Genetic architecture of environmental variance of somatic cell score using high density SNP data

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In recent years it has been shown that not only the phenotype is under genetic control, but also the environmental variance. Very little is, however, known about the genetic architecture of environmental variance. The objective of this study was therefore to perform a genome-wide association study and to quantify the accuracy of genome-wide breeding values for somatic cell score (SCS) in dairy cows. SCS was used because previous research has shown that the environmental variance of SCS is partly under genetic control and reduction of the variance of SCS by selection is desirable. In this study we used 37,590 SNP genotypes and 44,032 test-day records of 1,563 cows at experimental research farms in four countries in Europe. Using either a pedigree or a genomic relationship matrix, we calculated for both a residual variance per cow as a proxy for the environmental variance. In addition, we calculated the within-cow mean and phenotypic variance of somatic cell score. These four traits were analysed with a Bayesian stochastic search variable selection method. No SNP were found to be associated with environmental variance of SCS, whereas 34 SNP were found to be associated with mean SCS. Based on 10-fold cross-validation, the accuracy of genome-wide breeding values was 0.4-0.5 for both environmental variance and mean SCS. Environmental variance was estimated to be affected by ~2,000-2,500 independent chromosome segments, whereas ~1,700 independent chromosome segments were affecting the mean SCS. About 25-28% of 50-SNP windows were required to explain 50% of the genetic variance of environmental variance. It is concluded that environmental variance of SCS is likely to be determined by many genes and accuracy of genomic breeding values for environmental variance is comparable to that of genomic breeding values for mean SCS.