

intake protein (UIP). The balance of amino acids depends upon the proportion of UIP and the amino acid spectrum of the UIP. Therefore, it is absolutely essential to measure or predict the relative amounts of MP (metabolizable protein) from microbes and UIP in any given feeding scenario. Both the production potential of the beef animal and microbial protein synthesis are driven by energy. It is impossible to predict MP supplied to the lower gut and MP needs of the animal without having accurate estimates of energy needs, energy supplies and ruminal energy availability. While there are many variations on beef production systems, most are based on high grain (finishing) diets or high forage diets. Forage contains little UIP and that UIP appears to be poorly digested (<50%). Without supplements, essentially all of the MP in forage feeding situations is supplied by microbes. Site of carbohydrate digestion (NDF) is relatively predictable and methodology for measuring forage protein degradation is relatively precise (NDF-N). Degradable intake protein (DIP) may be deficient in some situations. Microbial protein synthesis efficiency decreases as diet TDN decreases from 60% down to 45 to 50%. Low microbial production and low forage UIP create MP deficiencies in many forage feeding situations. On high grain diets, energy supply is high but microbial efficiency is limited by low ruminal pH. Site of carbohydrate digestion (starch) varies with grain type and processing. Estimation of ruminal degradation of grain (starch and protein) is not precise. DIP is usually required. Byproducts reduce starch, raise pH and add protein (maybe DIP or UIP depending on byproduct). Corn is high in UIP and the UIP is highly digested (>90%). Therefore feedlot cattle generally have adequate supplies of MP. It is difficult to produce an amino acid deficiency in feedlot cattle. Growing cattle can be deficient in specific amino acids depending upon the amino acid balance in the UIP.

Key Words: Beef Cattle, Metabolizable Protein, Amino Acids

Swine Species Symposium. Improving Sow Productivity: Recent Developments in Gilt and Lactation Management

359 Increasing weaning age improves pig performance and profitability in a multi-site production system. R. G. Main*, S. S. Dritz, M. D. Tokach, R. D. Goodband, and J. L. Nelssen, *Kansas State University, Manhattan.*

Two trials were conducted to determine the effects of weaning age on growing pig biologic and economic performance in a multi-site production system. Trial 2 also evaluated the effects of modifying nursery feed budgets according to weaning age. In trial 1 (2,272 pigs), treatments included weaning litters at 12, 15, 18, or 21 d of age. In trial 2 (3,456 pigs), litters were weaned at 15, 16, 18, 19, 21, or 22 d of age and categorized into three treatments (15.5, 18.5, or 21.5 d of age). In trial 2, pigs in each age group were fed a nursery feed budget classified as more or less complex. Since feed budget did not affect ($P > 0.27$) performance, only weaning age effects are presented. Each trial was conducted as a randomized complete block design with four blocks of linked nursery and finishing sites (6 and 10 reps/block in trials 1 and 2, respectively). All wean age treatments were weaned from a 7,300-head sow farm on the same day into the same nursery. Each block remained intact as pigs moved from nursery to finishing site. Costs and revenue were measured for each pen. Increasing weaning age (12, 15, 18, or 21; and 15.5, 18.5, or 21.5 in trials 1 and 2, respectively) improved (linear, $P < 0.03$) wean-to-finish ADG (580, 616, 637, 687 ± 8 g/d; 676, 697, 722 ± 6 g/d), mortality rate (9.4, 7.9, 6.8, 3.6 ± 0.95 %; 3.9, 3.4, 2.5 ± 0.5 %), weight sold per pig weaned (94.1, 100.5, 104.4, 113.1 ± 1.3 kg, 107.6, 111.6, 116.2 ± 1.1 kg), income over costs (\$2.00, 5.11, 7.12, 11.19 ± 0.52 /pig; \$7.99, 10.04, 12.46 ± 0.46 /pig), and cost per hundred kg sold (\$86.19, 83.24, 81.49, 78.36 ± 0.46 ; \$80.80, 79.25, 77.50 ± 0.32). The improvements in growth and mortality largely occurred in the initial 42 d after weaning, with smaller growth improvements in finishing. These studies indicate that increasing weaning age up to 21.5 d predictably improves grow-finish throughput (1.80 ± 0.12 kg sold/pig/d of age) and profitability ($\$0.89 \pm 0.05$ /pig/d of age) within this multi-site production system.

Key Words: Weaning Age, Pigs, Economics

358 Mathematical models used to determine ruminant protein requirements and availabilities. R. A. Kohn*¹ and M. D. Hanigan², ¹University of Maryland, College Park, ²Land O' Lakes/Farmland Feeds, LLC, St. Louis, MO.

