Genetic and genomic analysis of groups of milk fatty acids measured by mid infrared spectroscopy in German Holstein dairy cows

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Summary

Milk components from 11,012 German Holstein cows (dataset 1) were measured by mid infrared spectroscopy during monthly milk recording. Genetic parameters for test day milk yield, fat content, protein content, fat:protein ratio, saturated FA (SFA) and unsaturated FA (UFA) concentrations predicted by mid infrared spectroscopy were in accordance with results from similar studies in the literature. SFA exhibited a 10 % higher genetic variance than fat content and a genetic correlation of 0.99 to fat content. SFA and UFA could serve as novel traits in breeding programs, and SFA could be used as an auxiliary trait for fat content. A subset of 5,022 cows (dataset 2) was genotyped and used as a reference population (RP) for genomic estimated breeding values (GEBV) of genotyped bulls. The correlation of the GEBV and the official national breeding values (EBV) for test day milk yield, fat and protein content was 0.57-0.69 for bulls without daughters in the RP. This correlation increased considerably when only bulls with a certain number of daughters in the RP were selected. The correlations of the bulls’ GEBV for SFA and UFA with those for the other milk traits were very similar to the genetic correlations of these traits in dataset 1. A relatively small RP of 5,022 cows can be used to derive meaningful GEBV, provided there is a sufficient number of daughter phenotypes available.

Keywords: milk fatty acids, mid infrared spectroscopy, heritability, genomic estimated breeding value

Introduction

Novel milk traits such as fatty acid (FA) concentrations, biomarkers for ketosis, mastitis and fertility (Bastin et al. 2016) or methane emission, energy intake and energy efficiency (McParland et al., 2014, van Gastelen and Dijkstra, 2016) are studied for genetic selection. A lower content of saturated and a higher content of unsaturated FA in dairy products could also decrease health risks in humans, e.g. the risk for cardiovascular diseases (Livingstone et al., 2012). These components can be predicted by mid infrared (MIR) spectroscopy, based on calibrated prediction equations. In contrast to the standard method gas chromatography, the MIR method is fast and easily available in many routine milk recording laboratories. We present genetic and genomic parameters for the content of saturated FA (SFA) and unsaturated FA (UFA) in the milk of German Holstein dairy cows and compare them with estimated breeding values (EBV) for milk traits from the national genetic evaluation.
Material and methods

In total, 59,230 monthly test day records from 11,012 Holstein cows in first lactation on 18 commercial contract testing herds between November 2014 and June 2016 were used (dataset 1). Milk fat content (%), protein content (%) and FA concentrations in g/100 g milk were analysed by Fourier transform infrared spectroscopy (FTIR) in a regional milk recording laboratory (Landeskontrollverband für Leistungs- und Qualitätsprüfung Mecklenburg-Vorpommern e.V., Güstrow, Germany) using a MilkoScan FT6000 (FOSS, Hilleroed, Denmark). The concentrations of SFA and UFA were predicted with the manufacturer’s own calibration equation and software (FOSS Integrator, FOSS). Pedigree data containing 83,059 animals were obtained from the national data recording centre Vereinigte Informationssysteme Tierhaltung (VIT). The statistical model was optimized with SAS 9.2 (SAS Institute, Cary, NC, USA). Variance components were estimated using VCE 6 (Groeneveld et al., 2008) using a two trait fixed regression test day model (1) for test day milk yield (kg), fat (%), protein (%), ratio of fat to protein (fat:protein), SFA and UFA (both in g/100 g milk):

\[
\text{trait 1 trait 2} = \mu + \text{HTD} + \text{AFC} + \text{CM} + \text{ls(dim)} + a + \text{pe} + e
\]  

(1)

where \(\mu\) is the overall mean, HTD is the fixed effect of herd-test day, AFC is the fixed effect of age at first calving in months, CM is the fixed effect of month of calving, \(\text{ls(dim)}\) is the Ali and Schaeffer polynomial regression on day in milk (Ali and Schaeffer, 1987), \(a\) is the random additive-genetic effect of the animal, \(\text{pe}\) is the random permanent environmental effect of the animal and \(e\) is the random residual effect.

