Session 32 Poster 22

Genome-wide association study for genetic heterogeneity for milk yield and somatic cell score

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Recently, genetic variation in residual variance was reported for both Swedish Holstein and Swedish Red. The aim of this study was to perform a genome-wide association study for this genetic heterogeneity. Breeding values for residual variance for milk yield and somatic cell score were available for 842 Swedish Red bulls. In addition, marker data were available for 701 bulls using the Illumina Bovine SNP50 BeadChip, which includes 54,001 single nucleotide polymorphisms (SNP) markers. After edits on minor allele frequency, call rates and GenCall scores more than 48,000 markers were available to be included in the analyses. A multi-locus Bayesian stochastic search variable selection model was used for the analysis. Here, allele effects follow a priori a mixture distribution, where a small fraction of the markers (prior probability of 5%) has a large effect and the remaining markers have virtually no effect. For milk yield in the Swedish Red breed, two regions with a Bayes factor larger than 10 were identified and a further five regions had a Bayes factor larger than three. For somatic cell score, the corresponding numbers were one and four, respectively. In conclusion, we found a few SNPs associated with residual variance of milk yield and somatic cell score in the Swedish Red breed.