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Chromosomal regions underlying noncoagulation of milk in Finnish Ayrshire cows

**Anna-Maria Tyrisevä, Kari Elo, Arja Kuusipuro,
Veijo Vilva, Isto Jänönen, Heidi Karjalainen, Tiina
Ikonen and Matti Ojala**

**Department of Animal Science
University of Helsinki
Email: kari.elo@helsinki.fi**



1. Background

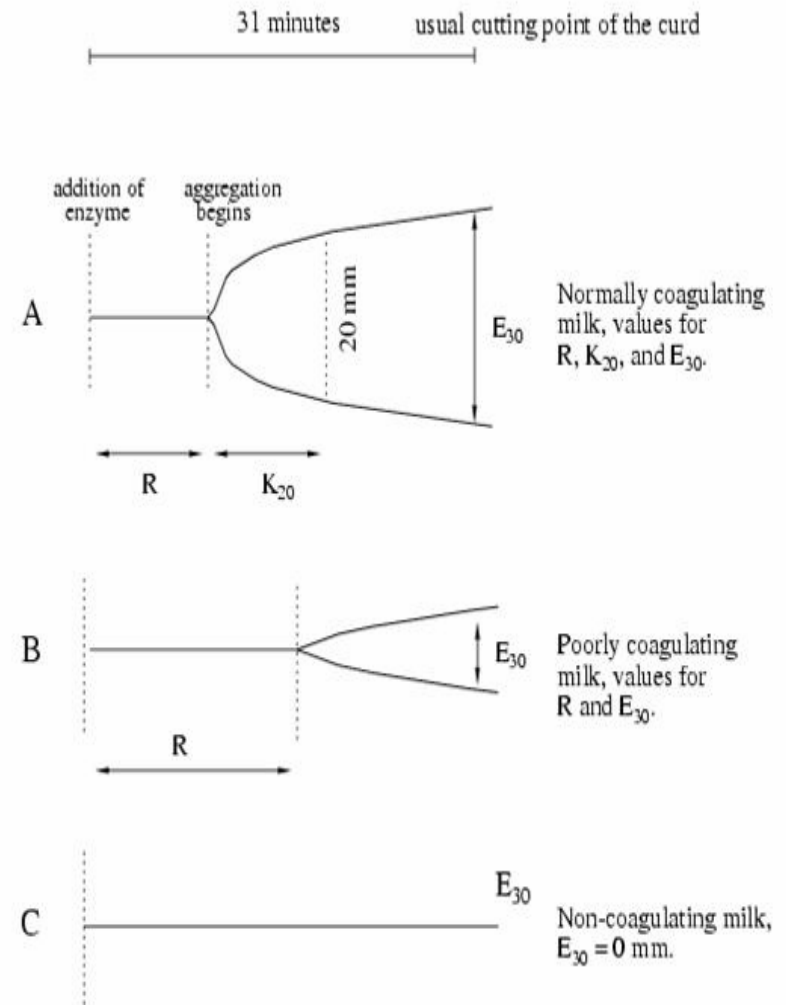
- Motivation to study milk coagulation properties ?
 - Milk coagulation is a critical step in cheese-making
 - 40% of milk is used for cheese production in Finland
 - Milk coagulation properties are impaired in Finnish Ayrshire (Tyrisevä 2008)





Measurement of milk coagulation properties

- Coagulation time R (min)
- Curd-firming time K_{20} (min)
- Curd firmness E_{30} (mm)
- Genetic correlations between the above traits are almost one





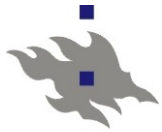
Definitions for noncoagulating and coagulating

- If $E_{30} = 0$ mm, milk is noncoagulating (NC)
- If $E_{30} < 20$ mm poorly coagulating
- If $E_{30} > 30$ mm excellently coagulating (E)



Percentages of poorly coagulating and noncoagulating milk

- About 12% of Finnish Holstein-Friesian and about 30% Finnish Ayrshire cows produce poorly coagulating milk (Tyrisevä et al. (2004))
- About 1% of Finnish Holstein-Friesian and about 10% Finnish Ayrshire cows produce noncoagulating milk (Ikonen et al. (1999), Tyrisevä et al. (2003), Tyrisevä et al. (2004))



Bulk milk - a mixture of excellently coagulating, poorly coagulating and noncoagulating milk

- If excellently coagulating, poorly coagulating and noncoagulating milk are mixed, the mixture has impaired coagulation properties → both quality and yield of cheese are impaired



Heritability and repeatability of R and E_{30}

■ Heritability estimates (with SE)

