234 SheepGenomics – An integrated gene discovery program.
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SheepGenomics (the Program) is a functional genomics program designed to discover genes and their functions and deliver products based on new genetic technologies for the benefit of the Australian sheep industry. There are four industry subprograms contained within the program, including wool biology, muscle growth and development, host resistance to internal parasites and reproductive efficiency. The research strategy of each of these industry subprograms uses positional and functional candidates for gene mapping with a view to identifying precise QTL regions for use in selection and then identification of candidate gene targets for therapeutic intervention of these traits. The most immediate outcome from the program is a series of DNA marker tests for muscle quality and quantity, parasite resistance and wool quality. Work is currently underway to validate existing marker tests and integrate allele effects into routine breeding value calculations so as to facilitate optimal use of genomic information in breeding decisions. SheepGenomics has placed particular emphasis on developing the tools needed to conduct genomic research in sheep including evaluation of bovine micro arrays, development of gene screening assays as well as building large well characterised sheep flocks to enable powerful gene mapping studies. A number of public domain outcomes arise from the Program, which are the result of significant international collaboration. They include development of a virtual sheep genome based on alignment of the end-sequences of BAC clones spanning the entire sheep genome with existing bovine sequence. Current research also involves development of a 1.5x ovine sequence, discovery of tens of thousands of new SNP and microsatellite markers as well as timely integration of this information into an informative sheep genome map. The scope for delivery of long-term benefits to the Australian sheep industry is enormous. Furthermore, each of the publicly available resources will be extremely beneficial to worldwide sheep genome related research efforts.

Key Words: Genomics, Sheep, DNA markers

235 Genomic regions associated with sheep muscle and carcass traits. C. Bidwell*[1] and N. Cockett[2], [1]*Purdue University*, *West Lafayette, IN*, [2]*Utah State University*, *Logan*.

Linkage maps for the sheep genome have been developed but to date no complete genome scan for muscle, adipose or carcass traits are in the public record. Genome scans of selected chromosomes have identified four regions affecting carcass traits in Suffolk and Texel breeds. Chromosomes 2 and 3 were reported to have quantitative trait loci for fat depth and chromosomes 1 and 18 had quantitative trait loci for muscle depth. Several loci affecting muscle growth traits have been identified in sheep. These include callipyge and rib-eye muscling (Carwell) on chromosome 18. The muscle hypertrophy locus in Texels maps near the myostatin locus on chromosome 2. The rib-eye muscling locus lies close to the callipyge region on chromosome 18 but the specific mutation is not known. The callipyge mutation has been identified as a single nucleotide polymorphism in an intragenic region of an imprinted gene cluster. The mutation has altered the expression of at least 5 genes surrounding the mutation. Two of the genes, DLK1 and PEG11 that have paternal allele-specific expression, are candidates for causing muscle hypertrophy in callipyge lambs. With the completion of whole genome sequences in several species including human, rodents, chickens and cattle, the role of noncoding RNA and micro RNA in regulating gene expression has become better understood. The imprinted gene cluster surrounding the callipyge mutation expresses several noncoding RNA and micro RNA that are likely to be involved in polar overdominant inheritance of the phenotype. Recently, a micro RNA that is normally expressed in sheep skeletal muscle has been reported to down-regulate a mutant myostatin allele in Belgian Texels resulting in the muscle hypertrophy phenotype. The callipyge allele and Belgian Texel myostatin allele provide examples of how single nucleotide mutations can have substantial phenotypic effects on muscle and carcass traits through genomic regulatory mechanisms.

Key Words: Sheep, Genomics, Muscle

ADSA – SAD Undergraduate Competition: Original Research

236 Probiotic ice cream manufactured with a weight loss ingredient. M. Brown* and K. J. Aryana, *Louisiana State University*, *Baton Rouge*.

