Breeding on polled genetics in Holsteins - chances and limitations

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Ethical aspects of breeding

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Background

- Ethical considerations about removing cattle horns after birth
  - Painful for animals

- Chance: Breeding on polled animals helps to solve ethical conflict on the long term

- Limitation: Only two polled sires and their offspring with high breeding values
  - Identification of polled Holstein animals in herdbook (Size of genetic base)
  - Increased inbreeding
  - Increased recessive alleles

- Objective: To investigate chances and limitations of breeding for polled cattle
Materials and Methods (1)

- Imputing procedure of horn state:
  - **Beagle**, Version 3.3 (Browning and Browning, 2010)

```
Training set
21202021222
21012121012

horn state inserted
derivation of haplotypes

Candidates / Validation
21012?21012

Imputing
21012121012

comparing imputed horn state with herdbook entries
21012121012 21012121012

error rate
```
Materials and Methods (1)

- Data Set for imputing horn state
- Localisation Chromosome 1
  - 78 SNPs from 54k-Chip

- Genotypes: 60,368 animals (54K Chip), **aug 2012**

- Animals with known horn state and genotypes (SNP):
  - 22,834 horned animals (pp), identified by pedigree information
  - 417 heterozygote polled animals (Pp), because of herdbook entry
  - 20 homozygote polled animals (PP), because of herdbook entry
Genomic breeding program for polled

- 250,000 cows with milk recording
- 2,500 sire dams (best 1%)
- 500 genotyped bull calves
- 30 genomic
- 199%-proven

Bull-sires:
- 95%
- 5%

Cow-sires:
- 94%
- 6%
Materials and Methods (2)

Breeding scenario for polled:

- **A**: Selection due to breeding values – assortative mating 500 bull-dams

- **A+BM**: Selection additional 100 polled bull-dams

- **G**: Selection only polled bull-dams (mostly PP)

- **G+A**: Selection within polled-bull dams due to breeding value

- **P**: Selection due to phenotype polled state
Comparison of herdbook entries and imputation results of validation animals

<table>
<thead>
<tr>
<th>Herdbook entries</th>
<th>Imputed pp</th>
<th>Imputed Pp</th>
<th>Imputed PP</th>
</tr>
</thead>
<tbody>
<tr>
<td>5.555 pp*</td>
<td>5.554</td>
<td>1</td>
<td>-</td>
</tr>
<tr>
<td>184 Pp</td>
<td>5</td>
<td>176</td>
<td>3</td>
</tr>
<tr>
<td>9 PP</td>
<td>-</td>
<td>-</td>
<td>9</td>
</tr>
<tr>
<td>68 P</td>
<td>3</td>
<td>65</td>
<td>-</td>
</tr>
</tbody>
</table>

- Genotype error rate: 0.2%

*) Because of pedigree- information
## Results (1)

Results of prediction for candidates

<table>
<thead>
<tr>
<th>Category</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td># reference animals</td>
<td>23.271</td>
</tr>
<tr>
<td># validation animals</td>
<td>37.097</td>
</tr>
<tr>
<td>Imputed PP</td>
<td>18</td>
</tr>
<tr>
<td>Imputed Pp</td>
<td>545</td>
</tr>
<tr>
<td>Imputed pp</td>
<td>36.534</td>
</tr>
</tbody>
</table>
Results (1)

- Distribution of polled status, allele frequencies of the recessive allele $p$ and Hardy-Weinberg-equilibrium by breed and sex

<table>
<thead>
<tr>
<th>Sub-population</th>
<th>PP animals</th>
<th>Pp animals</th>
<th>pp animals</th>
<th>Allele frequency $p$</th>
<th>Sub-population HWE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male HOL</td>
<td>11</td>
<td>313</td>
<td>41.781</td>
<td>0.996</td>
<td>No</td>
</tr>
<tr>
<td>Female HOL</td>
<td>7</td>
<td>124</td>
<td>11.724</td>
<td>0.994</td>
<td>No</td>
</tr>
<tr>
<td>Male RHF</td>
<td>10</td>
<td>372</td>
<td>4.620</td>
<td>0.960</td>
<td>Yes</td>
</tr>
<tr>
<td>Female RHF</td>
<td>8</td>
<td>145</td>
<td>981</td>
<td>0.929</td>
<td>Yes</td>
</tr>
</tbody>
</table>
Results (2)

Development of allele frequency of P in the whole population for the 5 scenarios over 15 generations.
Results (2)

Increase of mean breeding values of bulls over the investigated 15 generations and 5 scenarios

![Graph showing increase of mean breeding values of bulls over generations and scenarios.](image)
Conclusions

- Imputing powerful tool to identify more polled animals
  - Low error rate
  - Helps to check herdbook entries

- Selection on homozygote polled genotype for already SNP-genotyped animals is most effective way to increase polled allele & genetic gain in population

- Non-SNP-genotyped animals selection on their phenotype is sufficient

- Genotyping of the polled state is not mandatory
Acknowledgements

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Thank you for attendance!