

**Title:**

Genetic architecture of micro-environmental sensitivity of quantitative traits – application to bovine somatic cell score

**Abstract:** max 300 words (Your abstract must use Normal style and must fit into the box.)

In the last decade a number of studies have shown that not only the phenotypic trait value, but also micro-environmental sensitivity or environmental variance of traits is under genetic control. Micro-environmental sensitivity can be considered as differential sensitivity of individuals to unknown environmental factors observed as differences in micro-environmental variance. The availability of whole-genome SNP data on relatively large numbers of individuals makes it possible to perform genome-wide association studies to unravel the genetic architecture of micro-environmental sensitivity. The aim of this study was therefore to find SNP associated with micro-environmental sensitivity using a genome-wide association study and to quantify the predictive ability of genome-wide breeding values for micro-environmental sensitivity of bovine somatic cell score (SCS). Bovine SCS is a quantitative trait associated with mastitis and it is known that both its mean and micro-environmental sensitivity are partly under genetic control. A Bayesian stochastic search variable selection multi-SNP model was applied to different measures of micro-environmental sensitivity of SCS and mean SCS of 1563 cows located on research farms in four different countries. After quality control, genotypes of 37,590 SNP were used. No significant SNP were found to be associated with micro-environmental sensitivity, whereas 34 significant SNP were found for mean SCS. Based on 10-fold cross-validation, the accuracy of genome-wide breeding values was 0.4-0.5 for both micro-environmental sensitivity and mean SCS. Micro-environmental sensitivity was estimated to be affected by ~2000 - 2500 independent chromosome segments, whereas ~1700 independent chromosome segments were affecting the mean SCS. About 25-28% of 50-SNP windows were required to explain 50% of the total genetic variance of micro-environmental sensitivity. It can be concluded that micro-environmental sensitivity, at least for SCS, is likely to be determined by many genes and therefore the power to detect QTL for micro-environmental sensitivity is likely to be low.