DSN cattle including 2 parent-offspring trios. SVs were identified using sniffles2 v.2.5.3 and functionally annotated using the Ensembl Variant Effect Predictor. Additionally, previously identified QTLs for milk and meat traits in DSN were screened for locally relevant SVs. We identified a total of 56,820 SVs, with large indels being the predominant type. Genotype concordance in trios was 84.9% for PacBio Sequel II and improved to 97.3% with PacBio Revio HiFi, highlighting the higher data quality of the latter. Functional annotation of SVs revealed 1 start lost, 57 stop lost, and 130 frameshift SVs across the whole genome of the investigated cattle. In one of the previously identified meat QTLs on chromosome 5, we discovered a 7,504-bp deletion that resulted in the loss of exons 14–21 (out of 21) in the *WC1.3* (WC1.3 molecule) gene, including the stop codon. This deletion likely disrupts *WC1.3*, a gene involved in cargo receptor activity. Another 126 bp long insertion, found in a QTL on chromosome 10, caused a frameshift in exon 35 (out of 82) of the gene *VPS13C* (vacuolar protein sorting 13 homolog C), which is necessary for proper mitochondrial function and lipid transport. Both SVs had no linkage ($r^2 \leq 0.05$) to the top variants of the respective QTLs, but contribute to local genetic variation. This study provides novel insights into structural variations in cattle. Further investigations are necessary to evaluate the functional impact of these SVs on economically important traits and their potential role in breeding strategies.

Key Words: cattle, genome sequencing, GWAS, LD, structural variant

P456 Differential expression of circulating microRNAs in lactating Holstein and Jersey cows exposed to heat stress. T. Choi*[1], J. Lee[1], D. Kim[1], B. Lim[2], G. Ryu[1], H. Baek[1], J. Kim[3], S. Ha[4], S. Kim[1], S. Lee[5], and I. Choi[5], [1]*Dairy Science Division, National Institute of Animal Science, RDA, Cheonan, Chungnam, South Korea,* [2]*Department of Animal Science and Technology, Chung-Ang University, Anseong, Kyeongki, South Korea,* [3]*Dairy Biotechnology R&D Center, Seoul Milk Cooperation, Yangpyeong, Kyeongki, South Korea,* [4]*Animal Genetic Resources Research Center, National Institute of Animal Science, RDA, Hamyang, Kyeongbuk, South Korea,* [5]*Division of Animal and Dairy Sciences, College of Agriculture and Life Sciences, Chungnam National University, Daejeong, Chungnam, South Korea.*

Background: South Korea has recently faced record-high temperatures, which have adversely affected dairy production. Holstein cows, the primary dairy breed globally, are particularly sensitive to heat stress. In contrast, Jersey cows have shown greater heat tolerance, as demonstrated by phenotypic studies. Methods: We investigated physiological and molecular responses to heat stress in Holstein and Jersey cows by measuring rectal temperature, milk yield, and average daily gain, confirming Holstein cows' greater vulnerability. To explore molecular mechanisms, we analyzed circulating microRNA profiles from whole blood samples collected under heat stress and normal conditions using microRNA-sequencing. Differential expression patterns were compared between the 2 breeds to identify biological pathways associated with heat stress. Results: Four microRNAs (bta-miR-20b, bta-miR-1246, bta-miR-2284x, and bta-miR-2284y) were significantly differentially expressed in both breeds under heat stress ($|FC| \geq 2$, $P < 0.05$). Notably, bta-miR-20b and bta-miR-1246 were linked to corpus luteum function and progesterone biosynthesis, while bta-miR-2284x and bta-miR-2284y were associated with immune responses. A comparison of 11 potential heat stress-related microRNAs identified in previous studies of Holstein cows revealed consistent expression trends in Jersey cows, albeit with lower fold changes, suggesting their superior heat resilience. Conclusions: Our study highlights the physiological and microRNA-based differences in heat stress responses between Holstein and Jersey cows. Jersey cows exhibited greater resilience, supported by more stable microRNA expression profiles and improved heat stress indicators, making them a promising breed for dairy production in increasingly hot climates.

