

Phenotypic and Genetic Analysis Of Milk Fatty Acids in UK Holstein-Friesian Cows

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ABSTRACT: Applying calibration equations to mid-infrared (MIR) spectrometry has been shown to be an efficient method to predict fatty acid composition in bovine milk. Milk fatty acids were predicted from monthly milk MIR for approx. 30,000 cows with between 3 – 7 months of milk tests per animal. Results on approx. 60,000 test records showed that milk fatty acids varied with stage of lactation and time of year. Univariate linear sire models (repeated) were used to estimate heritabilities for a selection of the predicted fatty acids with heritabilities ranging from 0.09 – 0.33. The research demonstrates the practical application of this technique in the UK dairy herd and used to estimate genetic parameters and therefore has the potential to deliver genetic improvement tools for fatty acids routinely.

Keywords: dairy cattle; fatty acids; Milk production; genetics

Introduction

Research into the fatty acid profile of bovine milk has been limited in the past due to the expensive and time consuming nature of gas chromatography analysis. Mid-infrared (MIR) spectrometry is the method of choice for quantification of milk fat, protein, and lactose content of milk samples. Applying the Soyeurt et al. (2011) calibration equations to the MIR spectrum enables efficient analysis of fatty acid profiles for large datasets, not previously possible.

Fat content and composition of food is of growing consumer concern as consumption related health problems continue to be a heavy burden on society. Some fatty acids (FA) are known to have potential beneficial effects (e.g., the anticarcinogenic properties of C18:2 cis-9, trans-11) or potential deleterious effects (e.g., the hypercholesterolemic effects of C16:0) on human health. Cardiovascular disease (CVD), which is linked to high intake of saturated fatty acids (SFA), is the most common cause of death in the UK (Townsend et al. 2012). Milk and milk products are nutrient rich foods but suffer significant criticism as the main source of saturated fat in the diet, contributing approximately 31% and 22% of SFA in the British diet for 4-10 year olds and adults (19-64), respectively (Bates et al. 2011). Modifying the fatty acid profile of milk could be an effective way of reducing the SFA intake of the British population without requiring a change in dietary patterns.

In addition to human health attributes, milk is known to have technological and sensory qualities. Moreo-

ver, increasing C18:2 content makes butter softer, but with values higher than 20% the butter can be deemed to have not acceptable sensory attributed. Therefore better knowledge of the sources of variation of milk fat composition, and in particular the contribution of additive genetic variation to differences among animals in milk fatty acid content is useful to monitor and/or improve, through breeding and/or other management practices, the milk fatty acid content.

This study applies fatty acid predictions based on MIR to a large subset of national dairy herds in the UK, as part of the routine monthly milk recording. In addition, an initial estimate of the genetic parameters for fatty acids is performed.

Materials and Methods

Data. Daily milk yield, and components (fat and protein) were extracted from a UK milk recording organisation (National Milk Records) with associated animal parameters (e.g., lactation number, stage of lactation, age at first calving). A number of editing rules were applied to these data such that they could be included in genetic parameter estimation. These included tests from the first three lactations with ages at calving of 18-42 months, 30 – 60 months and 42-70 months respectively. Further data edits took place for the purposes of the genetic analysis including progeny group size and contemporary group size. Individual test day milk MIR spectra were obtained for these cows with each cow having between 3-7 monthly test day records. The prediction equations were initially presented by Soyeurt et al (2011) and are routinely updated as part of EU funded project OptiMir (www.optimir.eu). The prediction “accuracy” of the equations for the fatty acids, as measured with the cross-validation coefficient of determination, is reported as ranging from 0.81 – 0.99. Further limits were placed on the milk yields, fat and protein yields and the chosen fatty acid traits as presented in table 1 and descriptive analyses were performed.

Genetic analysis The dataset of predicted fatty acids were further edited for the purposes of genetic evaluations including minimum size of progeny and cotemporary groups. A total of 12,680 H-F cows remained in the edited dataset and a pedigree file was extracted for the cows with a total number of 108,985 individuals with five complete generations.

The model for initial genetic analyses followed the model developed based on analysis of a detailed recorded herd in the UK (Johnstone et al., 2013). The results presented below are for initial sire model estimates of the genetic parameters. Variances components were estimated for the fatty acid traits using single-trait sire models adjusting for the fixed effects of herd-year-season, lactation number, age at calving, calendar test date. Repeatability models were fitted to account for the repeated sample test date. Genstat and ASREML (Gilmour, et al., 2009) were used to undertake these analyses.

