proliferation, serum IgG, IgA, IgM,C3,C4 ($P \leq 0.05$), and increased IL-2,IL-18 ($P \leq 0.01$), decreased F/G and diarrhea ($P \leq 0.05$), while there was no significant difference between rPLFN group and antibiotics group. These results imply that rPLFN would be used as an additive to improve growth performance and immune functions of weanling pigs. This would seem to be a good method for defending weanling piglets from infections and weanling stress.

Key Words: recombine porcine Lactoferrin-N(rPLFN), growth performance, immune function

199 Effects of α-ketoglutarate on mucosal morphology and function of small intestine in piglets. Q. Hu, Y. Hou*, B. Ding, H. Zhu, Y. Liu, M. Wang, and H. Xiao, *Hubei key Laboratory of Animal Nutrition and Feed Science, Wuhan Polytechnic University*, *Wuhan, Hubei, P. R. China*.

Three experiments were conducted to evaluate the effects of dietary supplementation of α - ketoglutarate (AKG) on mucosal morphology and function of small intestine in piglets. Both the experiment 1 and experiment 2 included 32 piglets, and they were weaned at 21 ± 2 days and randomly allotted to 4 treatment groups with dietary supplementation of AKG at 0, 0.5%, 1.0% and 2.0% respectively. On the 14th day of the experiment, the piglets were infused 10% D-xylose solution at 1 ml per kg of body weight, after 60 minutes, blood samples were collected from anterior vena cava, the concentration of D-xylose and activity of diamine oxidase and the content of endotoxin in plasma were determined. In the experiment 3, twelve piglets were weaned at 21 ± 2 days and randomly divided into 2 treatment groups, one group was fed with basal diet and the other were fed with basal diet +1.0% AKG. On the 14th day, all pigs were sacrificed to observe the mucosal morphology. The small intestine was cut off three 5 cm segments at distal duodenum, mid-jejunum and mid-ileum. The segments were processed, embedded, and stained to make tissue sections, the villus height (VH) and the associated crypt depth (CD) were measured, and then the ratio of villus height to crypt depth (VH/CD) were calculated. Differences among groups were analyzed by one-way analysis of variance and subsequent Duncan's multiple range test. The results showed that, in the groups of 1.0% AKG, crypt depth and activities of diamine oxidase were decreased ($P < 0.10$), VH/CD was increased; compared to 0% group, in the groups of 1.0% AKG, the contents of endotoxin were decreased by 33.41% ($P < 0.05$), and plasma D-xylose contents were increased by 21.02% ($P < 0.05$). These results indicated that dietary supplementation of AKG could improve histological morphology and function of the small intestine of piglets and dietary supplementation of 1.0% AKG was better relatively.

Key Words: α-ketoglutarate, small Intestine, piglet

Breeding and Genetics: Whole Genome Selection - The New Frontier?

200 National and international genomic evaluations for dairy cattle. P. M. VanRaden*[1] and P. G. Sullivan[2], [1]*USDA Animal Improvement Programs Laboratory*, *Beltsville, MD*, [2]*Canadian Dairy Network*, *Guelph, ON, Canada*.

Genomic evaluations are rapidly replacing traditional evaluation systems used for dairy cattle selection. More than 35,000 dairy cattle worldwide have been genotyped for 50,000 markers. Reliabilities of 60-70% for young genotyped animals are now possible as compared to 35% for parent average. Gains depend on numbers of genotypes and are much less for Jerseys or Brown Swiss than for the large North American Holstein population. Accurate blending of genomic and non-genomic information is important because many animals are not genotyped. In U.S. evaluations, extra information from genotyped parents is transferred to non-genotyped descendants using the same formulas that adjust traditional evaluations for foreign parent data. Propagation from genotyped progeny to non-genotyped parents is more difficult because the extra information from genotyped progeny should not exceed the direct gain from genotyping the parent. Genomic information may be transferred across countries using simple conversion equations or by modifying multi-trait across-country evaluation (MACE) to account for correlated residuals and to account for genomic rather than pedigree relationships when deregressing national evaluations. In traditional MACE, residuals are independent because each daughter is measured in only one country. In genomic MACE, residuals may be correlated for two reasons: 1) multiple evaluation centers may include the same genomic and phenotypic data in national estimates of marker effects, and 2) genomic predictions act as repeated measures of the same portion of genetic merit rather than independent measures of total merit, especially for major gene marker(s) and low-density SNP panels. Marker effects in the U.S. and Canada are highly correlated because both countries share the same genomic data and include traditional MACE evaluations as input to their genomic equations. Residual correlations can be approximated using daughter equivalents from genomics as a fraction of the total in each country and proportions of common bulls shared. Economies of scale in genomics promote cooperation across country borders.

