help to produce coherence among conflicting sets of beliefs and values held by a moral agent or groups of moral agents, such as farmers and consumers who must consider "wicked problems," i.e., problems that are seemingly intractable in nature and which breed error, ignorance, confusion, transference of responsibility and learned helplessness. The development and implementation of animal welfare standards produce "wicked problems" that are complicated by social, economic and environmental constraints, empirical deficits and political struggle among different stakeholders in the food system. Implications of WRE for personal morality and public policy will be discussed.

Key Words: animal welfare, bioethics, ethics and deliberation

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0281 Farm animal welfare: Three essential ingredients from an international context. A. De Paula Vieira*, *Positivo University, Curitiba, Brazil.*

The animal food chain is characterized by an array of values that represent the interests of different stakeholders. These values are reflected in policies, practices, branding, and media. They highlight market share and profitability, food safety, quality assurance, traceability, sustainability, good governance, and trustworthiness. Animal welfare value is informed by animal welfare science, which brings the perspective of the animal into focus. This presentation will highlight (1) the centrality of animal welfare science and technology in innovating for animals' needs; (2) the importance of local contexts and engaging stakeholders in discussions when implementing substantial changes; and (3) the roles of shared value, well-informed communication and development of tools for monitoring, e-government and education, respectively.

(1) Animal welfare science is central in ensuring that policymakers, producers, consumers, retailers and industry agents continue to make the interests of farm animals a priority as the global system anticipates new challenges. Animal welfare scientists are essential in multidisciplinary teams to design new apparatuses, articulate the proper role of care for farm animals, and in transferring knowledge to producers.

(2) Engaging with all interested parties at the local level is key to contextualize the needs and challenges faced by animal producers in their home countries as they strive to be responsible custodians of their animals, promote respectable livelihoods and enhance food security and efficient use of resources, and minimize food loss and waste. Local producers and professionals such as animal welfare scientists should be given training and greater visibility as strategic collaborators for their significance in promoting animal welfare and "co-branding."

(3) There is increasing aspiration by consumers that animal production reflects common goals such as greater transparency and reflexivity by all in the food system, humaneness and social justice. Here, it is paramount that animal welfare scientists become conduits of innovation. Technology such as e-government platforms together with public policies will be crucial as the production sector embraces robust sustainability pathways and produces "responsible commodities" in the information age.

To sustain financial success and promote social benefit, animal value chains must consider the structure of their respective operations, be open to perform structural changes that is informed by the best science available and have strong ethical grounding, adopt new practices, design and model business and production processes that are personalized to their customers, and innovate their products and services to meet contextualized local and global expectations.

Key Words: farm animal welfare, sustainability, food chain

0282 Breaking down communication barriers to connect with stakeholders. R. Beck*, *The Center for Food Integrity, Gladstone, MO.*

The science is clear on antibiotics, animal housing, GMO feed, the global demand for protein, etc.—so why does it seem consumers don't understand or agree with any of it? The gap between consumer expectations and perceived industry performance presents grand challenges for those trying to stick to the science, but presenter Roxi Beck will lay the foundation for a big solution that serves to decrease that gap. In this session, attendees will:

(1) Gain an understanding of what U.S. consumers believe about animal agriculture and associated issues (animal care, antibiotics, GMOs, etc.)

(2) Expand awareness of why consumers distrust agriculture and the food system

(3) Review the Center for Food Integrity's peer-reviewed and published model to build consumer trust

(4) Learn effective approaches that allow stakeholders (including consumers) to consider complex and controversial science in their decision-making process

(5) Walk away with a toolbox of approaches and methods that complement CFI research to have meaningful stakeholder conversations

Key Words: consumers, industry performance, trust

ADVANCES IN BOVINE RESPIRATORY DISEASE

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283 Genetic approaches to selection for resistance to bovine respiratory disease. J. E. Womack*, *Texas A&M University, College Station.*

Advances in genomics, molecular genetics and genotyping technology offer unique opportunities to identify genetic

variation associated with complex traits, including host resistance to infectious diseases. The Bovine Respiratory Disease Consortium is a team of scientists and educators who are exploiting these technologies to identify genomic elements underlying resistance to the bovine respiratory disease complex and translating research findings for application by the beef and dairy industries. Genome-wide association studies (GWAS) in both dairy calves and beef feedlot cattle have been conducted, and numerous associated loci have been identified. Promise for successful translation to genomic selection and effective breeding of resistant animals comes from our discovery of higher than expected heritabilities and some loci with reasonably large effects. Challenge of animals with single BRD associated pathogens and subsequent RNA-seq and pathway analyses complement the GWAS studies and helps provide candidate genes for causal variation underlying susceptibility. Work is underway to identify optimal clinical criteria to identify BRD for use in EPDs and translation into predicted transmitting abilities for susceptibility. This program also includes development of educational courses and a study of economic impact of BRD to both beef and dairy industries. A comprehensive extension component of the project includes outreach at every level as evidenced through the project website (http://www.brdcomplex.org).

