Genetic variance in environmental sensitivity for milk and milk quality in Walloon Holstein cattle

J. Vandenplas\textsuperscript{1,2}, C. Bastin\textsuperscript{1}, N. Gengler\textsuperscript{1} and H. A. Mulder\textsuperscript{3,4}

\textsuperscript{1}University of Liege, Gembloux Agro Bio-Tech, Gembloux, Belgium
\textsuperscript{2}National Fund for Scientific Research, Brussels, Belgium
\textsuperscript{3}Wageningen UR Livestock Research, Lelystad, The Netherlands
\textsuperscript{4}Wageningen University, Wageningen, The Netherlands

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Introduction

• Dairy cows robust to environmental changes
  – Economically desirable for some traits (e.g., increase of homogeneity of dairy products)
Introduction

- Dairy cows robust to environmental changes
  - Economically desirable for some traits (e.g., increase of homogeneity of dairy products)
- But, variations of observations around the fitted curve during the lactation:

![Low variations graph](image)

![Large variations graph](image)
Introduction

• Dairy cows robust to environmental changes
  – Economically desirable for some traits (e.g., increase of homogeneity of dairy products)

• Environmental factors
  – Macro-environment
    • Identifiable (e.g., temperature)
  – Micro-environment
    • Unknown

⇒ The genetic variance in micro-environmental sensitivity can be studied through genetic variance in residual variance (Hill and Mulder, 2010).
Introduction

• Potential interesting traits
  – Milk yield
  – Somatic cells score (SCS)
  – Milk fatty acids (FA) composition
    • Saturated FA (SFA)
      – Cholesterol, cardiovascular diseases (Haug et al., 2007)
    • Unsaturated FA (UFA)
      – Healthier for humans (Haug et al., 2007)
      – Milk fat quality properties (Palmquist et al., 1993)
    • C18:1 cis-9
      – Major UFA
      – Body fat mobilization in early lactation (Barber et al., 1997; Van Haelst et al., 2008)
        ➔ poor fertility performances (Bastin et al., 2012)
Aim

To study genetic heterogeneity of residual variance for milk yield, SCS, SFA, UFA and C18:1 cis-9 separately

- Estimation of variance components and breeding values (EBV) in the residual variance part

- Using a double hierarchical generalized linear model (DHGLM; Rönnegård et al., 2010)
Data

• 26,887 Walloon Holstein first-parity cows
  – With a known sire
  – 747 herds
  – ≥ 5 cows / herd * test-day
  – ≥ 3 records / cow
  – 146,027 test-day records
  • Milk yield (kg), SCS
  • SFA (g/dL of milk), UFA (g/dL of milk), C18:1 \textit{cis}-9 (g/dL of milk)

• Pedigree
  – 86,410 animals
  – ≥ 10 cows with records / sire
Model

• Mean model

\[ y = X\beta + Zu + Zp + e \]

Fixed effects
- Herd * test-day
- Lactation stage (classes of 5 DIM)
- Gestation stage
- Age at calving * season of calving * major lactation stage (classes of 73 DIM)
Model

• Mean model

\[ y = X\beta + Zu + Zp + e \]

Random effects
- Additive genetic
- Permanent environmental

Random residuals
Model

- Mean model
  \[ y = X\beta + Zu + Zp + e \]

- Residual variance model
  \[ V(e) = \exp(X_v\beta_v + W_v h_v + Z_v u_v + Z_v p_v) \]

Fixed effects
- Herd * calving year
- Lactation stage
- Gestation stage
- Age at calving * season of calving * major lactation stage
Model

• Mean model

\[ y = X\beta + Zu + Zp + e \]

• Residual variance model

\[ V(e) = \exp(X_v\beta_v + W_h h_v + Z_u u_v + Z_p p_v) \]

Random effects
- Herd * test-day
- Additive genetic
- Permanent environmental
Model

- Mean model
  \[ y = X\beta + Zu + Zp + e \]

- Residual variance model
  \[ V(e) = \exp(X_v\beta_v + W_vh_v + Zvu_v + Zvp_v) \]