Obesity is directly related to about 300,000 deaths per year in the United States. The Surgeon General estimated obesity to cost $117 billion a year. A novel ingredient, namely "Super Citrimax", is being marketed as a weight loss ingredient (WLI). *Lactobacillus acidophilus* is one of the most effective forms of probiotic (good, helpful) bacteria discovered. The objective was to determine the effect of various amounts of the WLI on the physico-chemical, microbiological and sensory characteristics of probiotic ice cream. The WLI "Super Citrimax" was incorporated at the rate of 0, 1.5, 3.0 and 4.5g per 473 ml (pint) of ice cream. *L. acidophilus* was incorporated into all the pasteurized, homogenized and cooled ice cream mixes at the rate of 0.7% w/v mix. Product manufacture was replicated three times. The meltdown time for the first 15 ml of the ice creams with 3.0 and 4.5g WLI was significantly lower compared to the control. The meltdown volume of the control after one hour was significantly lower compared

to the ice creams with WLI at all concentrations. There were no significant (p<0.05) differences between the control and all treatments for standard plate counts. Control had significantly the highest lactobacilli counts followed by the ice creams with 1.5 g WLI. The ice creams with 3.0 and 4.5g WLI had significantly the lowest lactobacilli counts. The flavor scores for the ice creams with 0, 1.5, and 3.0g WLI were not different from each other but were higher than the ice cream with 4.5 g. Similar results were obtained for the flavor scores of the heat shocked ice creams. There were no differences in body and texture scores of any of the ice creams. The body and texture scores of the heat shocked ice creams with 0, 1.5, 3.0g WLI were not significantly different from each other, but scores for the ice creams with 4.5g were significantly lower than the ice creams with 0 and 1.5g. Incorporation of WLI up to 3 g per 473 ml of ice cream did not influence its flavor. The use of WLI decreased meltdown time, increased meltdown volume, did not alter the standard plate counts, lowered the lactobacilli counts and did not influence sensory body and texture.

Key Words: Probiotic, Obesity, Dairy

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237 Nitrogen and dry matter digestibility of high and low forage diets in dairy heifers. J. M. Daubert*, M. L. Moody, G. I. Zanton, and A. J. Heinrichs, *Pennsylvania State University, University Park.*

Diets fed to growing dairy heifers normally contain high levels of forages and are fed at ad libitum consumption. Feeding high concentrate diets in a restricted manner to achieve optimal ADG however can be more efficient because of reduced metabolic losses associated with digestion and lower feed costs per unit of energy. The objective of this experiment was to determine the DM and N digestibility of 2 diets with differing forage to concentrate ratios in dairy heifers. A 77% corn silage, 23% grain TMR (11.1% CP, 67.9% TDN, 40.9% NDF) and a 67% grain, 33% corn silage TMR (12.0% CP, 67.7% TDN, 37.9% NDF) were fed to 8 Holstein heifers (5 and 12 mo, 172 kg and 337 kg BW). Diets were fed at restricted intake (BW$^{.75}$) twice daily. A split plot design was used with the ages of heifers as the whole plot and the sub-plot of treatment, administered in a 2 period Balaam's design. Periods were 21d in length with 17d of adaptation and 4d total fecal and urine collection. Urine was collected via indwelling urinary catheters and feces were collected immediately at hourly intervals, stored in an airtight container, and weighed daily, mixed, sub-sampled, dried, and ground. DM digestibility was greater for low forage diets (74.3% vs. 70.7%; $P < 0.02$). DM digestibility was higher for older than younger heifers (74.3% vs. 70.7%; $P < 0.05$). N intake was 90.8g for the high forage diet and 100.9g for the low forage diet ($P < 0.04$). N digestibility was not different between treatments (57.5%, low forage vs. 55.1%, high forage; $P > 0.20$). Retained N was higher for low forage than high forage diets (35.5g vs. 26.2g; $P < 0.03$) and was higher for older than younger heifers (36.5g vs. 25.2g; $P < 0.05$). From these data we conclude that high concentrate diets are more digestible with greater retained N than high forage diets with equal nitrogen digestibility for both ages of heifers studied.