Key Words: bovine respiratory disease complex, complex traits, disease resistance, genomic approaches

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0284 Differential gene expression in cattle challenged with single pathogens of the bovine respiratory disease complex.

L. J. Gershwin[*1], A. Vaneenennaam[1], J. F. Taylor[2], J. Kim[2], R. L. Toaff-Rosenstein[3], H. L. Neibergs[4], and J. E. Womack[5], *[1]University of California, Davis, [2]University of Missouri, Columbia, [3]University of California, Berkeley, [4]Department of Animal Sciences, Washington State University, Pullman, [5]Texas A&M University, College Station.*

Bovine respiratory disease complex (BRDC) is an important infectious cause of mortality and morbidity in cattle. BRDC develops when stressed cattle are infected with one of several viruses followed by one or more bacterial pathogens. To evaluate the host response to each of these pathogens, we measured global transcript abundance using RNA sequence analysis, comparing infected steers with normal controls after single pathogen infections. At maximum clinical signs, steers were euthanized for necropsy and collection of lung, bronchial, nasopharyngeal, and retropharyngeal lymph nodes, and pharyngeal tonsils for RNA sequencing. Viral agents used for the challenge were: bovine respiratory syncytial virus (BRSV), infectious bovine rhinotracheitis (IBR), and bovine viral diarrhea virus (BVDV). Bacteria used to challenge included: *Mannheimnia hemolytica*, *Pasteurella multocida,* and *Mycoplasma bovis*. Differential expression of genes coding for non-specific defense innate immunity and the acute phase response was found among all pathogen infections. These included pattern recognition receptors, mucins, and host defense peptides; more specific immune response genes were differentially expressed in individual pathogen infections. Adaptive immune system pathways for both T and B cells were activated in BRSV infection. In general viral infections elicited a greater number of differentially expressed genes than bacterial pathogens. Tissues were compared and found to contain both differentially expressed genes shared among all tissues examined and specific to tissue type. Overall data obtained will have important implications for design of better therapeutic modalities; and will help further elucidate the complex pathogenesis of BRDC.

Key Words: BRDC, infection, RNA

0285 Genome-wide association study of bovine respiratory disease complex in U.S. feedlot cattle.

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Bovine respiratory disease complex (BRDC) is the leading natural cause of morbidity and mortality among feedlot cattle, and is responsible for substantial economic losses during commercial beef production. The primary objective of the present study was to estimate the heritability of two related BRDC traits in U.S. feedlot cattle (binary case-control; clinical severity scores), and identify quantitative trait loci (QTL) associated with differential susceptibility to BRDC. All beef cattle (Angus, Red Angus, Taurine Crossbreds, Charolais, Hereford) were sampled from commercial feedlots in Colorado (CO) and Washington (WA), with BRDC phenotypes assigned using the McGuirk diagnostic scoring system. Similar numbers of heifers (928) and steers (934) were genotyped using the Illumina BovineHD BeadChip, which included 932 BRDC cases, and 930 controls. Genome-wide association analyses were performed using a linear mixed model (EMMAX) with genomic relationship matrix (G), and accounted for the effects of month, season, breed, lot-pen, days-to-pull, sex, year sampled, and location in the combined cohort (CO+WA). Heritability estimates for the BRDC binary case-control and clinical score phenotypes ranged from 0.13–0.14 in CO, 0.25–0.20 in WA, and 0.20–0.22 in the combined cohort, respectively; thereby suggesting that a common set of susceptibility loci were likely to exist. QTL estimated to explain $\geq$ 2% of the variance in either of the BRDC phenotypes were detected in each individual population (CO, WA), whereas the most significant QTL detected for the combined cohort were estimated to explain $\geq$ 1% of the variance in both BRDC phenotypes. The genomic positions of several binary and clinical scores BRDC QTL

were found to overlap in all analyses (i.e., CO, WA, CO+WA); with the combined cohort producing overlapping QTL intervals (i.e., binary, clinical scores) on BTA1, BTA5, BTA8, BTA10, BTA13, and BTA27 thereby suggesting that genomic selection for reduced BRDC susceptibility in beef feedlot cattle is likely to help mitigate economic and production losses.
This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the USDA National Institute of Food and Agriculture.

