470   Association between lipid-related genes implicated in conceptus elongation and female fertility traits in dairy cattle. R. Abdollahi-Arpanahi*[1], M. R. Carvalho[2], E. S. Ribeiro[2], and F. Peñagaricano[1], [1]*University of Florida, Gainesville, FL,* [2]*University of Guelph, Guelph, ON, Canada.*

Elongation of the preimplantation conceptus is a requirement for pregnancy success in ruminants, and failures in this developmental phase seem to be highly associated with subfertility in dairy cattle. Identifying genetic markers that are related to early conceptus development and survival, and utilizing these markers in selective breeding can improve reproductive efficiency of dairy herds. The objective of this study was to evaluate the association of 1,679 single nucleotide polymorphisms (SNPs) within or close to 183 candidate genes involved in lipid metabolism of the elongating bovine conceptus with different female fertility traits in US Holstein dairy cattle. A total of 27,371 Holstein bulls with predicted transmitting ability (PTA) records for daughter pregnancy rate (DPR), cow conception rate (CCR), and heifer conception rate (HCR) were used as discovery population. The associations found in the discovery population were validated using 2 female Holstein populations (1,122 heifers and 2,138 cows) each with 4 fertility traits, including success to first insemination (SF), number of services per conception (NSC), fertility categorization (FertC), and age at first conception (AFC) for heifers or days open (DO) for cows. Marker effects were estimated using a linear mixed model with SNP genotype as a linear covariate and a random polygenic effect. After multiple testing correction, 39 SNPs flagging 27 candidate genes were associated with at least one fertility trait in the discovery population. Of these 39 markers, 3 SNPs were validated in the heifer population and 4 SNPs were validated in the cow population. The 3 SNPs validated in heifers are located within or near genes CAT, MYOF, and RBP4 while the 4 SNPs validated in lactating cows are located within or close to genes CHKA, GNAI1, and HMOX2. These validated genes seem to be relevant for reducing pregnancy losses, and the SNPs within these genes are excellent candidates to be included into genomic tests for improving reproductive performance in dairy cattle. Our findings emphasize the importance of lipid metabolism for bovine conceptus development.

Key Words: conceptus development, reproductive trait, validation study

471   Genomic prediction and marker selection using high-density genotypes from 5 dairy breeds. P. M. VanRaden[1], D. J. Null[1], J. R. O'Connell[2], J. B. Cole[1], and B. Li*[1], [1]*USDA Animal Genomics and Improvement Laboratory, Beltsville, MD,* [2]*University of Maryland School of Medicine, Baltimore, MD.*

Genotypes for 314,765 Jerseys (JE), 9,077 Ayrshires (AY; including Scandinavian Red), 39,191 Brown Swiss, 4,440 Guernsey, and 351,666 Holsteins (HO) were imputed to high density (HD). The separate HD reference populations included Illumina BovineHD genotypes for 410 JE, 527 AY, 181 BS, 147 GU, and 4,015 HO. The 641,459 variants included the HD SNPs and all 79,276 (80K) genetic markers and QTLs used in routine evaluations. The variants were not pruned for high linkage disequilibrium as in previous HD studies of only HO. Chromosome locations used the ARS-UCD1 map after removing some incorrectly placed regions. Imputation using findhap version 3 with 24 processors took <2 d for each breed. Before imputation, 90–97% of genotypes in each breed were unknown, and after imputation, 2.1% of JE, 3.6% of AY, 4.7% of BS, 2.8% of GU, and 0.7% of HO alleles remained unknown. Segments in chromosomes 1 and 2 had the most haplotypes in each breed, indicating possible map issues not discovered in earlier tests with fewer SNPs. Prediction and SNP selection results focus only on JE as an example. Allele effects for 26 traits were estimated using phenotypic reference populations that included up to 6,121 JE males and 99,426 JE females. Convergence took 4–8 d using 1 processor per trait and up to 800 iterations. Correlations of HD with 80K genomic predictions for young animals averaged 0.988; yield traits were highest with correlations of about 0.995; cow conception rate and dairy form were lowest at 0.982. Some HD effects were more than twice as large as the largest 80K SNP. On chromosome 11 at 104 Mbase, HD SNPs had the largest effects for fore udder attachment, front teat placement, rump width, and rump angle. For udder cleft and teat length, HD SNPs had higher effects than the highest SNP already in the 80K list. Large new effects were also discovered from HD for daughter pregnancy rate and cow conception rate. Surprisingly for protein, the β-Lactoglobulin gene test had smaller effects than 3 nearby HD SNPs. Previous studies selected and included markers with large effects for HO traits; adding these newly selected HD markers should also improve JE, AY, BS, GU, and crossbred genomic predictions.

Key Words: variant selection, imputation, minor breeds