user option. This step is extremely demanding for memory space. We developed a triangular memory storage technique that eliminated this memory requirement. Estimates for additive and dominance heritabilities of each SNP and for haplotype additive heritability of haplotype blocks are also available. These heritability estimates can be used for identifying SNPs, SNP pairs and haplotype blocks with high heritability estimates. With the many capabilities under highly complex models for genomic estimation and prediction, the EPIHAP program offers a computing capability to investigate and utilize complex genetic mechanisms.

Key Words: epistasis, haplotype, genomic prediction

P168 Genomic heritability and prediction accuracy of additive and nonadditive effects for daughter pregnancy rate in crossbred dairy cows. Z. Liang*[1], D. Prakapenka[1], P. VanRaden[2], and Y. Da[1], [1]*Department of Animal Science, University of Minnesota, Saint Paul, MN,* [2]*Animal Genomics and Improvement LaboratoryDA/ARS, Beltsville, MD.*

Genomic heritability and prediction accuracy of epistasis effects for daughter pregnancy rate (DPR) were evaluated using 79,294 SNPs and 9,565 crossbred dairy cows. Heritability was estimated under the model with SNP additive effects (A), SNP dominance effects (D), and second and third order epistasis effects of A × A, A × D, D × D, A × A × A, A × A × D, A × D × D and D × D × D. Heritability estimate was 0.162 for additive effects, 0.283 for dominance effects, 0.555 for A × A effects, and zero or nearly zero for A × D, D × D and the third-order epistasis effects. Genomic prediction included all SNP and epistasis effects with heritability greater than one percent, resulting in the prediction model with A, D and A × A effects only. Prediction accuracy as correlation between the genomic best linear unbiased prediction and the phenotypic values from a 10-fold validation study for each model was 0.268 for A-model, 0.363 for D-model, 0.438 for A × A, 0.446 for A+D, 0.455 for A+(A × A), 0.467 for D+(A × A), and 0.475 for A+D+(A × A). Relative to the A-model, the D-model increased the prediction accuracy by 35.6%, A × A by 63.6%, A+D by 66.4%, A+(A × A) by 69.8%, D+(A × A) by 74.3%, and A+D+(A × A) by 77.2%. The heritability estimates and prediction accuracies showed that A × A effects were the largest contributor to DPR heterosis, followed by dominance and additive effects. The high additive heritability (0.16) in crossbred dairy cows relative to the low additive heritability in Holstein cows (0.025 according to our own estimate) indicated that a larger collection of favorable alleles from different breeds in crossbreds than in purebreds was part of the genetic mechanism underlying DPR heterosis. The total heritability was almost 100%, indicating likely overestimates somewhere for unknown reasons. However, the prediction accuracies did support the conclusion that A × A effects were the largest contributor to DPR heterosis, followed by dominance and additive effects, and that prediction accuracy of DPR can be high in crossbred dairy cows. Combined with dominance and A × A effects, the results in this study support our GWAS finding in a separate study that genome-wide additive and nonadditive effects were the genetic mechanism of reproductive heterosis.

Key Words: heterosis, genomic prediction, heritability

P169 Genetic mechanisms of reproductive heterosis in crossbred dairy cows involve genome-wide additive and nonadditive effects. D. Prakapenka*[1], Z. Liang[1], P. VanRaden[2], J. Jiang[4], L. Ma[3], J. Garbe[5], C. Maltecca[4], P. Hansen[6], and Y. Da[1], [1]*Department of Animal Science, University of Minnesota, Saint Paul, MN,* [2]*Animal Genomics and Improvement LaboratoryDA/ARS, Beltsville, MD,* [3]*Department of Animal and Avian Sciences, University of Maryland, College Park, MD,* [4]*Department of Animal Science, North Carolina State University, Raleigh, NC,* [5]*Genomics Center, University of Minnesota, Minneapolis, MN,* [6]*Department of Animal Sciences, University of Florida, Gainesville, FL.*

Reproduction is one of the biological processes with strong heterosis in crossbred dairy cows. To identify the genetic mechanism for reproductive heterosis, we conducted a genome-wide association study for daughter pregnancy rate (DPR) using 79,294 SNPs and 9,565 crossbred dairy cows. Using a significance level of log(1/p) = 8 with the Bonferroni correction, the number of significant SNP effects was 16,449 for additive effects and 10,449 for dominance effects. This compares to only 112 additive and 2 dominance effects for DPR from a large-scale Holstein GWAS. The most significant additive effect had a log(1/p) of 53, whereas the most significant dominance effect had a log(1/p) of 203; 481 dominance effects had log(1/p) > 53. For pairwise epistasis effects, the cut-off significance level with the Bonferroni correction was log(1/p) = 12. This study only focused on the top 50,000 pairwise effects with minimal log(1/p) value of 29. Of these 50,000 effects, 50.2% were A × A effects, 37.6% A × D and D × A, and 12.2% D × D. Epistasis effects were 30% intra-chromosome and 70% inter-chromosome effects. Of the A × A effects, 82% were inter-chromosome and 18% were intra-chromosome effects. These results indicated that the genetic mechanism of reproductive heterosis involved both additive and nonadditive effects, and inter-chromosome A × A effects had a major role in reproductive heterosis. The large number of significant additive effects indicated a larger collection of favorable alleles for DPR in crossbred cows than in purebred Holsteins in comparison with previous GWAS results for Holsteins. The large numbers of significant dominance and epistasis effects indicated a major role of nonadditive effects underlying reproductive heterosis in crossbred dairy cows. The intra-chromosome and inter-chromosome epistasis effects as well as the significant additive and dominance effects involved all chromosomes, indicating that the entire genome contributed to reproductive heterosis.

Key Words: heterosis, GWAS, genetic mechanism

P170 Genomic heritability and prediction accuracy of epistasis effects for production and fertility traits in US Holstein cattle. Z. Liang*, D. Prakapenka, and Y. Da, *Department of Animal Science, University of Minnesota, Saint Paul, MN.*

Genomic heritability and prediction accuracy of epistasis effects were evaluated using 60,671 SNPs and 22,009 first-lactation Holstein cows for 5 production traits and 3 fertility traits, milk yield (MY), fat yield (FY), protein yield (PY), fat percentage (FPC), protein percentage (PPC), daughter pregnancy rate (DPR), cow conception rate (CCR), and heifer conception rate (HCR). Heritability was estimated for SNP additive effects (A), SNP dominance effects (D), and second and third-order epistasis effects. The additive heritability was 0.28 for MY, 0.24 for FY, 0.21 for PY, 0.51 for FPC, 0.56 for PPC, 0.025 for DPR, 0.038 for CCR, and 0.006 for HCR. Dominance heritability was 0.037 for MY, 0.035 for FY, 0.04 for PY, 0.016 for HCR, and was negligible the other traits. The A × A heritability estimate was 0.14 for MY, 0.16 for FY, 0.18 for PY, 0.08 for FPC, 0.07 for PPC, 0.19 for DPR, 0.07 for CCR and 0.08 for HCR. Other than HCR, A × D, D × D and third-order effects had low heritability estimates of 0–0.03. For HCR, epistasis heritability estimate was 0.10 for A × D, 0.03 for D × D, 0.10 for A × A × A, 0.04 for A × A × D, 0.02 for A × D × D, and 0.01 for D × D × D. These heritability estimates indicated that HCR had the most complex genetic mechanism among all 8 traits. For genomic prediction accuracy, the A+D model