Key Words: beef cattle, bovine respiratory disease complex, genome-wide association study, genomic selection

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0286 Identification of causal variants underlying pathogen susceptibility and translation to genetic improvement.
J. F. Taylor*[1], H. L. Neibergs[2], C. M. Seabury[3], A. Vaneenennaam[4], J. E. Decker[1], J. L. Hoff[5], P. C. Tizioto[6], J. E. Womack[7], and R. D. Schnabel[1], *[1]University of Missouri, Columbia, [2]Department of Animal Sciences, Washington State University, Pullman, [3]College of Veterinary Medicine, Texas A&M University, College Station, [4]University of California, Davis, [5]Division of Animal Sciences, University of Missouri, Columbia, [6]Embrapa Southeast Livestock, São Carlos, Brazil, [7]Texas A&M University, College Station.*

We have developed populations of 2781 preweaned Holstein calves (CA and NM) and 1862 Angus, Red Angus, Taurine Crossbred, Charolais and Hereford heifers and steers (WA and CO) that are approximately equally represented as cases or controls that are being used to train models for the prediction of additive genetic risk of Bovine Respiratory Disease (BRD). Analyzing BovineHD genotypes for these populations revealed heritabilities for BRD risk in the range from 20–23% and revealed numerous large effect QTL, many of which are located in genomic regions that also harbor genes that are differentially expressed between Angus × Hereford controls and animals challenged with single pathogens of the BRD Complex. To enable selection for increased resistance to the pathogens responsible for BRD, we seek to develop estimates of genetic merit that are robust to the breed composition of the tested animals and to the extent of their relatedness to these training populations. To accomplish this requires the identification of the causal variants that have a large effect on risk of BRD that were detected in Genome-Wide Association Analyses (GWAA). The strategy that we have followed involves the development of a functional variant assay known as the GGP-F250 that includes variants likely to alter the function of proteins through frameshifts, amino acid substitutions or altering the sequences of 5' and 3' untranslated regions. Variant discovery was performed using whole genome sequences (WGSs) for 262 taurines and RNA sequence data for 153 taurine animals. Variants were validated using 1000 Bull Genomes project data for 1147 sequenced animals and WGS data on 35 indicine or indicine × taurine composite animals. Holstein training population animals have been genotyped with this assay and the combined data have been imputed to WGS variation (~11M variants with minor allele frequency > 5%) for the purpose of performing GWAA. The beef populations are likewise being imputed to WGS, and we seek to identify variants that are consistently associated with risk of BRD across populations for which the direction of allele effects is conserved across populations. These variants will be migrated to assays commercialized by Zoetis and GeneSeek that are routinely utilized by the beef and dairy industries to enable the translation of project results.

This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the USDA National Institute of Food and Agriculture.

Key Words: BRD, GWAS, causal variants, estimated breeding values

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0287 Gene set enrichment analysis of bovine respiratory disease complex SNP data in feedlot cattle.
M. Neupane[1], J. F. Taylor[2], C. M. Seabury[3], J. E. Womack[3], and H. L. Neibergs*[1], *[1]Department of Animal Sciences, Washington State University, Pullman, [2]University of Missouri, Columbia, [3]Texas A&M University, College Station.*

Bovine Respiratory Disease Complex (BRDC) is responsible for annual deaths of more than 350,000 feedlot cattle and estimated losses of over $1 billion in the U.S. The objective of this study was to use gene set enrichment analysis of SNP data (GSEA-SNP) to identify pathways associated with susceptibility to BRDC in *Bos taurus* feedlot cattle. Cattle were sampled from commercial feedlots in Colorado and Washington, and cases were determined using the McGuirk diagnostic system. Approximately equal numbers of steers (933) and heifers (935) and cases (936) and controls (932) were genotyped with the Illumina BovineHD BeadChip and analyzed using an additive model with breed (Angus, Red Angus, Crossbred, Charolais and Hereford), days to pen removal, month and location as covariates in the genome-wide association analysis (GWAA). EIGENSTRAT principal component (PC) analysis was used to correct for population stratification using the first 10 PC resulting in $\lambda = 1.03$. GWAA was followed by GSEA-SNP utilizing 4388 pathways from Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes, Reactome, Biocarta and Panther. Haplotype block size was estimated and averaged across breeds to determine the size of the interval harboring each gene in which to search for a SNP that would serve as the proxy for the gene. The most significant SNP from the GWAA that was located within 7 kb of each gene was used as the proxy for each of the 19,723 genes mapped in the UMD 3.1 assembly. For each gene set, the significance value was calculated using the null distribution generated from 10,000 phenotype-based

