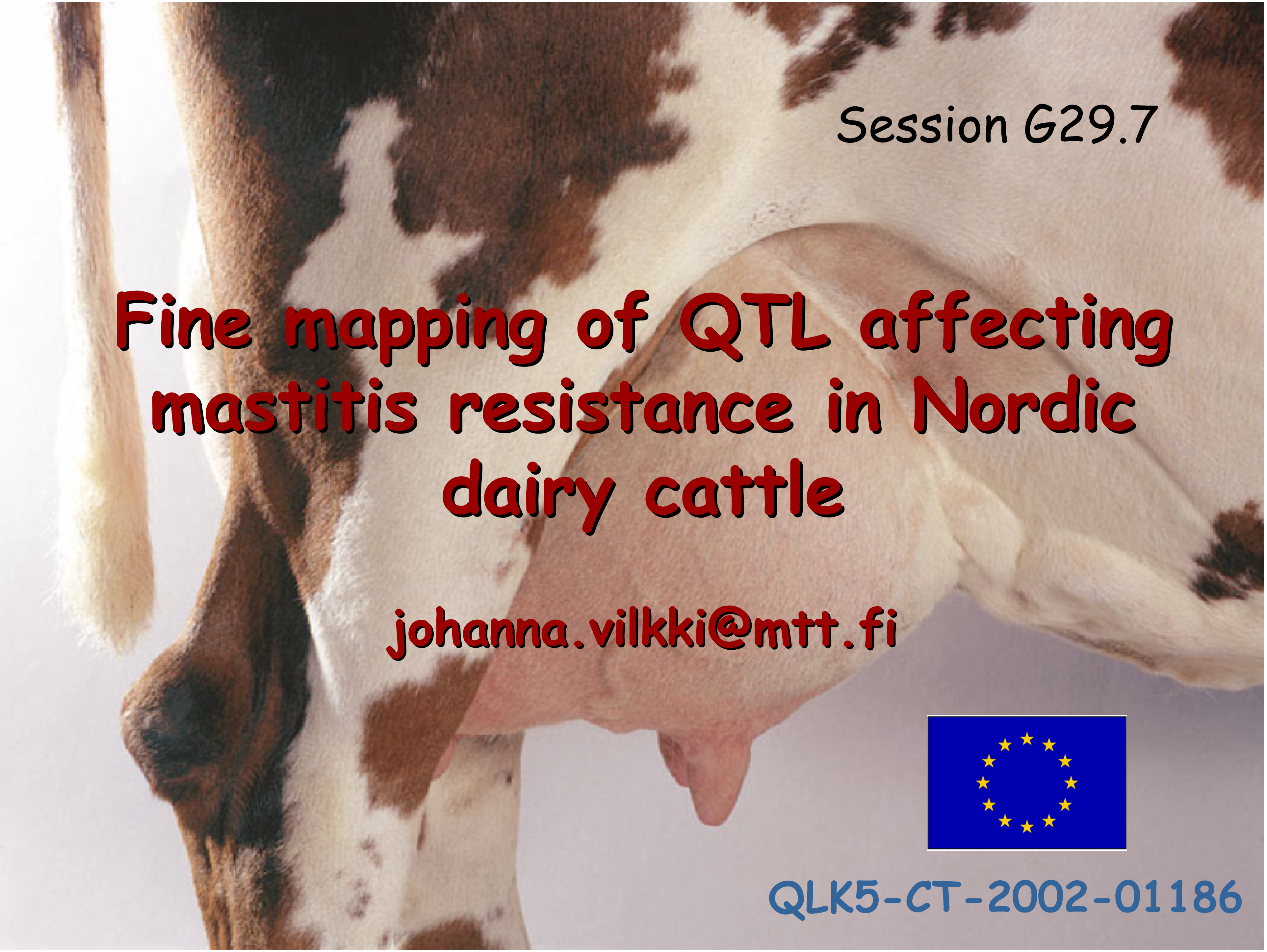

Session G29.7

Fine mapping of QTL affecting mastitis resistance in Nordic dairy cattle

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QLK5-CT-2002-01186

New breeding tools for improving mastitis resistance in European dairy cattle

Consortium (2002-2006):

