochemical assays. Then these piglets were anaesthetized with intravenous injection of pentobarbital sodium (15 mg/kg body weight) and slaughtered. Approximately 2 cm of ileal tissue was collected each piglet and stored at −80°C for real-time RT-PCR. Moreover, the chyme of ileum and colon were removed and stored at −80°C for microbial analysis. Data were analyzed using one-way analysis of variance (ANOVA) procedure of SPSS 20.0 (Chicago, IL, USA) and are reported as means ± SEM. The results showed that piglets fed YP diet had markedly higher overall ADG (470 ± 18 vs. 412 ± 12 g, P = 0.034) and G:F (0.72 ± 0.02 vs. 0.67 ± 0.01, P = 0.001). Serum concentration of urea was significantly decreased (166.58 ± 9.57 vs. 306.34 ± 26.89 mmol/L, P = 0.003) in piglets fed YP diet relative to piglets fed control diet. Moreover, serum activity of glutathione peroxidase (GP_X) was markedly increased (303.31 ± 7.22 vs. 255.54 ± 8.53 umol/L, P = 0.003) in piglets fed YP diet relative to piglets fed control diet. In addition, feeding YP diet significantly increased the DNA copy numbers (log^{10} Cfu/g of digesta) of lactobacilli (8.27 ± 0.13 vs. 7.20 ± 0.17, P = 0.021) and total bacteria (10.44 ± 0.06 vs. 10.26 ± 0.04, P = 0.044) in the colonic digesta of piglets. Furthermore, mRNA expression of the innate immunity-related genes (TLR4, NF-κB1 and IL-6) tended to increase (1.33 ± 0.11 vs. 1.00 ± 0.07, P = 0.057; 1.92 ± 0.15 vs. 1.00 ± 0.21, P = 0.024; 1.45 ± 0.10 vs. 1.00 ± 0.15, P = 0.041, respectively) in the ileum of piglets fed YP diet relative to piglets fed control diet. In conclusion, the diet with inclusion of YP improved growth performance, anti-oxidative capability and intestinal health of weaned piglets.

Key Words: growth, piglet, yeast

1952 (W382) Effects of added zinc during the grower and/or finisher phase on growth performance and carcass characteristics of finishing pigs fed diets with or without ractopamine HCl. C. B. Paulk*, M. D. Tokach, S. S. Dritz, J. M. DeRouchey and R. D. Goodband, *Kansas State University, Manhattan*

A total of 1197 pigs (PIC 337 × 1050) were used in a 72-d study to determine the effects of added Zn from ZnO fed during the grower (d 0–45; initially 58.8 kg) and finisher (d 45–72; initially 99.0 kg) in diets with or without racto-

Table 1952. Effects of added zinc during the grower and/or finisher phase on growth performance and carcass characteristics of finishing pigs fed diets with or without ractopamine HCl

Added Zn d 0–45:	-	-	-	-	+	+	+	+	
Added Zn d 45–72:	-	+	-	+	-	+	-	+	
Added RAC d 45–72:	-	-	+	+	-	-	+	+	SEM
d 0 to 72									
ADG, kg	0.89	0.88	0.95	0.95	0.89	0.88	0.97	0.96	0.01
ADFI, kg	2.65	2.60	2.60	2.63	2.69	2.68	2.71	2.72	0.05
G:F	0.34	0.34	0.37	0.36	0.33	0.33	0.36	0.35	0.00
Final BW, kg	118.7	118.0	122.9	123.6	119.4	118.0	124.0	124.2	2.7
Carcass Characteristics									
HCW, kg	86.0	86.0	88.2	90.0	85.4	87.1	88.7	89.5	2.2
Yield,[1%]	74.09	74.12	74.64	75.35	73.09	75.52	73.98	74.08	1.35
Backfat thickness,[2] mm	16.75	15.69	13.81	14.86	16.29	16.28	14.13	13.67	0.63
Loin depth,[2] mm	62.64	61.71	64.59	63.12	61.99	61.58	65.52	66.06	1.13
FFLI,[2%]	53.13	53.70	55.13	55.13	53.52	53.33	55.01	55.94	0.57