Key Words: circulating microRNA, heat stress, Holstein, Jersey, lactation

P457 From data to decisions: Using genomics and sensors to monitor Holstein behavior and welfare. Boris Lukic*[1], Ino Curik[2,5], Karlo Nyarko[3], Tina Bobic[1], Marko Oroz[1], Mihaela Oroz[1], Mario Shihabi[2], David Kranjac[1], Marija Spehar[4], and Nikola Raguz[1], [1]*Faculty of Agrobiotechnical Sciences Osijek, University of Josip Juraj Strossmayer of Osijek, Department for Animal Production and Biotechnology, Osijek, Croatia,* [2]*Faculty of Agriculture, University of Zagreb, Department of Animal Science, Zagreb, Croatia,* [3]*Faculty of Electrical Engineering, Computer Science and Information Technology Osijek, Department of Computer Engineering and Automation, 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, Kaposvar, Hungary.*

With the rapid advancement of high-tech approaches, new opportunities are emerging to enhance productivity and welfare in livestock farming. With the rising global demand for animal-based food, precision livestock farming (PLF) has become essential for optimizing resources while reducing environmental impact. A central aspect of this analysis is genomics, which enables early identification of superior cattle by mapping genomic regions linked to production, reproductive, and health traits. Genotyping 900 Holstein cows using a 700K SNP array will provide valuable insights into genetic variability, allowing for improved breeding strategies. Alongside genomic data, biometric monitoring through thermal imaging, video surveillance, pedometers, and environmental sensors tracks locomotion, behavior and physiological responses, ensuring continuous health and welfare assessment in large herds. Artificial intelligence (AI) and machine learning play a crucial role in analyzing big data sets, integrating genomic and biometric information to develop predictive models for disease susceptibility, productivity, and stress resilience. By combining traditional statistical approaches with AI-driven analytics, this study aims to improve risk assessment and decision-making. Preliminary results reveal significant correlations between genomic markers and behavioral traits, highlighting a genetic basis for activity levels and adaptability. By merging genomics, digital phenotyping and AI, this project seeks to revolutionize livestock management. The integration of these technologies enables early health detection, optimized breeding, and a more efficient, sustainable, and welfare-oriented approach to dairy farming. The Next Generation Animal Production project, within the NextGenerationEU framework, applies these cutting-edge technologies and research to address the key challenges in modern livestock farming.

Key Words: cattle, genomics, PLF, machine learning, behavior

P458 Genetic control of DNA methylation in bovine sperm cells. Y. Tang* and Y. Yu, *Key Laboratory of Animal Genetics, Breeding and Reproduction, Ministry of Agriculture & National Engineering Laboratory for Animal Breeding, College of Animal Science and Technology, China Agricultural University, Beijing, China.*

In dairy cows, the sperm quality of bulls is crucial for the reproductive performance of the herd. DNA methylation of sperm cells is a key molecular phenotype that affects the sperm quality of bulls. However, the extent of its genetic influence remains unclear. Here, we conducted whole-genome bisulfite sequencing (WGBS) and whole genome-wide re-sequencing (WGS) on sperm cells from 125 bulls. Taking Chromosome 1 as an example, the heritability of DNA methylation explained by *cis*-SNPs from the starting position of phenotype was estimated using the GCTA "reml" method. The results showed that the heritability of DNA methylation levels in blocks was higher than that of CpG sites. Given that methylation of DNA blocks have higher heritability and can reduce the number of tests, we performed meSNP (SNPs significantly associated with block methylation levels) mapping on DNA methylation blocks. Linear regression was performed using tensorQTL on the residuals of DNA methylation blocks after correcting for covariates and SNPs. First, using a permutation method, more than 40,000 significant SNP-associated DNA methylation blocks were identified (FDR <0.05). Subsequently, a stepwise regression method was used to identify over 40,000 independent meSNPs. Enrichment analysis of the meBlocks using regioneR revealed significant enrichment in re-