Table 1. Summary statistics, genetic and phenotypic variance and heritability of the groupings of monounsaturated (MONO), polyunsaturated (POLY), short, medium and long chained (SCFA, MCFA, LCFA respectively) fatty acids expressed as proportion of milk fat (%fat) and component weight (Wgt).

| % fat | MONO | POLY | SCFA | MCFA | LCFA |
|----------------|-------|------|-------|-------|-------|
| Mean | 29.02 | 4.48 | 8.58 | 53.73 | 38.41 |
| StdDev | 4.07 | 0.80 | 1.20 | 5.93 | 7.16 |
| VarP | 16.53 | 0.63 | 1.45 | 35.21 | 51.33 |
| Min | 12.78 | 0.01 | 0.01 | 16.20 | 16.22 |
| Max | 43.42 | 9.27 | 13.62 | 75.02 | 93.92 |
| VarG | 2.48 | 0.08 | 0.29 | 7.04 | 4.62 |
| h ² | 0.15 | 0.12 | 0.20 | 0.20 | 0.09 |
| Wgt | | | | | |
| Mean | 1.17 | 0.18 | 0.35 | 2.16 | 1.56 |
| StdDev | 0.29 | 0.04 | 0.08 | 0.48 | 0.53 |
| VarP | 0.09 | 0.00 | 0.01 | 0.23 | 0.28 |
| Min | 0.08 | 0.00 | 0.00 | 0.23 | 0.20 |
| Max | 2.60 | 0.46 | 1.07 | 5.30 | 5.85 |
| VarG | 0.02 | 0.00 | 0.00 | 0.05 | 0.04 |
| h ² | 0.20 | 0.19 | 0.24 | 0.23 | 0.15 |

Table 2. Summary statistics, genetic and phenotypic variance and heritability of saturated fatty acids (SAT) and C16, C18 and C18_1 fatty acids expressed as proportion of milk fat (%fat) and component weight (Wgt).

| % fat | C16 | C18 | C18_1 | SAT |
|----------------|-------|-------|-------|-------|
| Mean | 29.89 | 8.10 | 24.34 | 66.58 |
| StdDev | 4.61 | 3.89 | 4.41 | 4.52 |
| VarP | 21.27 | 15.13 | 19.48 | 20.47 |
| Min | 6.59 | 0.00 | 3.58 | 55.00 |
| Max | 78.84 | 50.74 | 51.03 | 77.00 |
| VarG | 3.40 | 2.95 | 2.29 | 4.50 |
| h ² | 0.16 | 0.20 | 0.12 | 0.22 |
| Wgt | | | | |
| Mean | 1.22 | 0.34 | 0.99 | 2.70 |
| StdDev | 0.38 | 0.26 | 0.30 | 0.63 |
| VarP | 0.15 | 0.07 | 0.09 | 0.40 |
| Min | 0.04 | 0.00 | 0.03 | 0.43 |
| Max | 6.17 | 3.08 | 3.10 | 7.07 |
| VarG | 0.05 | 0.02 | 0.01 | 0.13 |
| h ² | 0.33 | 0.23 | 0.11 | 0.32 |

Results and Discussion

Fatty acids in the national dairy herd. Important trends can be visualised across a larger dataset of over 24,000 (note: this is prior to edits for genetic parameter estimation) first parity animals with fatty acid data between 0 and 305 days in milk in 2013 which has been subject to quality control data edits. Within this fat component the average mono and polyunsaturated fatty acid are significantly lower in winter than they are in summer (student's t test, $p < 0.001$), whilst the amount of saturated fat does not change significantly (Figure 1). These differences between seasons could represent the changes in diets as cows move from winter feeding indoors to grazing in the summer months. Diet was shown to have a significant effect on many fatty acids by Johnstone et al (2013). Another way of grouping the fatty acid components is by branch length and here it is apparent that the short-chain fatty acids are present in much smaller amounts and with less variation than the medium and long chain fatty acids (Figure 2). There was significant variation in profile over the course of lactation, especially evident in later parities where patterns are more settled (not shown). The low SFA percentages in early lactation corresponded to when cows were producing peak milk yield (Coffey et al, 2004) and therefore typically in negative energy balance. To compensate for this imbalance, fat stores in adipose tissue, which are rich in C18:1cis9 MUFA, are mobilised and released into the udder and make up a greater proportion of the milk fat (Stoop et al. 2009).

