

with a boar; gilts not exhibiting estrus by 180 d of age were considered non pubertal. There was no relationship between growth rate at 100d of age and age at puberty ($P=.67$, $r=.04$). As a consequence, inherent differences in age at puberty (lmean \pm sem) (Early, 150.4 \pm 1.0 d; n=28: Intermediate, 158.4 \pm 6 d; n=74: Late, 174.2 \pm .9 d; n=33: or non pubertal, n=13) affected ($P\leq.05$) weight (109.7 \pm 2.3, 115.7 \pm 1.4, 126.9 \pm 2.1 and 134.0 \pm 3.5 kg, respectively) and backfat depth (12.0 \pm .8, 14.1 \pm .5, 15.2 \pm .7 and 15.2 \pm 1.0 mm, respectively) but not growth rate ($P\geq.05$) (.72 \pm .01, .72 \pm .01, .73 \pm .01 and .76 \pm .02 kg/d, respectively) at puberty. Additionally, the Late puberty group averaged 33.1 \pm .9 d from stimulation to first estrus. Litter of origin affected age at puberty ($P\leq.04$) and is clearly an important contributing factor to inherent differences in the rate of sexual maturity. These results indicate that: 1) with average growth rates exceeding .7kg/d to puberty, gilts would need to cycle by 171 days (31 days after start of stimulation at 140d) to be "selected" below market weight; 22% of gilts failed to meet this target. 2) Later maturing (≥ 175 d) and faster growing ($\geq .8$ kg/d) gilts weighed ≥ 140 kg at first estrus and constitute potentially overweight gilts at breeding and farrowing.

Key Words: Gilts, Puberty, Growth rate

444 The effects of including a blend of encapsulated organic and inorganic acids in diets for weanling pigs. H. H. Stein*¹, D. Peters¹, B. T. Christopherson¹, and E. Cerchiaro², ¹South Dakota State University, ²SODA Feed Ingredients, Monaco.

One hundred and twenty weanling pigs were used in a five-week nursery experiment to evaluate the effect of including the acidifier Aciprol[®] in

the phase 1 and the phase 2 diets for nursery pigs. Aciprol[®] consists of a blend of organic and inorganic acids that have been encapsulated during the manufacturing process. Four experimental groups were included in the experiment. Treatment group 1 was the negative control group # pigs in this group were fed unsupplemented phase 1 and phase 2 diets. Treatment group 2 was the Aciprol[®] supplemented group (0.5 and 0.3% in the phase 1 and the phase 2 diet, respectively) while pigs on treatment groups 3 and 4 were fed diets supplemented with 3000 ppm of zinc oxide and 50 ppm carbadox, respectively. Pigs were weaned at an age of 20 d, and they were placed in groups of five pigs per pen. There were six pen replicates per treatment group. The phase 1 diet was offered on an ad libitum basis during the initial two weeks post-weaning, while in the next three weeks, the phase 2 diet was provided. During the initial two weeks post-weaning, pigs fed the diet containing zinc oxide grew faster ($PP < 0.05$) and had a higher ($P < 0.05$) daily feed intake than had pigs fed any of the other diets. However, during the following 3 weeks and overall for the entire experimental period, no differences ($PP > 0.05$) between the four groups were observed for daily gain or for average daily feed intake. Pigs fed the Aciprol[®] supplemented diets had a greater ($P < 0.1$) gain to feed ratio during the second phase of the experiment and overall for the entire experimental period than had pigs fed diets 1 and 3. The results for the Aciprol[®] supplemented diet were not different ($PP > 0.1$) from those obtained for the carbadox-supplemented diet. From the present investigation, it is concluded that the dietary supplementation with Aciprol[®] during the nursery phase may be as beneficial as the supplementation with carbadox. [®]

Key Words: Protected acids, Weanling pigs

Alpharma Beef Cattle Nutrition Factors Affecting Feed Intake in Beef Cattle

445 The multifactorial nature of food intake control. J.M. Forbes*, Centre for Animal Sciences, University of Leeds, England.

In some situations it is apparent that intake of forage by ruminant animals is limited by the capacity of the digestive tract while in others it seems that metabolic factors control intake. It has sometimes been argued that physical limitation on intake is more apparent than real because positive relationships between rate of digestion and intake can be ascribed to causes other than gut capacity. However, there are receptors in the rumen wall sensitive to stretch and their afferent pathways converge with those from other classes of receptor thereby providing the means for several types of stimulus to be combined before reaching the controlling circuits of the brain. In addition there is experimental evidence of additivity of intake-limiting factors in sheep and dairy cows. The fact that various signals affecting intake (physical, metabolic, behavioral, environmental) are in different currencies has proved a barrier to the development of models; it is proposed that abdominal stimuli resulting from the ingestion of food, as well as climatic and social factors, generate discomforts which animals prefer to avoid and learn to minimize. There is considerable evidence that ruminants can learn to avoid toxic or imbalanced foods and to choose between two foods of different nutritional value in order to avoid either an excess or a deficiency of the nutrient in which the two foods differ. From this it can be deduced that the intake of a single food may be eaten in quantities that minimize the total discomfort whereas when two or more foods are available both the mixture of foods and their total intake are varied to achieve this state. Animals fed ad libitum have naturally fluctuating daily intakes which allows their daily intake to settle in the region of their most comfortable state. While these theories have not yet been properly quantified they provide a framework for integrating the various factors known to affect intake and should lead the way to better understanding and, possibly, prediction of voluntary feed intake and diet selection by beef cattle.