Key Words: Dairy heifers, Forage: concentrate, Digestibility

238 Nutritional management practices and current trends on Virginia Grade A dairy farms. J. Leech*, S. Sink, C. Stallings, K. Knowlton, and G. Groover, *Virginia Polytechnic Institute and State University, Blacksburg.*

The objective of this study is to describe current management practices, trends, and plans of Virginia Grade A dairy farms and then compare and contrast these practices based on residency in the Chesapeake Bay Watershed (CBW). In September of 2005 surveys were mailed to 806 Grade A permit holders. Using the Dillman (1978) protocol, follow-up postcards and surveys were mailed based on a predetermined calendar. By January of 2006, 56% of the surveys were returned. CBW herds participating in this survey reported 60,370 dairy animals, including replacement heifers, inside the CBW and 45,382 outside of the CBW. Formal nutrient management plans (NMP) were found on 72% of farms in the CBW, compared to 58% of farms outside out the CBW. Average milking herd size with a NMP is 140 cows and 73 cows without a NMP. Average milk production with a NMP is 63 lbs/cow/day, while farms without a NMP average 53 lbs/cow/day. This analysis indicates that higher levels of management are associated with higher milk production. Thirty-seven percent of the respondents reported plans to expand their herd size in the next 3 years and 52% plan to stay the same size. Of the expanding herds, 68% currently have a NMP in place, while 31% do not. Average herd size on farms planning to expand is currently 141 milking cows. Mixed rations are fed by 96% of the surveyed dairies and these rations are formulated by the feed companies a majority of the time (59%) and by independent nutrition consultants less often (28%). Results of the project have helped to characterize Virginia Grade A dairy farms and highlight differences between management across an environmentally sensitive watershed.

Key Words: Nutrient management

239 A critique of RFV: Comparing RFV to degradation parameters and proposal of an alternative model. T. J. Hackmann* and J. N. Spain, *University of Missouri, Columbia.*

Relative feed value (RFV) is an index used to describe forage quality. RFV scores are calculated using DM concentrations of forage NDF and ADF. Rate and extent of digestion are not directly incorporated into RFV. It has not been determined whether RFV accounts for variation in these parameters across forages. The objectives of this study were to evaluate RFV relative to degradation parameters and to develop an alternative model. Forty-six alfalfa, 16 grass, and 19 mixed grass/legume forage samples were collected from duplicate hay bales submitted to the 2002 and 2003 MO State Fair Hay Contests. Sub-samples were placed in duplicate in situ bags and incubated at 0, 6 or 8, 12, 24, and 48 h. Residues were analyzed for DM, ADF, NDF and CP. PROC NLIN of SAS fit degradation data best to an age-dependent model based on the second-order Erlang distribution. Forage degradation parameters were sorted according to forage (alfalfa, grass, grass/legume). PROC CORR was used to determine correlation coefficients between these parameters and RFV. RFV was correlated to digestible NDF for alfalfa (r = 0.30, $P < 0.05$) and grass/legume (r = 0.52, $P < 0.03$). RFV was correlated to digestible hemicellulose in the grass/legume class (r = 0.57, $P < 0.05$). No correlations between RFV were observed for grasses (NDF: $P > 0.25$; hemicellulose: $P > 0.24$). For all forage classes, there were no relationships between RFV and rates of degradation of any chemical fraction ($P > 0.22$). This suggests that RFV is inadequate in describing forage quality, particularly of grasses. An alternative mechanistic model was formulated that incorporates a library of digestion rate and digestibility values measured in this study. Based on a previously published model, the model is contained in a spreadsheet and designed to be accessible to producers. In sum, this study demonstrates that RFV has little correlation with degradation parameters. RFV possesses shortcomings that limit its accuracy in describing forage quality. A mechanistic model has been developed that may serve as an effective alternative in predicting forage quality.

