



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

H.A. Mulder^{1,2}, R.E. Crump², M.P.L. Calus², R.F. Veerkamp²

Background

- Micro-environmental sensitivity is differential sensitivity to unknown environmental factors
- Observed as differences in micro-environmental variance/environmental variance/residual variance within an animal.

Objectives

- To identify genomic regions affecting micro-environmental sensitivity and the mean of bovine somatic cell score (SCS)
- To quantify the predictive ability of genome-wide estimated breeding values (GW-EBV) for micro-environmental sensitivity and mean of bovine somatic cell score

Material and Methods

Data

- 1563 first-parity cows >5 SCS records at 5 research farms.
- Genotyped with Illumina BovineSNP50 BeadChip

GWAS/GW-EBV analyses

- Univariate Bayesian SSVS method (Calus et al., 2008)
- Posterior genetic variance per 50-SNP window
- Ten-fold cross-validation to assess accuracy GW-EBV
- Number of independent chromosome segments (Daetwyler et al., 2008)

Genetic analysis

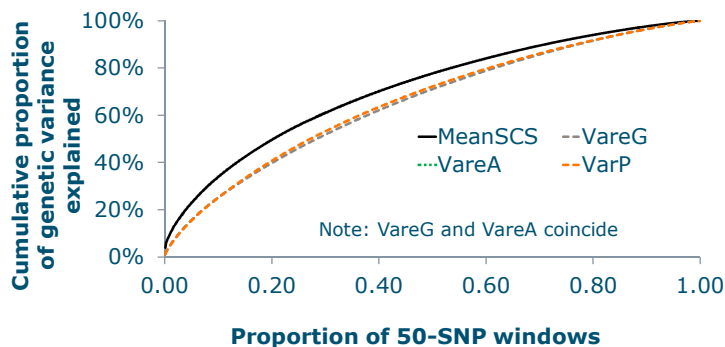
- Double hierarchical generalized linear model model in ASREML (Rönnegård et al., 2010)
- Genomic (G) or numerator (A) relationship matrix

Phenotypes used for GWAS/GW-EBV

- MeanSCS: raw mean SCS per cow
- VareG: Residual variance per cow using G-matrix
- VareA: Residual variance per cow using A-matrix
- VarP: Raw phenotypic variance of SCS per cow

Micro-environmental sensitivity

Results



Accuracy (r) of GW-EBV and pedigree EBV and number of independent chromosome segments

Trait	r GW-EBV	r EBV	Number of chromosome segments
meanSCS	0.444	0.402	1688
VareG	0.447	0.503	1959
VareA	0.445	0.504	1975
VarP	0.418	0.480	2447

GWAS

- 5 SNP with very strong or decisive Bayes Factors for meanSCS
- No evidence for SNP associated with micro-environmental sensitivity of SCS

Conclusions

- Inheritance of micro-environmental sensitivity of SCS follows approximately infinitesimal model.
- Accuracy of (GW)-EBV are similar for micro-environmental sensitivity of SCS and mean SCS.

References

- Calus, M. P. L., T. H. E. Meuwissen, A. P. W. De Roos, and R. F. Veerkamp. 2008. Accuracy of genomic selection using different methods to define haplotypes. *Genetics* 178:553-561.
- Daetwyler, H. D., B. Villanueva, and J. A. Woolliams. 2008. Accuracy of predicting the genetic risk of disease using a genome-wide approach. *PLoS ONE* 3(10):e3395.
- Rönnegård, L., M. Felleki, F. Fikse, H. A. Mulder, and E. Strandberg. 2010. Genetic heterogeneity of residual variance: estimation of variance components using double hierarchical generalized linear models. *Genet. Sel. Evol.* 42:8.
- VanRaden, P. M. 2008. Efficient methods to compute genomic predictions. *J. Dairy Sci.* 91:4414-4423.

Acknowledgements

This project was financed by the RobustMilk project, which is financially supported by the European Commission under the Seventh Research Framework Programme, Grant Agreement KBBE-211708. The content of this paper is the sole responsibility of the authors, and it does not necessarily represent the views of the Commission or its services.