- Milk coagulation time R (min) 0.28 (0.03)
- Curd firmness E_{30} (mm) 0.39 (0.04)

■ Coefficients of repeatability

- Milk coagulation time R (min) 0.66
- Curd firmness E_{30} (mm) 0.68



2. Objective

- To locate chromosomal regions affecting noncoagulation of milk in Finnish Ayrshire



3. Materials and methods

- Studied traits:

- curd firmness (E_{30})
- somatic cell score
- pH of milk

- Two stages:

- (1) genome scan
- (2) verification of the genome scan



Genome scan

- Genome scan with 194 microsatellite markers using selective DNA pooling method (Darvasi and Soller 1994)
- Pooled DNA samples
 - 33 NC-milk producing cows
 - 49 E-milk producing cows
- Allele intensities were tested for homogeneity between the two pools using the method of Sham and Curtis (1995)



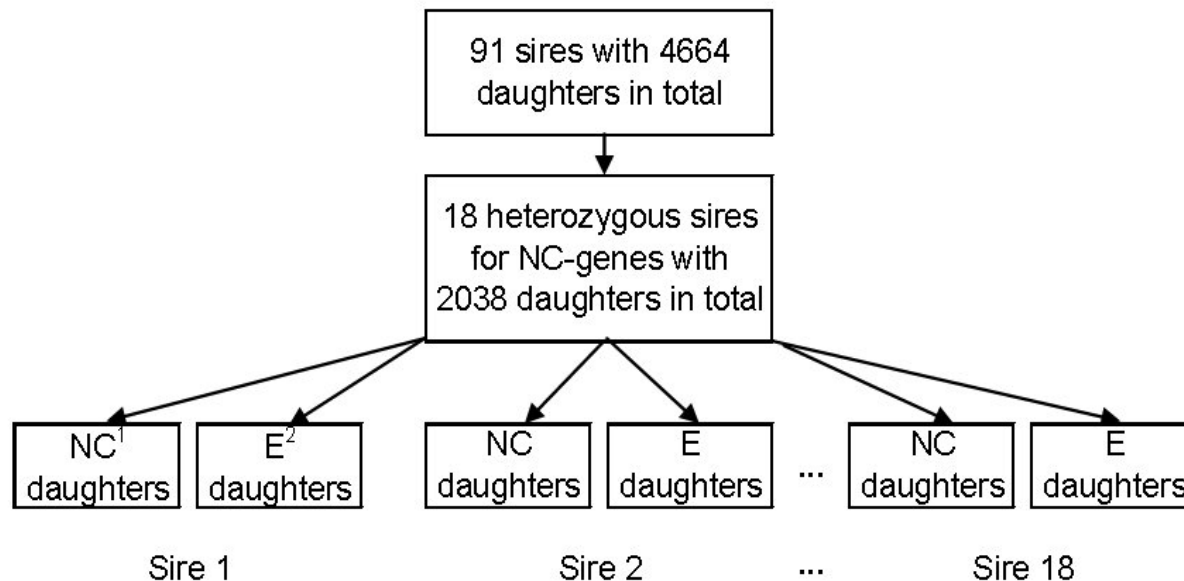
Verification of the genome scan

- 16 regions on 11 chromosomes were selected
- 47 microsatellite markers
- 18 sires and 477 daughters individually genotyped
 - 188 NC-milk producing cows
 - 289 E-milk producing cows
- Maximum likelihood method (ANIMAP, Georges et al. 1995)
- Nonparametric method (HSQM, Coppieters et al. 1998)