Key Words: Forage, RFV, In situ degradation

240 Effects of dietary addition of unsaturated fat, vitamin E, and sorbitol on performance of dairy cows and fatty acid concentrations in milk. A. Todd*, M. L. Eastridge, C. V. D. M. Ribeiro, J. Engel, and B. Mathew, *The Ohio State University, Columbus.*

Dietary addition of soybean oil will increase conjugated linoleic acid (CLA) in milk but not to the extent that results from feeding fish oil. Data are limited on CLA in milk from feeding a combination of soybean and fish oils to provide different sources of fatty acids (FA). There is some evidence that increasing dietary concentration of vitamin E may affect milk CLA when feeding unsaturated fat. Sorbitol is being used in commercial feed, but limited published data are available. Eight lactating dairy cows (4 Holstein and 4 Jersey) were used in a Latin square design. Each period consisted of 3 wk, with wk 3 being used for data analyses. Rumen samples were taken from the Holstein cows (one with rumen cannula and via stomach tube for the other 3 cows). Diets consisted of 44% forage (80% corn silage and 20% alfalfa hay), were mixed once daily as TMR, and fed twice daily. The cows

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were fed 4 diets: 1) control diet (CNTL; 500 IU vitamin E), 2) 2% fish oil, 0.5% soybean oil, and 500 IU of vitamin E (FSO), 3) 2% fish oil, 0.5% soybean oil, and 2000 IU of vitamin E (FSOE), and 4) 1% sorbitol (SORB, dry form; 500 IU vitamin E). Diets with oil reduced DMI (18.8 versus 22.7 kg/d), but DMI was similar between CNTL and SORB. Milk yield (31.7 kg/d) and MUN (17.0 mg/dl) were similar among diets. Diets with oil reduced milk fat and protein percentages (3.87, 2.50, 2.58, and 3.96%; 3.38, 3.09, 3.16, and 3.32% for CNTL, FSO, FSOE, and SORB, respectively). Rumen VFA were similar among diets. Concentrations of vaccenic acid (3.49, 8.03, 11.8, and 1.96% of FA, respectively) and CLA (0.63, 1.28, 2.00, and 0.39%, respectively) in milk were increased with the diets containing oil; concentrations of vaccenic acid tended to be higher and CLA was higher for FSOE versus FSO. Both breeds responded similarly to the dietary treatments with respect to performance and individual milk FA. Addition of soybean and fish oils increased CLA in milk, but the higher concentration of vitamin E in combination with the oils further increased milk CLA. Feeding the sorbitol resulted in similar responses as to feeding the CNTL diet.

Key Words: Fish oil, Sorbitol, Vitamin E

241 The effect of lactoferrin on the appearance of immunoglobulins in the peripheral blood of Holstein calves. W. Knauer* and J. M. Smith, *University of Vermont, Burlington*.

The objective of this study was to determine the effect of a single dose of lactoferrin on the appearance of immunoglobulins in the peripheral blood of Holstein bull calves. Shortly after birth, all calves were fed 3.8 L of whole milk supplemented with bovine serum immunoglobulin and with lactoferrin according to treatment. Treatment 1 (n=3) received 4 g lactoferrin; treatment 2 (n=3) received 8 g lactoferrin; treatment 3 (n=3) served as the control and received no supplemental lactoferrin. Subsequently, all calves were fed a 26% crude protein, 18% crude fat milk replacer, mixed at a 15% concentration, to provide dry matter at 2% of body weight per d, for 6 wk. Calves were offered starter grain from 3 d of age and were weaned at d 42. Ten ml of blood were drawn from each calf at 0, 2, 4, 6, 8, 12, 16, 24, 32, and 42 h after the first feeding and at wk 1, 3, 5, 7, and 9. At 24 h, plasma immunoglobulin measured by radial immuno-diffusion did not differ, being 1430 ± 268, 1020 ± 607, and 960 ± 664 mg/dl, respectively, for treatments 1, 2, and 3. This study will be repeated with 3 more blocks of calves before we can conclude whether lactoferrin affects immunoglobulin absorption in neonatal calves.

