GWAS using a Bayesian approach for litter size and piglet mortality in Danish pigs

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Outline

- Introduction
- Materials & Methods
- Results & Discussion
- Conclusions
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  - Results & Discussion
- Conclusions
Litter size & mortality

- Litter size & mortality
  - reproductive traits of major economic importance

- Total number born
  - litter size at weaning↑ mortality↑

- Litter size at d 5
  - litter size at weaning↑ mortality↓
Objective

- Identify QTL for the litter size and piglet mortality in Danish Landrace and Yorkshire pigs.
- Propose a novel method based on Bayesian mixture model to detect QTL regions.
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Data

- Phenotypes
  - TNB: total number of piglets born
  - LS5: litter size at five days after birth
  - Mort: mortality rate before day 5

- Genotypes
  - Illumina PorcineSNP60 BeadChip
# Size of data

<table>
<thead>
<tr>
<th></th>
<th>Landrace</th>
<th>Yorkshire</th>
</tr>
</thead>
<tbody>
<tr>
<td>Marker</td>
<td>37,060</td>
<td>36,058</td>
</tr>
<tr>
<td>Animal</td>
<td>5,977</td>
<td>6,000</td>
</tr>
<tr>
<td>Boar</td>
<td>1,788</td>
<td>1,761</td>
</tr>
<tr>
<td>Sow</td>
<td>4,189</td>
<td>4,239</td>
</tr>
<tr>
<td>Birth</td>
<td></td>
<td>1998 to 2014</td>
</tr>
</tbody>
</table>
Bayesian Mixture Model (BM)

\[ y_c = 1\mu + \sum_{i=1}^{m} x_i g_i + Zu + e \]

> \( y_c \): corrected phenotypic value

> \( g_i \sim \begin{cases} N(0, \sigma_{g_0}^2) & \text{with probability } \pi_0 \\ N(0, \sigma_{g_1}^2) & \text{with probability } \pi_1 = 1 - \pi_0 \end{cases} \)

> \( u \): polygenic effect

> BayZ Package
QTL region analysis

- Sliding window

- Posterior probability of interval ($PP_{int}$)

  the proportion of samples where at least one SNP within the window was falling into the second distribution
## Interval posterior probability ($PP_{int}$)

<table>
<thead>
<tr>
<th></th>
<th>M1</th>
<th>M2</th>
<th>M3</th>
<th>M4</th>
<th>M5</th>
<th>M6</th>
<th>M7</th>
<th>M8</th>
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</thead>
<tbody>
<tr>
<td>S1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>S2</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>S3</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>S4</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>S5</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

$PP_{snp}$: 0/5 1/5 0/5 2/5 0/5 0/5 2/5 1/5
QTL region analysis

- $PP_{\text{int}} > 0.8$
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Several peaks when using sliding window with 1Mb
The narrowest region among three scenarios was chosen as the QTL region.
### Overlap with reported region

- 15 QTL regions on SSC1, 2, 3, 6, 7, 9, 13 and 14

<table>
<thead>
<tr>
<th>Reproduction</th>
<th>corpus luteum number</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>teat number</td>
</tr>
<tr>
<td></td>
<td>non-functional nipples</td>
</tr>
<tr>
<td></td>
<td>age at puberty</td>
</tr>
<tr>
<td></td>
<td>litter weight</td>
</tr>
<tr>
<td></td>
<td>embryo weight</td>
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Common QTL regions

<table>
<thead>
<tr>
<th>SSC</th>
<th>Breed 1</th>
<th>Trait 1</th>
<th>QTL 1</th>
<th>Breed 2</th>
<th>Trait 2</th>
<th>QTL 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>Landrace</td>
<td>TNB</td>
<td>6.34 ~ 7.34 Mb</td>
<td>Yorkshire</td>
<td>TNB</td>
<td>5.48 ~ 6.48 Mb</td>
</tr>
<tr>
<td>7</td>
<td>Landrace</td>
<td>LS5</td>
<td>34.74 ~ 35.74 Mb</td>
<td>Landrace</td>
<td>MORT</td>
<td>34.74 ~ 35.74 Mb</td>
</tr>
</tbody>
</table>

> 6 common QTL regions on SSC2, 3, 6, 7 and 13

> SSC3: both Landrace & Yorkshire

> SSC7: positive for LS5 & negative for MORT
Candidate genes

- **KPNA7**: suggested the requirement for cleavage development
- **SPESP1**: involved in the sperm–oocyte binding and fusion in pigs
- **GDF9**: expression higher in oocytes than in cumulus/granulosa cells
Conclusions

- 15 QTL regions were identified on SSC1, 2, 3, 6, 7, 9, 13 and 14.

- 6 regions located on SSC2, 3, 6, 7 and 13 were associated with more than one trait.

- The QTL regions detected overlapped with the regions previously reported for reproduction traits.
Thanks for your attention

Tage Ostersen
Luc Janss
Take-home messages

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