GM2.7
New breeding tools for improving mastitis resistance in European dairy cattle

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MASTITIS RESISTANCE

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- ROSLIN (UK)/ John Williams, John Woolliams, Nicola Hastings
- ID-Lelystad (NL)/ Lucia Kaal, Luc Janss, Herwin Eding

Mastitis resistance - aiming at MAS!

- the most common disease in dairy cattle (up to 40%)
- low heritability
- difficult to improve by selection
- difficult to measure
- veterinary records available only in Nordic countries

Objectives

- Combine different genome scans into a multi-population, multiple trait analysis
- Improve statistical methodology for fine-mapping
- Identify marker haplotypes associated with QTL alleles (-> MAS)
- Dissect the genetic basis of mastitis by :

(i) disease etiology correlated to specific QTL alleles and pathogens,
(ii) positional candidate gene sequence variation,
(iii) pleiotropic effects of each QTL
(iv) gene expression

Material

- Nordic QTL scans (old & new families)
- DYDs for clinical mastitis and SCC
- pathogen data of milk samples
- bovine RH-panel and BAC libraries (Roslin, DIAS)

BREED	N sires	N bulls
"Red" group:		
Ayrshire	24	900
Swedish R&W	20	750
Red Danish	9	300
Holstein-Friesian	25	2100
Total	78	4050

Statistical developments

- Multiple trait analysis (CM and SCC)
  - to increase power and accuracy
  - distinction between pleiotropy and linkage

- Longitudinal analysis (SCC)
  - non-constant QTL effects
  - information from fitting time dependent QTL (Lund et al. 2002)

QTL regions for fine-mapping

- 6 chromosome regions with best support from previous QTL scans (40 families, 3 countries) were chosen

- 78 families genotyped with common marker set at 20 cM intervals

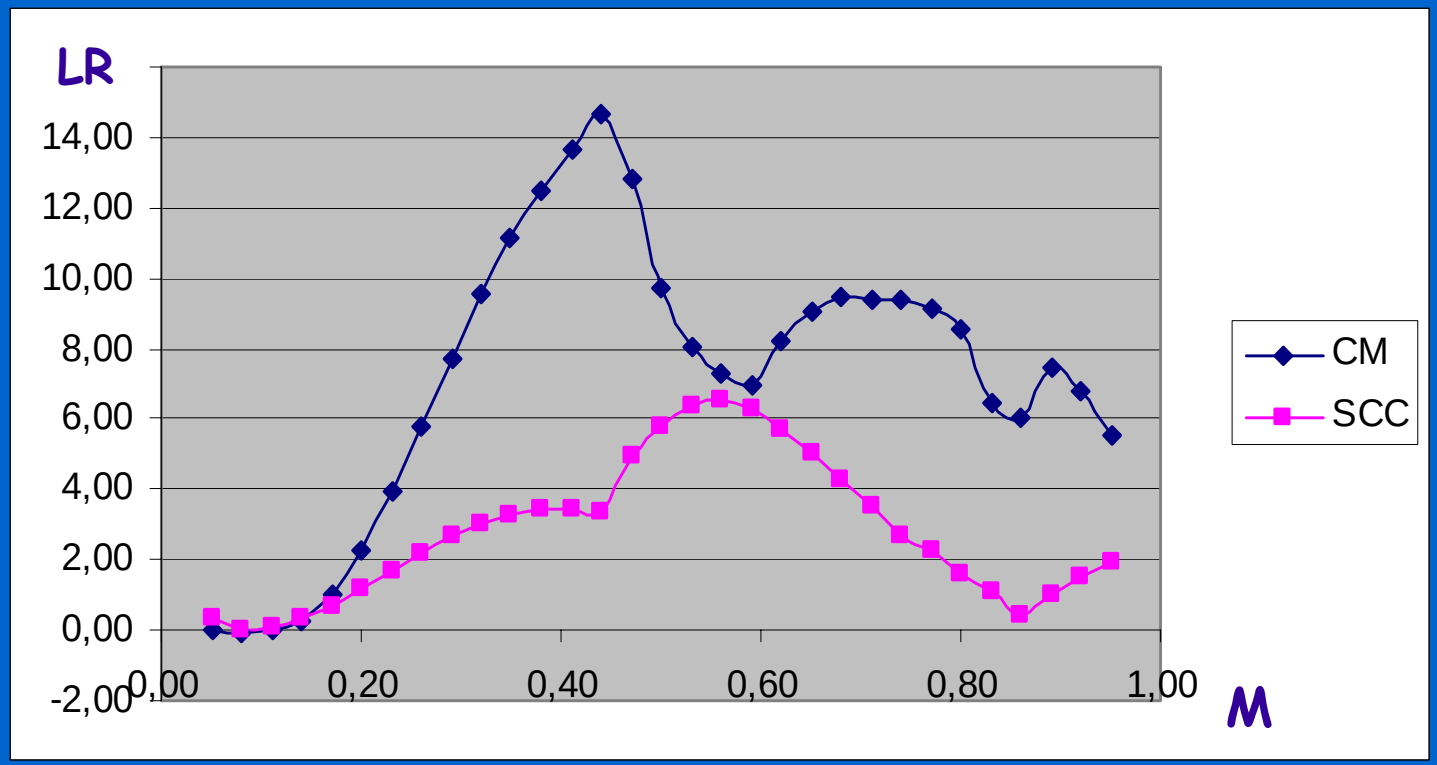
- segregating families ($p < 0.1$, single trait least squares analysis) genotyped at 5 cM marker intervals for best regions - 15 to 25 families/ region

