Session 15

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Mapping of fertility traits in Finnish Ayrshire by genome-wide association

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Introduction

- Fertility disorders lead to
  - Veterinary treatments
  - Involuntary culling

→ High costs

Objectives

- Detect associations between dense SNP markers and fertility traits

- Confirm previously detected fertility QTL in Finnish Ayrshire

Animals

- 340 Ayrshire bulls
- 18 half-sib families
- 39 to 2 sons per family, median=18
- 10 bulls not included in the families

Traits

- De-regressed estimated breeding values for
    - Non-return rate heifers (nrrh)
    - Non-return-rate cows (nrrc)
    - Time from first to last insemination heifers (iflh)
    - Time from first to last insemination cows (iflc)
    - Number of inseminations heifers (aish)
    - Number of inseminations cows (aisc)
    - Time from calving to first insemination (icf)

Markers and quality control

- Illumina BovineSNP50 BeadChip

- Excluded markers
  - Maf < 5 %
  - Poor clustering performance
  - Pedigree errors
  - Not assigned to any chromosome
  - Assigned to the X-chromosome

- 35630 SNPs included in the analyses

Association analysis

- Mixed model approach
- Fixed SNP effect, random polygenic effect
- Number of daughters as weights
- Software package DMU (Madsen et al, 2006)

Significance thresholds

- Method by Lander and Kruglyak, 1995 for genome-wise significance
- Chromosome-wise Bonferroni correction, $p=0.05$
- Interval-wise Bonferroni correction, $p=0.05$ for confirmation of old QTL peaks

Results

Significant SNP

- Total of 11 cromosome-wise significant SNP
- On 7 different chromosomes
- Four genome-wise significant

Non-return rate heifers	2	1
Non-return rate cows	1	-
Time from first to last insemination heifers	1	-
Time from first to last insemination cows	1	-
Number of inseminations heifers	1	1
Number of inseminations cows	2	-
Time from calving to first insemination	3	2

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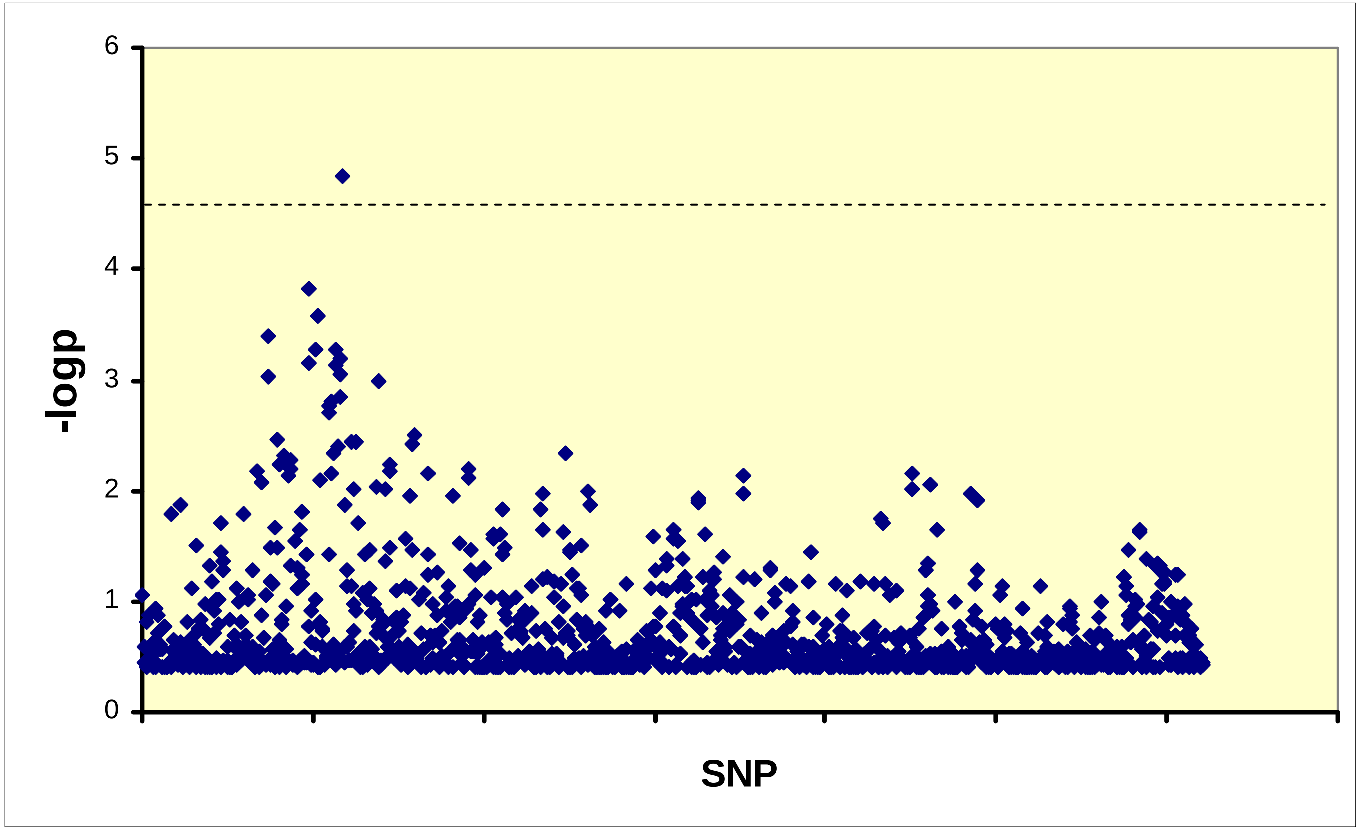
Time from calving to first insemination