[1] Calculated by dividing HCW by live weight obtained at the packing plant.
[2] Adjusted using HCW as a covariate.

pamine HCl (RAC; Elanco Animal Health, Greenfield, IN) on growth performance and carcass characteristics. There were 25 pigs per pen and 6 pens per treatment. Pens were randomly assigned to a 2 × 2×2 factorial arrangement in a split-plot design. The whole plot consisted of diets with or without 75 ppm added Zn from d 0 to 45 and the subplots were diets with or without 75 ppm added Zn and with or without 10 ppm RAC from d 45 to72. All diets contained 50 ppm Zn supplied from the premix. No interactions were observed. Addition of 75 ppm Zn during either period or both did not influence pig growth performance or carcass characteristics. Pigs fed RAC had improved ($P < 0.03$) ADG, G:F, final BW, HCW, loin depth, and fat-free lean index compared with pigs fed the control diet. In conclusion, feeding RAC improved the performance of grow-finish pigs; however, additional Zn did not.

Key Words: growing-finishing pigs, ractopamine HCl, zinc

1953 (W383) Postnatal nutrition restriction affects growth and immune response of intrauterine growth restricted piglets. L. Hu, L. Che*, Y. Liu, Y. Xuan, F. Han, Z. Fang, Y. Lin, S. Xu and D. Wu, *Institute of Animal Nutrition, Sichuan Agricultural University, Chengdu, China*

Epidemiological studies and experimental models show that intrauterine growth restriction (IUGR) followed by accelerated postnatal growth is associated with increased susceptibility to diseases in later life. We hypothesized that postnatal nutrition restriction may improve intestinal development and immunity of IUGR neonates. Piglets with a birth weight near the mean litter birth weight (SD 0.5) were identified as NBW, whereas those with at least 1.5 SD lower birth weight were defined as IUGR. Twelve pairs of normal-birth weight (NBW) and IUGR piglets at 7 d of age were randomly assigned to adequate (ANI) or restricted nutrition intake (RNI) for a period of 21 d, which produced 4 experimental groups (birth weight/nutrition intake) as NBW-ANI, IUGR-ANI, NBW-RNI and IUGR-RNI ($n = 6$ per group). The NBW-ANI and IUGR-ANI piglets had free access to formula milk, while the NBW-RNI piglets had same intake of formula milk as IUGR-ANI piglets. To achieve the same degree of nutrition restriction as NBW piglets, the formula milk intake of IUGR-RNI piglets was based on the calculation that the formula milk intake of IUGR-ANI piglets multiplied by the formula milk intake of NBW-RNI piglets and divided by the formula intake of NBW-ANI piglets. At d 28, blood and intestinal samples were collected at necropsy and analyzed for cellular immune response and expression of innate immunity and DNA methylation-related genes. Data were analyzed by SPSS software using the MIXED procedure. The results indicated that both IUGR and postnatal nutrition restriction decreased (-26%, $P = 0.002$) ADG during the experimental period, but there was comparable ADG between IUGR-ANI and NBW-RNI piglets. The relative weight of intestine, heart or brain to body weight was higher (+9%, $P = 0.091$; +23%, $P = 0.025$ and +41%, $P = 0.001$; respectively) in IUGR than that in NBW piglets. Irrespective of body weight, number of peripheral leucocytes, lymphocytes and monocytes were significantly decreased (-25%, $P = 0.006$; -37%, $P = 0.001$ and −82%, $P = 0.009$; respectively) by RNI, whereas the ratio of $CD4^+$ to $CD8^+$ in blood was significantly increased (+27%, $P = 0.034$) by RNI, however, it did not markedly differ between NBW-ANI and IUGR-RNI piglets. Likewise, ileal mRNA expression of innate immunity and DNA methylation-related genes (*TLR-9* and *DNMT1*) were up-regulated in piglets with RNI (+31%, $P = 0.004$ and +57%, $P = 0.001$; respectively), particularly increased in IUGR-RNI relative to IUGR-ANI piglets. In conclusion, the present study indicated that postnatal nutrition restriction may affect systematic and intestinal immune response of IUGR piglets.

