Runs of homozygosity and levels of inbreeding in cattle breeds

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In this study we used:

- Brown Swiss cattle, 463 bulls
- Norwegian red cattle, 498 bulls
- Simmental cattle, 502 bulls
- Tyrol Grey, 215 bulls
...on which we tried to

- predict levels of inbreeding
- compare levels of autozygosity
- explain their inbreeding history
Genomic inbreeding coefficient

Level of homozygosity

\[ F_{\text{hom}} : \frac{H_e - H_o}{H_e} \]

Runs of homozygosity

\[ F_{\text{ROH}_k} : \frac{\sum_k \text{length (ROH}_k)}{L} \]
Runs of homozygosity (ROH)

Observable inbreeding?
GENERATIONS & CROSSING OVERS
Illumina Bovine SNP50TM Beadchip

We exclude:
- SNP with gc_score < 0.2
- SNP with MAF < 0.01
- SNP with >0.05 of missing genotypes
- animals > 0.05 of missing genotypes
Pedigree data (6.46 – 9.02 CGE)

36273 SNP

ROH lengths (k):

PEDIG

PLINK

PLINK

SAS

$F_{\text{pedT}}$ & $F_{\text{ped5}}$

$F_{\text{hom}}$

Five ROH lengths (k):

>$1\text{Mb}$, >$2\text{Mb}$, >$4\text{Mb}$, >$8\text{Mb}$, >$16\text{Mb}$

$F_{\text{ROH1}}$, $F_{\text{ROH2}}$, $F_{\text{ROH4}}$, $F_{\text{ROH8}}$, $F_{\text{ROH16}}$
What are inbreeding levels?

<table>
<thead>
<tr>
<th></th>
<th>$F_{\text{pedT}}$</th>
<th>$F_{\text{ped5}}$</th>
<th>$F_{\text{ROH8}}$</th>
<th>$F_{\text{ROH16}}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brown Swiss</td>
<td>4.1 (2.2)</td>
<td>2.1 (1.8)</td>
<td>6.6 (3.1)</td>
<td>3.3 (2.4)</td>
</tr>
<tr>
<td>Simmental</td>
<td>1.4 (1.3)</td>
<td>0.9 (1.2)</td>
<td>1.6 (1.6)</td>
<td>0.8 (1.2)</td>
</tr>
<tr>
<td>Norwegian Red</td>
<td>2.1 (1.4)</td>
<td>1.0 (1.2)</td>
<td>3.3 (2.7)</td>
<td>1.5 (1.6)</td>
</tr>
<tr>
<td>Tyrol Grey</td>
<td>2.4 (2.2)</td>
<td>1.6 (2.0)</td>
<td>3.0 (2.6)</td>
<td>1.6 (2.0)</td>
</tr>
<tr>
<td>Mean(SD) %</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
...but ancient inbreeding?

<table>
<thead>
<tr>
<th></th>
<th>$F_{ROH1}$</th>
<th>$F_{ROH2}$</th>
<th>$F_{ROH4}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brown Swiss</td>
<td>14.2 (3.6)</td>
<td>11.5 (3.6)</td>
<td>9.3 (3.5)</td>
</tr>
<tr>
<td></td>
<td>8.5 (2.0)</td>
<td>5.2 (1.9)</td>
<td>3.0 (1.7)</td>
</tr>
<tr>
<td></td>
<td>9.6 (2.5)</td>
<td>7.2 (2.5)</td>
<td>5.3 (2.4)</td>
</tr>
<tr>
<td></td>
<td>7.8 (2.7)</td>
<td>5.3 (2.7)</td>
<td>4.1 (2.7)</td>
</tr>
</tbody>
</table>

Brown Swiss  Simmental  Norwegian Red  Tyrol Grey  Mean(SD) %
## Correlations?

<table>
<thead>
<tr>
<th></th>
<th>$F_{\text{ped}T}$</th>
<th>$F_{\text{ped}5}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$F_{\text{ped}5}$</td>
<td>0.94 – 0.98</td>
<td>–</td>
</tr>
<tr>
<td>$F_{\text{ROH}1}$</td>
<td>0.60 – 0.71</td>
<td>0.49 – 0.70</td>
</tr>
<tr>
<td>$F_{\text{ROH}2}$</td>
<td>0.60 – 0.71</td>
<td>0.49 – 0.70</td>
</tr>
<tr>
<td>$F_{\text{ROH}4}$</td>
<td>0.62 – 0.72</td>
<td>0.52 – 0.72</td>
</tr>
<tr>
<td>$F_{\text{ROH}8}$</td>
<td>0.61 – 0.71</td>
<td>0.53 – 0.71</td>
</tr>
<tr>
<td>$F_{\text{ROH}16}$</td>
<td>0.51 – 0.69</td>
<td>0.50 – 0.71</td>
</tr>
</tbody>
</table>

Brown Swiss  Norwegian Red  Simmental  Tyrol Grey
...level of homozygosity?

**Inbreeding**

<table>
<thead>
<tr>
<th>Breed</th>
<th>( F_{\text{hom}} ) Mean(SD)%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brown Swiss</td>
<td>13.8 (3.6)</td>
</tr>
<tr>
<td>Simmental</td>
<td>6.6 (2.7)</td>
</tr>
<tr>
<td>Norwegian Red</td>
<td>6.6 (2.6)</td>
</tr>
<tr>
<td>Tyrol Grey</td>
<td>7.2 (3.6)</td>
</tr>
</tbody>
</table>

**Correlations**

| \( F_{\text{ped}T} \) | 0.56 – 0.63 |
| \( F_{\text{ped}5} \)  | 0.49 – 0.64  |
| \( F_{\text{ROH}1} \)   | 0.84 – 0.93  |
| \( F_{\text{ROH}2} \)   | 0.80 – 0.92  |
| \( F_{\text{ROH}4} \)   | 0.76 – 0.91  |
| \( F_{\text{ROH}8} \)   | 0.69 – 0.87  |
| \( F_{\text{ROH}16} \)  | 0.61 – 0.81  |
ROH structure

The graph shows the relationship between the total length of ROH (>
1Mb) and the number of ROH (> 1Mb). The data points are differentiated
by color, with Brown Swiss in black and Simmental in red.

- Y-axis: number of ROH (> 1Mb)
- X-axis: total length of ROH (> 1Mb)
Conclusions about ROH & $F_{ROH}$

- Useful especially if pedigree is missing or incorrect
- Demonstrated as optimal way for identification of ancient inbreeding in humans (Keller et al. 2011)
- ROH give information about level of inbreeding and its age
- Observational approach: most likely provide more accurate information than probabilistic approaches
We are very grateful to owners of the genotype data for providing them:

Geno  – breeding organization for Norwegian Red
AGOEF  – Association of Austrian Fleckvieh Breeders
ArGe Braunvieh
ArGe Grauvieh
Thank you for your attention

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