Genetic analysis of milk fatty acids composition of Italian Brown Swiss cows

A. Cecchinato[1], F. Tagliapietra[1], S. Schiavon[1], M. Mele[2], J. Casellas[3] and G. Bittante[1]

[1]Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), University of Padova, Viale dell'Università 16, 35020 Legnaro, Padova, Italy
[2]Department of Agricolture, Food and Environment,, Università di Pisa, Via del Borghetto, 80, 56124 Pisa, Italy
[3]Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, 08193 Bellaterra, Spain

Corresponding author: alessio.cecchinato@unipd.it

AIMS

The aims of this study were to infer variance components and heritabilities for 47 milk fatty acids (FA) (including conjugated linoleic acid) and for Δ9 desaturation ratios in the Italian Brown Swiss population and to asses the statistical relevance of the genetic background of FA by using the Bayes factor (BF) procedure

DATA AND STATISTICAL ANALYSIS

- **1,270 cows** were sampled once in 85 herds;
- Milk samples collected during the evening milking concurrently with the monthly test-day milk recording;
- Each sample was analyzed for single FA percentages (computed as FA weight as a proportion of total weight) by gas chromatography;
- A Bayesian univariate animal model was implemented via Gibbs sampling. The model accounted for the effect of days in milk, parity, herd and animal additive genetic effect (the pedigree file included 8,845 animals);
- The statistical relevance of the heritability parameter was evaluated through the Bayes factor (BF) test developed by Garcia-Cortes et al. (2001) and Varona et al. (2001)

Table 1. Bayes factor, genetic standard deviation and heritability estimates for FA categories and for Δ9 desaturation ratios

Trait	BF	σ_a	Heritability Mean	Heritability PSD
SFA	22.71	1.500	0.15	0.05
MUFA	4.39	1.179	0.13	0.06
PUFA	17.19	0.261	0.11	0.03
Short-chain FA	0.04	0.389	0.06	0.03
Medium-chain FA	36.66	1.903	0.15	0.05
Long-chain FA	1.74	1.706	0.13	0.05
Branched-chain FA	1.31	0.116	0.08	0.03
Trans FA C18:1	22.12	0.174	0.11	0.04
C10:1/C10	5.96	0.009	0.23	0.07
C14:1/C14	76.06	0.013	0.44	0.09
C16:1/C16	1.65	0.005	0.26	0.08
C18:1/C18	11.37	0.019	0.22	0.06
RA/VA	0.05	0.016	0.10	0.05

BF: Bayes factor of the model with additive polygenic effects (numerator model) against the same model without additive polygenic effects (denominator model), where greater-than-1 BF favored the numerator model and less-than-1 BF favored the denominator model; **Mean**: mean of the marginal posterior density of the parameter; **PSD**: posterior standard deviation; **RA** = rumenic acid; **VA** = vaccenic acid

RESULTS

- Heritability ranged from moderate, for long chain and unsaturated FA, to high for fatty acids, which origin from de novo mammary synthesis, such as medium chain FA.
- Within the FA categories, the greatest BF was reached by C14:1/C14 ratio (BF 76.06), confirming a strong genetic determinism of mammary SCD enzyme, which is responsible of desaturation of several FA, including C18 and C18:1 t11. Similarly, C18:1/C18 ratio, PUFA, TFA 18:1, SFA, and MCFA showed strong evidence favoring the numerator model (BF>10)
- Within the single FA, C18:3 n-3 and C10 showed substantial evidence favoring the numerator model (3.16<BF<10), whereas C16:1 *c9*, C18, C12, C16 and C14:1 *c9* showed strong evidence of genetic background, as a consequence of their strict relationship with mammary enzyme involved in the synthesis and desaturation of milk FA (BF>10)

CONCLUSIONS

Results highlight the existence of important and exploitable genetic determinism for FA related to mammary neo-synthesis and desaturation, suggesting interesting perspectives for the improving of nutritional properties of milk fat by selective breeding. Long chain and unsaturated FA (including CLA) showed the lowest values of heritabilities as a consequence of the strong influence of environmental factors

Table 2. Bayes factor, genetic standard deviation and heritability estimates for individual FA

Trait	BF	σ_a	Heritability Mean	Heritability PSD
C4	0.02	0.159	0.03	0.02
C6	0.02	0.074	0.04	0.03
C8	0.05	0.080	0.12	0.06
C10	8.49	0.276	0.20	0.07
C10:1 *c9*	0.05	0.029	0.12	0.05
C11	0.10	0.013	0.13	0.06
C12	35.13	0.357	0.24	0.07
C13	0.03	0.011	0.08	0.04
C13 *iso*	0.02	0.006	0.03	0.03
C14	0.04	0.461	0.10	0.06
C14 *iso*	0.06	0.019	0.13	0.04
C14:1 *c9*	70.66	0.175	0.36	0.09
C15	0.05	0.075	0.10	0.04
C15 *iso*	0.04	0.024	0.09	0.03
C15 *ante*	0.05	0.039	0.12	0.04
C16	51.19	1.828	0.26	0.06
C16 *iso*	0.04	0.025	0.08	0.03
C16:1 *c9*	32.99	0.155	0.24	0.08
C16:1 *t9*	0.02	0.005	0.03	0.02
C17	0.06	0.035	0.09	0.04
C17 *iso*	0.03	0.018	0.05	0.03
C17 *ante*	0.06	0.028	0.10	0.04
C17:1 *c9*	0.04	0.019	0.07	0.04
C18	33.38	0.830	0.22	0.07
C18:1 *t4*	0.02	0.003	0.02	0.02
C18:1 *t6-8*	0.04	0.018	0.06	0.04
C18:1 *t9*	0.04	0.017	0.08	0.04
C18:1 *t10*	0.03	0.024	0.06	0.03
C18:1 *t11*	0.06	0.104	0.07	0.03
C18:1 *c9*	0.06	0.896	0.09	0.05
C18:1 *c12*	0.05	0.028	0.08	0.03
C18:1 *t16*	0.03	0.020	0.06	0.03
C18:2 *t9,t12*	0.02	0.074	0.03	0.02
C18:2 *t11, c15*	0.02	0.015	0.03	0.02
C18:2 n-6	0.05	0.148	0.06	0.02
C18:2 *c9, t11*	**0.06**	**0.057**	**0.07**	**0.03**
C18:3 n-3	4.75	0.054	0.09	0.03
C18:3 *c9, t11, c15*	0.02	0.005	0.03	0.02
C20	0.08	0.014	0.10	0.05
C20:1 *c8*	0.03	0.009	0.06	0.04
C22	0.02	0.006	0.03	0.02
C20:3 n-6	0.24	0.018	0.11	0.05
C20:4 n-6	0.09	0.016	0.08	0.04
C20:5 n-3	0.03	0.005	0.05	0.03
C24	0.03	0.004	0.03	0.03
C22:4 n-6	0.03	0.005	0.05	0.03
C22:5 n-3	0.03	0.006	0.04	0.03