
40 PRLR and PCCA variants associated with hair length in Brangus heifers. Kaitlyn M. Sarlo Davila¹, Alyssa Howell¹, Andrea Nunez¹, Arseia Orelie¹, Victoria Roe¹, David Rodriguez¹, Eduardo Rodriguez¹, Serdal Dikmen², Raluca G. Mateescu¹, ¹University of Florida, ²Bursa Uludağ University

Thermal stress limits beef cattle production and results in a loss of \$370 million in the U.S. annually due to reduced animal performance. A shorter hair coat is a key thermoregulative adaptation that allows cattle to lose heat more efficiently through conductive, convective, and evaporative cooling at the hair-skin interface. The objective of this study was to identify genetic variants associated with the length of the topcoat and undercoat of cattle. Hair samples were collected from the shoulder, 4 inches down from the spine from 2,161 heifers in 2016, 2017 and 2018. ImageJ software was used to measure hair length. The length of the topcoat and undercoat were evaluated for each individual by averaging five long and five short hairs, respectively. DNA was extracted from blood samples and genotyped with the Bovine GGP F250 array. After quality control, 132,225 SNP were available for association analyses using Golden Helix SVS. Year of collection was fitted as a fixed effect and the genomic relationship matrix was fitted to account for the genetic covariance among animals. To correct for multiple tests, the Benjamini-Hochberg false discovery rate was constrained to 0.1. Four SNP in the PRLR gene were significantly associated with topcoat length, including a missense mutation that explained 4% of the variation in topcoat length. PRLR has previously been demonstrated to significantly impact hair length in cattle. Seven SNP in the PCCA gene were significantly associated with undercoat length. PCCA belongs to the biotin transport and metabolism pathway. Biotin deficiency has been reported to cause hair loss. These genetic variants may contribute to a shorter hair coat and more thermotolerant animals.

Keywords: beef cattle thermotolerance hair

48 Genetic study of horn fly abundance in beef cattle. Ashley Ling¹, Taylor Krause², Bradley Heins², Nancy Hinkle², Dean Pringle², Samuel E. Aggrey², Romdhane Rekaya², ¹University of Georgia, Department of Animal and Dairy Science, ²University of Georgia

Disturbing the non-symbiotic relationship between horn flies and cattle is of economic, health, and animal welfare importance. Reliance on management and insecticides has proven inadequate. In the United States, horn flies are estimated to cause more than \$1 billion in economic losses on pastured cattle annually. Although insecticides provide temporary control, their efficacy is hampered by several factors. Intensive insecticide use has led to horn fly resistance and decreased predation on horn flies by other insects. Due to the cost and logistic complexity of measuring fly resistance traits under commercial conditions, the genetic basis of these traits remains largely unknown. Only a few heritability estimates are available based on small-scale studies. Currently, the economic injury threshold (EIT) due to horn fly abundance (onset of production decay) is set at around 200 flies for beef cattle. This threshold is largely heuristically set. Additionally, the rate of decay in performance as a function of fly abundance after injury onset is unknown. It is also likely that EIT is breed and animal specific. Data used in this study was collected during the summer of 2019. Animals were not treated or managed in any way to control horn flies prior to data collection. Animals were assessed subjectively and based on image counts for horn fly abundance. Estimates of heritability of horn fly abundance ranged between 0.14 and 0.22 for subjective and image-based phenotypes. The lowest heritability was for the subjective assessment, likely due to the excessive variation between evaluators. Change-point model-based analysis showed that EIT is variable between sire families, ranging from 265 to 413 flies. Furthermore, there was significant difference in the decay of performance after the onset of injury. The rate of decay ranged between -0.0003 and -0.00018. Collectively, these results indicate the potential to improve horn fly resistance/tolerance using genetic tools.

Keywords: horn flies, heritability, change-point model