Genetic parameters for pathogen-specific mastitis in Danish Holstein Cattle

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Nordic udder health index

- Direct and indirect measures of udder health
  - Mastitis treatments
  - Lactation average somatic cell score
  - Fore udder attachment
  - Udder depth

- Improvement?
  - Adding pathogen information?
  - Bacteriological culturing of milk samples
Motivation

Pathogen information may prove beneficial in a breeding context because:

- Direct measure of an infection of the udder and the pathogen causing the infection
- Mastitis caused by different pathogens may be considered as different traits
- $r_a$ between pathogen-specific mastitis and SCS may depend on causative pathogen
- Economic values of mastitis caused by different pathogens may differ
Objectives of study

- To estimate genetic variation and $h^2$ of pathogen-specific mastitis traits
- To estimate $r_a$ among different pathogen-specific mastitis traits
Data I

Editing

- Minimize bias of pathogen data
- Reduce extreme category problems
- Removal of unreliable data

Final data set: 168,158 first lactations from 1529 herds
Data II

- Mastitis incidence, before editing in ():
  - Unspecific: 0.230
  - *Strep. dysgalactiae*: 0.152 (0.100)
  - *E. coli*: 0.140 (0.112)
  - CNS: 0.140 (0.119)
  - *Staph. aureus*: 0.155 (0.145)
  - *Strep. uberis*: 0.187 (0.160)
  - Other: 0.144 (0.147)
  - Culture negative: 0.236 (0.216)

- Mastitis with pathogen information: 0.72
- Frequency of culled animals: 0.172 (0.191 vs 0.166)
Threshold model

$$\lambda_{ijklm} = YM_i + AGE_j + b \cdot t_{ijklm} + hys_k + sire_l + e_{ijklm}$$

where

- $\lambda_{ijklm}$ = liability to mastitis
- $YM_i$ = “fixed” effect og yr×mo of calving
- $AGE_j$ = “fixed” effect of calving age
- $hys_k$ = random effect of herd×yr×season
- $sire_l$ = transmitting ability of sire
- $b$ = “fixed” regression coefficient of $\lambda$ on the length of period at risk
- $t_{ijklm}$ = period at risk, defined as the number of d from 15 d before calving to the date of culling or to the end of the period at risk.
- All cows treated for mastitis were assigned a full period
  
  (Heringstad et al., 2001)
- $e_{ijklm}$ = residual $\sim$ iid $N(0,1)$

Full Bayesian approach via Gibbs sampling implemented in the DMU package

(Madsen and Jensen, 2006)
### Results I ($h^2$)

<table>
<thead>
<tr>
<th>Mastitis trait</th>
<th>$h^2$</th>
<th>95% CI</th>
<th>ESS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Unspecific</td>
<td>0.114</td>
<td>[0.086;0.138]</td>
<td>1527</td>
</tr>
<tr>
<td><em>Strep. dysgalactiae</em></td>
<td>0.044</td>
<td>[0.017;0.064]</td>
<td>238</td>
</tr>
<tr>
<td><em>E. coli</em></td>
<td>0.050</td>
<td>[0.021;0.077]</td>
<td>256</td>
</tr>
<tr>
<td>CNS</td>
<td>0.052</td>
<td>[0.022;0.077]</td>
<td>312</td>
</tr>
<tr>
<td><em>Staph. aureus</em></td>
<td>0.039</td>
<td>[0.018;0.058]</td>
<td>277</td>
</tr>
<tr>
<td><em>Strep. uberis</em></td>
<td><strong>0.079</strong></td>
<td>[0.043;0.112]</td>
<td>356</td>
</tr>
</tbody>
</table>
## Results II ($r_a$)

<table>
<thead>
<tr>
<th></th>
<th>$E. \ coli$</th>
<th>CNS</th>
<th>$Staph.\ aureus$</th>
<th>$Strep.\ uberis$</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Strep. dysgalactiae</strong></td>
<td>0.637</td>
<td>0.640</td>
<td>0.714</td>
<td>0.768</td>
</tr>
<tr>
<td><strong>E. coli</strong></td>
<td>0.602</td>
<td></td>
<td>0.452</td>
<td>0.628</td>
</tr>
<tr>
<td><strong>CNS</strong></td>
<td></td>
<td></td>
<td>0.608</td>
<td>0.745</td>
</tr>
<tr>
<td><strong>Staph. aureus</strong></td>
<td></td>
<td></td>
<td></td>
<td>0.631</td>
</tr>
</tbody>
</table>
Posterior density of $r_a$

$r_a$ between *E. coli* and *Staph. aureus*
Economic values

- Including pathogen information in the genetic evaluation of udder health may prove beneficial – especially as the cost of mastitis caused by different pathogens varies:
  - Contagious pathogen: €483/case
  - Environmental pathogens: €272/case

(Østergaard et al., 2008)
Conclusion

- $h^2$ of unspecific mastitis consistent with other studies of similar populations
- Pathogen-specific $h^2$ of mastitis were low – in most cases consistent with other studies
- $r_a$ in all cases different from unity → different pathogen-specific mastitis traits may be considered as different traits