permutations. Enrichment scores (ES) were calculated using running sum statistics. Five GO gene sets had normalized ES > 3 and were found to be associated with susceptibility to BRDC: GO:0005887 Integral Component of Plasma Membrane, GO:0031324 Negative Regulation of Cellular Protein Metabolic Process, GO:0005496 Steroid Binding, GO:0030162 Regulation of Proteolysis and GO:0008277 Regulation of G Protein Coupled Receptor Protein Signaling Pathway. No other gene sets were found to be associated with BRDC susceptibility. Of the 228 leading edge genes, 79 were differentially expressed between cases and controls and represent putative BRDC functional candidate genes which will be further investigated to determine how they may be best used in the selection of feedlot cattle that are more resistant to BRDC.

Key Words: GSEA-SNP, bovine respiratory disease complex

0288 Calculation of genomic predicted transmitting abilities for bovine respiratory disease complex in Holsteins. C. P. VanTassell*[1], G. Spangler[2], D. M. Bickhart[3], G. R. Wiggans[4], J. B. Cole[5], J. F. Taylor[6], H. L. Neibergs[7], C. M. Seabury[8], A. L. Van Eenennaam[9], and J. E. Womack[10], *[1]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [2]USDA-ARS, Beltsville, MD, [3]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [4]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [5]Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD, [6]University of Missouri, Columbia, [7]Department of Animal Sciences, Washington State University, Pullman, [8]College of Veterinary Medicine, Texas A&M University, College Station, [9]University of California, Davis, [10]Texas A&M University, College Station.*

Bovine Respiratory Disease Complex is a disease that is very costly to the dairy industry. Genomic selection may be an effective tool to improve host resistance to the pathogens that cause this disease. Use of genomic predicted transmitting abilities (GPTA) for selection has had a dramatic effect on rates of genetic improvement in Holsteins, particularly for lowly heritable traits. Data were collected on 2682 calves located in California (n = 1978) and New Mexico (n = 705). DNA was extracted and animals were genotyped using the BovineHD BeadChip. A total of 22 individuals were excluded based on genotype call rate and breed designation other than Holstein. Of the remaining animals, 708 had unidentified sires, the remaining 1952 animals were the offspring of 578 sires which were identified by genotype matching. There were 38 bulls with at least 10 offspring, 343 with at least 2 progeny, and 235 bulls with a single offspring in the data set. A standardized scoring system considering animal body temperature, cough severity, nasal discharge, and eye discharge or ear scores was used to characterize the disease status of all calves according to the McGuirk classification system. Currently, GPTA are being calculated from these data using a heritability value of 0.20, which will be validated from the data. Estimated genetic marker effects will be compared with results from previous genome-wide association studies.

This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the USDA National Institute of Food and Agriculture.

Key Words: BRD, genomic selection, predicted transmitting abilities

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0289 The value of genetic selection in reducing economic losses from bovine respiratory disease complex in beef cattle feedlots. J. S. Neibergs*[1] and H. L. Neibergs[2], *[1]Washington State University, Pullman, [2]Department of Animal Sciences, Washington State University, Pullman.*

The U.S. inventory of beef cattle has declined since its peak in the 1980s to levels present in the early 1960s. Low cattle inventories have contributed to record high prices since 2009. The increased cattle values have also resulted in a subsequent increase in economic losses from disease. Reducing losses due to disease has become increasingly important in managing thin profit margins at feedlots. The objective of this study was to develop a bio-economic model to evaluate the economic cost of bovine respiratory disease complex (BRDC) in beef feedlots and estimate the potential net economic gain from using selection approaches to reduce BRDC prevalence. Treatment cost, mortality, and harvest data from approximately 1000 heifers and 1000 steers with similar numbers of cases and controls were taken from two commercial feedlots and two commercial processing facilities at harvest. These data were used to develop a Reed-Frost epidemiological model that simulated BRDC prevalence in a population of cattle on feed. Treatment cost was computed as a function of days on feed and the prevalence of cases. Losses due to mortality, and carcass quality discounts were also included to estimate total economic losses. Based on market prices, and carcass discounts, the average economic loss per BRDC case was estimated. To estimate the potential net economic gain from selection, the rate of genetic gain was estimated using a 16.2% national BRDC prevalence rate obtained over a 15-yr period and an estimated heritability for BRDC susceptibility of 21% from the 2000 cattle evaluated in this study. An @ Risk model was used to estimate a 20-yr time frame of genetic selection with stochastic BRDC prevalence rates using historical USDA data. The model compared net economic gains for cattle feedlots that used selection to reduce BRDC and feedlots that approached reducing BRDC without selection. This project was supported by Agriculture and Food Research Initiative Competitive Grant no. 2011–68004–30367 from the

USDA National Institute of Food and Agriculture.