The objective of this presentation is to review the functional differences between mathematical models that are used to formulate diets for beef and dairy cattle with respect to protein and amino acid requirements. An ideal model for diet formulation would require minimal data input to accurately predict the amount and form of protein required by the animal and supplied by available feedstuffs. Where appropriate, there should be a means to incorporate feed analysis results into the model to improve predictions. All current models divide dietary crude protein into two parts: that required by ruminal microbes and that required at the small intestine as true feed protein that has not been digested by ruminal microbes. The most recent models have established specific requirements and availabilities of the first limiting amino acids (e.g. lys, met). The Cornell model (CNCPS) also formulates for required amino acid and peptide protein (as opposed to non-protein nitrogen) for rumen fermentation. The 2001 NRC can incorporate soluble protein information, and the CNCPS can use protein solubility in buffers and detergents as indicators of protein degradation. When several models (NRC, 1989; CNCPS, CPM Dairy) were compared for their ability to predict protein flows to the small intestine for typical diets and cows, there were no obvious advantages for any one model. However, the NRC, 1989 was best able to predict losses in milk production due to underfeeding of protein to dairy cows. The 2001 NRC increased both RDP and RUP requirements for dairy cows without affecting the supply. As a result, the total CP recommended in diets increased for the 2001 NRC compared to the 1989 version. However, the amount recommended in the 1989 NRC was adequate. The various models that currently are available differ substantially in their level of complexity and the number and type of feed analyses that can be used. But, there is little evidence that this increased complexity has improved the accuracy of model predictions for typical farm conditions.

Key Words: Protein Requirements, Mathematical Models

360 Behavior of sows during lactation. J. McGlone*, *Pork Industry Institute, Texas Tech University, Lubbock.*

Sow behavior is influenced by their genes and by their environment. During lactation, sows undergo significant changes in physiology that cause large behavioral changes. The objective of this review is to summarize the literature on sow behavior during lactation and the effects of management practices (such as weaning age and housing system) on sow behavior. Also, this review will summarize sow behaviors that lead to problems with the lactating sow or piglets. Sows undergo four major phases of behavior in the peri-lactation phase. First, prior to farrowing, sows undergo nest-building behavior that may involve building of an actual nest if sows are given building materials or expression of phantom nest-building behaviors in the absence of building materials. The second phase involves the establishment of the maternal-neonatal bond. This phase requires 12 to 24 h and is critical for piglet survival and growth. Maternal pheromones are secreted and the piglet is able to suckle in the presence of maternal pheromones. The piglet also is able to recognize its mother by her odor signature. The third phase is the lactation phase in which sows and piglets organize suckling with an interval of 40 to 50 min between nursing bouts. As piglets become larger, they will have larger, but less frequent meals - this trend continues from birth through market age. If given the opportunity, sows will spend less time with piglets as lactation progresses. The fourth phase is the weaning phase which can be gradual or abrupt and includes weaning and the weaning to estrus interval. Natural weaning by the sow can take place at any time from 3 d to 6 months of age. Sow genotype and the housing system can have major impacts on pig behavior during each phase. Weaning age will significantly impact phase 3 and 4 sow behaviors. Sow welfare including stress-related behaviors, wounds, scratches, injuries, weight loss and body condition are influenced by the behavior sows express as a result of their genotype, housing system and management practices.

Key Words: Pigs, Lactation, Behavior

361 Field experience with gilt age and lactation length. L. V. Himmelberg*, *Danbred North America, Seward, NE.*

The objective of this presentation will be to relate field experiences regarding the impact of gilt age and lactation length on sow productivity. Over time the largest percentage of females to farrow within a herd are parity one and therefore overall herd productivity is greatly influenced by the results achieved by them. Gilt age and weight at first service have a direct impact on these results. Field observations show that increasing gilt age and weight by approximately 30 days and 20 kilograms respectively, over traditional targets of 210 days and 125 kilograms can improve first parity born alive by as much as .75 pig per litter. Early

weaning programs designed to increase sow productivity and improve health have driven weaning averages below 21 days of age. Many producers have noted that weaning this early has a negative impact on subsequent parity born alive. To explore this, commercial production herds containing Danish genetics were examined. Born alive per litter was treated as a dependent variable and previous lactation length as an independent variable within each herd. The results of this analysis showed an average decrease in subsequent parity born alive of .12 pig per day for each day decrease in weaning average between 21 and 15.

Key Words: Gilt, Lactation

Breeding and Genetics: Genetics Methodology 2

362 Pedigraph 2.0: A software tool for the graphing and analysis of large complex pedigrees. J. R. Garbe* and Y. Da, *Department of Animal Science, University of Minnesota, St. Paul.*

Pedigree graphing and analysis are important tasks in animal breeding and genetics. However, pedigree graphing and analysis are difficult for large complex pedigrees. Pedigraph version 2.0 provides rapid graphical visualization and analysis of large, complex pedigrees with a variety of options and features. The program produces artistic pedigree drawings with options to draw the full pedigree, a summarized pedigree with three options, or an extracted pedigree for a selected individual. The user has control over drawing style, fill color, line color, page size, pedigree size, title of the pedigree, gap between two generations, display of trait status, genotype, or inbreeding coefficient, and the minimal number of offspring required for a family to be included in the pedigree. The program can also calculate inbreeding coefficients for all individuals and the coefficient of coancestry between each pair of individuals. The program has been tested using two large and complex populations for its capability of pedigree graphing and its computational feasibility to calculate inbreeding and coancestry coefficients. The program has not encountered limitations in sample size or complexity of the pedigree. The only limitation encountered so far is the ability to print a potentially huge pedigree drawing. These tests plus over a years trial indicate that Pedigraph could be a versatile and capable tool for pedigree visualization and analysis.

