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 bended by applying the weighted bending 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 | |
| | | | Within lactation | | Across lactation | | | |
	Estimate	SE	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 witht 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.**

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