Collection of data sets

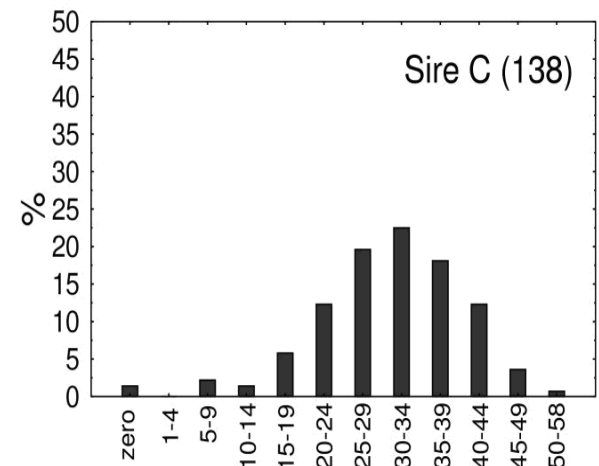
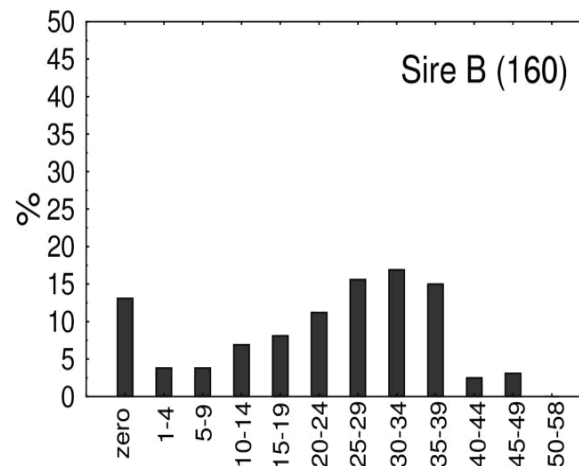
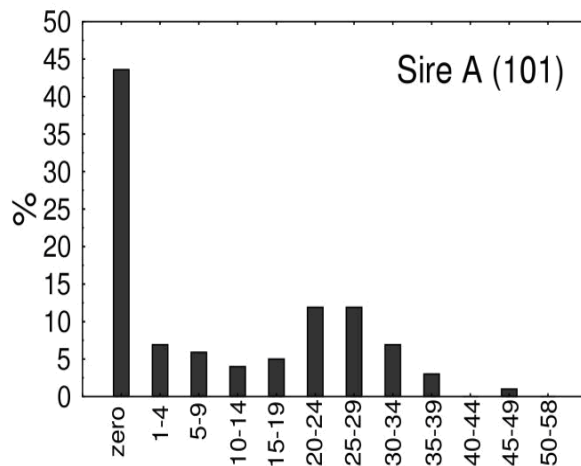
- Sire families were a sub-sample from Ikonen et al. (2004)
- Only sires assumed to be heterozygous for the hypothesized NC-genes and sires with large daughter groups were selected for genome scan

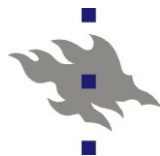




Classification of sires

- Based on daughters' distribution of milk coagulation ability, sires can be classified to homozygous (A), heterozygous (B) and non-carriers for the NC-genes (C)





4. Results

- In genome scan, 16 markers in 11 chromosomes reached the 1% statistical significance threshold
- In verification study, the most significant findings on chromosomes 2, 18 and 24 for noncoagulation
- Putative findings for pH and milk coagulation ability on chromosomes 24 and 27



Interval mapping using nonparametric method (1)

■ Mapping results across families

Chr	Marker	-log(p)	Experimentwise risk level
2	BMS1126	4.3	0.001
18	BMS1355	4.3	0.001



Interval mapping using nonparametric method (2)

■ Mapping results on chromosomes 24 and 27

Chr	Trait	Family	Max position	-log(p)	Experimentwise risk level
24	NC	38651	BM7151	4.3	<0.001
24	pH	38585	AGLA269	2.4	<0.05
27	NC	38585	DIK5134	2.9	<0.05
27	pH	38651	DIK5134	3.7	<0.01



Interval mapping using maximum likelihood

■ Estimates for effects

Family	Chr	Marker position	LOD	Experimentwise risk level	Effect (phenotypic SD)
38651	18	BMS1355	2.7	0.05	1.9
38651	24	BM7151	4.2	0.01	1.8



5. Conclusions (1)

- Regions on chromosomes 2 and 18 affect noncoagulation of milk
- Putative findings
 - chromosomes 18 and 24 associated with noncoagulation of milk in single families
 - markers on chromosomes 24 and 27 associated with coagulation ability and pH of milk



5. Conclusions (2)

- Further mapping needed on chromosomes 2 and 18 before marker assisted selection is viable option to improve milk coagulation ability by elimination of carrier bulls of NC-genes
 - Dissection of candidate chromosomal regions is ongoing using SNP markers



6. References

- Coppieters et al. (1998) – Genetics 149: 1547
- Darvasi and Soller (1994) – Genetics 138: 1365
- Georges et al. (1995) – Genetics 139: 907
- Ikonen et al. (1999) – Journal of Dairy Science 82: 205
- Ikonen et al. (2004) – Journal of Dairy Science 87: 458
- Sham and Curtis (1995) – Annals of Human Genetics 59: 97
- Tyrisevä et al. (2003) – Journal of Dairy Research 70: 91
- Tyrisevä et al. (2004) – Journal of Dairy Science 87: 3958
- Tyrisevä (2008) Options for selecting dairy cattle for milk coagulation ability. PhD thesis, <http://urn.fi/URN:ISBN:978-952-10-3692-7>