A subset of 5,022 cows with 30,710 test day records (dataset 2), serving as a reference population (RP), and 1,030 bulls were genotyped on a BovineSNP50 BeadChip (Illumina, San Diego, CA, USA). The pedigree comprised 58,055 animals. The same model as in (1) and an H-matrix in a single-step approach (BLUPF90, Misztal et al. (2014)) were used to estimate the SNP effects. From these SNP effects, genomic breeding values (GEBV) for the bulls were calculated. Estimated breeding values (EBV) from the national genetic evaluation for Holstein bulls were obtained from VIT. A genome wide association study (GWAS) for SFA and UFA was also conducted with the BLUPF90 package.

Results and Discussion

The estimates of heritability (\(h^2\)) for SFA and UFA and their genetic correlations (\(r_g\)) (table 1) were in the range reported in other studies (Bastin et al., 2013, Penasa et al., 2015, Narayana et al., 2017). SFA and UFA were genetically negatively correlated with milk yield (−0.48 and −0.37, respectively), which was not surprising, since fat content had a negative genetic correlation with milk yield (−0.49). Fat content was more genetically correlated with SFA (0.99) than UFA (0.83).

The saturated FA C4:0 – C14:0 and partly C16:0 are synthesized de novo in the mammary gland. A part of C16:0, C18:0 and C18:1 are taken up into the mammary gland from the blood and originate from tissue mobilization or from microbial production in the rumen. The higher \(h^2\) of SFA supports the hypothesis that de novo synthesized FA are under stronger genetic regulation than the ones from tissue or feed (Moore and Christie, 1979).

With 10.07 %, the additive-genetic coefficient of variation (\(s_g\)) (table 2) of SFA was higher than the one of milk, fat content and fat:protein ratio. The \(s_g\) % of UFA was still higher than the one of protein content. Together with the low to moderate \(h^2\) for SFA and UFA, this
suggests that these groups of FAs have sufficient genetic variation and heritability to be used as new traits for genetic selection.

Table 1. Heritability (diagonal), genetic correlation (above diagonal) and phenotypic correlation (below diagonal) of the milk components

<table>
<thead>
<tr>
<th>Trait</th>
<th>milk (kg)</th>
<th>fat (%)</th>
<th>protein (%)</th>
<th>fat:protein</th>
<th>SFA¹</th>
<th>UFA</th>
</tr>
</thead>
<tbody>
<tr>
<td>milk</td>
<td>0.23</td>
<td>-0.49</td>
<td>-0.60</td>
<td>-0.27</td>
<td>-0.48</td>
<td>-0.37</td>
</tr>
<tr>
<td>fat</td>
<td>-0.41</td>
<td>0.31</td>
<td>0.69</td>
<td>0.89</td>
<td>0.99</td>
<td>0.83</td>
</tr>
<tr>
<td>protein</td>
<td>-0.40</td>
<td>0.47</td>
<td>0.30</td>
<td>0.29</td>
<td>0.66</td>
<td>0.58</td>
</tr>
<tr>
<td>fat:protein</td>
<td>-0.24</td>
<td>0.87</td>
<td>-0.02</td>
<td>0.22</td>
<td>0.90</td>
<td>0.71</td>
</tr>
<tr>
<td>SFA</td>
<td>-0.37</td>
<td>0.95</td>
<td>0.49</td>
<td>0.78</td>
<td>0.33</td>
<td>0.74</td>
</tr>
<tr>
<td>UFA</td>
<td>-0.27</td>
<td>0.74</td>
<td>0.18</td>
<td>0.75</td>
<td>0.59</td>
<td>0.13</td>
</tr>
</tbody>
</table>

¹SFA = Saturated fatty acids; UFA = Unsaturated fatty acids

Table 2. Additive-genetic standard deviation (sₐ) and coefficient of variation (sₐ %)

