

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. Spangler², D. M. Bickhart³, G. R. Wiggans⁴, J. B. Cole⁵, J. F. Taylor⁶, H. L. Neibergs⁷, C. M. Seabury⁸, A. L. Van Eenennaam⁹, and J. E. Womack¹⁰, 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

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. Neibergs², 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