



FRS

Genetic Parameters of the Major Fatty Acid (FA) Contents in Cow Milk

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1. Aim and Objectives

Fatty acids profile influences the **technological properties of butterfat** and presents some interests for **human health**.

Feed impact is well known; **lack of information about genetic parameters**.

Chromatographic analysis are expensive → Limited numbers of samples.

→ **ALTERNATIVE : MIR Spectrometry to predict the FA contents + Quantitative Models.**

2. Material and methods

Animal Population

- 7,700 samples in 25 herds and from 7 breeds were collected between April 2005 to May 2006 and analyzed on MilkoScan FT6000.

Prediction of FA contents

- Calibration equations established previously by Soyeurt et al. (JDS 2006) were applied to 7,700 recorded spectra.

- Prediction of C12:0, C14:0, C16:0, C18:0, C18:1, C18:2 9-cis, 12-cis, saturated FA (SAT) and monounsaturated FA (MONO) in g/dl of milk. Conversion in g/100 g of milk and in g/100 g fat.

Estimation of Genetic Parameters

- Added 40,007 records on milk yields, %fat, %protein

- Multi-trait mixed model :

Fixed effects : herd*date of test * class of lactation number; class of days in milk * class of lactation number; age * class of lactation number.

Random effects : residual effect, animal additive, permanent environment within and across lactations.

- Variance components were the average values measured from the 5 runs. Correlation matrices were banded by applying the weighted banding procedure reported by Jorjani et al. (JDS 2003).

3. Results and discussion

Heritabilities ranged between **9 to 28 %**.

Total content of **SAT** in fat is **less heritable than MONO**. Selection based on MONO content in fat could be investigated.

However the major saturated FA (**C14:0**, **C16:0** and **C18:0**) showed **higher heritability values** than C18:1.

Table 1. : Average estimate and standard error (SE) of variances (in % of phenotypic variance) for genetic, 2 permanent environments and residual effect with a multi-trait model including milk yield, the contents of fat, protein and fatty acids in milk fat (g/100 g fat).

| Trait | Heritability | | Permanent environments | | | | Residual | |
|---------------------|--------------|-----|------------------------|-----|------------------|-----|----------|-----|
| | Estimate | SE | Within lactation | | Across lactation | | Estimate | SE |
| | | | Estimate | SE | Estimate | SE | | |
| Milk (kg/day) | 18 | 1.7 | 31 | 0.7 | 9 | 1.5 | 42 | 0.2 |
| Fat (%) | 32 | 1.8 | 5 | 0.2 | 5 | 1.2 | 58 | 0.1 |
| Protein (%) | 28 | 2.2 | 12 | 0.4 | 9 | 1.7 | 51 | 0.3 |
| SAT (g/100 g fat) | 14 | 1.5 | 27 | 1.5 | 3 | 0.7 | 55 | 0.4 |
| MONO (g/100 g fat) | 24 | 2.3 | 25 | 1.7 | 8 | 1.6 | 43 | 0.4 |
| C12:0 (g/100 g fat) | 9 | 1.2 | 24 | 1.2 | 5 | 1.0 | 61 | 0.4 |
| C14:0 (g/100 g fat) | 19 | 1.7 | 20 | 1.3 | 7 | 1.6 | 52 | 0.4 |
| C16:0 (g/100 g fat) | 20 | 2.2 | 8 | 0.9 | 12 | 1.8 | 60 | 0.5 |
| C18:0 (g/100 g fat) | 28 | 2.3 | 14 | 1.4 | 9 | 2.0 | 50 | 0.6 |
| C18:1 (g/100 g fat) | 15 | 1.6 | 28 | 1.5 | 4 | 1.0 | 53 | 0.3 |
| C18:2 (g/100 g fat) | 15 | 1.8 | 15 | 1.6 | 6 | 1.4 | 64 | 0.8 |

Table 2. : Genetic (above the diagonal) and phenotypic (below the diagonal) correlations among milk yield, content of fat, content of protein, saturated (SAT), monounsaturated (MONO), C12:0, C14:0, C16:0, C18:0, C18:1 and C18:2 9-cis, 12-cis in milk fat.

| Trait | Milk | Fat | Protein | SAT | MONO | C12:0 | C14:0 | C16:0 | C18:0 | C18:1 | C18:2 |
|---------------------|-------|-------|---------|-------|-------|-------|-------|-------|-------|-------|-------|
| Milk (kg/day) | | -0.35 | -0.48 | -0.09 | 0.22 | -0.34 | -0.02 | 0.01 | -0.15 | 0.11 | -0.01 |
| Fat (%) | -0.18 | | 0.63 | 0.76 | -0.22 | 0.55 | -0.06 | 0.60 | 0.83 | -0.78 | -0.37 |
| Protein (%) | -0.32 | 0.38 | | 0.51 | -0.34 | 0.77 | 0.15 | 0.20 | 0.52 | -0.59 | -0.02 |
| SAT (g/100 g fat) | 0.04 | 0.13 | 0.21 | | -0.44 | 0.67 | 0.37 | 0.55 | 0.66 | -0.90 | -0.66 |
| MONO (g/100 g fat) | -0.06 | 0.03 | -0.18 | -0.73 | | -0.70 | -0.84 | -0.34 | -0.44 | 0.67 | 0.67 |
| C12:0 (g/100 g fat) | 0.00 | -0.03 | 0.37 | 0.75 | -0.84 | | 0.60 | 0.20 | 0.52 | -0.78 | -0.54 |
| C14:0 (g/100 g fat) | 0.09 | -0.19 | 0.11 | 0.65 | -0.90 | 0.84 | | 0.00 | 0.10 | -0.46 | -0.68 |
| C16:0 (g/100 g fat) | -0.03 | 0.10 | 0.05 | 0.44 | -0.23 | 0.16 | 0.12 | | 0.61 | -0.62 | -0.28 |
| C18:0 (g/100 g fat) | 0.00 | 0.65 | 0.23 | 0.30 | -0.24 | 0.11 | 0.01 | 0.29 | | -0.78 | -0.38 |
| C18:1 (g/100 g fat) | -0.03 | -0.13 | -0.27 | -0.93 | 0.83 | -0.85 | -0.73 | -0.47 | -0.33 | | 0.70 |
| C18:2 (g/100 g fat) | -0.10 | -0.23 | 0.21 | -0.50 | 0.53 | -0.34 | -0.50 | -0.23 | -0.32 | 0.53 | |

Genetic correlations FAT and FA were highest with saturated FA except for C14:0.

Genetic correlations between some FA were high. These correlations seemed to reflect the metabolic process of production of FA (*de novo* synthesis, biohydrogenation,...)

4. Conclusion

Genetic variability of FA exists. Thanks to the MIR prediction of FA, **these traits** could be **easily included in the routine Walloon genetic evaluation system.**