Key Words: pigs, intestine, innate immunity

1954 (W384) Effects of dietary omega-3 polyunsaturated fatty acids on growth and immune response of weanling pigs. Q. Li, J. H. Brendemuhl, K. Jeong and L. Badinga*, *University of Florida, Gainesville*

The recognition that *omega*-3 polyunsaturated fatty acids (*n*-3 PUFA) possess potent anti-inflammatory properties in human models has prompted studies investigating their efficacy for animal growth and immunity. The objective of this study was to examine the effect of feeding an *n*-3 PUFA-enriched diet on growth and immune response of weanling piglets. Newly weaned pigs (averaging 27 ± 2 d of age and 8.1 ± 0.7 kg of BW) were assigned randomly to receive a control (3% vegetable oil, $n = 20$) or *n*-3 PUFA-supplemented (Omega, $n = 20$) diet for 28 d after weaning. Diets were formulated to be isocaloric (3.3 Mcal/kg of diet) and isolysinic (14 g Lys/kg of diet). A diet × gender × week interaction was detected ($P < 0.04$) for body weight. Female pigs consuming the *n*-3 PUFA-enriched diet were lighter ($P < 0.01$) at wk 4 post-weaning than their counterparts fed the vegetable oil-supplemented diet. Newly weaned pigs gained more weight ($P < 0.01$), consumed more feed ($P < 0.01$) and had better G: F ($P < 0.01$) between d 14 and 28 than between d 0 and 14 post-weaning. Peripheral IGF-1 concentration decreased ($P < 0.01$) between d 0 (87.2 ± 17.0 ng/mL) and 14 (68.3 ± 21.1 ng/mL) after weaning and then increased again by d 28 (155.2 ± 20.9 ng/mL) post-weaning. In piglets consuming the vegetable oil-enriched diet, plasma TNF- α concentration increased ($P < 0.04$) from 37.6 ± 14.5 to 102.9 ± 16.6 pg/mL between d 0 and 14 post-weaning and remained high through d 28 (99.0 ± 17.2 pg/mL) post-weaning. The TNF-α increase detected in the piglets fed vegetable oil was not observed in the piglets fed *n*-3 PUFA (d 0 = 33.0 ± 17.2

pg/mL; d 14 = 29.1 ± 21.7 pg/mL; d 28 = 36.7 ± 21.4 pg/mL). With the exception of blood platelets and eosinophil cells, dietary *n*-3 PUFA had minimal effects on hematological characteristics. Fecal consistency scores improved ($P < 0.01$) with increasing weeks after weaning, but were similar between the two dietary treatments. Results indicate that weaning induces considerable immune stress on piglets and that this stress can be mitigated by dietary supplementation of *n*-3 PUFA.

Key Words: *n*-3-PUFA, growth, immunity, pig

TEACHING/UNDERGRADUATE AND GRADUATE EDUCATION

1955 (W385) Examining demographics and student interests in an introductory animal science course. D. A. Nichols* and M. R. Hay McCammant, *Kansas State University, Manhattan*

