each experimental animal was infected with 10,000 L_3 of *H. contortus* per kg of body weight per oral route. Fecal samples were obtained to determine fecal egg count using the modified McMaster technique. Blood samples were collected from the jugular vein with sterile vacuum tubes with sodium heparin to evaluate blood package cell volume (PCV) and levels of IgA, IgM and IgG. DNA was purified from blood samples using DNeasy Blood & Tissue Kit (Qiagen). One SNP in the OLA-DRA20 segregating in this population was analyzed using High Resolution Melting assays and three genotypes were observed (AA, GA, GG). A GLM was fitted with MPCV, DMI, ADG, RFI, IgM, IgG, IgA levels and genotype as predictors and the square root of the mean of FEC as the response variable. According the results, the best significant predictors to fit the model were Genotype, Breed (Species), MPCV, DMI, ADG and genotype ($p < 0.05$). In conclusion, the polymorphism in the OLA-DRA20 gene could have an important role in the immune mechanisms against *H. contortus* infections in sheep and goats. Indeed, these results provided evidence that there is a significant effect among the square root of the mean of FEC and production traits between breeds within species.

Key Words: *Haemonchus contortus*, small ruminants, OLA-DRA20 gene

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0333 Genomic analysis of lactation persistency in four breeds of dairy cattle. J. B. Cole[1], D. J. Null[*1], and K. L. Parker Gaddis[2], [1]*Animal Genomics and Improvement Laboratory, USDA-ARS, Beltsville, MD,* [2]*Department of Animal Sciences, University of Florida, Gainesville.*

The objectives of this study were to determine gains in reliability from the addition of genomic information to genetic evaluations for best predictions of lactation persistency in U.S. Ayrshire (AY), Brown Swiss (BS), Holstein (HO), and Jersey (JE) cattle, and to identify genomic regions with large effects on those traits. Data consisted of lactations initiated by calvings on or after January 1, 1997, stored in the national dairy database (NDDB) at the Council on Dairy Cattle Breeding (Bowie, MD). Persistencies were computed by multiple-trait best prediction for milk (PM), fat (PF), and protein (PP) yields. Genetic analyses were conducted on a within-breed basis using identical repeatability animal models and breed-specific (co)variance components. Traditional and genomic PTA and reliabilities were computed by GBLUP using the national genomic evaluation system. Gain in reliability from the addition of genomic information was calculated as the difference between the realized genomic reliability and the reliability of traditional PA using a cutoff study. Predictor populations consisted of animals with traditional genetic evaluations in April 2014, and validation sets included animals with traditional genetic evaluations in August 2009. Allele effects were converted to additive genetic standard deviations, and closestBed 2.17.0 was used to obtain a list of genes that contained SNP or were within 25 kbp of a genotyped SNP. Gene names and coordinates were those published in Cow Ensembl Release 79. Reliability gains averaged 8% in AY, 5% in BS, 12% in HO, and 12% in JE. The SNP ARS-BFGL-NGS-4939 at 1801,116 bp on BTA14, downstream of the *DGAT1* gene, had the largest effects on PM and PF in HO and PM in JE of any marker in the analysis. BovineHD1600000386 at 1554,597 bp on BTA16 had largest effect on PF and PP in JE, in a region previously reported to effect fat and protein yields and percentages. The SNP with the largest effects in AY were located on the X chromosome in regions reported to affect fat and protein yields and percentages in HO. The largest effect for PM in BS was in a region of BTA19 associated with MY in Chinese Holsteins, while the largest PF and PP effects were in regions of the X chromosome reported to affect fat and protein yield in U.S. Holsteins. Genetic correlations of yield with persistency range from −0.32 to 0.26, so loci with large effects on yield also can affect persistency.

Key Words: association analysis, best prediction, reliability

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0334 Genome-wide association study for tick count and infection level of *Babesia bovis* traits in Angus cattle. L. Cavani[*1], C. H. Santana[1], R. Giglioti[1], T. B. Bilhassi[1], M. C. D. S. Oliveira[2], R. Carvalheiro[1], and H. N. Oliveira[1], [1]*State University of São Paulo, Faculty of Agriculture and Veterinary Sciences, Jaboticabal, Brazil,* [2]*Embrapa Southeast Livestock, São Carlos, Brazil.*

Tick and tick-borne diseases, including babesia (*B. bovis*), constitutes a major drawback to improve productivity of beef cattle in the tropics, especially for systems where *Bos taurus* cattle animals and their crosses are used. To identify highlight regions highly associated with the studied traits, genome-wide association studies (GWAS) were performed. Tick counts and blood sample were taken in two occasions from each of 355 Angus cattle at a farm located at Rio Grande do Sul State, Brazil. Blood samples were collected, in tubes containing EDTA for DNA extraction. *B. bovis* quantification was performed using both qPCR technique from genomic DNA of each animal with specific primers for this protozoary and the absolute quantification method. Animals were genotyped by using Illumina GeneSeek GGP Bovine 150K. Quality control criteria were: MAF < 2%, call rate < 92%, and animal call rate (with less than 90% of SNPs called). After edits, 144,924 SNPs and 350 animals were available. Fixed effects in the model included contemporary groups and effect of data collection period, as well as additive genetic direct and permanent environmental effects as random. Variance components and genetic parameters were estimated by Bayesian inference in a bivariate analysis using GIBBS2F90 software, and the effect of each SNP was estimated using methods Bayes C as implemented in the GS3 software. Also, it was