Quantitative trait loci for udder conformation and other udder traits in Finnish Ayrshire

Nina Schulman
MTT Agrifood Research Finland
Nina.schulman@mtt.fi
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Background

- Udder traits are genetically correlated with clinical mastitis which causes major economic losses to the dairy farms
- Good udder conformation is also important for an easy and uniform milking routine
- Quantitative trait loci (QTL) could be used in breeding schemes to improve these important traits

Objective

- Are there QTL for udder conformation, milking speed, and leakage on chromosomes where udder health QTL have earlier been detected?

Traits

- Analysed traits were:
  - Udder depth (UD)
  - Fore udder attachment (FUA)
  - Central ligament (CL)
  - Distance from udder to floor (DUF)
  - Udder balance (UB)
  - Rear udder height (RUH)
  - Fore teat length (FTL)
  - Milking speed (MS)
  - Leakage (LE)

Phenotypes and Animals

- EBV from the Finnish Animal Breeding Association, spring evaluation 2004
- A GDD with 12 sire families
- 360 sons, 21 to 48 sons /family

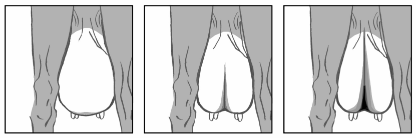
Markers and Genotypes

- BTA9, 11, 14, 18, 20, 23, and 29 were analysed
- 2 SNP (GHR and PRLR) and 33 microsatellite markers
- maps were constructed with CRIMAP
- 3 to 7 markers/chromosome
- The average spacing was 11 cM

Statistical Analysis

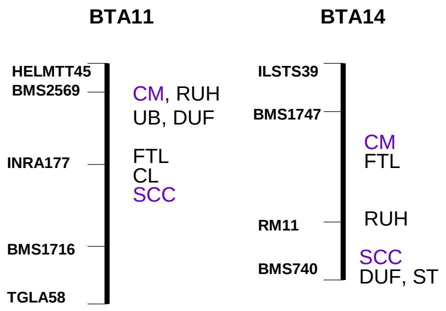
- Multiple linear regression between and within families
- Traits and chromosomes were analysed separately
- Significance thresholds and p values by permutation
- Genome-wise p values by Bonferroni correction

Results and Discussion



Significance levels and locations of udder trait OTL

	BTA11			BTA14			BTA23		
Trait[1]	P_{chr}^2	P_{gen}^3	markers	P_{chr}^2	P_{gen}^3	markers	P_{chr}^2	P_{gen}^3	markers
FTL	0.03	ns	BMS2569 -INRA177	0.01	ns	BMS1747 -RM11	<0.01	ns	BM1818 -BM1443
UB	<0.01	ns	BMS2569 -INRA177				<0.01	0.01	RM185
RUH	<0.01	<0.01	BMS2569	<0.01	ns	BMS1747 -RM11			
DUF	0.05	ns	BMS2569 -INRA177	0.02	ns	RM11 -BMS740	0.01	ns	RM185 -BM1818
CL	0.01	ns	INRA177				<0.01	0.04	BM1818 -BM1443
MS							0.02	ns	RM185



BTA11

BTA14

HELMTT45

BMS2569

CM, RUH

UB, DUF

INRA177

FTL

CL

SCC

BMS1716

TGLA58

ILSTS39

BMS1747

CM

FTL

RM11

RUH

BMS740

SCC

DUF, ST

Conclusions

- Genome-wise significant QTL were detected for udder balance on BTA23, rear udder height on BTA11, and central ligament on BTA23
- 13 chromosome-wise QTL were suggested
- Udder trait QTL are overlapping with previously detected QTL for mastitis and SCC on BTA11 and 14

Thank you for your attention!

Team
Johanna Vilkki
Nina Schulman
Sirja Viitala
Jouni Virta
Tiina Jaakkola

Collaboration
FABA breeding
FABA
Ministry of Agriculture and Forestry