Over the past 9 yr, the Department of Animal Sciences and Industry at Kansas State University has seen tremendous growth in undergraduate programs (2005 n = 704, 2013 n = 1197). One of the courses impacted by enrollment growth is ASI 102, Principles of Animal Science (2005 n = 263, 2013 n = 438). This course is required for Animal Sciences & Industry majors and is a service course to students in the Colleges of Agriculture, Business Administration and Arts & Sciences. Over 9 yr, surveys were given to the students enrolled in ASI 102 during the Fall semester, examining demographics and student interest. These questions examined gender, ethnicity, age, residency, and both primary and secondary specie of interest. Gender distribution has held relatively steady over the years with 61% of the class being female in 2005 and 68% female in 2013. Age distribution held steady with 61% of the class being ages 17–18 yr of age in 2005 and 63% in 2013. Subtle changes in student ethnicity have been shown as the class went from being 92% White/Non-Hispanic to 85% White/Non-Hispanic with the most significant growth in both the Black/Non-Hispanic population (1% in 2005 to 5% in 2013) and the Hispanic/Spanish American/Latin/Mexican population (2% in 2005 to 6% in 2013). The change in residency came from the increase of out-of-state students (18% in 2005 to 23% in 2013), while international students remained 1% each year. Student primary specie of interest in 2005 showed that the most popular specie was beef cattle at 37% of the class, with companion animals close behind at 31%, then horses at 29%, swine or sheep (these were combined because of bubble sheet limitations) at 2% and dairy cattle at 1%. In 2009, the percentage of students with a primary specie interest in companion animals (35%) surpassed those with a beef cattle interest (34%). Companion animals continue to be the most popular species of interest with 39% of the students reporting them as their primary species of interest in 2013, however, beef cattle have held steady at 34%. When students were asked about their secondary specie of interest, horses consistently were the most popular (36% in 2007 and 31% in 2013). Survey results have been extremely useful to categorize students. Examining demographics has allowed us to identify student interest and focus on areas of the course that need greater clarification and emphasis.

Key Words: undergraduate, demographics, teaching

1956 (W386) Development of a science education experience for adolescents based on stress physiology and a growing interest in smartphone technology. P. A. Eichen*, B. Scharf, G. D. Martin, R. Mott and D. E. Spiers, *University of Missouri, Columbia*

Interest in STEM (i.e., Science, Technology, Engineering, and Mathematics) education is increasing among all age groups. In a recent survey of Missouri beef and dairy producers, 98% indicated willingness to use technology to improve management of heat stress in their herds, with about 80% having access to wireless internet and 60% having smartphones. In contrast, only half thought understanding heat stress was important, while 90% of extension livestock specialists noted it is a significant issue. This discrepancy suggests the need for education on this important topic at an early age. To this end, a 2-d "Science Boot Camp" for pre-college students was developed several years ago to stimulate interest in environmental stress issues. A brief survey of the students participating in this camp showed that 90% agreed that science is important, and science education can benefit everyone. In contrast to producers, a majority of the teens had wireless internet and smartphones. Building on the results of this event, we have developed at the University of Missouri a 4-d science camp for adolescents in 2014 (Summers@Mizzou, "The Stress of Life,"). The goal of the camp is to increase understanding and appreciation of science research through experiential learning. A smartphone heat stress app for livestock (i.e., ThermalAid) has been developed in our laboratory, along with a website thermalnet.missouri.edu. It is incorporated into the camp to illustrate the real-world value of science. Students will be introduced to research methods, and then use state-of-the-art technologies (e.g., ThermalAid, iPads, and iButtons) to collect data on themselves under different environmental conditions. They will then learn to statistically analyze and interpret the results. This information, along with data from cattle at the University research farm, will be incorporated into a final determination of the impact of stress. Students will work in teams to collect videos throughout the camp to be combined with their results into a final presentation. Developing and presenting these videos will give them an opportunity to practice presentation skills, apply new information they have learned, and gain confidence in working with others. Entry and exit surveys will be administered, to assess students' views on science and technology and the life skills they developed throughout this camp. Future projects will build on the educational discoveries of this camp.

Key Words: heat stress, education, technology

1957 (W387) Student assessment through a survey instrument of a horse management laboratory course. M. C. Nicodemus* and T. L. Bova, *Mississippi State University, Mississippi State*