Key Words: Ruminants, Feed intake, Minimal Total Discomfort

446 Effects of roughage source and level on intake by feedlot cattle. M. L. Galyean*¹ and P. J. Defoor², ¹Texas Tech University, ²Nutrition Service Associates, Pratt, KS.

Intake by beef cattle fed high-concentrate, grain-based diets is likely controlled by metabolic factors and not limited by bulk fill. Small changes (e.g., 5% of DM or less) in the level of bulky roughage and changing from

less fibrous to more fibrous sources of roughage typically increase DMI by feedlot cattle. Reasons for increased DMI with changes in roughage level and source are not fully understood. Energy dilution effects caused by added dietary fiber might be responsible for altered DMI, but the quantity of dietary NEg provided by roughage shows little relationship to changes in DMI with roughage source and level. Altered rate of ruminal fermentation and/or acid production as a result of roughage source and level might affect DMI via various mechanisms, including: 1) increased chewing and/or rumination, with increased saliva flow; 2) inherent buffering properties of roughages; and 3) altered ruminal and/or intestinal digesta kinetics. We hypothesized that much of the effect of roughage source and level on DMI by feedlot cattle could be accounted for by changes in dietary NDF. Data from 11 trials in the published literature involving roughage source and level effects on intake by feedlot cattle were compiled. The dataset included 48 treatment means with roughage sources including hays, straws, byproducts, and silages. Roughage level ranged from 0 to 30% of DM. Effects of dietary roughage level (% of DM), NDF (% of dietary NDF from roughage), or effective NDF (eNDF, % of dietary eNDF from roughage) and the random effects of trial on DMI (% of BW) were evaluated using the MIXED procedure of SAS (SAS Inst., Inc., Cary, NC). Tabular values were used to obtain estimates of NDF and eNDF. Using trial-adjusted means, dietary roughage level accounted for 69.9% of the variation in DMI, whereas the percentage of dietary NDF and eNDF supplied by roughage accounted for 92.0 and 93.1%, respectively, of the variation in DMI. The relationship between dietary NDF (% supplied by roughage) and DMI (% of BW) for trial-adjusted data was given by: $DMI = 1.8562 - 0.02751 \times NDF$ ($P < 0.01$; $RMSE = 0.0447$). Based on these results, percentage of dietary NDF supplied by roughage seems useful for predicting effects of roughage source and level on DMI by feedlot cattle.

Key Words: Feedlot cattle, Feed intake, Neutral detergent fiber

447 Metabolic consequences of feeding behavior and intake in feedlot cattle. T.A. McAllister*¹, K.S. SchwartzkopfGenswein², K.A. Beauchemin¹, D.J. Gibb¹, M.N. Streeter³, D.D. Hickman¹, and D.H. Crews, Jr.¹, ¹Agriculture and Agri-Food Canada, Lethbridge, AB, ²Alberta Agriculture, Food and Rural Development, Lethbridge, AB, ³Alpharma Inc., Fort Lee, NJ.

Nutritionists and feedlot managers commonly attribute metabolic digestive disturbances such as subclinical acidosis to abnormal feeding

behavior and erratic feed intake by cattle. This perception is based on the belief that variability in intake of high grain diets compromises the maintenance of ruminal pH at levels high enough for optimal fibre digestion and rumen function (i.e., >5.6 to 5.8). Periodic abundance in starch availability allows amylolytic bacteria (e.g., *Ruminobacter amylophilus*, *Streptococcus bovis*, *Lactobacillus* spp.) to proliferate and produce excessive quantities of fermentation acids. It has been proposed that heightened VFA production stimulates satiety receptors in cattle, which in turn results in the commonly observed "off-feed" or low intake syndrome. Despite this well accepted relationship, comparatively few studies have actually demonstrated that variability in ad libitum feed intake impairs growth performance of cattle. Ruminal pH profiles differ substantially among cattle, even among those with identical diet composition, feed quantity and delivery schedules. It is apparent, therefore, that factors other than meal size and feeding regime determine an animal's susceptibility to subclinical acidosis and ultimately, its growth performance. Feedlot management practices developed to regulate feeding behavior and reduce variations in feed intake by penned cattle include programmed feeding, multiple feed deliveries per day, and consistent timing of feed delivery. However, the efficacy of these practices is assessed largely on the basis of intake per pen, with little or no appreciation of the variation in feed intake among individuals. Further characterization of this variability in feeding behaviors among penmates could provide the foundation for effective refinement of present feeding practices.

