

Genetic Evaluation for Milk Fat Composition in the Walloon Region of Belgium

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Abstract

A genetic evaluation system for milk fat composition is currently under development in the Walloon Region of Belgium. Based on data for test-day saturated and monounsaturated fatty acid content in milk together with correlated traits as milk, fat and protein yields, EBV could be estimated dUNSAT and dMONO, two indices that represent the desaturation of milk fat compared to the expected level. A total of 1904 sires for dUNSAT and 1583 sires for dMONO had EBV with reliabilities of 0.50 and more. The range of these breeding values was 4.96 and 4.28 genetic standard-deviations which indicate the potential for selection.

Introduction

Currently there is no cattle selection program in the Walloon Region of Belgium or elsewhere in the world that is considering milk fat composition. However the interest of dairy industry for differentiated products is increasing and selective collection of milk has started at several places to provide milk for specific products. Recent advances were made in determination of content of fatty acids using Mid-Infrared Spectrometry (**MIR**) (e.g., Soyeurt *et al.*, 2010). Obtaining data can be considered as the first steps towards a selection program for milk fat composition. The objective of this report was to describe the current status toward the development of genetic evaluation system for milk fat composition in the Walloon Region of Belgium and to update on the plans for further developments.

Material and Methods

Fatty acids and milk recoding data

After an experimental phase from March 2005 to March 2006 on 25 farms, the recording of spectral data recording increased gradually. In April 2010, spectral data from regular milk recording was available for nearly all cows and test-day records in the Walloon Region of Belgium. This represents a total of 864,835

spectral records. Moreover, a total of 15,403,130 standard test-day records for milk, fat and protein recorded since 1975 were also available. For genetic evaluation, fat content (**PFAT**) and (**PPROT**) was excluded because of the fact that they are not INTERBULL traits, variation in fat and protein being already described by milk, fat (**FAT**) and protein yields (**PROT**). Milk fat composition was represented by saturated (**SAT**) and monounsaturated (**MONO**) fat content in milk. These fatty acids were predicted from the spectral data using the newest equations available developed by Soyeurt *et al.* (2010).

Model and variance component estimation

The development of an adapted model useful for genetic evaluation is still underway. The model currently used is a single lactation multi-trait test-day random regression model (SL-MT-TD-RRM) similar to the standard model used for genetic evaluation of production traits in the Walloon Region of Belgium. Co)variance components were obtained using results from previous studies (e.g., Soyeurt *et al.*, 2008) and from those currently used in the Walloon genetic evaluation and were validated by running Gibbs Sampling on four sub-sets of the data representing each time 1/4 of the available data. Used (co)variance components were averages of these computations.

Computations and expression of results

Computations were done using the standard genetic evaluation software used in the Walloon Region of Belgium which allows elimination of outliers. Records that showed more than 5 residual SD during computations were put to missing and between 3 and 5 residual SD values were scaled back to 3. This approach was considered more robust than the simple use of pre-computational filters. EBV were expressed to a base of cows born in 2000 with records. Reliabilities (**REL**) were computed using the Effective Daughter Contribution (**EDC**) method used for routine INTERBULL computations.

Expression of results as traits of interest should follow the definition of breeding goals. For milk fat composition there is not yet a global consensus about the traits that could have a place in breeding goals. However, it is clear that these traits should express milk pricing (i.e., SAT) and potential human health issues (i.e., MONO) and that they should have no deleterious effects on other important traits. As milk fat composition is expected to be correlated with MILK, FAT and PROT, it is logical to express milk fat composition as a relative deviation from expected compositions at certain level of MILK, FAT and PROT. For this reason milk fat composition was reported in this study as **dUNSAT** and **dMONO** defined as the relative deviations. For **dUNSAT** the scale was inversed, higher values expressing less saturation (more unsaturation). Expected values for SAT and MONO for given levels of MILK, FAT and PROT could have been defined in different ways. In this study multiple regression of EBV for SAT or MONO on EBV of MILK, FAT or PROT were used. Regression coefficients were theoretical coefficients obtained from the genetic covariance matrix. Alternative coefficients obtained from sire proofs were similar, especially for **dUNSAT**. Values of **dUNSAT** and **dMONO** were standardized using theoretical genetic standard deviations. REL for **dUNSAT** and **dMONO** were based on REL from contributing traits using standard formulas.

When defining new traits, it is important to assess the effect of selection for these new traits on other, already selected traits. Correlations for sires with MACE proofs between EBV for traditional traits, partial and global indexes, and EBV for new traits were computed.

Results and Discussions

Table 1 gives descriptive statistics about the available traits. A total of 6.7 millions test-day records were used from 795,718 cows. Out of these cows, 68,425 had also at least one test-day records for a detailed milk fat composition trait (SAT or MONO).

Table 1. Test-day data available for genetic evaluation of milk fat composition.