Inclusion of a hands-on laboratory to the Mississippi State University horse management course, ADS 3223 Horse Management, was done in the spring of 2008, and due to it's popularity, this year the course offering will be expanded to both the spring and summer semesters. With course expansion, an understanding of the course impact on students is needed to determine areas that should be explored in future laboratories, and thus, the study objective was to assess through the application of a survey instrument the effectiveness of a horse management laboratory course in developing student's horse handling abilities. Students (n = 35) enrolled in ADS 3223 Horse Management were given a researcher-developed, 19 forced-choice question survey instrument at the beginning (B) and end (E) of the semester. Each question described a horse management activity that students rated 1 to 5 for their ability to perform. A score of 5 indicated the student had a perceived high proficiency level for performing all aspects of the described activity. The average score for each question was determined and compared using a one-way ANOVA to determine the impact of the course on handling abilities ($P < 0.05$). While all questions indicated students believed their abilities had improved through completion of the course, a significant impact on skill level according to students' scores was seen in the following areas: basic handling of European (B: 3.2, E: 4.2) and pony (B: 3.3, E: 4.5) breeds and performance-related handling of society-type (B: 2.4, E: 3.4) breeds ($P < 0.05$). Students were acclimated to various breeds through laboratory activities. The highest score given at the end of the semester was associated with the most common laboratory activity, catching, haltering, and leading of adult, well-trained horses (4.75), while the lowest score was associated with an activity not covered in laboratories, handling untrained, young horses (2.7). At the end of the semester, students were able to select suggested future topics to be covered in which training younger horses was the most popular topic (35%). While this topic is covered in another course, the majority of the students were all upperclassmen (70%) that were not taking another equine course that same semester (80%), nor had they taken another equine course in past semesters (55%), and thus, topics not covered proficiently in this course may leave these students lacking in those particular horse handling skills.

Key Words: horse management, survey

1958 (W388) Educational outcomes of an online course: Pharmaceutical use in cattle. E. Blythe*, *West Texas A&M University, Canyon*

Objective: To assess the effectiveness of a distance-based, online course entitled "Pharmaceutical Use in Cattle" by measuring the cognitive knowledge of agricultural science students (n = 27) as felt in their confidence level to explain; legal and regulatory issues that affect responsible pharmaceutical use and food safety principles, basic pharmacokinetics, veterinary drug informatics and classes of pharmaceuticals used in the therapeutic treatment of disease states in cattle. The course goal is to provide any interested animal science, dairy science, meat science, agricultural education, and pre-veterinary medicine student an opportunity to obtain knowledge and skills that can positively impact educational, veterinary and economic outcomes by applying drug knowledge resources to beef and dairy cattle operations. Methods: Quantitative and qualitative methods were utilized to assess the effectiveness of the curriculum. A one group, pre-post, quasi-experimental design was used to evaluate the confidence level and application skills of the students. A 5-point Likert scale was used to measure confidence levels. Improvement in confidence is expressed by standard deviations and confidence intervals. Results: Cognitive post-course scores improved significantly over the pre-course scores on all 11 survey questions. The analysis for each question indicated an increase in the cognitive measure as a result of completing the course curriculum. The reflective commentary on how students will utilize concepts learned in the course was positive. Students reported that increased knowledge in all topic areas would enhance their ability to; implement patient safety and food safety principles, serve as the basis for educating others under their supervision, and ultimately benefit the end consumer and industry. Additionally students reported; increased awareness of the depth of drug control regulations, the desire to demystify drug use in cattle, desire to strengthen working relationship with their attending veterinarian, and improve overall herd health, quality and performance. Students also reported applying what they learned to their personal cattle, to the job market, competitive internships and graduate thesis work. The large majority of students reported a near complete lack of self-awareness on the many facets of pharmaceutical use in cattle before this class. Conclusion: This online course can be used to increase the confidence level of the student's cognitive knowledge and skills after completion of the curriculum. The online offering of this course is an effective method to educate any interested agricultural science students in the United States on topics specific to pharmaceutical use in cattle.

Key Words: cattle, pharmaceuticals, education

1959 (W389) Using community engagement to enhance student learning in animal science: Farm to fork-at home and abroad. T. Montgomery*, *University of Wisconsin-Platteville, Platteville*