Statistical analyses

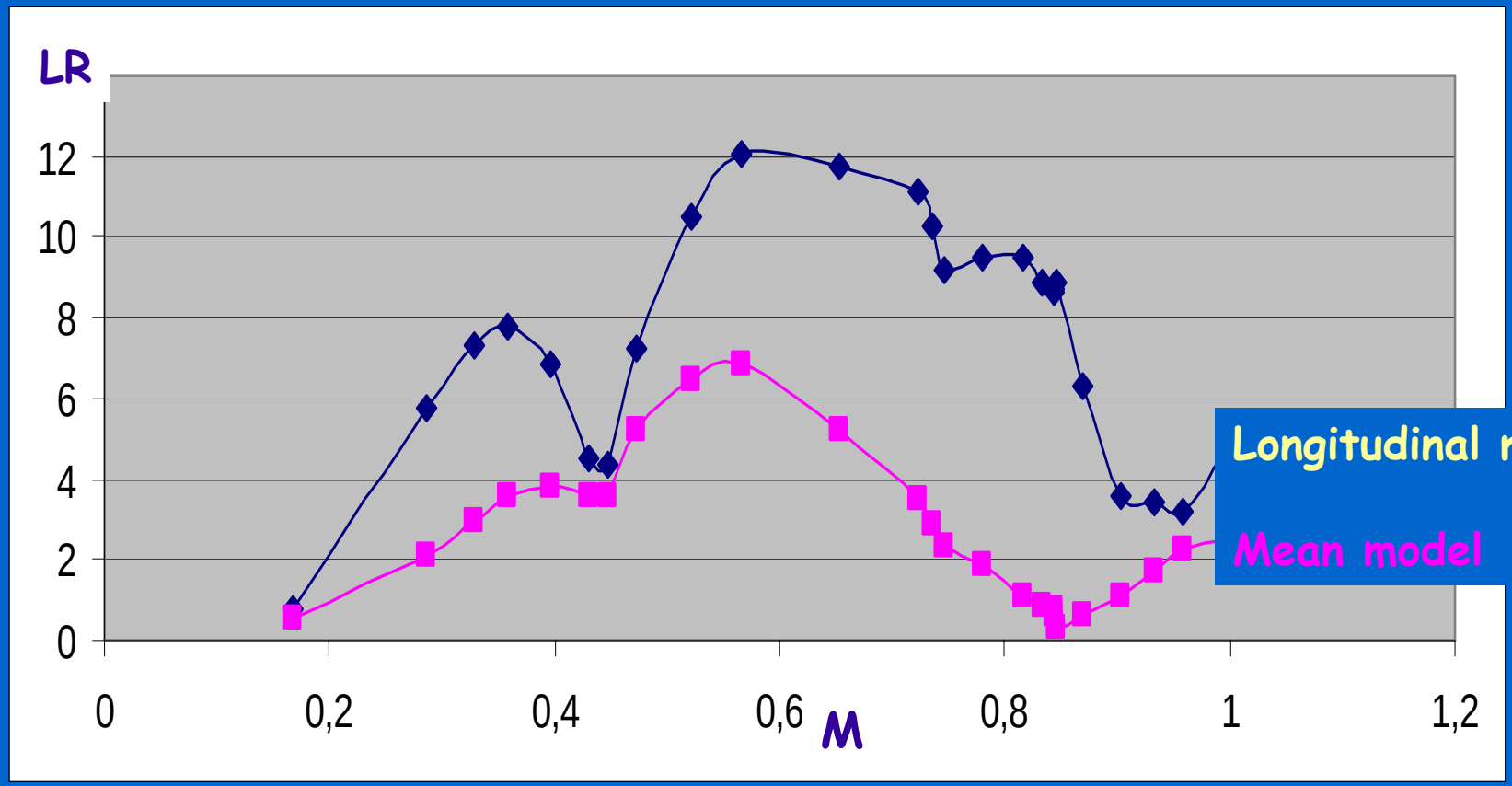
- Least squares analyses within and across families