- MTT (Finland)/ Johanna Vilkki
- SLU (Sweden)/ Lena Andersson-Eklund
- EAU (Estonia)/ Haldja Viinalass
- DIAS (Denmark)/ Mogens Sando Lund
- ROSLIN (UK)/ John Williams
- ID-Lelystad (NL)/ Lucia Kaal

Mastitis

- the most common and costly disease in dairy cattle (up to 40% affected)
- difficult to record
- low heritability
- genetic correlation with milk production
- selection / SCC

Clinical mastitis

- Nordic countries are the only countries with well-established national health recording
  - Norway 1975
  - Finland 1982
  - Sweden 1984
  - Denmark 1990

- Genome scans made in all these countries for health traits, including clinical mastitis

Aims

- Joint analysis of Nordic data

- Improvement of statistical methodology

- To identify marker haplotypes associated with QTL alleles (-> marker assisted selection)

- To dissect the genetic basis of mastitis as:
(i) correlated to specific pathogens
(ii) positional candidate gene sequence variation,
(iii) pleiotropic effects of each QTL

Material (red breeds)

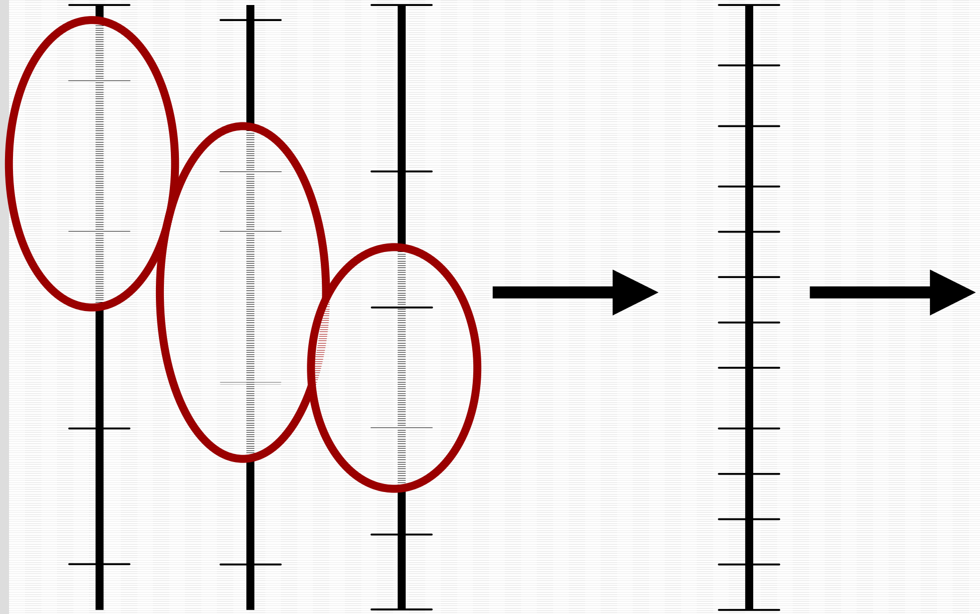
- 53 grandsires, 1900 bulls

(Finnish Ayrshire, Danish Red, Swedish Red and White)

