Genetic evaluation of mastitis liability and recovery through longitudinal models of somatic cell count

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Mastitis is most frequent and costly diseases.

Genetic evaluation is performed either with cross-sectional or longitudinal methods\(^1\).

Cross-sectional methods are the most commonly used.

In cross-sectional methods lactations are considered as a static process.

\(^1\) Franzén et al. 2012
Longitudinal methods enable us to model changes throughout a lactation:

- Getting infected
- Recovery after infection

SCC (Somatic Cell Count) is used as a proxy to label clinical mastitis.
Objective

Develop better longitudinal models that capture as much genetic information as possible in both directions of the disease.
Data with five dairy traits were generated in Fortran.
- SCC and TBV for mastitis liability and recovery

Two population sizes:
- 24,000 and 60,000 first-parity cows from 1,200 herds
- 400 unrelated sires (60 or 150 daughter/sire)

28% and 95% mastitis incidence rates per lactation

Genetic correlations between infection and recovery:
- $rg = 0.00$, $rg = 0.02$, $rg = -0.02$

Designed to generate a representative of the real life dairy population and alternative herd structure.$^1$

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$^1$ Franzén et al. 2012
Data Creation

- Binary data {0, 1} were created to define:
  - Disease (D) or Healthy (H) state

\[ B(\tau) = m \times L(\tau) \]

\[ f_{ijkt}^{(H \text{ to } D)} = 1 \]
Transition probability model

- Possibilities of mastitis contract and recovery model

\[ T_i = \begin{bmatrix} \pi^{(H \to D)} & 1 - \pi^{(H \to D)} \\ 1 - \pi^{(D \to H)} & \pi^{(D \to H)} \end{bmatrix} \]

- \( T_i \) = transition probabilities for individual \( i \) going from a healthy (H) to a disease (D) state or the other way.

- A desired structure of the transition matrix is

  - High values of \( \pi^{(H \to H)} \) and \( \pi^{(D \to H)} \)
  - Low values \( \pi^{(H \to D)} \) and \( \pi^{(D \to D)} \)
The transition probability of getting infected:

\[ f_{ijkt}^{(H \to D)} \sim Ber(\pi_{ijk}^{(H \to D)}) \]  and

\[ \text{probit}(\pi_{ijk}^{(H \to D)}) = \beta^{(H \to D)} + S_j^{(H \to D)} + h_k^{(H \to D)} + e_{ijk}^{(H \to D)} \]

- \( f_{ijkt}^{(H \to D)} = 1 \) if a transition in time interval \( t \). otherwise = 0.
- \( \beta = \) liability of mastitis during period \( i \) for an average cow
- \( h_j = \) fixed herd effect ; \( s_k = \) random sire effect
- \( e_{ijk} = \) random residual effect for a cow

The transition probability of recovery \( \pi_{ijk}^{(D \to H)} \):

\[ f_{ijkt}^{(D \to H)} \sim Ber(\pi_{ijk}^{(D \to H)}) \]  and

\[ \text{probit}(\pi_{ijk}^{(D \to H)}) = \beta^{(D \to H)} + S_j^{(D \to H)} + h_k^{(D \to H)} + e_{ijk}^{(D \to H)} \]
Breeding values were estimated.

RJMC¹ package in DMU
  - single trait genetic analysis

MCMCglmm² package in R
  - multitrait genetics analysis.

Correlations between TBV and EBV were calculated as the reliability of estimates.

¹Madsen et al. 2010
²Hadfield, 2010
More reliable estimates in the HD direction

<table>
<thead>
<tr>
<th>Cases per lactation</th>
<th>Scenario 1 (28%)</th>
<th>Scenario 2 (95%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transition direction</td>
<td>HD</td>
<td>DH</td>
</tr>
<tr>
<td>$r_g = 0$</td>
<td>0.73</td>
<td>0.40</td>
</tr>
<tr>
<td>$r_g = 0.2$</td>
<td>0.72</td>
<td>0.37</td>
</tr>
<tr>
<td>$r_g = -0.2$</td>
<td>0.71</td>
<td>0.56</td>
</tr>
</tbody>
</table>

So far: single-trait analysis, ignoring genetic correlation between contracting and recovery.
Results and Discussion

- Estimates from the MCMCglmm analysis

<table>
<thead>
<tr>
<th>Direction</th>
<th>rTBV,EBV</th>
<th>h²</th>
<th>correlation</th>
</tr>
</thead>
<tbody>
<tr>
<td>HD</td>
<td>0.543</td>
<td>0.191</td>
<td></td>
</tr>
<tr>
<td>DH</td>
<td>0.240</td>
<td>0.001</td>
<td>0.119</td>
</tr>
</tbody>
</table>

- Bivariate model considering both traits at the same time enable us to calculate the possible genetic correlation between the traits.
Conclusions

- Selection accuracy as good as the estimations based on clinical mastitis for the HD direction.
- The transition probability model enables us to generate breeding values for DH direction.
- An option to include the whole disease course in the genetic evaluation of udder health.