- Variance components analyses:
  - linkage analysis (LA)
  - LA/LD
  - Multitrait: CM + SCC
  - Longitudinal data: SCC

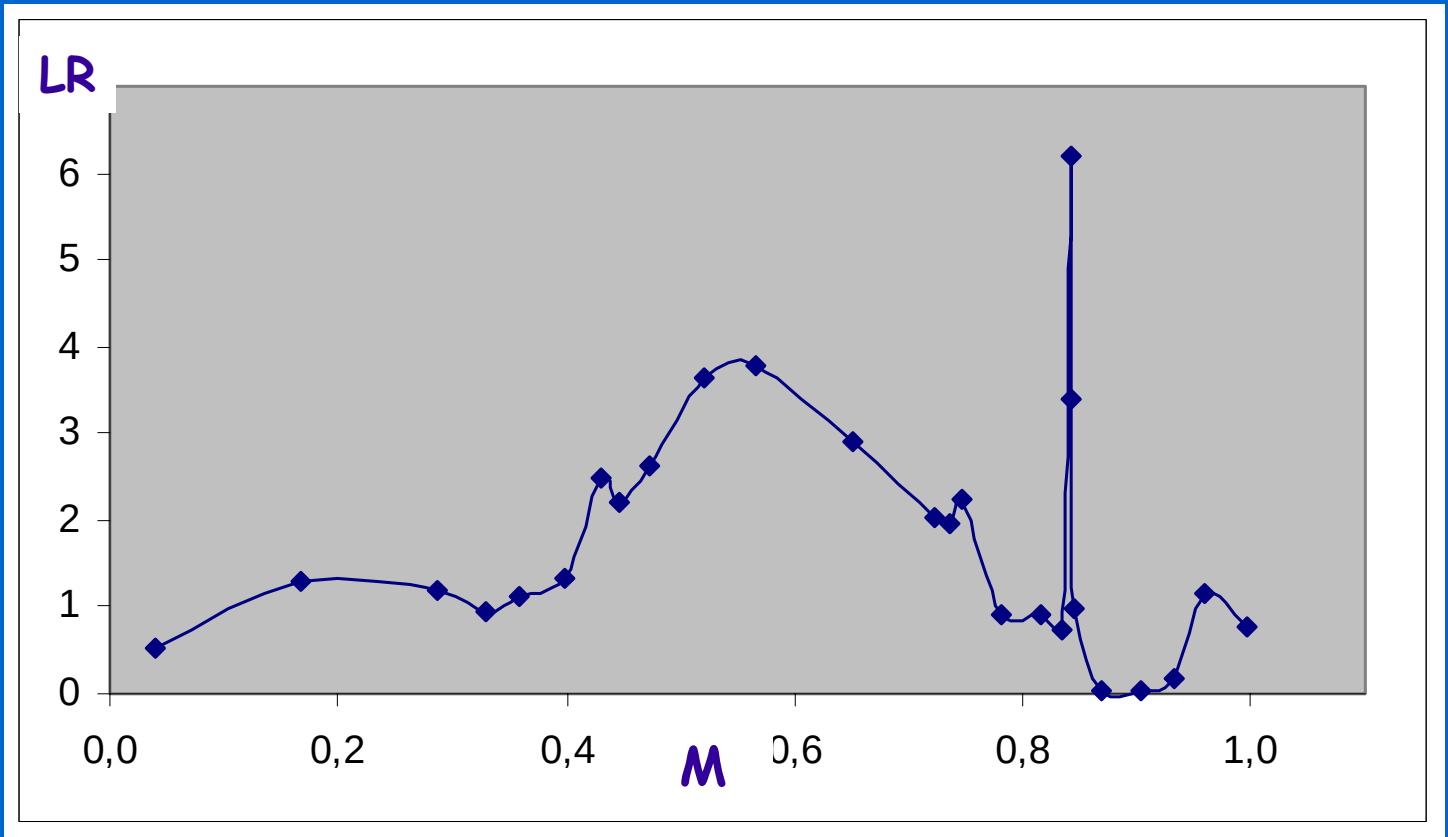
"Multitrait" analysis of CM and SCC



SCC field data
- preliminary results



Linkage/Linkage disequilibrium



Fine-mapping

Development of a dense marker map for the defined short regions:

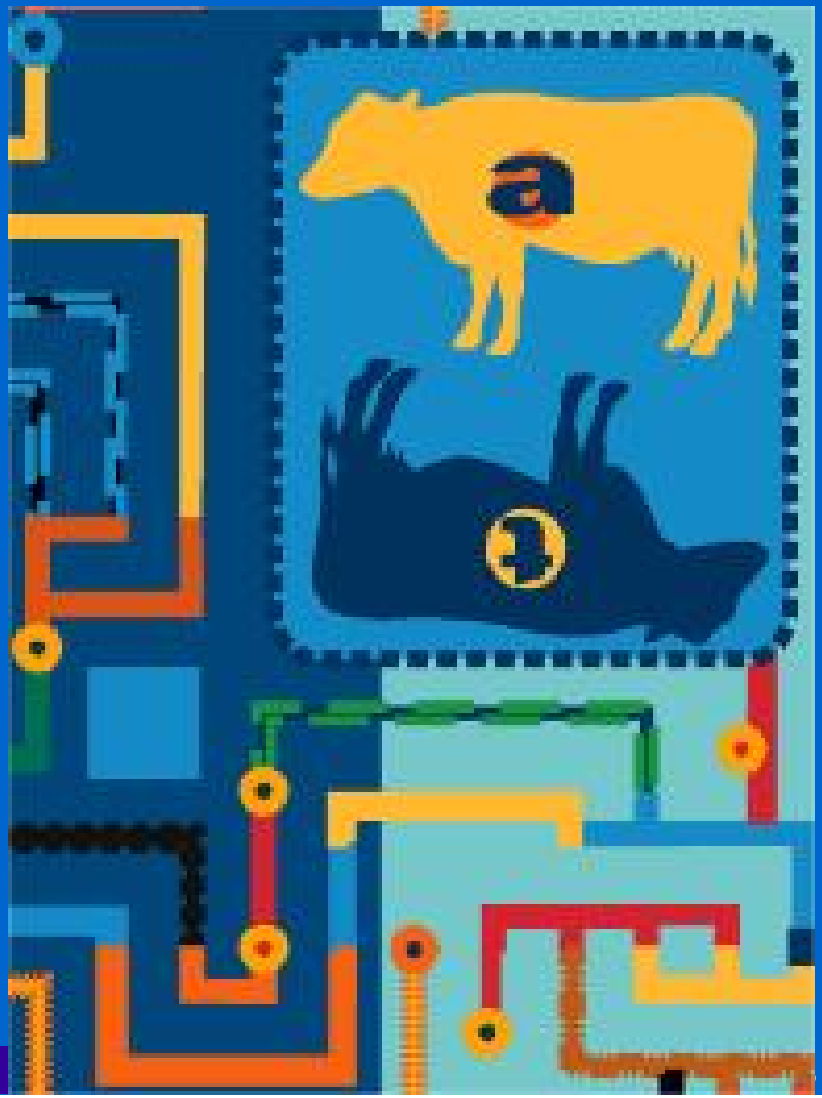
- new microsatellites from bovine sequence trace archives
- comparative mapping of BACs in QTL regions to human map
- sequencing of genes (BACs & human orthologues in bovine WGS) -> SNPs

Basis for further studies

- A list of candidate genes, based on their position, including knowledge of sequence variation (SNPs)
- Animals with known QTL genotypes
- Knowledge of differences in pathogen specificity of identified QTL alleles

→ Material for functional analysis

Strategy for use



- pleiotropic effects of each QTL on other important traits known -> a strategy for the use of these QTL in breeding programs.
- developing a set of guidelines to aid introgression programmes