- Estimation of variance components and breeding values
  - DHGLM method (Rönnegård et al., 2010)
    - Iterations between the mean model and the residual variance model
  - Modified REMLF90 (Misztal, 2012)
## Results

<table>
<thead>
<tr>
<th>Trait</th>
<th>GCV</th>
<th>$h^2_v$</th>
</tr>
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<tbody>
<tr>
<td>Milk yield</td>
<td>0.17</td>
<td>1.99*10^{-3}</td>
</tr>
<tr>
<td>SCS</td>
<td>0.16</td>
<td>3.47*10^{-3}</td>
</tr>
<tr>
<td>SFA</td>
<td>0.12</td>
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- Low genetic coefficients of variation for residual variances ($GCV$; $\approx$ genetic SD of the residual variance model)

- In the lower range of GCV for other species (Hill and Mulder, 2010)

→ Presence of some genetic variance in environmental sensitivity
## Results

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- **Low heritabilities for residual variances** ($h^2_v$)
  
  Lower than estimates in other species (0.02-0.05; Hill and Mulder, 2010)

- **Accurate EBV**$_v$ **estimated from a large data set** with enough information per animal (Mulder et al., 2007)
• Low EBV<sub>v</sub> sire: **less variation in observations** within its daughters group than the high EBV<sub>v</sub> sire
Results

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<tr>
<td>Mean model</td>
<td>σ²_p</td>
<td>1.11</td>
<td>0.70</td>
<td>0.41</td>
<td>0.14</td>
</tr>
<tr>
<td></td>
<td>σ²_u</td>
<td>0.57</td>
<td>0.15</td>
<td>1.34</td>
<td>0.30</td>
</tr>
<tr>
<td>Residual variance</td>
<td>σ²_h_v</td>
<td>0.13</td>
<td>0.18</td>
<td>0.14</td>
<td>0.20</td>
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<td>model</td>
<td>σ²_p_v</td>
<td>0.53</td>
<td>0.95</td>
<td>0.42</td>
<td>0.33</td>
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<td>σ²_u_v</td>
<td>0.29*10⁻¹</td>
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- Herd * test-day and permanent environmental effects
  ➔ **Substantial contributions** to heterogeneity of residual variance

  ➔ The DHGLM method may **provide interesting information** for **management purposes** in terms of variation.
Results

Pearson correlations between EBV and $EBV_v$

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• Positive correlations
  • Higher EBV $\rightarrow$ higher $EBV_v$ $\rightarrow$ ↑ residual variance
Results

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• Positive correlations
  • Higher EBV $\Rightarrow$ higher EBV_v $\Rightarrow$ ↑ residual variance

• Milk yield
  • Highest correlation
## Results

### Pearson correlations between EBV and EBV<sub>v</sub>

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- **Positive correlations**
  - Higher EBV $\Rightarrow$ higher EBV<sub>v</sub> $\Rightarrow$ ↑ residual variance

- **Milk yield**
  - Highest correlation

- **SCS**
  - Selection of lower EBV would reduce the average level of SCS but also the residual variance of SCS, both involving fewer mastitis cases.
Results

Pearson correlations between EBV and EBV

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• Positive correlations
  • C18:1 cis-9
    • Desirable: high contents in milk with few variation during the lactation
  • But, selection of low EBV would decrease the average content in milk of this FA.
Results

Pearson correlations between EBV and EBV\textsubscript{v}

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• Positive correlations
  • C18:1 \textit{cis}-9
    • \textbf{Desirable}: high contents in milk with few variation during the lactation
    • But, selection of low EBV\textsubscript{v} would decrease the average content in milk of this FA.

• Correlations ≠ 1.00
  ➡️ \textbf{Selection feasible} in a desired direction with proper weighting of both EBV in total merit indices
Conclusion

For all studied traits in the Walloon Holstein dairy cattle:

– Genetic and non-genetic heterogeneity of residual variance

– Genetic variance in environmental sensitivity
  ➔ Selection feasible to change micro-environmental sensitivity

– Substantial contributions of non-genetic effects
  ➔ Interesting information for management purposes in terms of variation
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