Community engagement in the animal sciences takes many different forms. Our Pioneer Academic Center for Community Engagement (PACCE) was founded as a way to help faculty from all across campus to engage students with community

partners to increase learning opportunities that involve problem-solving. PACCE projects are funded through segregated student fees and allow each faculty member to design projects that will engage students without a significant financial burden on the course. Many disciplines, such as engineering and business, have community partners looking for the specific expertise of the course and the students within. Animal science courses have historically been less able to attract community partners and so we have had to seek them out more intentionally and controversy exists as to whether this approach compromises the engagement process. Surveys and interviews were conducted in animal science, agribusiness, and agriculture engineering technology to determine if differences in approach to finding community partners changed the experiences and outcomes for faculty, students, and community partners in the different disciplines. From on-farm projects creating standard operating procedures to exploring ice cream flavors for a local business to doing community service during study abroad experiences (such as Ghana and Romania), students that engage in these activities have an increased investment in the course, a greater sense of civic responsibility, and an overall awareness of how they fit into the larger community regardless of discipline. Community partners felt equally engaged throughout the projects. Struggles for faculty include finding time to organize these projects as well as garnering acceptance from colleagues that these projects are worthy of the same weight as grant-writing and research publications.

Key Words: community engagement, study abroad, farm to fork

1960 (W390) An animal handling course for today's animal science student. A. P. Fidler*, *University of Arkansas, Fayetteville*

An increasing number of students with limited exposure to animal husbandry and plans to practice companion animal veterinary medicine are enrolling as Animal Science majors at the University of Arkansas. Without adjusting the curriculum to reflect the needs of the incoming student body, the department is at risk of graduating students lacking the knowledge and skills expected of an Animal Science graduate. Chief among those is the general livestock husbandry principles and practices which previous generations of animal science students might have been expected to already have become familiar with before matriculation. Simultaneously, the knowledge base and technologies continues to grow in a number of animal science disciplines, necessitating their inclusion into courses in our curriculum, often at the expense of the more time-consuming and logistically difficult live animal handling laboratory experiences. To address this disparity, a course has been developed at the University of Arkansas to provide animal science students with the opportunity to learn and practice safe and humane animal handling, restraint, and husbandry procedures of a variety of domestic species. The course utilizes live animal demonstrations and hands-on activities with cattle, horses, sheep, swine, dogs, cats, and laboratory rodents. Students learn methods of safe, effective, and humane handling and restraint as well as typical husbandry procedures which may be performed by an animal scientist. Examinations combine a written portion to test comprehension of basic principles as well as a practical portion to test ability to perform basic procedures. Students are thereby given the opportunity to learn, practice, and demonstrate animal handling knowledge and skills that may be lacking in their previous experience or academic history.

Key Words: handling, husbandry, student

1961 (W391) Experiential learning experience for undergraduate students in livestock and fisheries work in India. S. Robinson, M. Shelby, C. Prakash, O. Bolden-Tiller and N. Gurung*, *Tuskegee University, Tuskegee, AL*

The Tuskegee University (TU), as a collaborating partner, for the Agricultural Innovation Partnership project funded by USAID in India with Cornell University as the lead institution, was responsible for developing new and enhancing existing animal science courses at select Universities in India for advanced learning to prepare market ready students to improve their employability with market knowledge and market access as well as to develop curricula to address the needs of small and landless farmers to improve their livelihood. Three faculty members and two undergraduate students from TU travelled to India in December of 2012. The project partners in India were Sardar Vallabhbhai Patel University of Agriculture and Technology (SVPUA&T) in Meerut, India, Banaras Hindus University (BHU), Varanasi, India and Assam Agricultural University in Guwahati, India. Over the project period, the team assisted with the development of new curriculum and revised the existing curriculum in animal science and veterinary science programs, diplomas, certificate programs and experiential learning programs. Based on our work, the BHU launched a program for Bachelor of Veterinary Science and Animal Husbandry (B.V.SC. and A.H) effective July 13, 2013. Two other short courses were successfully completed in the hygienic production of milk-based desserts and vegetable processing at BHU. Since 2010, several faculty exchange visits have been made between Tuskegee University and SVPUA & T and BHU. The faculty members from India spent several weeks in the US for developing new curricula and improving the exiting one. In addition to the curricula development for the Indian universities, The TU students visited numerous fish markets, both dry and wet, becoming sensitive to the challenges faced in post-harvest processing, value addition and marketing for such markets in India. Further, TU students observed first-hand various challenges facing animal production systems in rural India. Students prepared white papers describing their international experiences with comparisons of challenges faced by

limited resource producers in rural America (Alabama Black Belt). Collectively, these experiences provided and continue to provide a platform for enhanced intellectual consideration in their training subsequent to the program.