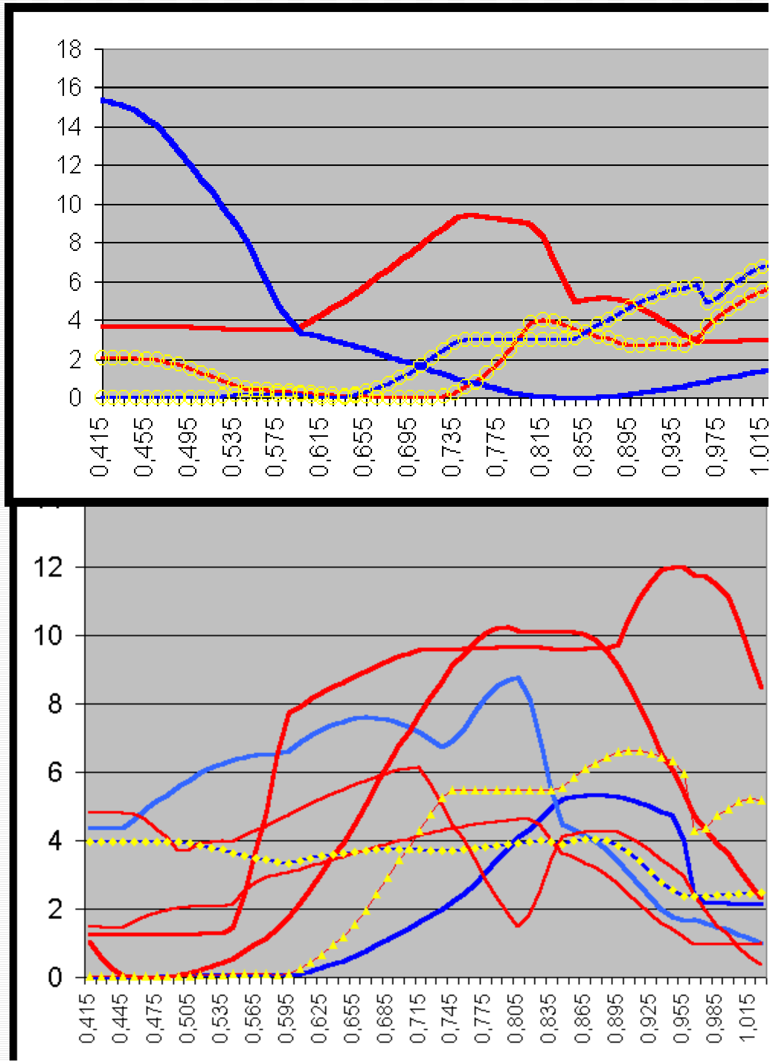
- Nordic QTL scans
- DYDs: clinical mastitis and SCS
- pathogen data of milk samples

Combining the Nordic results

Fin; Swe; Dnk all



53 families



Dense maps

- 4 regions on BTA9 and BTA11
- old (USDA/MARC) & new microsatellites and gene SNPs
- RH-mapping (Roslin 3000 Rad) and linkage mapping
- marker order problematic: the linkage maps do not completely agree with RH-map or genomic sequence assembly (Ensembl Btau 2.0)

Genotyping

- BTA9 linkage map: 59 markers, 97.7 cM
- BTA11 linkage map: 38 markers, 85.1 cM

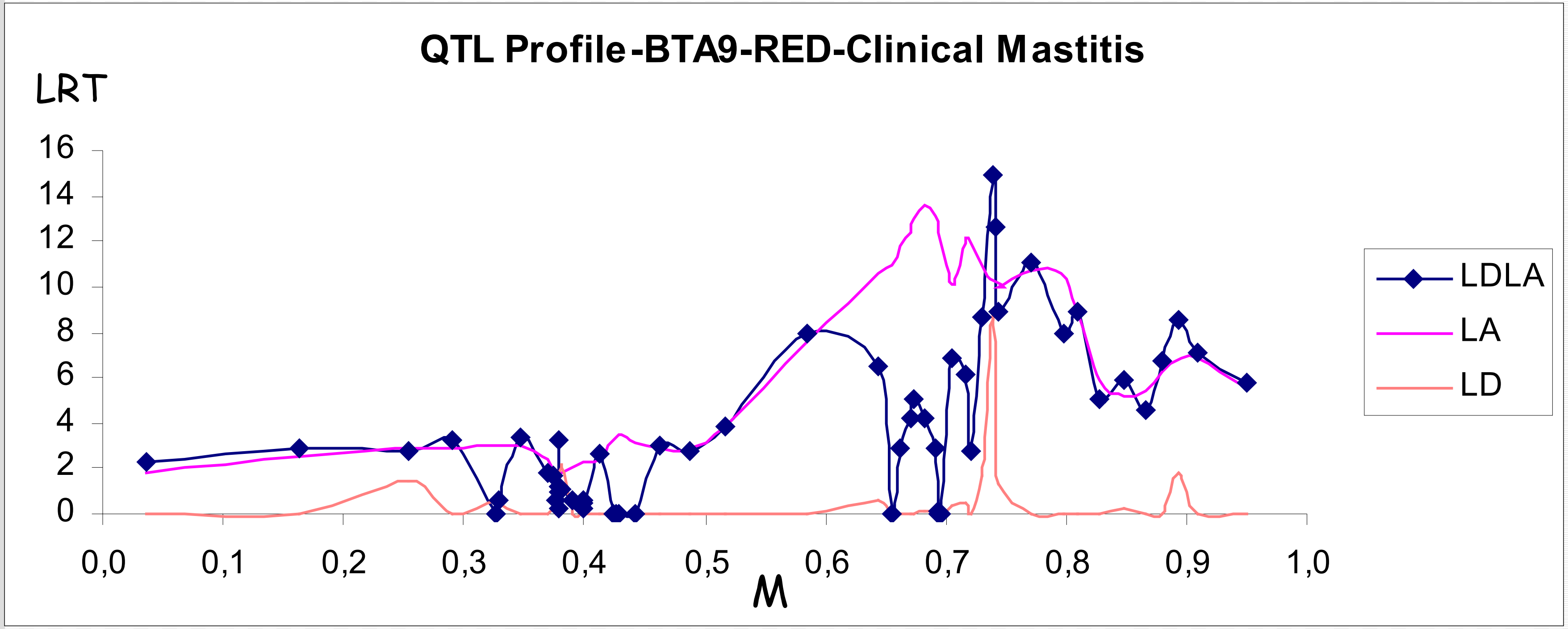
- part of nonsegregating families also genotyped (for maternal haplotypes); in total 34 families