Key Words: bovine respiratory disease complex, economics, epidemiology, genetics

0290 How might genomic information get translated into industry outcomes? A. L. Van Eenennaam*, *University of California, Davis.*

The 5-yr USDA-funded Bovine Respiratory Disease Complex Coordinated Agricultural Project (BRD CAP; USDA-AFRI 2011–68004–30367) aims to develop genetic markers associated with bovine respiratory disease (BRD) to enable the genetic identification of cattle that are less susceptible to BRD. Ultimately the aim of this project is to integrate predictive markers for BRD susceptibility into genetic tests and national cattle genetic evaluations. The research team is activity working to identify regions of the genome associated with BRD susceptibility in both dairy and beef cattle. Initial results have identified multiple genomic regions that were significantly associated with BRD susceptibility. Genomic selection has been introduced into dairy cattle breeding programs globally and within breed genomic estimated breeding values (GEBV) are published in a number of countries. Work is ongoing to integrate BRD information into dairy cattle evaluations at the appropriate economic weighting. However the incorporation of genomic information into beef cattle evaluations has been more problematic due to the presence of numerous breeds and the importance of crossbreeding in the commercial cattle population. Linkage disequilibrium between markers and quantitative trait loci (QTL) is not consistent across breeds, and so markers that were identified in one breed were frequently uninformative in other breeds. However, the sequencing of a large number of animals has opened up the possibility of identifying the actual SNP variations that are causing genetic variation. It is envisioned that by imputing the genotypes of reference animals collected by the BRD CAP up to full sequence and further fine mapping and analyses, the causative genetic variants associated with BRD susceptibility will be identified, and that inclusion of these markers on genotyping platforms will provide a reliable selection criterion to enable for the selection of both beef and dairy cattle that are less susceptible to BRD. There are several advantages associated with using causative SNP makers in selection panels including persistence of the marker effect across generations, and an increased likelihood that causative polymorphisms will be similarly associated with variation across multiple breeds. Ultimately, prospective marker panels will need to be tested in independent cattle populations to ensure they are predictive of BRD phenotype. Toward this end the BRD CAP is working in collaboration both breed associations and commercial feedlots to develop populations of BRD phenotyped animals. Ultimately selection against BRD susceptibility will depend on breeder inclusion of this disease trait in their breeding objective and selection decisions. See http://www.brdcomplex.org for more information.

Key Words: cattle, respiratory disease, extension

BREEDING AND GENETICS

0291 APY inverse of genomic relationship matrix–theory, analyses and questions. I. Misztal*, I. Pocrnic, D. Lourenco, and Y. Masuda, *University of Georgia, Athens.*

Genomic relationship matrix (GRM) can be inverted by Algorithm for Proven and Young (APY) based on recursion on a random subset of animals. While a regular inverse has a cubic cost, the cost of the APY inverse can be close to linear, allowing inexpensive computations with millions of genotyped animals. Theory proposed for APY assumes that optimal size of the subset (maximizing accuracy of genomic predictions) is due to a limited rank of GRM, which is a function of independent chromosome segments (Me) and subsequently of effective populations size (Ne). Simulation studies have shown that (1) the dimensionality is almost a linear function of Ne but for large Ne can be depressed by limited number of genotyped animals and SNP markers, (2) accuracy of predictions with APY inverse is higher than with a regular inverse, and (3) the distribution of independent chromosome segments is skewed. Tests using commercial data sets confirmed results by simulation. Comparisons of eigenvalue plots between simulated and commercial populations indicated an effective population size of 157 for Holsteins, 115 for Angus, 107 for Jerseys, 41 for broiler chicken and 30 for pigs. Experiences with the APY inverse raise a few questions. Can the rank provide information on the minimum SNP chip size that eliminates the polygenic component (or missing heritability)? Is the rank of GRM for a large two-breed population twice that of a single population? In simulation studies where QTL are on SNP markers, the best correlation of a simulated QTL effect is not with the actual SNP effect but with an average of adjacent SNPs. Is the optimum number (window size) of adjacent SNP a function of Ne and dictates the maximum resolution in GWAS? With all causative SNP are identified and their variances known, and appropriate weighted GRM (with APY inverse applicable) has the rank of the number of causative SNPs. Is the rank of weighted GRM with incomplete identification of QTLs (e.g., via GWAS or BayesB) smaller than that of a regular GRM? The APY inverse solves the problem of large-scale genomic computations and provides new insight into the genomic information.

Key Words: genomic selection, single-step GBLUP, APY inversion