Key Words: experiential learning, undergraduate students, livestock, fisheries

---

1962 (W392) *Fine Focus*: A new international journal for undergraduate microbiology research.

J. L. McKillip*, *Ball State University, Muncie, IN*

The American Association for the Advancement of Science (AAAS) recently disseminated a call to action underscoring the need for a re-evaluation of undergraduate biology education. Development of creative student-centered research into existing curricula is a major theme of this announcement, as well as 'community-based participatory research.' Ball State University is well positioned to take advantage of many of these rapidly evolving objectives in undergraduate science education, largely due to an established track record of excellence through our Biotechnology Certificate Program, an active Chapter of Sigma Xi (the Scientific Research Society), and the only ASM chapter in Indiana. This proposed immersive learning course utilizes the skill sets of 12 undergraduates in four departments to develop a peer-reviewed journal that will publish findings of undergraduate microbiology research internationally. This journal, entitled *Fine Focus*, will be the first of its kind, and will be produced in print form and electronically. Participating students gain a multitude of experiences through collaborations with professionals from ASM National and other professional coalitions. Such experiences will include acquisition of a working knowledge on scientific writing, editing, peer review, graphic design, and advertising, as they relate to dissemination of microbiological research data through an academic journal with international scope. Students will leave the course having also established permanent professional contacts in varied subdisciplines of microbiology worldwide. To be successfully implemented, contemporary undergraduate research in the biosciences must incorporate not only the bench skills, and experimental design principles, but the other vital aspects of doing original research, including professional dissemination. It is this unique niche that *Fine Focus* will fill. Our proposed work here is the first undergraduate journal specifically in microbiology. In a time when limited research budgets prevent undergraduates from attending national conferences to present their data, a venue such as *Fine Focus* allows interested students the opportunity to see their research efforts to fruition and learn about the entire research process at the same time.

Key Words: undergraduate research, microbiology, immersive learning, peer-review

PHYSIOLOGY AND ENDOCRINOLOGY: INTERRELATIONSHIPS BETWEEN ENVIRONMENTAL, METABOLIC AND PHYSIOLOGICAL PROCESSES I

1963 Non-targeted plasma metabolomic profile at early and late lactation in parity 1 dams with diverging body composition at weaning. L. A. Rempel* and J. R. Miles, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Following Lactation is an extremely energy demanding event, impacting naïve dams to a greater extent as they are still physiologically immature. The objective of the current study was to determine if a unique plasma metabolome exists at early and late lactation from first parity gilts having similar body measurements and litter sizes post-farrow (PF) with divergent body condition measurements at weaning. Farrowing data, body composition traits (bodyweight, backfat thickness, and loin eye area), and a plasma sample were collected PF (2.7 ± 1.45 d) and 1d prior to weaning (WN) from composite Landrace-Duroc-Yorkshire gilts bred with Yorkshire semen. Twenty-seven gilts were identified from 68 first parity farrowings with similar farrowing ages (P = 0.9442), PF body weight (P = 0.6789), PF backfat thickness (P = 0.8549), and litter size ($P \geq 0.2263$). Dams were fed to appetite from d3 PF through WN. Of the 27 dams, 10 with the greatest (Hi) and 10 with the least (Lo) body weight loss ($P < 0.0001$; 26.1 ± 1.90 kg and 8.6 ± 1.48 kg, respectively) and backfat thickness loss (P = 0.0094; 4.7 ± 0.86 mm and 1.3 ± 0.67 mm, respectively) had plasma samples submitted for non-targeted profiling by UPLC-MS and GC-MS techniques. Raw spectral data was processed using XCMS package in R to generate feature detection and alignment followed by grouping of features into compounds. Samples were blocked by time of collection (PF and WN) and body condition loss (Hi and Lo) and ANOVA was performed on each compound in R with a Benjamini-Hochburg false discovery rate adjustment. Several compound changes ($P \leq 0.05$) in the metabolome occurred from PF to WN under both detection techniques (UPLC-MS, 112; GC-MS, 59). While changes ($P \leq 0.05$) in compounds between Hi loss and Lo loss also occurred, the prevalence was much less (UPLC-MS, 21; GC-MS, 11). Interestingly, the interaction of time by body condition loss yielded unique compound profiles for both detection techniques (UPLC-MS, 16; GC-MS, 20). Of the 36 compounds significant for interactions, 11 compound signatures may prove to be relevant as predictors for animals that will or won't lose excessive weight and backfat thickness during the course of lactation. Further investigations into the specific identities and validation of all significant compounds will provide potential nutraceuticals to offset intensive depletion of energy stores in young dams during lactation. *USDA is an equal opportunity provider and employer.*

