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**ADSA<sup>®</sup> Annual Meeting**  
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## Breeding and Genetics Virtual Posters with Live Q&A

**2466V Comparison of 2 methods of genomic epistasis relationship matrices using daughter pregnancy rate in US Holstein cattle.** Z. Liang\*, D. Prakash, and Y. Da, *Department of Animal Science, University of Minnesota, Saint Paul, MN.*

This study compared 2 methods of genomic epistasis relationship matrices (GERM) for heritability estimation, accuracy of predicting the phenotypic residuals of daughter pregnancy rate (DPR) after removing fixed nongenetic effects, and computing time. The 2 GERM methods are the genomic version of Henderson's Hadamard products between additive and dominance relationships, to be referred to as approximate GERM (AGERM); and the exact GERM (EGERM) that removes the intra-locus epistasis effects contained in AGERM. A total of 60,671 SNPs and 22,022 first-lactation Holstein cows were used. The full prediction model included additive (A) dominance (D),  $A \times A$ ,  $A \times D$ ,  $D \times D$ ,  $A \times A \times A$ ,  $A \times A \times D$ ,  $A \times D \times D$  and  $D \times D \times D$  effects; and the reduced model included A and  $A \times A$  effects. The accuracy of predicting the DPR phenotypic residuals was the correlation between the predicted total genetic values and the phenotypic residuals in each validation population and then averaged across 10 validation populations. The data analysis used the EPIHAP computing package that implements both AGERM and EGEM. The results showed that AGERM and EGEM had the same heritability estimates and prediction accuracy, but EGEM required 21 times as much computing time as required by AGERM, which required 1.32 times as much time for the genomic additive relationship matrix. The same prediction accuracy of the 2 methods should favor AGERM for its mathematical simplicity and computing efficiency. The full model had 5 effect types with heritability estimates of 0.008–0.199 but had the same prediction accuracy as the reduced model, indicating that  $A \times D$ ,  $A \times A \times A$  and  $A \times A \times D$  with heritability estimates 0.008–0.02, as well as D,  $D \times D$ ,  $A \times D \times D$  and  $D \times D \times D$  with zero heritability, had no contribution to the prediction accuracy. The full or reduced model increased the prediction accuracy over the additive model by 13.3%. The AGERM and EGEM methods also had the same estimates of intra- and inter-chromosome heritabilities, 0.031 intra-chromosome  $A \times A$  heritability, and 0.178 inter-chromosome  $A \times A$  heritability. These results were consistent with previous GWAS results that inter-chromosome  $A \times A$  effects were the main genetic effects of DPR.

**Key Words:** epistasis, heritability, prediction accuracy

**2467V Genetic parameters of milk mid-infrared spectra-based methane predictions and their relationships with production traits in Walloon dairy cattle.** H. Atashi<sup>1,2</sup>, A. Vanlierde<sup>3</sup>, S. Vandrick<sup>1</sup>, H. Wilmot<sup>1,4</sup>, H. Soyeur<sup>1</sup>, and N. Gengler\*<sup>1</sup>, <sup>1</sup>*ULiège-GxABT, Gembloux, Belgium*, <sup>2</sup>*Shiraz University, Shiraz, Iran*, <sup>3</sup>*Walloon Agricultural Research Center, Gembloux, Belgium*, <sup>4</sup>*National Fund for Scientific Research, Brussels Belgium*.

Beyond global warming issues, direct CH<sub>4</sub> emissions are also a loss of energy. Genetic selection of low CH<sub>4</sub> emitting cows is a promising cost-effective and permanent strategy. However, CH<sub>4</sub> emission traits must be well defined, genetically variable and heritable, and their genetic correlations with other important traits known. Proposed traits include CH<sub>4</sub> production, defined as the daily production (g/d); CH<sub>4</sub> yield, defined as the amount of CH<sub>4</sub> produced per unit of dry matter intake; CH<sub>4</sub> intensity, defined as CH<sub>4</sub> produced per unit of product (milk or meat), and residual CH<sub>4</sub>. Research has found that milk mid-infrared (MIR) spectra based predictors could explain approximately 70% of

the daily CH<sub>4</sub> emissions. This study estimated genetic parameters of MIR-based CH<sub>4</sub> and its relationships with production traits. Edited data were 1,529,282 test-day milk yield (MY), fat percentage (FP), protein percentage (PP), lactose percentage (LP), milk urea concentration (MU), and somatic cell count (SCS) from 229,465 first-parity cows distributed in 1,530 herds collected from 2006 to 2021. Milk MIR spectra were used to predict CH<sub>4</sub> emissions (PME, g/d) using existing equations. The trait log-transformed CH<sub>4</sub> intensity (LMI) was defined as the log-transformed ratio of PME divided by the daily MY (kg/d) recorded on the same test-day achieving a more normal distribution. Random regression test-day models were used to estimate variance components. Means (SD) PME and LMI were 326.8 (67.65) g/d, and 2.64 (0.35), respectively. Mean daily h<sup>2</sup> estimated for PME and LMI were 0.14 (0.05) and 0.24 (0.05), respectively. Mean genetic correlation estimated between PME and LMI was 0.55 (0.03). Mean genetic correlation between PME and the included milk traits ranged from –0.14 (MY) to 0.40 (FP). The corresponding values estimated using LMI ranged from –0.88 (MY) to 0.58 (PP). MU and SCS showed close to zero genetic correlations with the studied CH<sub>4</sub> traits. Breeding for reduced CH<sub>4</sub> emissions seems to be possible, but relationships to other traits need also to be considered.

**Key Words:** greenhouse gases, methane emissions, sustainable agriculture

**2468V Genotype by climate zone interactions for fertility, somatic cell score, and production in Iranian Holsteins.** F. Atrian-Afiani\*<sup>1</sup>, S. Joezy<sup>2</sup>, and J. Jensen<sup>3</sup>, <sup>1</sup>*Aarhus University, Aarhus, Denmark*, <sup>2</sup>*Shahr-e-Qods Branch, Islamic Azad University, Qods, Tehran Province, Iran*, <sup>3</sup>*Aarhus University, Aarhus, Denmark*.

The objective of this study was to investigate genetic variation and genotype by environment (G × E) interactions for fertility (including age at first calving and calving interval), somatic cell score (SCS), and milk production traits for Iranian Holsteins. Different environments were defined based on the climatic zones (cold, semi-cold, and moderate) and considering the herd location. Data were collected between 2003 and 2018 by the National Animal Breeding Center of Iran (Karaj). Variance and covariance components and genetic correlations were estimated using 2 different models, which were analyzed using Bayesian methods. For both models, performance of traits in each climate were considered as different traits. Fertility traits were analyzed using a trivariate model. Furthermore, SCS and production traits were analyzed using trivariate random regression models (records in different climate zones considered as different traits). For the fertility traits, the largest estimates of heritability were observed in cold climate. Fertility performance was always better in cold environment. Genetic correlations between climatic zones ranged from 0.85 to 0.94. For daily measurements of SCS and production traits, heritability ranged from 0.031 to 0.037 and 0.069 to 0.209, respectively. Results indicated heterogeneous variance components for all the studied traits across various climatic zones. Estimated genetic correlations for SCS revealed that the genetic expression of animals may vary by climatic zone. Results indicated the existence of G × E interaction due to the climatic condition, only for SCS. Therefore, in Iranian Holsteins, the effect of G × E interactions should not be neglected, especially for SCS, as different sires might be optimal for use in different climatic zones.

**Key Words:** G×E interactions, fertility, SCS