- BTA9 4-marker haplotype region: 20 SNPs

Statistical analyses

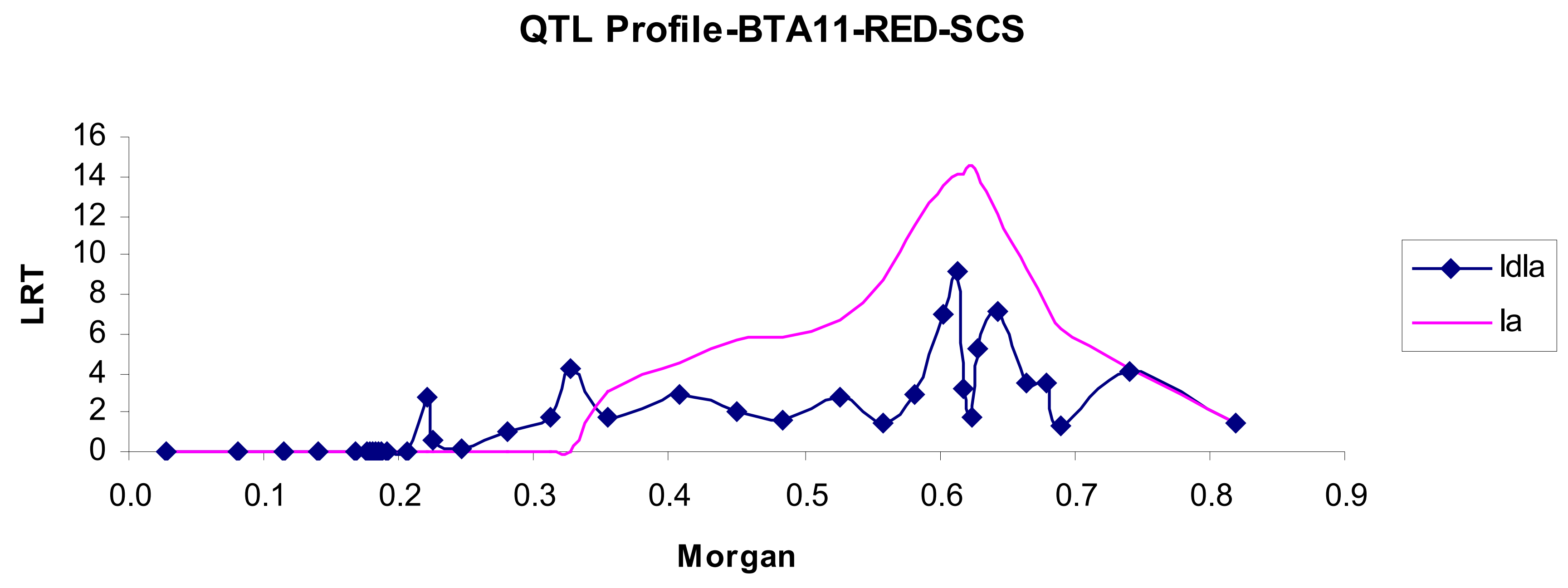
- Linkage mapping (least squares and variance components)
- Combined linkage/linkage disequilibrium (LA/LD)
  - haplotypes of sires and sons (GDQTL)
  - IBD matrix (Wang et al 1995)
  - IBD probabilities (Meuwissen & Goddard 2001)
  - hypothesis testing by likelihood ratio test (LRT)
  - Multi-trait model used when QTL for both CM and SCC in the same region (Lund 2003)