Key Words: Pedigree, Genealogy, Visualization

363 Multiple-breed genetic inference using a heavy-tailed structural model for heterogeneous residual variances. F. F. Cardoso, G. J. M. Rosa, and R. J. Tempelman*, *Michigan State University, East Lansing.*

Multiple-breed genetic models have been recently demonstrated to effectively specify the heterogeneous genetic variances that exist between different beef cattle breed groups. We extend these models to allow for heterogeneous residual variances that may be a function of fixed effects (e.g. sex, breed proportion, or breed group heterozygosity) and random effects such as contemporary groups (CG). We additionally specify the residual distributions to be either Gaussian or based on a heavy tailed alternative such as the Student t , in order to distinguish potential outliers from individuals in high variance environments. For either of these two distributions and their homoskedastic counterparts, we analyzed 22,717 post weaning gain records from a Nelore-Hereford population based on a Markov chain Monte Carlo animal model implementation. The heteroskedastic Student t error model (with estimated degrees of freedom 7.33 ± 0.48) was clearly the best fitting model based on a Pseudo-Bayes factor criterion. Sex and breed group heterozygosity, but not breed proportion, appeared to be marginally important sources of residual heteroskedasticity. Specifically, the male residual variance was estimated to be 1.13 ± 0.09 times that for females whereas, for example, the residual variance in F_1 animals was estimated to be 0.70 ± 0.16 times that for purebreds. The CG effects were important random sources of residual heteroskedasticity; that is, the standard deviation of ratios of CG-specific residual variances relative to the baseline average was estimated to be 0.72 ± 0.06 . Purebred Nelores were estimated to have a larger genetic variance ($124.87 \pm 21.75 \text{kg}^2$) compared to Herefords ($40.89 \pm 6.70 \text{kg}^2$) under the heteroskedastic Student t error model; however, the converse was observed from results based on a homoskedastic Student t error model ($46.24 \pm 10.90 \text{kg}^2$ and 60.11 ± 8.54

kg^2 , respectively). These results naturally have important implications for multiple breed genetic evaluations.

Key Words: Bayesian Inference, Genetic Predictions, Outlier Robustness

364 Genetic evaluation of male fertility using a threshold model with emphasis on accurate estimation of conception rate. G. Abdel-Azim*¹, S. Schnell¹, G. Gelbert¹, and H. Rycroft², ¹Genex Cooperative, Inc., *Shawano, WI*, ²Cooperative Resources International, *Shawano, WI.*

A threshold model for male fertility evaluation was applied to a data set of size 2,233,377 records. The model included herd, year-season, bull age, cow parity, as fixed factors, and service bull, inseminated cow, and inseminator as random factors. Variance components estimated as ratios of the total phenotypic variance were 2.8, 11.1, and 5.2% for service bull, cow and inseminator, respectively. The main objective of the study was to transform bull solutions into percentages of conception rates, a more interpretable value to indicate male fertility. The transformation implemented avoids problems arising when linear combinations of estimates are used in a nonlinear parametric function, a practice that is currently in use to report national calving ease evaluations estimated by a threshold model. The transformation we implemented takes into account the accuracy of estimating breeding values and other factors in the model, hence, current practices that do not take accuracy into account were shown to consistently overestimate the probability of success in the binomial setting studied.

Key Words: Fertility, Conception Rate, Genetic Evaluation

365 Application of a random regression model to gene expression profiling. S. L. Rodriguez-Zas*, J. J. Looor, J. K. Drackley, and H. A. Lewin, *University of Illinois, Urbana.*

The patterns of gene expression recorded on individuals over a period can be studied using discrete or continuous representations of time. Within the later representation, the profile of expression can be modeled using common (fixed) and individual (random) polynomial coefficients in time. We evaluated the potential of random regression models to describe the fluctuations in the gene transcription levels recorded at successive time points. The data consisted of fluorescence intensities on more than 6000 unique genes recorded using spotted cDNA microarray technology. Liver samples were obtained at -65 d, -30d, -14d, +1d, +14d, +28d and +49d relative to calving on 8 Holstein cows. A reference design was implemented with each cow-day sample represented in two reverse-dye microarrays and each gene double spotted on each microarray. Fluorescence intensity measurements on 106 microarrays were filtered for weak signals and were normalized using a log2 transformation on the loess-adjusted values. The random regression model included linear to quartic polynomials on days and accounted for heteroscedasticity between days. Three percent of the genes had at least one significant ($P < 0.0001$) regression coefficient in days. The majority of these genes had significant quadratic trends alone or in combination with a significant quartic trend. Hierarchical and disjoint clustering of these coefficient estimates indicated the presence of 5 clusters. Four of these clusters were approximately characterized by significant (positive and negative) quadratic regression coefficients in combination with significant (positive and negative) quartic regression coefficient within each signed quadratic group. The last cluster was characterized by significant linear and cubic regression coefficients. Results from this study