

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



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Objective

Identify genomic regions affecting genetic heterogeneity for milk yield and somatic cell score in Swedish Red cattle

Background

Genetic heterogeneity = Environmental sensitivity
Animal-specific response to short-term changes in environment

Results

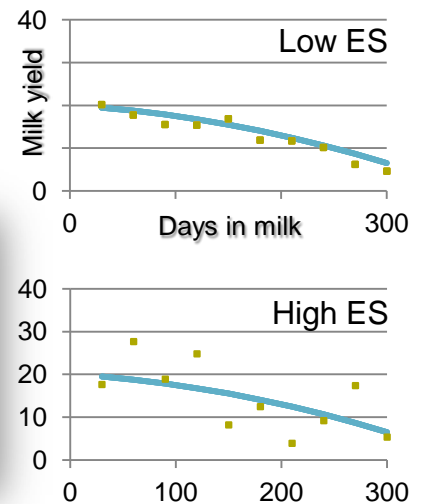
Table: Number of SNPs with signal

Evidence	Milk yield	Cell score
Strong	2 (2)	1 (0)
Substantial	5 (0)	3 (0)

In brackets: number of SNPs also affecting mean performance, suggesting a scaling effect

Data

- 701 Swedish Red bulls
- Illumina Bovine SNP50 BeadChip
- Breeding values for environmental sensitivity
 - Test-day observations for milk yield and somatic cell score
- Approx. 300 thousand Swedish Red cows
- Analyzed with double hierarchical generalized linear model



Conclusions

- Several regions identified
- Partly due to scaling effect

Methods

- All SNPs fitted simultaneously
- Bayesian variable selection
 - Allele effects follow a 2-component mixture distribution
 - Prior probability of large effect: 0.05
- Bayes factors:
 - > 3: substantial evidence
 - > 10: strong evidence

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