Genetic management without pedigree: effectiveness of a breeding circle in a rare sheep breed

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EAAP 2016
Rare breeds

- Numerically small (especially males)
  - High inbreeding rate
  - Loss of genetic diversity
  - Inbreeding depression and genetic defects

- Genetic management needed
  - Pedigree: management of relatedness and inbreeding
  - No pedigree: breeding circle

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Breeding circle

- Each herd receives rams from the previous herd in the circle
- Each herd provides rams to the next herd in the circle
- Ewes stay in own herd
- Pattern remains the same over the years
- Relatively simple
- Theoretically effective in reducing inbreeding rates
- Practically effectiveness not tested
Veluws Heideschaap

- Rare sheep breed
- Dates back to middle ages
- 8 large herds remain
- Used for heath conservation
- Inbreeding problems before
- Breeding circle since 1980’s

Unique case to test effectiveness of breeding circle in practice
Aim of study

- How effective is the breeding circle in the “Veluws Heideschaap”?
  - Mathematical
  - Computer simulation
  - DNA analysis
Keep track of average kinship ($f$) within and between herds

$f$ between herds depends on kinship between parental herds in previous generation

$$f_{x,y(t)} = \frac{1}{4} (f_{x,y} + f_{x,y-1} + f_{x-1,y} + f_{x-1,y-1})_{t-1}$$

$f$ within herds on effective population size + kinship between parental herds

$$f_x(t) = \frac{1}{N_{e,x}} (1 - F_x(t-1)) + \left(\frac{1}{2}\right) f_x(t-1) + \frac{1}{2} f_{x,x-1(t-1)}$$

$F$ on kinship in parental herds

$$F_x(t) = f_{x,x-1(t-1)}$$

Based on Nomura and Yonezawa (1996)

GSE 28:141

$$\frac{1}{N_e} = \frac{1}{4n_m} + \frac{1}{4n_f}$$
### Mathematical 2

- Kinship matrix in excel based on formulas
- For 8 herds with herd sizes equal to Veluws Heideschaap in 2015

**Inbreeding rates calculated from inbreeding levels**

<table>
<thead>
<tr>
<th>Herd</th>
<th>Nm</th>
<th>Nf</th>
<th>Ne</th>
<th>ΔF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Loenen</td>
<td>9</td>
<td>175</td>
<td>34</td>
<td>1.47%</td>
</tr>
<tr>
<td>Ermelo</td>
<td>14</td>
<td>271</td>
<td>53</td>
<td>0.94%</td>
</tr>
<tr>
<td>Epe-Heerde</td>
<td>7</td>
<td>141</td>
<td>27</td>
<td>1.85%</td>
</tr>
<tr>
<td>Lemelerberg</td>
<td>7</td>
<td>110</td>
<td>26</td>
<td>1.92%</td>
</tr>
<tr>
<td>Rheden</td>
<td>9</td>
<td>140</td>
<td>34</td>
<td>1.47%</td>
</tr>
<tr>
<td>Hoog Buurlo</td>
<td>7</td>
<td>147</td>
<td>27</td>
<td>1.85%</td>
</tr>
<tr>
<td>Ede I</td>
<td>14</td>
<td>279</td>
<td>53</td>
<td>0.94%</td>
</tr>
<tr>
<td>Ede II</td>
<td>9</td>
<td>170</td>
<td>34</td>
<td>1.47%</td>
</tr>
<tr>
<td><strong>total</strong></td>
<td>76</td>
<td>1433</td>
<td>289</td>
<td>0.17%</td>
</tr>
</tbody>
</table>

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Result Mathematical inbreeding rates

- Initially divergent inbreeding rates between herds up to 0.47%
- After 40 years all rates 0.18%

Very effective!
Result Mathematical inbreeding rates

- Initially decrease in inbreeding rates
- After 30 years all rates 0.18%
Computer simulation

- Simulation tool that calculates inbreeding (Windig & Oldenbroek, 2015)
- Takes into account overlapping generations and variation due to chance
- Input
  - Population structure (population size, number of herds, number of sires and dams, litter size, age breeding animals, exchange of rams between herds etc.)
- Rams 1 year old, Ewes up to 6 years
- 25 runs, 100 years
- Output: Inbreeding level and rate
Results Computer simulation

<table>
<thead>
<tr>
<th></th>
<th>ΔF</th>
<th>Min.</th>
<th>Max.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mathematical</td>
<td>0.18%</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Simulation</td>
<td>0.10%</td>
<td>0.09%</td>
<td>0.12%</td>
</tr>
<tr>
<td>Ewes 2 year</td>
<td>0.15%</td>
<td>0.013%</td>
<td>0.16%</td>
</tr>
<tr>
<td>No overlapping</td>
<td>0.17%</td>
<td>0.16%</td>
<td>0.19%</td>
</tr>
<tr>
<td>generations</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Use of older ewes reduces inbreeding rate
- Computer simulations and mathematical calculations agree

Very effective!
Real inbreeding rates: DNA analysis

- 12 DNA samples per herd, 8 herds
  - Rams 1 year old
  - Ewes 6 years old
- 10k SNP-chip
- DNA edit: 96 samples → 90 samples
  - 12,785 SNPS → 11,432 SNPs
- Level of heterozygosity → inbreeding rate per generation

\[
\Delta F = \left(1 - \frac{H(t)}{H(t-x)} \right)^{1/x} \cdot L ; \quad \Delta F = \left(1 - \frac{H(rams)}{H(ewes)} \right)^{1/6} \cdot L
\]
Results – DNA analysis

- **ANOVA:**
  - Significant difference between sexes
  - No significant difference between herds

- **Estimated ΔF**
  - 1.35%

Not effective!
Possible reasons

- **Sampling**
  - Sampling simulated - $\Delta F$: 0.07 - 0.17
- **Dominant rams**: not all rams equal chance siring offspring
  - Simulated 2 dominant rams siring 90% offspring
  - $\Delta F$: 0.38
- **Selection**
  - Strong selection on scrapie resistance in past 10 years
  - Old simulations: $\Delta F$ from 0.09 -> 0.36 with scrapie selection
Conclusions

• Theory does not always match practice
• Breeding circles theoretically effective
• High inbreeding rate in practice
• Caused by selection and dominant rams (?)

Acknowledgements
Rare breeds trust
Myrthe Maurice
Saskia Visser

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