Key Words: gilts, lactation, metabolome

ASAS EARLY CAREER WINNER

Small RNA expression and function during oocyte maturation and embryo development in the pig. B. J. Hale, C.-X. Yang, E. C. Wright, and J. W. Ross* *Department of Animal Science, Iowa State University, Ames.*

Following germinal vesicle breakdown (GVBD), the genome of an immature oocyte becomes transcriptionally inactive and changes in mRNA and protein abundance rely on interactions with the surrounding cumulus oophorus and cellular processes occurring within the oocyte and early embryo prior to the maternal to zygote transition. Thus, molecular events regulating oocyte recruitment and maturation may have a significant impact on the developmental ability of subsequent embryos. MicroRNA (miRNA), in addition to several RNA binding proteins, have a demonstrated ability to regulate both mRNA and protein repertoires through their ability to confer post transcriptional gene regulation (PTGR). To better understand the biological roles of miRNA in the pig oocyte during meiotic progression and during early embryonic development, we characterized expression patterns of miRNA and other small RNA molecules using deep sequencing. Following mapping of our sequencing reads to the pig genome, we identified the expression of several hundred miRNA in cumulus cells, oocytes and in the 4- to 8-cell stage and blastocyst stage embryos following in vitro fertilization. In addition to miRNA, we were able to identify the expression patterns of other small, non-coding RNA, such as piwi-interacting RNA (piRNA), and siRNA. Based on total small RNA expression in the oocyte and the ability of those small RNA to map to intronic and exonic regions of mRNA, we were able to predict mRNA that may be subject to small RNA mediated PTGR in the oocyte. We have also pursued the characterization of miRNA, including MIR21 and its target, programmed cell death 4 (PDCD4), during in vitro maturation and the implications of MIR21 inhibition for developmental competency. We have demonstrated a temporal relationship between MIR21 and PDCD4 protein abundance exists and can be altered during in vitro maturation by prematurely elevating MIR21 abundance or through the use of MIR21 antagonists. We have also further characterized expression of dead end homolog 1, an RNA binding protein with the potential to interact with specific mRNA and spare those molecules from miRNA mediated PTGR, during follicle development, in vitro maturation and during early embryo development. *These projects were supported by USDA National Institute of Food and Agriculture grant no. 2008-35205-05309 and 2008-35205-18712.*

AUTHOR INDEX

Numbers following names refer to abstract numbers. The author index is created directly and automatically from the submitted abstracts. If an author's name is entered differently in multiple abstracts, the entries in this index will reflect those discrepancies. Efforts have been made to make this index consistent; however, error from author entry contributes to inaccuracies.

A

B

C

D

E

F

G

H

I

J

K

L

M

N

O

P

Q

R

S

T

U

V

W

X

Y

Z

KEYWORD INDEX

Numbers following keywords refer to abstract numbers. The keyword index is created directly and automatically from the submitted abstracts. Efforts have been made to make this index consistent; however, error from author entry contributes to inaccuracies.

A

B

C

D

E

F

G

H

I

J

K

L

M

N

O

P

Q

R

S

T

U

V

W

X

Y

Z