Key Words: cattle and related species, lethal gene, SNP

P489 Development of an early prediction model for Hanwoo carcass traits using genomic estimated breeding values and weather data. S. W. Yoon*, Y. S. Kim, H. J. Beak, E. S. Hong, O. C. Kwon, N. R. Choi, Y. M. Jo, and D. W. Seo, *TNT Research Co., Ltd., Jeonju-si, Jeollabuk-do, Korea.*

This study aimed to develop and evaluate a machine learning model for the early prediction of key economic traits in Hanwoo, specifically carcass weight and marbling score. Genomic estimated breeding values (GEBVs) for carcass traits were estimated using the Genomic Best linear unbiased prediction (GBLUP) method based on a 26,760-animal reference population, and EBVs for 5,000 animals were utilized. Weather data (monthly average temperature, average humidity, and total precipitation) were collected from the Korean Statistical Information Service and used to calculate average monthly values for each animal's rearing period. To identify optimal rearing environments, monthly average temperature and humidity were categorized at 1°C and 1% intervals, respectively. A Bayesian Ridge model was employed, with carcass weight and intramuscular fat as dependent variables, and the following as independent variables: the EBVs of these traits, monthly average weather data, and slaughter age (months). Of the 5,000 animals, 3,500 were used for training and 1,500 for validation. A 10-fold cross-validation was conducted to evaluate and tune the model, and final performance was assessed using the validation set. The model yielded coefficients of determination (R^2) of 0.369 and 0.401 for carcass weight and marbling score, respectively, confirming the effectiveness of incorporating weather data and genomic EBVs in an early prediction model. These findings are expected to serve as a basis for improving Hanwoo through optimized environmental settings and provision of carcass trait predictive information.

Key Words: Hanwoo, carcass trait, genomic estimated breeding value (GEBV), weather data, machine learning

P490 A synonymous SNP in *DGAT1* affects milk fat percentage of dairy sheep by regulating the stability of the mRNA to change the viability, proliferation triglyceride levels of ovine mammary epithelial cells. H. Zhen*, J. Wang, Z. Hao, M. Li, and C. Ren, *Gansu Agricultural University, Lanzhou, Gansu, China.*

Diacylglycerol O-acyltransferase1 (DGAT1) is a rate-limiting enzyme that catalyzes triglycerides synthesis originated from diacylglyc-

P491 Genome-wide signatures of selection and functional characterization of Croatian Holstein cattle. M. Shihabi*[2], I. Curik[2,5], T. Bobic[1], M. Oroz[1], D. Kranjac[1], K. Nyarko[3], M. Spehar[4], N. Raguz[1], and B. Lukic[1], [1]*Faculty of Agrobiotechnical Science Osijek, University of Josip Juraj Strossmayer of Osijek, Osijek, Croatia,* [2]*Faculty of Agriculture, University of Zagreb, Zagreb, Croatia,* [3]*Faculty of Electrical Engineering, Computer Science and Information Technology Osijek, Osijek, Croatia,* [4]*Centre for Livestock Breeding, Department for Genetic Evaluation, Zagreb, Croatia,* [5]*Institute of Animal Sciences, Hungarian University of Agriculture and Life Sciences, Kaposvár, Hungary.*

Holstein cattle are the most widespread dairy breed globally, shaped by intensive artificial selection. Despite a large census population, the breed exhibits low genetic diversity, necessitating genetic monitoring in local subpopulations. Identifying genomic regions under selection is essential for understanding past breeding practices and guiding future genetic improvement. This study aimed to identify genomic regions under positive selection in Croatian Holsteins and functionally characterize them. The dataset included 417 cows genotyped with the Illumina BovineSNP50 BeadChip, retaining 26,887 autosomal SNPs after quality control. Four complementary methods, extreme Runs of Homozygosity islands (eROHi), integrated Haplotype Score (iHS), number of Segregating Sites by Length (nSL) and Haplotype Richness Drop (HRiD), were applied to detect selection signals. Genes and QTLs within candidate regions were annotated using Ensembl and Animal QTLdb databases, based on the UCD 1.2 bovine reference genome. The analysis identified 3 eROHi signals (on chromosomes 1, 2 and 6), 2 iHS signals, one nSL signal (both iHS signals on chromosome 10, with one overlapping nSL) and 4 HRiD signals (on chromosomes 4, 21, 23 and 24). Within these 9 regions, a total of 87 candidate genes were annotated. QTL annotation revealed that 68.22% of the 1,592 mapped QTLs were associated with Milk traits, and enrichment analysis confirmed their significant overrepresentation. Among individual regions, the eROHi region on chromosome 6 was strongly linked to Milk QTLs, while HRiD regions on chromosomes 4, 21 and 23 were associated with Health, Exterior, Production, Meat and Carcass QTLs. Notably, ADGRL3 was the only candidate gene within the most significant region, the eROHi region on chromosome 6. These results suggest that selection in Croatian Holsteins is primarily driven by milk production, with additional pressure on health, exterior and production traits, providing insight into the genetic mechanisms shaping this population.

Key Words: selection, cattle and related species, genetic improvement, genotyping, population genomics