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Genetic Analyses of Pathogen-Specific Mastitis

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Aims

To investigate whether there is a genetic variability regarding cow´s resistance to different mastitis pathogens

To examine the effects of a previously identified QTL for general mastitis resistance on pathogen-specific mastitis

Data

Bacteriological data (field data collected 1993-2004) on mastitis pathogens were obtained from the Swedish National Veterinary Institute. The data were mainly from subclinical cases of mastitis and it comprised 21,834 cows with 38,607 diagnoses.

Haplotypes of a previously identified QTL with effect on mastitis (Sahana *et al.*, 2008. Animal Genetics 39:354-62) were available on 114 bulls that had daughters with bacteriological data.

Analyses

Variance components were estimated for incidence of the six most frequent pathogens. A threshold sire model was used and the analyses were based on MCMC methodology.

An allele substitution model was used to study the effect of QTL-haplotype.

Results

Estimated genetic variation on the liability scale for acquired infections of different pathogens ranged from 0.006 (*E.coli*) to 0.047 (CNS).

No significant QTL-haplotype substitution effects on the resistance to pathogen-specific mastitis were found. However, the effects inbetween two of the QTL-haplotypes differed regarding the risk of acquiring a *Str. dysgalactiae* infection.

Prevalence and sire variance for the most common mastitis causing pathogens in Sweden

Pathogen	%	Sire variance	
		Mean	SD
S. aureus	35	0.026	0.005
CNS	29	0.047	0.008
Str. uberis	13	0.038	0.008
Str. dysgalactiae	11	0.028	0.007
E. coli	4	0.006	0.004
Str. species	2	0.013	0.009

Conclusion

We found evidence for genetic variation regarding resistance to specific mastitis pathogen but no overall effect of "mastitis-QTL"