<table>
<thead>
<tr>
<th>Trait</th>
<th>milk (kg)</th>
<th>fat (%)</th>
<th>protein (%)</th>
<th>fat:protein</th>
<th>SFA¹</th>
<th>UFA</th>
</tr>
</thead>
<tbody>
<tr>
<td>sₐ</td>
<td>2.81</td>
<td>0.35</td>
<td>0.14</td>
<td>0.08</td>
<td>0.25</td>
<td>0.07</td>
</tr>
</tbody>
</table>

¹SFA = Saturated fatty acids; UFA = Unsaturated fatty acids

The Pearson correlation of the bulls’ EBV and GEBV (r(EBV/GEBV)) for milk, fat and protein content were intermediate to high, but increased with the number of daughters per bull in the RP. Single outliers and the low number of bulls could have led to the varying r(EBV/GEBV) above 20 daughters per bull. The r of the EBV for fat content with the GEBV for SFA was higher than r(EBV/GEBV) for fat content. SFA also had a higher sₐ than fat content and an r of fat content with fat content of almost 1.00. This suggests that SFA could be used for the genetic selection on fat content with a higher genetic gain, if this is desired.

Table 3. Pearson correlation coefficients (r) of GEBV with EBV of bulls for milk traits

<table>
<thead>
<tr>
<th>No. of daughters in RP¹ per bull</th>
<th>No. of bulls</th>
<th>r(EBV/GEBV)²</th>
<th>r(EBV fat/GEBV SFA³)</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>493</td>
<td>0.57</td>
<td>0.69</td>
<td>0.63</td>
</tr>
<tr>
<td>1 – 5</td>
<td>67</td>
<td>0.63</td>
<td>0.72</td>
<td>0.73</td>
</tr>
<tr>
<td>6 – 10</td>
<td>23</td>
<td>0.69</td>
<td>0.84</td>
<td>0.84</td>
</tr>
<tr>
<td>11 – 20</td>
<td>29</td>
<td>0.82</td>
<td>0.93</td>
<td>0.89</td>
</tr>
<tr>
<td>21 – 30</td>
<td>31</td>
<td>0.79</td>
<td>0.87</td>
<td>0.86</td>
</tr>
<tr>
<td>31 – 40</td>
<td>6</td>
<td>0.95</td>
<td>0.91</td>
<td>0.89</td>
</tr>
<tr>
<td>41 – 50</td>
<td>7</td>
<td>0.48</td>
<td>0.84</td>
<td>0.98</td>
</tr>
<tr>
<td>&gt;50</td>
<td>20</td>
<td>0.75</td>
<td>0.91</td>
<td>0.90</td>
</tr>
</tbody>
</table>

¹Reference population of 5,022 genotyped cows
²EBV = Official national estimated breeding value; GEBV = Genomic estimated breeding value
³Saturated fatty acids

The Pearson correlations between the GEBV of 237 bulls with daughters in the RP between SFA, UFA, fat content, protein content and milk yield were very similar to the r of between these traits in data set 1 (data not shown).

The GWAS confirmed several significant SNPs on chromosome 14 in the DGAT1 gene.
which has been described to have a major effect on milk fat (Grisart et al., 2004) and FA content (Li et al., 2014). This served to validate our method. Other genomic regions associated with SFA and UFA content were found on chromosomes 5 and 11, but no suitable candidate gene was identified so far.

Conclusion

SFA and UFA can easily be measured during the routine milk recording on a large number of cows. SFA and UFA show genetic variation and heritability, so that they can be used as novel traits in breeding programs. The correlations of GEBV with EBV from bulls were similar to the r_g for milk traits. SFA could be used as an auxiliary trait for fat content. A relatively small RP of 5,022 cows seems to be sufficient for the estimation of GEBV, provided that there is a minimum number of daughters with genotypes and phenotypes available.

Acknowledgments

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List of References


