Impact of genomic selection on genetic diversity in 5 European local cattle breeds

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Genetic diversity in local cattle populations

- Strong selection can lead to high inbreeding rates
  - associated los of genetic diversity
  - + inbreeding depression
  - + risk expression genetic defect
- Especially in small populations
- Genomic selection (GS) now applied in local breeds
- Main question
  - Did inbreeding rates change after the introduction of GS in 5 local breeds?
Changes in inbreeding rate after introduction GS

- **Genomic selection (GS):** starting ~2008 (VanRaden, 2008)
- Larger genetic gains, shorter generation intervals
- Expectation $\Delta F$ to go down

**Up**
- Holstein
  - the Netherlands (Doekes et al. 2018)
  - USA (Forutan et al. 2018; Makanjuola et al. 2020)
  - Poland (Topolski and Jagusiak 2020)
  - France (Doublet et al. 2019)
  - Australia (Scott et al. 2021)
  - Italy (Ablondi 2022)
- Jersey (Makanjuola et al. 2020)
- Finnish Ayrshire (Sarviaho et al. 2023)

**Not up**
- Normande
- Mont Beliarde
  - Doublet et al. 2019
- Aberdeen Angus
  - Lozada-Soto et al. 2021
5 cattle populations

- Abondance (F)
- MRY (NL)
- Tarentaise (F)
- Norwegian Red (N)
- Vosgienne (F)
## Some data

<table>
<thead>
<tr>
<th>Breed</th>
<th>Calf/year</th>
<th>Pedigree</th>
<th>Genotypes</th>
<th>Years analysed</th>
<th>Introduction GS</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRIJ</td>
<td>5,053</td>
<td>205,934</td>
<td>4,645</td>
<td>1975-2021</td>
<td>2018</td>
</tr>
<tr>
<td>Tarentaise</td>
<td>9,514</td>
<td>259,150</td>
<td>8,882</td>
<td>2000-2020</td>
<td>2014</td>
</tr>
</tbody>
</table>
MRY inbreeding and kinship levels

- All animals in pedigree

- Steady increase up to 2013
- Decrease 2013 – 2018
- Increase since introduction GS in 2019

\[ \Delta F = 0.46\% \]

- F (inbreeding)
- f (kinship)

- F all animals
- F (inbreeding)
- f (kinship)
MRY inbreeding and kinship levels

- Genotyped animals only

- Steady but irregular increase up to 2013
- Decrease F(ROH) but not F(ped) 2013 – 2018
- Increase since introduction GS in 2019

\[ \Delta F = 0.66\% \]

\[ -0.05\% \]

\[ -1.13\% \]

\[ 1.56\% \]
Norwegian Red inbreeding and kinship levels

- All animals in pedigree

- Steady increase of inbreeding
- Kinship decreases since 2009
- Inbreeding continues to increase since introduction GS in 2016
- Kinship continues to decrease
Norwegian Red inbreeding and kinship levels

- Genotyped animals only

- F(ROH) stable, slight increase since introduction GS
- Kinship decrease after 2014, stable after 2016
- F(ped) increase but less after 2014
French breeds

- Steady increase in all levels
- After introduction GS (2014)
  - Abondance
    - Less steep
    - Especially $F(ROH)$
  - Tarentaise
    - Steeper
    - especially $F(Ped)$
  - Vosgienne
    - Clearly less steep
    - Especially $F(ROH)$
## Change in inbreeding and kinship rates

<table>
<thead>
<tr>
<th>Breed</th>
<th>$F_{\text{ped}}$</th>
<th>$F_{\text{ROH}}$</th>
<th>$f$</th>
</tr>
</thead>
<tbody>
<tr>
<td>MRIJ all</td>
<td>Stable/Up</td>
<td>-</td>
<td>Stable/Up</td>
</tr>
<tr>
<td>MRIJ genotyped</td>
<td>UP</td>
<td>UP</td>
<td>Stable/Up</td>
</tr>
<tr>
<td>NR all</td>
<td>Stable</td>
<td>-</td>
<td>Down/up</td>
</tr>
<tr>
<td>NR genotyped</td>
<td>Down/Stable</td>
<td>UP</td>
<td>Down/up</td>
</tr>
<tr>
<td>Abondance</td>
<td>Down</td>
<td>Down</td>
<td>Down</td>
</tr>
<tr>
<td>Tarentaise</td>
<td>Up</td>
<td>Up</td>
<td>Up</td>
</tr>
<tr>
<td>Vosgienne</td>
<td>Down</td>
<td>Down</td>
<td>Down</td>
</tr>
</tbody>
</table>

- Mixed pattern: rates can go
  - up
  - or down
  - or remain stable
- after introduction of GS
Genetic management can reduce kinship

- MRIJ and Norwegian Red both use optimal contributions to select sires
- After introduction of OC a clear reduction in kinship
Summary

- Inbreeding rates ($\Delta F_{\text{gen}}$):
  - Increased  (MRIJ, Tarentaise)
  - More or less stable  (Norwegian Red)
  - Decreased  (Abondance, Vosgienne)

- Genomic Selection:
  - shorter generation intervals
  - screening more individuals
  - preselection of less sires

Main take-home message

- genetic management of local breeds more important than implementation of genomic selection per se