Using on-farm milk progesterone levels to define new fertility traits for dairy cows

Sorg D, Wensch-Dorendorf M, Schöpke K, Martin G, Swalve HH

diana.sorg@landw.uni-halle.de
Background

- low heritability of conventional fertility traits
- declining cow fertility
- progesterone-based new fertility traits are promising...
Background

- low heritability of conventional fertility traits
- declining cow fertility
- progesterone-based new fertility traits are promising…

...BUT:
- Biological fertility of the cow not easy to measure automatically
- No common standard on definition of progesterone-based fertility traits (e.g. sampling frequency, progesterone threshold for luteal activity, method of measurement … )
Objective

- Analyzing progesterone-based fertility traits for dairy cows that could be included in a breeding program in the future

→ Which progesterone-based traits can be easily measured on-farm?

→ Which traits are suitable for genetic selection?

→ What influence do method and sampling frequency have?
Progesterone-based traits

Commencement of Luteal Activity = first rise above threshold

Proportion of Luteal Activity = proportion of samples above threshold

CLA

PLA
Commencement of Luteal Activity
= first rise above threshold

Proportion of Luteal Activity
= proportion of samples above threshold

**CLA**
- **CLA1**: Visual inspection of profile
- **CLA2**: prog_mean
- **CLA3**: 3 ng/ml
- **CLA_Opt**: herd-optimized threshold (with visual CLA as reference)

**PLA**
- **PLA2**: prog_mean
- **PLA3**: 3 ng/ml
- **PLA_Opt**: herd-optimized threshold
Progesterone profiles

- Week 2 – 9 pp.
- on-farm ELISA measurement (eProCheck from FrimTec, Oberostendorf, Germany) in skimmed milk
- 5 large commercial dairy herds in Eastern Germany forming 2 data sets:

<table>
<thead>
<tr>
<th></th>
<th>data set 1</th>
<th>data set 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of profiles</td>
<td>1,446</td>
<td>296</td>
</tr>
<tr>
<td>Herd #</td>
<td>1,2,3,4</td>
<td>5</td>
</tr>
<tr>
<td>Parity</td>
<td>1-3</td>
<td>1-12</td>
</tr>
<tr>
<td>305-d milk yield</td>
<td>10,300 kg</td>
<td>11,900 kg</td>
</tr>
<tr>
<td>Progesterone</td>
<td>1 per week</td>
<td>2 per week</td>
</tr>
<tr>
<td>measurements</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Progesterone profiles

Graph showing progesterone levels (ng/ml) over weeks 1 to 8. The peak level is labeled CLA1.
Progesterone profiles

![Graph showing progesterone profiles with CLA1 and CLA2 highlights. The graph plots progesterone levels (ng/ml) against weeks. The progesterone mean line is also shown.]
Progestosterone profiles

The graph shows the Progesterone levels (ng/ml) over 8 weeks. The red line represents individual profiles, while the blue line indicates the mean Progesterone level. The profile peaks at CLA1 around week 5, with a notable decline at CLA2. The mean Progesterone level is shown as a blue horizontal line at 3 ng/ml. The graph highlights the variability in Progesterone levels across different weeks.
Statistical analysis

- Mixed model with SAS proc mixed and cow as random effect (accounting for repeated records) to examine fixed effects

- Genetic analysis with VCE and full relationships
Single trait animal model – genetic analysis

\[ y_{ijk} = \mu + HYS_i + P_j + a_{ijk} + e_{ijk} \]

- \( y_{ijk} \) = trait (CLA1, CLA2, CLA3, CLAOpt, PLA2, PLA3, PLAOpt, prog_mean)
- \( \mu \) = intercept
- \( HYS_i \) = fixed effect of herd-year-season of calving
- \( P_j \) = fixed effect of parity (\( j = 1 \) for lactation 1, \( j = 2 \) for lactation 2 and above)
- \( a_{ijk} \) = animal’s random additive genetic effect
- \( e_{ijk} \) = random residual effect
Two trait animal model – genetic analysis

\[ y_{1ijk} \ y_{2ijk} = \mu + HYS_i + P_j + a_{ijk} + e_{ijk} \]

- \( y_{ijk} \) = trait (CLA2, CLA3, CLAOpt, PLA2, PLA3, PLAOpt, prog_mean)
- \( \mu \) = intercept
- \( HYS_i \) = fixed effect of herd-year-season of calving
- \( P_j \) = fixed effect of parity (j = 1 for lactation 1, j = 2 for lactation 2 and above)
- \( a_{ijk} \) = animal’s random additive genetic effect
- \( e_{ijk} \) = random residual effect
LSMeans

CLA in weeks pp.

<table>
<thead>
<tr>
<th>Method</th>
<th>Frequency</th>
<th>Herd 1-4</th>
<th>Herd 5</th>
<th>Herd 5</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1x weekly</td>
<td>4.5</td>
<td>4.7</td>
<td>5.2</td>
</tr>
<tr>
<td></td>
<td>2x weekly</td>
<td>4.3</td>
<td>5.0</td>
<td>4.9</td>
</tr>
<tr>
<td></td>
<td></td>
<td>4.0</td>
<td>4.7</td>
<td>5.4</td>
</tr>
</tbody>
</table>

n = 1,446, n = 296

method, frequency p<0.0001
method*frequency p<0.0001
LSMeans

PLA (%)