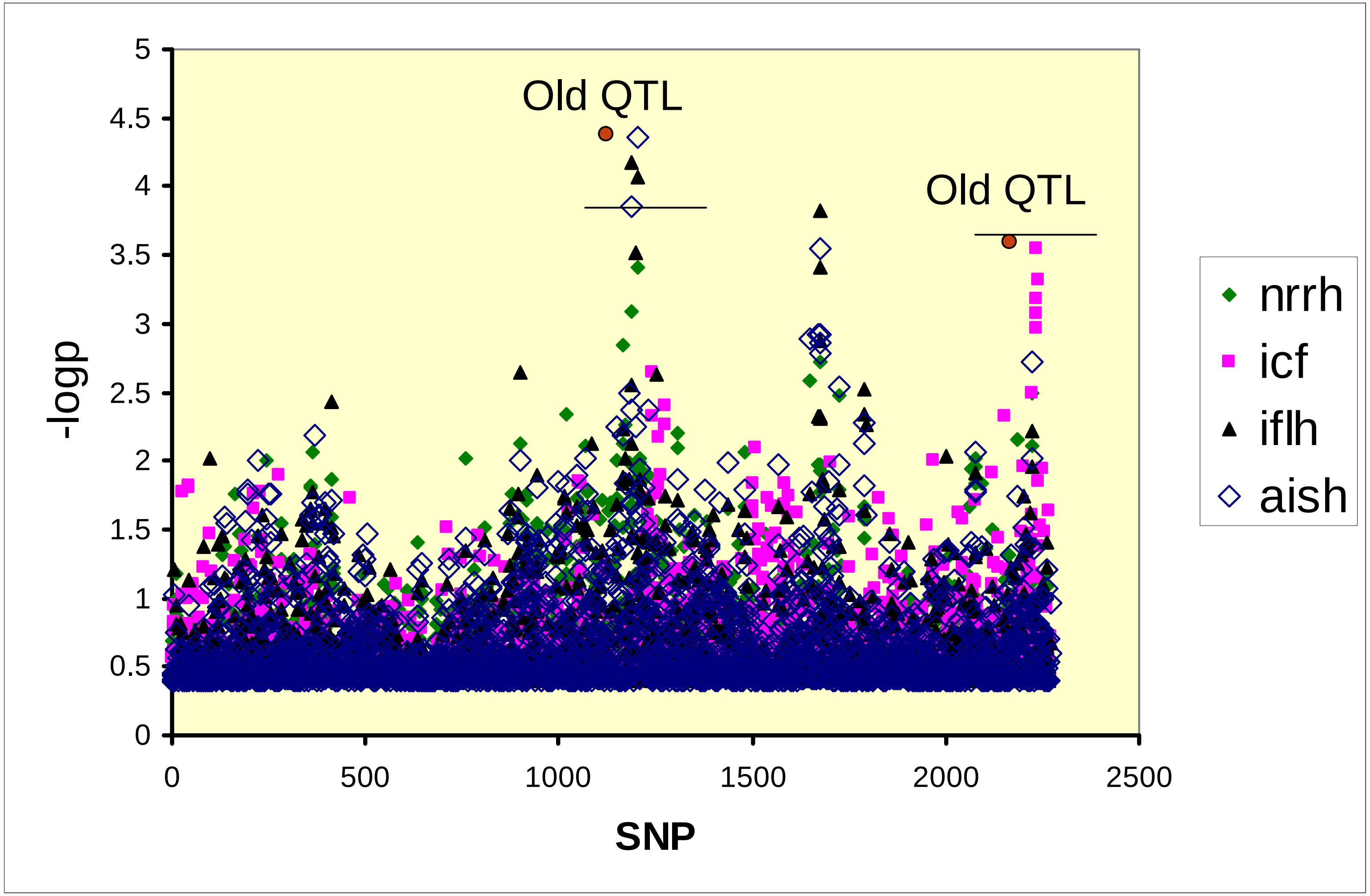


Comparison to previously detected fertility QTL in Finnish Ayrshire

- Old QTL were affecting days open and/or fertility treatments
- Evidence for associations was detected at positions close to the old QTL

BTA	Trait	p-value
1	iflh, aish	$p=6.5 * 10^{-5}$, $p=4.3* 10^{-5}$
2	nrrc	$p=1.6 * 10^{-4}$
14	nrrc	$p=1.2 * 10^{-4}$
20	icf	$p=2.2 * 10^{-5}$

BTA1


Old QTL
Old QTL
-logp
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
5
0
500
1000
1500
2000
2500
SNP
nrrh
icf
iflh
aish

Conclusions

- Fertility trait associations were detected
- Four old fertility QTL were confirmed
- Sample size needs to be increased in order to get higher power for future confirmation