Brisbane, Queensland, Australia, [4]CSIRO Agriculture and Food, Queensland Bioscience Precinct, Brisbane, Queensland, Australia, [5]Colorado State University, Department of Animal Science, Fort Collins, CO, USA.

Pleiotropy drives genetic correlations between complex traits. The combination of SNP effects from genome-wide association studies (GWAS) may lead to the identification of key-regulators of pleiotropic effects. A total of 35,041 SNP effects from GWAS were combined for 16 traits related to meat quality, fatness, body composition and feed efficiency. Preliminary analyses were performed using 800 animals composed by different proportions of 6 beef breeds (Angus, Charolais, Simmental, Piedmontese, Limousin, Gelbvieh). A multi-trait statistic was calculated for each SNP following: $\chi^2 = t'_i V^{-1} t_i$; where t_i was the vector of signed t-values of SNP_i for the traits and t'_i was its transposed, V^{-1} was an inverse of the correlation matrix among the traits, and P-values obtained from a χ^2 distribution with 16 degrees of freedom. In total, 74 SNPs distributed across all the autosomes were significantly associated (P-value $<10^{-3}$) with pleiotropic effects. BTA6 (12) and BTA14 (6) were the chromosomes with the highest number of significant pleiotropic SNPs. Furthermore, 31 SNPs showed significant pleiotropic effect with 6 or more traits (absolute t-value >3). Interestingly, the most important SNP located in BTA6 (P-value $<10^{-5}$), close to a transcription factor, showed the highest number of related traits (13) with pleiotropic effect. In addition, clusters of QTLs were estimated using the correlation between the t-values for each pair of significant markers on BTA6 and BTA14. Two clusters of SNPs were identified on BTA6 (6 SNPs/each) and BTA14 (3 SNPs/each). Clear differences were observed between traits for the percentage of related SNPs within clusters on BTA14, e.g., lean carcass composition (cluster1 = 100%; cluster2 = 33%). Further research is warranted to validate these results and will be done using a larger population of ~15,000 animals including representation of several Taurine (*Bos taurus*) and Indicine (*Bos indicus*) breeds and over 30 traits related to meat quality, fatness, body composition, feed efficiency, reproduction and health. The results could help to avoid the unfavorable indirect genetic selection of genetically correlated traits in beef cattle.

Key Words: cattle and related species, genetic improvement, comparative genomics, functional genomics, complex trait

P438 Mammary RNA-seq data can better understand the genetic architecture of milk production traits in dairy cattle. W. Cai*[1,2], L. Fang[2], J. Cole[3], P. VanRaden[3], S. Zhang[2], and J. Song[1], *[1]University of Maryland, College Park, MD, USA, [2]China Agricultural University, Beijing, China, [3]USDA, Beltsville, MD, USA.*

Even with genome-wide association studies (GWAS) observed thousands of genomic variants associated with milk production traits in dairy cattle, the differentially expressed genes (DEGs) and long non-coding RNA (lncRNAs) in mammary gland across lactations on which those genomic variants act remain largely unknown. Here, we used multi-variance component approaches to test whether variants in DEGs regions and lncRNAs across lactations will explain more variance in milk production traits than others. To investigate the landscape and dynamic changes of genes and long non-coding RNA across lactations in dairy cattle, we reanalyzed 115 mammary RNA-seq samples, including 49 lactating and 66 nonlactating samples, which were collected from available data sets. Accounting for study effect, we identified 8,553 genes and 5,140 lncRNAs differentially expressed between nonlactating period and lactating period. Our population data set consisted of 3.2 million SNPs in 19,575 dairy cattle with records for 5 milk production trait phenotypes from USDA. We found that genomic variants in DEG regions captured the dynamic proportions of the variance ranged from 26.0% to 72.4% for different traits. Genomic variants in DE lncRNAs regions could explain 7.3% ~32.4% of the variance depends on different traits. Upregulated lncRNAs seemed more important than downregulated lncRNAs based on their SNPs explanation proportions. Then, we divided the DEGs into 8 groups based on their fold change values. We found that sequence variants in small fold change groups (−2~2) captured the greatest across all traits. The upregulated DEGs could explain a higher proportion of the variance than downregulated DEGs. We also found genomic variants in fold change >8 group regions, captured 16% of the variance for protein percentage trait. For per genomic variant, variants in fold change >8 group regions explain the highest proportion of variance for protein percentage, fat percentage, and milk traits. The proportion of variance captured by DEG regions with a fold change < −4 was very small. Overall, the results underscore that the use of mammary biological priors such as DEGs and lncRNAs enhances our insight into the genetic architecture underlying phenotypic diversity. Variants found in differentially expressed lncRNAs regions, explained considerable variation in milk production traits, should be further explored in detail.

