Differences in bovine milk fat composition among dairy breeds in The Netherlands

Myrthe Maurice – Van Eijndhoven, Henk Bovenhuis, Hélène Soyeurt, and Mario Calus
Background

- **Differences in milk fatty acid (FA) composition between breeds** is of interest because it is associated with:
  - Processability
  - Human health
  - Methane emission
  - Unique breed characteristic (selection / conservation)

- Different cattle breeds used in dairy industry in the Netherlands:
  - Holstein Friesian (HF)
  - Jersey (JER)
  - Meuse-Rhine-Yssel (MRY)
  - Dutch Friesian (DF)
  - Groningen White Headed (G)
Measuring FA composition

- Gas chromatography (GC)
  - Highly accurate
  - High cost per sample

- Mid-infrared (MIR) profiles
  - (Somewhat) lower accuracy
  - Very low cost per sample (measured during routine milk recording)

=> MIR is optimal for large-scale breeding applications
Aim of this study

Investigate differences in bovine milk fat composition between different cattle breeds in the Netherlands

=> Milk fat composition predicted from MIR spectra using RobustMilk prediction equations (Soyeurt et al., 2011)
Data

MIR profiles obtained during routine milk recording

On farms with MRY, DF, GWH, and JER (and HF):
- 24,445 cows (41,404 records) from 445 farms
- 7,626 cross-bred cows
- 1,769 purebred (≥ 87.5%) MRY, DF, GWH, and JER
- 15,050 purebred (≥ 87.5%) HF
Model

- Only FA included that were predicted accurately
  - validation $R^2 > 0.6$ (on Dutch data)
- All FA components analysed as g/dL milk
- FA+ & FA- model
  - FA- includes no regression on fat%
  - FA+ includes regression on fat%
    - $\Rightarrow$ To correct for differences in total Fat%
- Fixed effects
  - Regression on breed fractions
  - Heterosis & recombination
  - Further: age, hys, dim, etc.
Results – groups of FA

- Generated through de novo synthesis
  - short and medium chain FA

- Affected by Δ9-desaturases
  - C14:1

- Arising in milk directly from cows diet
  - C18:2cis9,12 and C18:3cis9,12,15
FA generated through de novo synthesis

Short chain FA (SCFA; C4-C10)

<table>
<thead>
<tr>
<th>Breed</th>
<th>g/dL milk</th>
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<tbody>
<tr>
<td>HF</td>
<td>b</td>
</tr>
<tr>
<td>MRY</td>
<td>b</td>
</tr>
<tr>
<td>DF</td>
<td>b</td>
</tr>
<tr>
<td>GWH</td>
<td>a</td>
</tr>
<tr>
<td>JER</td>
<td>c</td>
</tr>
</tbody>
</table>

The graph shows the comparison of short chain fatty acids (SCFA) concentration in different breeds. The breeds are abbreviated as follows: HF, MRY, DF, GWH, and JER. The bars indicate the concentration of SCFA in g/dL milk, with different letters (a, b, c) indicating significant differences among the breeds.
FA generated through de novo synthesis

Short chain FA (SCFA; C4-C10)

Same trends observed for Medium chain FA (MCFA; C12:0, C14:0, C16:0)
FA affected by Δ9-desaturases (C14:1)
FA affected by Δ9-desatururases (C14:1)
FA arising from the cows diet

- Some significant differences, despite low concentration in milk

Using FAT+ model (correcting for Fat%):

- C18:2cis9,12
  - JER: Lower compared to other breeds

- C18:3cis9,12,15
  - Results inconsistent with other studies
Conclusions

FA composition:
- Similar for HF, MRY, and DF; different for GWH & JER

- Short & medium chain FA:
  - GWH: lowest concentration
  - JER: highest concentration

- Is related to total fat percentage in all breeds; especially short and medium chain FA
  - FA- or FA+ model
Acknowledgements

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