Key Words: Acidosis, Bunk Management, Rumen

448 Controlling variation in feed intake through bunk management. R. H. Pritchard*¹, ¹South Dakota State University.

Controlling variation of daily feed intake stems from the obvious concern that a significant aberration in grain intake can lead to clinical acidosis

or death. Less dramatic aberrations also occur when cattle have unrestricted access to feed. A cyclic pattern of higher and lower daily DMI can cause gain efficiency to be less than that predicted from the mean DMI since ADG responses to changes in DMI are not linear. If bunk management (BM) is a means of ameliorating either of these events, it is presumed that management ascribed to the pen is affecting variability in daily DMI by individuals within the pen. Two likely mechanisms are limiting availability of feed to prevent overconsumption events, or affecting animal behavior so that daily intake is more consistent. BM approaches that have been evaluated for their impact on production rates and in some instances on day to day variability in DMI include: limiting the quantity of feed available or the amount of time feed is available each day, the timing and frequency of feed deliveries, linear bunk space allocation, and mixed diet or segregated ingredient feeding. When BM approaches do alter responses, it may be that the approach has a direct biological and/or behavioral impact on the animal, or that the approach itself involves less variation, which is consequently favorable to the animal (or the data). The causes of variable results in BM research can be ambiguous. Management and feeding systems are difficult to standardize which can cause the definitions of controls, the characterizations of treatments, and the context of responses to be inconsistent. A rudimentary limitation is that in systems where individual daily DMI is known, competition for access to feed is usually not comparable to typical pen feeding. There is evidence of favorable responses to some BM approaches that could be used commercially. Impact on production efficiency in these studies is of significant biological and economic importance. These mechanisms must be more fully characterized to allow broad application.

Key Words: cattle, management, feedlot

Breeding and Genetics Applications of Functional Genomics in Animal Breeding and Genetics

449 Novel approaches for complex trait analysis. B Bowen*, *Lynx Therapeutics, Inc.*

Complex traits include the majority of human diseases and commercially important targets of selection in agriculture, such as yield or hybrid vigor. Unlike monogenic traits, they are controlled or influenced by the interplay of multiple genes and environmental factors. Although it is not clear to what extent complex traits are controlled by alleles that qualitatively affect the function of proteins or quantitatively affect gene expression, both types of genetic variation are likely to be important. Lynx's Massively Parallel Signature Sequencing (MPSS™) technology is a gene expression profiling system that can help understand the genetic architecture of complex traits at the molecular level by addressing two fundamental questions in quantitative genetics:

1. How much variation in gene expression between individuals is controlled by cis-acting alleles vs. segregation of trans-acting factors? 2. How many genes that differ in expression between parents and offspring behave non-additively?

I will demonstrate how an understanding of these two questions can be exploited to help identify candidate genes for quantitative trait loci controlling a complex trait in a model plant species on the one hand and candidate genes for heterosis in a poorly characterized animal species on the other.

Key Words: Gene Expression, Quantitative Trait Loci, Genetic Variation

450 Integrating molecular marker information into national beef cattle evaluation. R. L. Quaas*, *Cornell University, Ithaca, New York.*

Information from molecular markers has the potential to increase the accuracy of genetic evaluation, especially for traits for which phenotypes are difficult and/or expensive to obtain. Several problems remain for this potential to be realized. The purpose of this paper is to discuss some of these and offer some suggestions. Among these problems is the likelihood that the number of animals in the pedigree will exceed the number with phenotypes which will greatly exceed those with genotypes. Suggestions as to how to combine many phenotypic data with

limited marker data will be discussed in more detail. Emphasis is on approximations practicable for routine national beef cattle evaluation.

Key Words: Genetic Markers, Genetic Evaluation, National Beef Cattle Evaluation

451 Using gene expression profiling to study disease resistance in the chicken: honing in on candidate genes. J. Burnside*¹, R. Morgan¹, and H. Cheng², ¹Delaware Biotechnology Institute, University of Delaware, ²USDA/ARS, Avian Disease and Oncology Laboratory.

Poultry disease is a major threat to chickens raised in a production environment, where birds are exposed to a variety of pathogens. Of particular economic importance is Marek's Disease (MD), which is caused by the MD virus (MDV), an oncogenic herpesvirus of chickens that latently infects T lymphocytes and induces T-cell lymphomas. A study of the gene regulatory pathways that control development of the immune system as well as an understanding of the host response to MDV will improve our understanding and our control of this disease. Using a functional genomics approach, we have sequenced over 6,000 ESTs from chicken lymphoid libraries and used a selected subset of these ESTs for the preparation of DNA arrays for gene expression profiling studies. These arrays have been used to assess developmental changes in gene expression in the immune system. Expression of cell surface markers (MHC class I, MHC class II invariant chain, CD8, CD18, and beta-2 microglobulin), and genes involved in the innate immune response (NK lysin) increased with age, and these patterns were consistent with an increase in the immune-responsiveness of young chicks. We also evaluated changes in viral and cellular gene expression that accompany infection of chicken embryo fibroblasts (CEF) with MDV. MIP, quiescence specific protein and MHC class I genes were among the host genes that were induced by infection with MDV. In parallel studies, these arrays have been used to identify genes that confer genetic resistance to MD, by comparing expression profiles in genetically resistant and susceptible birds. Differential expression of candidate genes has been detected, and at least one maps near a QTL conferring resistance to MD. Using