Accuracy of genomic breeding values from endocrine and traditional fertility traits in dairy cows

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Context

• Important for production efficiency

• Poor fertility:
  ▪ Involuntary herd replacement
  ▪ Increased inseminations
  ▪ Longer calving intervals (CI) or CFS

• Traditional fertility traits for selection (e.g. CI or CFS)
  ▪ Biased by farm management
  ▪ Low heritability ($h^2 < 0.1$)
  ▪ Low rate of genetic gain
  ▪ Do not directly reflect cows own physiology
Endocrine fertility traits

PLA = $n_1 / (n_1 + n_2)$

- Less influenced by farm management
- Higher heritability (e.g. 16 – 28% for CLA)
- But expensive and labour intensive
Endocrine fertility traits

• New technologies reduce labor and cost

• Automatic sampling of milk P4 by Herd Navigator

• Applicable on a larger scale
Objective

Evaluate the added value (accuracy) of using endocrine fertility traits along with traditional traits in genomic prediction of fertility
Materials and Methods

Phenotypes
• 2,447 cows (5,339 lactations)
• 14 commercial herds
• 4 experimental herds
• Endocrine traits: CLA, PLA
• Traditional trait: CFS

Genotypes
• 80K (commercial herds)
• 50K (experimental herds)
• Imputation to 100K
• 85k SNP after QC

GEBV from GBLUP in univariate and bivariate models
G-matrix constructed as in VanRaden, 2008

\[ G = ZZ' / 2 \sum p_i (1 - p_i) \]
Genomic prediction

**Training population**
- Known Genotypes
- Phenotypes

**Selection candidates**
- Known genotypes

**Prediction equation**
Genomic breeding value (GEBV) = $W_1X_1 + W_2X_2 + W_3X_3 \ldots \ldots$

**Selected breeders**
- Using GEBV
Scenario 1 evaluates accuracy of prediction when:

- All training animals are phenotyped for endocrine traits
- and (or not) for traditional traits
Scenario 2

Genotyped cows

Training set

Phenotypes available for both CLA and CFS

Validation set

CLA and CFS masked during training and prediction

- Scenario 2 evaluates if phenotyping all training animals for both traits improves accuracy
Cross validation

Accuracy = Corr(GEBV, Phen)
Realized accuracy = Accuracy/\sqrt{h^2}
<table>
<thead>
<tr>
<th>Trait</th>
<th>Genomic</th>
<th></th>
<th>Pedigree</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n</td>
<td>$h^2$</td>
<td>SE</td>
<td>$h^2$</td>
</tr>
<tr>
<td>CLA (d)</td>
<td>3,524</td>
<td>0.10</td>
<td>0.02</td>
<td>0.14</td>
</tr>
<tr>
<td>PLA (%)</td>
<td>3,597</td>
<td>0.12</td>
<td>0.03</td>
<td>0.15</td>
</tr>
<tr>
<td>CFS (d)</td>
<td>3,634</td>
<td>0.11</td>
<td>0.03</td>
<td>0.10</td>
</tr>
</tbody>
</table>
### Accuracy GEBV scenario 1

<table>
<thead>
<tr>
<th>Trait</th>
<th>Training</th>
<th>Validate</th>
<th>Cows Training</th>
<th>Cows Validate</th>
<th>Accuracy (SD)</th>
<th>Realized accuracy (SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Univariate model</td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CLA</td>
<td>CLA</td>
<td>1,855</td>
<td>464</td>
<td></td>
<td>0.15 (0.05)</td>
<td>0.46 (0.16)</td>
</tr>
<tr>
<td>PLA</td>
<td>PLA</td>
<td>1,887</td>
<td>472</td>
<td></td>
<td>0.14 (0.02)</td>
<td>0.42 (0.07)</td>
</tr>
<tr>
<td>CFS</td>
<td>CFS</td>
<td>1,329</td>
<td>332</td>
<td></td>
<td>0.04 (0.07)</td>
<td>0.13 (0.21)</td>
</tr>
<tr>
<td>Bivariate model</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CLA and CFS</td>
<td>CFS</td>
<td>1,855</td>
<td>258</td>
<td></td>
<td>0.14 (0.07)</td>
<td>0.41 (0.21)</td>
</tr>
<tr>
<td>PLA and CFS</td>
<td>CFS</td>
<td>1,887</td>
<td>284</td>
<td></td>
<td>0.10 (0.03)</td>
<td>0.31 (0.09)</td>
</tr>
</tbody>
</table>

Accuracy increased in bivariate analyses where endocrine and traditional traits were used.
### Accuracy GEBV scenario 2

<table>
<thead>
<tr>
<th>Trait</th>
<th>Training</th>
<th>Validate</th>
<th>Cows Training</th>
<th>Cows Validate</th>
<th>Accuracy (SD)</th>
<th>Realized accuracy (SD)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLA</td>
<td>CLA</td>
<td></td>
<td>1,199</td>
<td>300</td>
<td>0.13 (0.08)</td>
<td>0.40 (0.26)</td>
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<tr>
<td>PLA</td>
<td>PLA</td>
<td></td>
<td>1,202</td>
<td>301</td>
<td>0.14 (0.04)</td>
<td>0.42 (0.12)</td>
</tr>
<tr>
<td>CFS</td>
<td>CFS</td>
<td></td>
<td>1,131</td>
<td>283</td>
<td>0.04 (0.05)</td>
<td>0.11 (0.15)</td>
</tr>
<tr>
<td><strong>Bivariate model</strong></td>
<td><strong>CLA and CFS</strong></td>
<td><strong>CFS</strong></td>
<td><strong>1,128</strong></td>
<td><strong>282</strong></td>
<td><strong>0.18 (0.04)</strong></td>
<td><strong>0.55 (0.13)</strong></td>
</tr>
<tr>
<td><strong>Bivariate model</strong></td>
<td><strong>PLA and CFS</strong></td>
<td><strong>CFS</strong></td>
<td><strong>1,129</strong></td>
<td><strong>282</strong></td>
<td><strong>0.07 (0.06)</strong></td>
<td><strong>0.20 (0.17)</strong></td>
</tr>
</tbody>
</table>
Conclusions

• Accuracy of GEBV increased in bivariate predictions where endocrine and traditional fertility traits were used.

• Better predictive ability of CFS in bivariate analysis with CLA than with PLA.

• Further studies with larger training populations may show bigger improvements.
Acknowledgements

**Data**
Lattec
CRV
RobustMilk project

**Funding**
European Graduate School in Animal-Breeding and Genetics (EGS-ABG)
EU PROLIFIC project