PSXV-5 Incorporating Breed of Origin and Runs-of-Homozygosity Information in a Genome-Wide Association for Meat Traits in a Brangus Commercial Herd. Gabriel A. Zayas[1], Eduardo Rodríguez[1], Kaitlyn Sarlo Davila[2], Andrea N. Nunez Andrade[1], Aakilah Hernandez[1], Fernanda M. Rezende[1], Raluca Mateescu[1], [1]*University of Florida,* [2]*USDA*

Abstract: Heterosis is the tendency of crossbreed animals performing better than the average of the purebred parents. Heterosis retention is essential in crossbreeding and composite breeding systems. However, not every genomic region benefits from heterosis, with certain traits showing an improvement when certain genomic regions are kept fixed for a certain breed. The objectives of this study were to detect such regions in a commercial Brangus herd, using genotypes, and Breed of Origin (BO) genotypes to identify runs of homozygosity (ROH) and investigate their effects on meat traits. The Brangus herd was genotyped with the Bovine GGP F250 array, after quality control, 99,669 variants, and 1,046 cattle remained. These genotypes were converted into BO genotypes with LAMP-LD, which describes the origin of the markers either from Angus or Brahman ancestry. The new BO genotypes and original genotypes were then used to identify ROH using the –homozyg function PLINK. The ROH genotypes were fit into a single locus mixed model for hot carcass weight (HCW) and marbling (MARB) using the EMMAX procedures in Golden Helix. The same single locus mixed model was used on both genotypes and Breed of Origin genotypes using the EMMAX procedures in Golden Helix. Using BO alleles, and ROH alongside traditional genotypes can help identify regions with significant effects on carcass traits. Providing important information for crossbreeding/composite breed systems about regions which should remain fixed for breeds.

Keywords: animal genomics, heterosis, meat quality

PSXV-1 Genetic Variants of the Ghrelin, Ghsr1a, Mboat4 and NPY Genes Related to Feed Efficiency Traits and Ghrelin Plasma Concentration in Hampshire Lambs. José G. Pérez-Álvarez[1], Francisco J. Jahuey-Martínez[1], José A. Martínez-Quintana[1], Ana M. Sifuentes-Rincón[2], Guadalupe N. Aguilar-Palma[1], Francisco A. A. Paredes Sánchez[2], Joel Domínguez-Viveros[1], Felipe A. Rodríguez-Almeida[1], [1]*Universidad Autónoma de Chihuahua, Facultad de Zootecnia y Ecología,* [2]*Instituto Politécnico Nacional-Centro de Biotecnología Genómica*

Abstract: Reports in the literature suggest that a transient surge of ghrelin secretion (TSGS) just before a scheduled meal may be triggered by an appetite mechanism. Also, it is known that circulating ghrelin concentrations fluctuate relative to nutritional status and influence feeding behavior. The aim of the present study was to search for genetic variants in five selected genes (GHRL, GHSR1a, MBOAT4, NPY and AgRP) within the ghrelin gene (GHRL) interaction network. gDNA was extracted from the six highest- and six lowest-RFI Hampshire non-castrated male lambs, out of a total of 25 lambs in a 56-d GrowSafe Systems© feeding trial and the complete genes were amplified by PCR. Libraries were prepared and sequenced in the ILLUMINA platform MiniSeq Sequencing System. Variations were identified using the genomic variant call format (GVCF) workflow with HaplotypeCaller using the reference genome oviAri 4 - Oar_v4 (GCA_000298732.2). One hundred and ninety-two SNPs were found in the five analyzed genes. Most of them had been reported in the SNPs data base. Linear models including each SNP genotype at a time as fixed effects, in addition to ADG and mid test metabolic body weight as covariates for some variables, were adjusted. Forty-three of these SNPs had different genotype frequencies in the two RFI groups, and appear to be associated ($p < 0.05$) with traits such as RFI, feed intake (FI), feed conversion (FC) and ghrelin hormone concentration in plasma (GHRL) at the TSGS; especially SNPs rs399405301, rs421869734, rs604106535, rs417836509, rs600356564, rs590893697 at the MBOAT4 gene which resulted highly significant ($p < 0.01$) for RFI and GHRL. The SNP rs423156356 at the GHSR1a gene was highly significant ($p < 0.01$) for FI and FC. These SNPs (Table 1) have the potential to be used as genetic markers for improvement of