Fine Mapping a QTL for Somatic Cell Score in the German Holstein

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Introduction

Somatic Cell Score (SCS)
- indicator trait for mastitis
- $h^2 = 16 - 17\%$
- marker assisted selection

😊 Over 50 QTL for SCS reported

😢 Large confidence intervals
Objectives

- Investigate chromosomal region on BTA27 affecting SCS:
  - ↑ marker density
  - ↑ number of families
  - linkage disequilibrium

- Identify haplotypes associated with increases or decreases in SCS
Experimental Design

Pedigree

– GDD (6 families)
– 492 sires → 492 DYD for SCS
– 4,622 animals

Linkage Map

– 19 Microsatellites (~95 SNP) spanning 33.8 cM
– 6.84 alleles / marker
– Marker interval: 1.78 cM
– Putative QTL at midpoint of every marker interval
Observations for sire $i$ (DYD for SCS)

$$y_i = X\beta + Zu + Wv + e$$

- **$\beta_{(k \times 1)}$**
  - Fixed Average
  - Random polygenic effects which have nothing to do with the QTL
- **$u_{(n \times 1)}$**
  - Random gametic (QTL) effects
- **$v_{(\text{gam} \times 1)}$**
  - Random residual
- **$X_{(m \times k)}Z_{(m \times n)}W_{(m \times \text{gam})}$**
  - Design matrices
Analysis

Restricted log likelihood ratio test statistic for all QTL positions (\(pos=1-18\)):

\[
RLRT^{Pos} = -2 \left[ \ln(L_0) - \ln(L_1^{Pos}) \right]
\]

\[
\begin{align*}
L_0 & \quad \Rightarrow \quad y_i = X\beta + Zu + e \\
L_1^{Pos} & \quad \Rightarrow \quad y_i = X\beta + Zu + Wv + e
\end{align*}
\]
Analysis

- Pedigree
- Marker Positions
- Genotypes

- Pedigree
- Phenotypes

- ASReml
  \[ y_i = X\beta + Zu + Wv + e \]

- Allele Frequencies
- Transmitting Probabilities

- Allele Frequencies
- Marker Positions

BTA27

Graph showing likelihood quotients for different genotypes and positions in cM.
Analysis of Haplotype Effects

Estimated Effect on SCS DYD

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Haplotype
Analysis of Haplotype Effects

Sum of Absolute Haplotype Estimates / Standard Error
Analysis of Haplotype Effects

Difference in Absolute Haplotype Estimates / Standard Error
Summary

- Chromosomal region on BTA27 affecting udder health further investigated
- Sharper curves and higher peaks
- Specific haplotypes identified
- Basis for comparative sequencing
Financial support from the EAAP and the FUGATO M.A.S.-Net project is gratefully acknowledged!!!
Analysis

Pedigree
Marker Positions
Genotypes

- Allele Frequencies
- Transmitting Probabilities

Allele Frequencies
Marker Positions

ASReml
\[ y_i = X\beta + Zu + Wv + e \]

\[ G \& G^{-1} \]

BTA27

Position in cM

Likelihood Quotient

LA
LD
LA + LD

0 5 10 15 20 25 30 35
0 1 2 3 4 5 6 7 8 9 10 11 12
Analysis: 2-QTL Model

<table>
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<tr>
<th>Position in cM</th>
<th>Pos1</th>
<th>Pos2</th>
<th>LogL</th>
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