<table>
<thead>
<tr>
<th>Method</th>
<th>Herd 1-4</th>
<th>Herd 5</th>
<th>Herd 5</th>
</tr>
</thead>
<tbody>
<tr>
<td>PLA2</td>
<td>47</td>
<td>39</td>
<td>41</td>
</tr>
<tr>
<td>PLA3</td>
<td>59</td>
<td>28</td>
<td>30</td>
</tr>
<tr>
<td>PLAOpt</td>
<td>66</td>
<td>34</td>
<td>70</td>
</tr>
</tbody>
</table>

- Herds 1-4:
  - 1x weekly: n = 1,446
  - 2x weekly: n = 296

- Herd 5:
  - 1x weekly: n = 296

method, frequency: p<0.0001
method*frequency: p<0.0001
### Genetic results herds 1-4

**Single trait model**

<table>
<thead>
<tr>
<th>Trait</th>
<th>$h^2$</th>
<th>SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLA1</td>
<td>0.04</td>
<td>0.05</td>
</tr>
<tr>
<td>CLA2</td>
<td>0.07</td>
<td>0.06</td>
</tr>
<tr>
<td>CLA3</td>
<td>0.08</td>
<td>0.06</td>
</tr>
<tr>
<td>CLAOpt</td>
<td>0.07</td>
<td>0.04</td>
</tr>
</tbody>
</table>
## Genetic results herds 1-4

### Single trait model

<table>
<thead>
<tr>
<th>Trait</th>
<th>$h^2$</th>
<th>SE</th>
<th></th>
<th>Trait</th>
<th>$h^2$</th>
<th>SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLA1</td>
<td>0.04</td>
<td>0.05</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CLA2</td>
<td>0.07</td>
<td>0.06</td>
<td></td>
<td>PLA2</td>
<td>0.18</td>
<td>0.06</td>
</tr>
<tr>
<td>CLA3</td>
<td>0.08</td>
<td>0.06</td>
<td></td>
<td>PLA3</td>
<td>0.18</td>
<td>0.07</td>
</tr>
<tr>
<td>CLAOpt</td>
<td>0.07</td>
<td>0.04</td>
<td></td>
<td>PLAOpt</td>
<td>0.13</td>
<td>0.06</td>
</tr>
</tbody>
</table>
# Genetic results herds 1-4

## Single trait model

<table>
<thead>
<tr>
<th>Trait</th>
<th>$h^2$</th>
<th>SE</th>
<th>Trait</th>
<th>$h^2$</th>
<th>SE</th>
<th>Trait</th>
<th>$h^2$</th>
<th>SE</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLA1</td>
<td>0.04</td>
<td>0.05</td>
<td>CLA2</td>
<td>0.07</td>
<td>0.06</td>
<td>PLA2</td>
<td>0.18</td>
<td>0.06</td>
</tr>
<tr>
<td>CLA3</td>
<td>0.08</td>
<td>0.06</td>
<td>PLA3</td>
<td>0.18</td>
<td>0.07</td>
<td>PLAOpt</td>
<td>0.13</td>
<td>0.06</td>
</tr>
<tr>
<td>CLAOpt</td>
<td>0.07</td>
<td>0.04</td>
<td>PLAOpt</td>
<td>0.13</td>
<td>0.06</td>
<td>Prog_mean</td>
<td>0.25</td>
<td>0.07</td>
</tr>
</tbody>
</table>
### Genetic results herds 1-4

Two trait model

<table>
<thead>
<tr>
<th>Trait 1</th>
<th>Trait 2</th>
<th>$h_1^2$</th>
<th>$h_2^2$</th>
<th>$r_g$</th>
<th>$r_p$</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLA2</td>
<td>PLA2</td>
<td>0.09</td>
<td>0.19</td>
<td>-1.0</td>
<td>-0.47</td>
</tr>
<tr>
<td>CLA3</td>
<td>PLA3</td>
<td>0.06</td>
<td>0.18</td>
<td>-1.0</td>
<td>-0.67</td>
</tr>
<tr>
<td>CLAOpt</td>
<td>PLAOpt</td>
<td>0.06</td>
<td>0.13</td>
<td>-1.0</td>
<td>-0.64</td>
</tr>
<tr>
<td>PLA2</td>
<td>Prog_mean</td>
<td>0.20</td>
<td>0.25</td>
<td>0.95</td>
<td>0.55</td>
</tr>
</tbody>
</table>
Conclusions

1. Progesterone-based fertility traits can be measured on-farm and once weekly in a commercial setting, but method of detection and sampling frequency have a significant influence on phenotypic levels of CLA and PLA

→ Exact and standardized definition of progesterone-based new fertility traits necessary
Conclusions

1. Exact definition of progesterone-based new fertility traits necessary!
   - High genetic correlation of PLA with CLA
   - PLA easy to detect with a computer algorithm
   - Higher heritability than CLA

2. High genetic correlation of PLA with CLA
   - PLA easy to detect with a computer algorithm
   - Higher heritability than CLA

→ using PLA as a proxy for CLA?
Conclusions

1. Exact definition of progesterone-based new fertility traits necessary!
2. Using PLA as a proxy for CLA?

3. \texttt{Prog\_mean} had the highest heritability and can be easily calculated

→ new interesting trait

→ Further studies needed on physiological implications of \texttt{prog\_mean}
Conclusions

1. **Exact definition of progesterone-based new fertility traits necessary!**

2. **Using PLA as a proxy for CLA?**

3. **Prog_mean new interesting trait**

We thank our sponsors for the support:

- **Federal Ministry of Food and Agriculture**
- **Federal Office for Agriculture and Food**
- **SACHSEN-ANHALT**

*diana.sorg@landw.uni-halle.de*