

# Genome-wide Scan for Long Chain Milk Fatty Acids

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**Aim:** to identify Quantitative Trait Loci (QTL) for long chain milk fatty acids.

## Materials & Methods

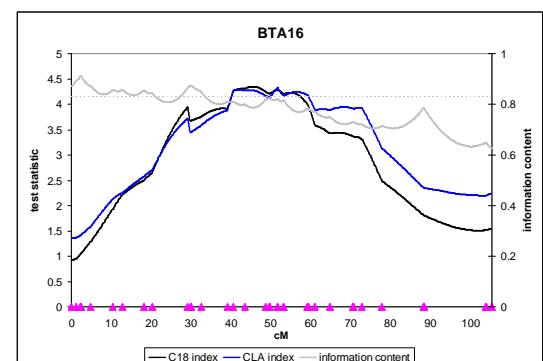
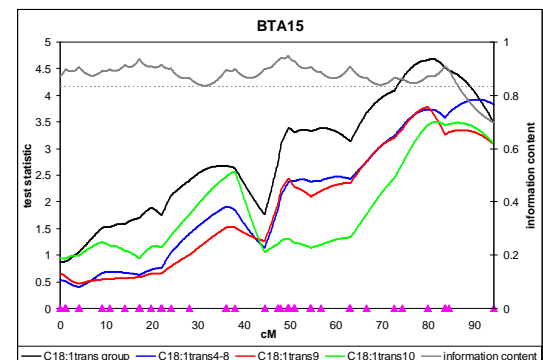
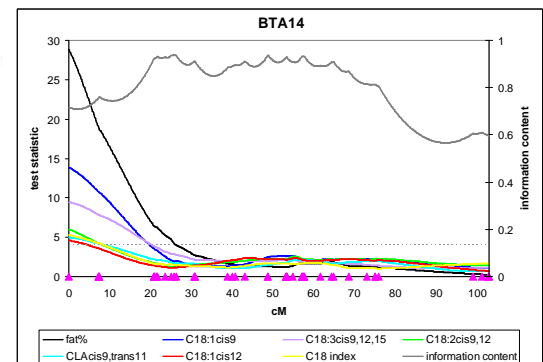
- 7 half-sib families (n = 856) were genotyped for 1,379 SNP.
- Multi-marker interval mapping was used in a weighted across-family QTL regression, on
- Phenotypes from 1905 Dutch Holstein Friesian heifers, pre-corrected for systematic environmental effects.



## Results

Trait	Mean	$\sigma_D$	$V_{QTL}$ (% of $V_p$ )
<b>BTA14</b>			
Fat%	4.36	0.64	19
C18:1 <i>cis</i> 9	18.18	1.57	10
C18:1 <i>cis</i> 12	0.20	0.03	4
C18:2 <i>cis</i> 9,12	1.20	0.18	5
CLAcis9,trans11	0.39	0.07	4
C18:3 <i>cis</i> 9,12,15	0.41	0.06	7
C18 index*	67.62	3.49	4
<b>BTA15</b>			
C18:1 <i>trans</i>	1.50	0.24	4
<b>BTA16</b>			
C18 index*	67.62	3.49	3
CLA index*	33.72	3.73	3

$$* index = \frac{cis9FA}{cis9FA + saturatedFA} * 100$$



## Conclusions

- Significant QTL ( $P_{genome-wide} < 0.05$ ) for long-chain fatty acids were detected on BTA14, 15 and 16.
- Pre-correction for the DGAT1 K232A mutation eliminated the QTL at BTA14, suggesting that this mutation is responsible for the QTL on BTA14.
- The identification of QTL for long chain fatty acids, and in particular for C18:1 *trans* fatty acids, strongly supports the hypothesis of a genetic component for these fatty acids.