Key Words: genomic evaluation, MACE, SNP

201 Beef cattle industry structure: Implications for whole genome selection. A. Van Eenennaam*, *University of California*, *Davis*.

The breed diversity, lack of vertical-integration, and segmentation of the beef cattle industry present unique challenges for the implementation of whole genome selection. Under the current model of genetic improvement, the costs involved in phenotyping and objectively ranking breeding animals are mostly incurred by the seedstock sector in partnership with breed associations. Record-keeping focuses on traits that are of importance to bull-buyers who understandably select on traits that directly impact their profitability. However, downstream segments of the beef industry (feeder, processor, retailer) each have their own set of economically relevant traits, and market failure means breeders and cow-calf producers receive little or no reward for including traits that are of importance to these segments (e.g. tenderness) in their selection decisions. The promise of genomic selection to improve traits that are currently intractable (feedlot health, feed efficiency, eating experience) will require the development of training populations with appropriate phenotypes. Research suggests that the development of accurate genomic prediction equations will require training populations of thousands of phenotyped and genotyped animals. Developing these populations will be expensive and require increased collaboration between industry segments. Additionally, marketing systems will have to begin to appropriately reward the costs associated with the incorporation of new traits into breeding and cattle evaluation programs. Finally, genomic prediction equations will need to be validated in populations raised in different environments and made up of various breed combinations. These variables have frustrated the validation of the first generation of

DNA-marker tests for quantitative traits in beef cattle. If the scientific validation of this approach shows that it is able to consistently deliver accurate genetic merit estimates for young beef sires, producer education and integration of genomic data into national cattle evaluation will be requisite for the ultimate adoption of whole genome selection.

Key Words: beef cattle, genomic selection, industry structure

202 Utilization of next generation sequencing technologies for development of a high-density pig SNP genotyping platform. R. P. M. A. Crooijmans*[1], M. A. M. Groenen[1], and L. B. Schook[2], [1]*Wageningen University, Wageningen, the Netherlands*, [2]*University of Illinois, Urbana*.

The Illumina Genome Analyzer (Solexa) and Roche 454 FLX 'next generation' sequencing platforms were identify porcine SNPs from diverse commercial breeds. The combined approach permitted increased sequence depth and longer 454 reads to obtain adjacent SNP sequence information to design the primers for the genotyping assay. Considering that only approximately 70% of the pig genome had been sequenced at the time of SNP discovery and beadchip design, the utilization of the longer 454 reads further allowed coverage of the genome at the same SNP density as for the remaining 30% not sequenced or assembled. The only caveat in this approach is the fact that because no information was available regarding the position of these SNPs, it was not possible to predict even SNP distribution. Thus, to maximize SNP spacing, the position of such SNPs on the porcine genome was predicted based on the human-porcine comparative map and end sequences of BACs present on the highly robust BAC contig map. Mapping results on build 8 of the pig genome clearly underscored the success of this approach. The importance of this strategy can be extended to other species where the reference genome and the genomic resources are less developed and/or for which there is no genome sequence available. The number of new porcine SNPs identified in this study exceeded 375,000, which demonstrated that the identification of large numbers of novel SNPs is now feasible in a highly efficient manner. The overall confidence of the SNPs identified by this approach using the porcine SNP60 beadchip demonstrated > 95% of the predicted SNPs were validated. These SNPs were subsequently used to design an Illumina iSelect pig DNA chip (60,000 SNPs). This Illumina iSelect chip was used to SNP genotype global wild boar (35 samples from Europe and Asia) and ten European, North American and Asian domesticated breeds. The average heterozygosity and MAF ranged from 21.6 to 31 and 0.15 to 0.23 respectively for Western breeds, from 14.3 to 17.3 and 0.08 to 0.19 respectively for Chinese breeds, and from 8 to 17.6 and 0.09 to 0.24 for global Wild boar populations. Considering that the breeds used for the discovery of these SNPs included the four main breeds used in pig production (Duroc, Pietrain, Landrace and Large White) as well as the wild boar, the ancestor of all modern pig breeds, it is anticipated that the porcine SNP60 beadchip will be highly efficient to be used for genomic selection by the pig breeding industry.