Key Words: cattle, RNA-seq, DEGs, long non-coding RNA, SNPs explanations

P439 Investigation of genomic variation of coat color genes in Italian goat breeds. S. Frattini*[1], M. Cortellari[1], A. Talenti[2], A. Negro[1], M. Caprioglio[1], and P. Crepaldi[1], *[1]Department of Veterinary Medicine, University of Milan, Milan, Italy, [2]The Roslin Institute, University of Edinburgh, Easter Bush Campus, Midlothian, United Kingdom.*

Coat color, a distinctive trait described in the breed standards, allows the identification of many native and cosmopolitan breeds.The aim of this work is to evaluate the presence of signals of selection in genes involved in pigmentation processes of *Capra hircus*.Starting from genotyping data (GoatSNP50 BeadChip) of 423 goats belonging to 25 Italian breeds/populations provided by the Italian Goat Consortium. For every breed, an Integrated Haplotype Score (iHS) analysis was performed. Animals were then classified in 5 groups depending on their coat colors patterns (solid eumelanic, solid pheomelanic, pied eumelanic, pied pheomelanic and white). A reduced data set consisting of 467 SNPs included in regions surrounding 40 candidate genes (+0.25 Mb) was generated. Using this data set, a canonical discriminant and allelic frequencies analyses on the 5 groups previously defined were performed.The iHS, calculated with the Selscan software, allowed the identification of 44 relevant signal (>0.6) in 17 out of 25 breeds. These signals of selection are about 4% of all the genomic regions investigated, and fall in 26 genes. The canonical analysis highlighted that genes involved in the dilution of the eumelanins (e.g., *OCA2* and *MYO5A*) and in the formation of the white patches (e.g., *DOCK7* and *PAX3*) have a major role in differentiating these groups of breeds. The analysis of the allele frequencies of the 467 SNP was focused on extreme frequencies (<0.2 or >0.8) and allowed the identification of 13 genes with at least 67% of extreme SNPs in 8 different breeds. Another noteworthy result is the high level of extreme SNPs observed for the *EDNRB* gene (white patches) only in the Maltese population and in the Vallesana breed which are characterized by a wide white extension in their coat.In conclusion, the results show that, despite the lack of selection signals within breed likely due to a reduced standardization of coat color in goat, canonical discriminant analysis highlight the relevance of regions around genes involved in withe patches and eumelanin dilution. However, the pigmentation control in the species is a complex system that deserves to be better studied from a phenotypical/genomic point of view.

Key Words: goat and related species, genetic identification, genotyping, coat color, breed standardization

P440 A complex structural variant at the *KIT* locus in Alpine cattle with a unique white spotting pattern. L. Küttel[1], A. Letko[1], I. Häfliger[1], S. Joller[1], G. Hirsbrunner[2], H. Signer-Hasler[3], G. Mészáros[4], J. Sölkner[4], C. Flury[3], and C. Drögemüller*[1], *[1]University of Bern, Vetsuisse Faculty, Institute of Genetics, Bern, Switzerland, [2]University of Bern, Vetsuisse Faculty, Clinic for Ruminants, Bern, Switzerland, [3]Bern University of Applied Sciences, School of Agricultural, Forest and Food Sciences HAFL, Zollikofen, Switzerland, [4]University of*