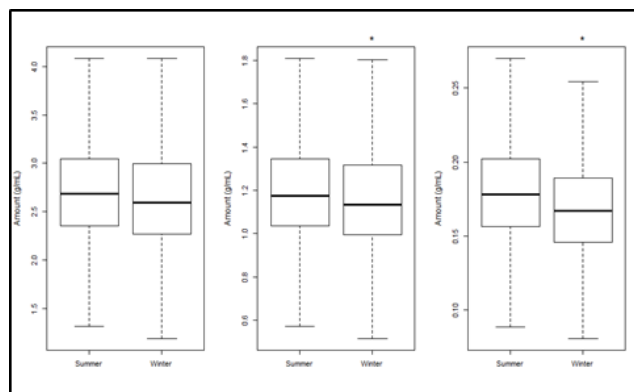


Figure 1. Distribution of the three main groups of fatty acid (saturated, monounsaturated and polyunsaturated fatty acids respectively) in summer and winter.

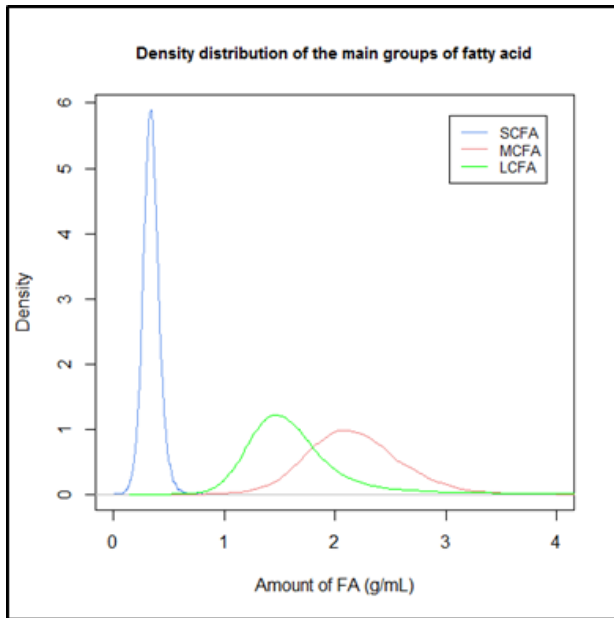


Figure 2. Density distribution of the three main groups of fatty acid from 0 – 305 DIM first parity Holstein Friesian cows.

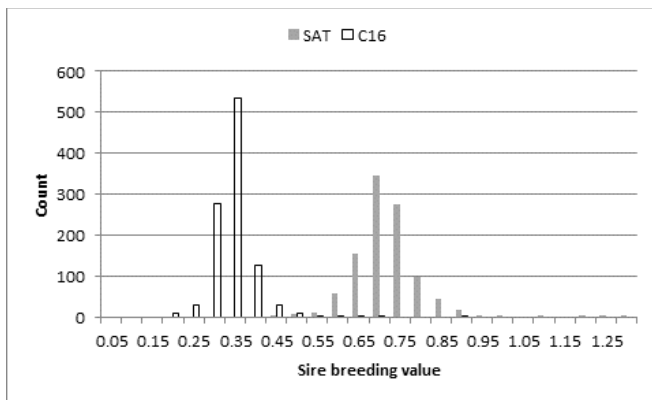


Figure 3. Distribution of the sire solutions for saturated fatty acid and C16 for approx. 1,000 in the genetic analysis.

Heritabilities for fatty acids. The heritability estimates are in the range of those quoted in the literature (e.g., Bastin et al, 2011, Stoop et al 2008). The lowest heritability was for long chain fatty acid expressed as a proportion of fat (0.09 ± 0.015) and the highest was for weight of C16 (0.33 ± 0.01). The heritabilities for the traits when expressed in grams was higher than when expressed as a percentage of fat which was also seen by Bastin et al (2011). For example the heritability from saturated fat as a percentage of fat was 0.22 but weight of saturated fat was 0.32. The results of this study had a slightly lower range of heritabilities than other studies but it important to note that these record span only seven months (and not necessarily for all animals) and therefore the data does not reflect a full calendar year or a full lactation. It would be appropriate to apply

random regression models to the genetic analyses of the fatty acid traits when we have sufficient temporal records at an animal and herd level to capture the individual variation that may exist at a cow level as the fatty acid profiles change over the year and the lactation.

Conclusion

Individual cow fatty acids are now routinely available to UK dairy farmers as part of selected milk recording programmes with between 30,000-50,000 test day records being collected per month. These results represented the first application of MIR predicted fatty acids in UK dairy cattle. The traits were shown to vary over lactation and with time of the year. Initial heritability estimates are in line with the literature and show that the key fatty acids display genetic variance and are therefore likely to be suitable for selection such that selection for altered fatty acids could be part of a routine genetic improvement programme.

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