LA/LD - CM - BTA9 - across breeds



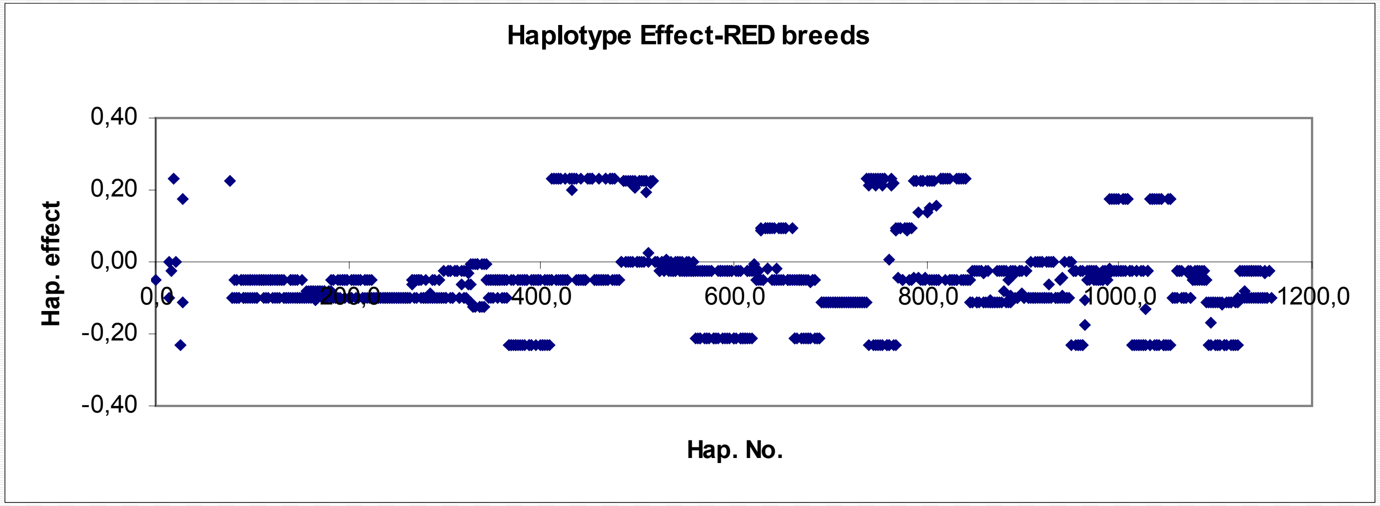
Multi-trait model suggests a pleiotropic QTL affecting both CM and SCC

LA/LD - SCS - BTA11 - across breeds



Haplotype effects at BTA9 QTL

- clustering of the founder haplotypes and haplotype effects:



- preliminary analyses suggest association of extreme haplotypes with frequency of *Escherichia coli* and/or *Staphylococcus aureus* in affected daughters

Pleiotropic effects/ BTA9

- joint Nordic breeding values (NAV)
- milk, protein, fat yields:

→ 2 linked QTL with possible pleiotropic effects 5 cM apart (69 cM: milk, protein + CM; 74 cM: CM and SCC)

- udder conformation traits: no evidence of segregating QTL

Basis for further studies

- three positional candidate genes (and SNPs); more genes expected after better annotation of bovine genome sequence?
- animals with known QTL genotypes
- possible differences in pathogen specificity of identified QTL alleles

→ Material for functional analysis (FP6: SABRE)

Conclusions

- on all studied chromosomes, at least two or more QTL seem to be segregating
- for one QTL, a narrow haplotype was identified, other regions remained larger
- the 4-marker haplotype can be used for marker-assisted selection in the Nordic red breeds
- further analyses are required to elucidate pleiotopic effects and pathogen associations