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 chromosome-wise significant SNP
- On 7 different chromosomes
- Four genome-wise significant

<table>
<thead>
<tr>
<th>Category</th>
<th>Heifers</th>
<th>Cows</th>
</tr>
</thead>
<tbody>
<tr>
<td>Non-return rate</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>Time from first to last insemination</td>
<td>1</td>
<td>-</td>
</tr>
<tr>
<td>Number of inseminations</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Time from calving to first insemination</td>
<td>3</td>
<td>2</td>
</tr>
</tbody>
</table>
Significant SNP

- Total of 11 chromosome-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
Time from calving to first insemination

SNP

-logp

SNP
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

<table>
<thead>
<tr>
<th>BTA</th>
<th>Trait</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>iflh, aish</td>
<td>p=6.5 * 10^{-5}, p=4.3* 10^{-5}</td>
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<tr>
<td>2</td>
<td>nrrc</td>
<td>p=1.6 * 10^{-4}</td>
</tr>
<tr>
<td>14</td>
<td>nrrc</td>
<td>p=1.2 * 10^{-4}</td>
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<tr>
<td>20</td>
<td>icf</td>
<td>p=2.2 * 10^{-5}</td>
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</tbody>
</table>
BTA1

SNP

-logp

nrrh

icf

iflh

aish

Old QTL

Old QTL
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