Key Words: Immunoglobulin, Lactoferrin, Dairy calf

242 Dairy farmers' perceptions and attitudes about lameness. A. M. Edgecomb*, C. L. Wickens, A. J. Zanella, and D. K. Beede, *Michigan State University, East Lansing*.

Lameness reduces productivity and welfare of dairy cattle. Incidence rates (IR) and severity of lameness in some herds are unacceptable. Various management strategies are recommended to reduce lameness; however, success is not observed in many instances. Our objective was to try to better understand the perceptions and attitudes of dairy farmers about lameness. A survey was mailed to all Michigan dairy farmers in July (n = 1,280) and December (n = 1,008). The survey asked four Likert Scale and 22 forced-choice questions. Survey return rate was 33%. Herd size profile of respondents was similar to Michigan's overall herd size profile. Data were analyzed using Statistical Package for the Social Sciences ® 13.0. Ninety-nine percent of respondents believed lame cows feel pain. Overall, 43% 'strongly agreed' or 'agreed' that lameness was a problem in their herds; 23% 'neither agreed nor disagreed', and 31% 'disagreed or strongly disagreed'. However, 53% of farmers indicated that their IR was <10%; 35% believed it was between 11 to 30%; and, only 7% believed their IR was ≥31%, suggesting that lameness was not perceived as a major issue. The actual severity and frequency of lameness in the survey herds was not known. Furthermore, 69% of respondents indicated that they do not use a specific method to record occurrence of lameness. In 38% of herds a professional hoof trimmer was not used, yet only 2% indicated a person on-staff who trimmed hooves. The owner was identified as the main person (79%) responsible for managing lameness; yet, 37% indicated that no other person was responsible to help the owner with lameness in their herd (e.g., no team approach). We conclude based on survey responses that Michigan dairy farmers may underestimate the potential seriousness of lameness on cow productivity and welfare; or, what they might do to reduce lameness. Thus, careful consideration should be given for the best approaches in extension education and research to affect perceptions and attitudes of dairy farmers about lameness to improve animal health, welfare and productivity.

Key Words: Farmers' perceptions, Animal welfare, Dairy lameness

Companion Animals: Advances in Companion Animals - BioMarkers

243 Gut microbial and immunological responses of dogs to diets containing alternative carbohydrates with properties similar to those of dietary fibers. I. S. Middelbos*, N. D. Fastinger, M. R. Godoy, and G. C. Fahey, Jr., *University of Illinois, Urbana*.

Several blends of carbohydrates containing fructooligosaccharides (FOS) and/or mannanoligosaccharides (MOS) from yeast cell wall were evaluated as proxies for traditional dietary fibers in animal protein-based diets fed to dogs. Six mixed breed dogs with hound bloodlines were fitted with ileal "T"-type cannulas. In a 6 x 6 Latin square design with 14 d periods, six diets with different carbohydrate sources were tested. Dogs were offered 175 g twice daily of a brewer's rice and poultry byproduct meal-based diet supplemented with: no additional fiber (CO); 2.5% cellulose (CL); 2.5% beet pulp (BP); 1.0 % cellulose + 1.5% FOS (CF); 1.0% cellulose + 1.2% FOS + 0.3% MOS (CFM1); or 1.0% cellulose + 0.9% FOS + 0.6% MOS (CFM2). Chromic oxide was provided in gelatin capsules as a digestion marker at each feeding. On d 11 through 14 of each period, ileal samples and total feces excreted were collected. On d 14, a blood sample was collected for a complete blood count. Additionally, a fresh fecal sample was collected for bacterial enumeration by serial dilution and plating on selective agars. Treatment least squares means were compared using a Tukey adjustment. Feed intake, fecal score, and fecal pH were similar among treatments, but wet fecal output tended (P = 0.09) to be higher for dogs fed BP compared with CFM1. Fecal *Bifidobacterium* concentrations were higher for CF (P = 0.02) and CFM2 (P = 0.09) than for CL, and tended to be higher (P = 0.06) for CF than for CO.

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