203 Bioinformatics requirements to apply whole genome prediction in livestock. D. Garrick*, *Iowa State University*, *Ames.*

The traditional method of evaluation adjusts records for non-genetic effects then combines adjusted deviations on the individual of interest and its relatives. The emphasis attributed to various relatives is dictated by their covariance, derived from pedigree information based on expected identity by descent. The prediction has three potential sources, the collective knowledge of its parents genetic merit, the individuals own information relative to its contemporaries, and the average merit of any offspring, adjusted for the merit of mates. Individuals without their own or progeny information can only be estimated from the average merit of their parents and reliability (r^2) cannot exceed 0.5. Whole genome prediction involves tracking inheritance of chromosome regions to infer identity by descent and thereby derive genetic covariances between members of the population. A consequence of this approach is that merits of relatives other than parents and progeny can directly influence the evaluation of a young selection candidate so that it can depart from parent average before individual or progeny information is collected, increasing reliability above the 0.5 threshold. The application of whole genome prediction requires a bioinformatics system to store, access and analyze genotypes, phenotypes and relationships. One computational approach directly uses genotypes to construct the variance-covariance matrix using knowledge of the appropriate emphasis that should be attributed to each chromosomal region. That information can be obtained from prior Bayesian analyses known as training, that estimates the genetic variance of each region, or equivalently, estimates the effect associated with each marker. In circumstances whereby the marked genomic regions collectively account for less than 100% additive variation, predictions can be improved by accounting for covariation between relatives due to residual polygenic effects, not captured by genomic relationships. Prediction of genomic and residual polygenic contributions can be undertaken jointly, or in separate analyses with results subsequently combined into single predictions of merit.

Key Words: genomic analysis, genetic evaluation, Bayesian analysis

Companion Animals: Dietary Supplements in Companion & Exotic Animal Nutrition - Use, Regulations & Safety

204 Navigating the FDA's regulation of animal feed "supplements". J. B. Murphy*, *U.S. Food and Drug Administration's Center for Veterinary Medicine, Rockville, MD*.

The Center for Veterinary Medicine (CVM) is the branch of the U.S. Food and Drug Administration (FDA) that is responsible for the regulation of products (food, drugs, and devices) intended for animals, which includes both livestock and pet animals. The use of food products for both humans and animals is governed by the provisions of the Federal Food, Drug and Cosmetic Act (FFDCA). CVM regulates two classes of orally ingested products intended for animals: food or drugs. The Dietary Supplement Health and Education Act (DSHEA) created a third class of products for humans, the dietary supplements. In 1996, FDA determined that DSHEA does not apply to animals and that the use of the term "dietary supplement" and associated labeling practices are not permitted for animal products. Therefore, depending on the intended use, an animal "supplement" is considered either a food or drug under the FFDCA. The evolution of the pet product market over the past several years has led to an exponential increase in the number of pet supplements available for consumers. Many of these products contain ingredients, claims, and labeling practices that are associated with human dietary supplements that are not permitted for animal products. In addition, CVM is concerned about the inclusion of dietary supplement-type substances, such as herbs and their extracts in pet products. Many of