Trait*	N	Mean	SD
	6,749,2		
MILK (kg)	39	16.96	6.83
	6,746,9		
FAT (kg)	93	0.68	0.29
	6,727,5		
PROT (kg)	24	0.56	0.22
	6,746,9		
PFAT(%)	93	4.02	0.72
	6,727,5		
PPROT(%)	24	3.33	0.40
	220,39		
SAT(%)	7	2.79	0.49
	220,39		
MONO(%)	6	1.15	0.24

* FAT = fat yield, PROT = protein yield, PFAT = fat content, PPROT = protein content SAT = saturated fatty acid content in milk and MONO = monounsaturated fatty acid content in milk

Results in Table 1 show that phenotypic variation of these traits was considerable, with the new trait SAT being even more variable than PPROT.'

Table 2 gives details on the genetic correlations used expressed on a lactation basis. As SAT and MONO are both representing fractions of milk fat, the observed correlations corresponded to expectations. Differences between SAT and MONO content showed up in their correlations with MILK and FAT.

Table 2. Genetic correlations among yields and major milk components.

Trait	Trait			
	FAT	PROT	SAT	MONO
MILK	0.57	0.83	-0.42	-0.31
FAT		0.70	0.50	0.38
PROT			-0.11	-0.11
SAT				0.80

Corresponding heritabilities on a lactation basis were 0.31, 0.33, 0.26, 0.61 and 0.51 for MILK, FAT, PROT, SAT and MONO, respectively.

Table 3. Mean and SD of EBV and REL for sires with a minimum REL of 0.50 for different traits.

Trait	N	EBV		REL	
		Mean	SD	Mean	SD
Milk (kg)	1844	450	424	0.78	0.14
FAT (kg)	1929	16.1	16.6	0.80	0.13
PROT (kg)	1780	18.9	11.9	0.77	0.14
SAT(%)	1949	0.005	0.207	0.82	0.12
MONO (%)	1583	0.008	0.053	0.75	0.14
dUNSAT	1904	-1.02	0.69	0.80	0.13
dMONO	1583	0.34	0.62	0.80	0.11

A total of 1949 sires for SAT and 1583 sires for MONO, which had also official EBV in the Walloon Region of Belgium, reached REL of 0.50 and above for these traits. Table 3 gives additional details. It has to be noticed that SAT and MONO were expressed in content, dUNSAT and dMONO were expressed in genetic SD. The genetic correlation between dUNSAT and dMONO was 0.93. Heritabilities of dUNSAT and dMONO were 0.21 and 0.42, respectively. This difference can be explained by the fact that these are heritabilities of residual variations and the residual variation is larger for dMONO than it is for dUNSAT which has higher correlations to MILK, FAT and PROTEIN. Still the range (maximum – minimum values) of the relative EBV for dUNSAT and dMONO were 4.96 and 4.28. EBVs for all traits were put to a common base that were cows born in 2000. However, the sires with a reliability of 0.50 and more were clearly a selected group. This is also reflected in the means for dUNSAT and dMONO, the values for SAT and MONO being much closer to zero. The means for dUNSAT (negative)

and dMONO (positive) might reflect some correlated response to ongoing selection increasing expected saturation (lower dUNSAT values are considered unfavorable), however at the same time increasing dMONO which is favorable. A way to check this hypothesis is by analyzing correlations of EBV for dUNSAT and dMONO with economic indexes currently used for sire selection. Correlations for EBV for SAT, MONO, dUNSAT and dMONO with official EBV for individual traits and indexes are shown in Table 4. Results showed that correlations with *a priori* unrelated traits remained rather low. Quiet remarkable were that dUNSAT and dMONO had positive correlations to the global index V€G. Unfavorable are the negative correlations of dUNSAT with longevity (LONG) and of dMONO with female fertility (FFERT). Both results are obviously preliminary and have to be investigated further. Still all correlations remained low and these results did not corroborate the hypothesis that we see in Table 3 of a correlated response to selection.

Conclusions and Perspectives

The first results indicate that the development of a genetic evaluation system for milk fat composition in the Walloon Region of Belgium is well underway. The chosen traits showed high heritabilities and genetic variability exists. With the present, still limited data, 1904 sires had EBV with REL of 0.50 and more for dUNSAT, a composite trait that represents the desaturation of milk fat compared to the expected level.

Next steps in the development will be:

- Adding more data: currently 500,000 records a year are currently added;
- Going to a multi-lactation model: better use of already existing data from later lactations;
- Adding new traits: additional fatty acids will be added;
- Integration of external information: different possibilities will be explored to integrate MACE EBV for MILK, FAT and PROT;
- Genomic selection: specific situation of this evaluation makes it very well suited to use a one step approach (Aguilar *et al.*, 2010).

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Table 4. Correlations of EBV for milk composition traits with official individual traits and Indexes used in the Walloon Region of Belgium

	Individual Trait*								Index			
	MILK	FAT	PROT	PFAT	PPROT	SCS	LONG	FFERT	V $\u20ac$ L	V $\u20ac$ T	V $\u20ac$ F	V $\u20ac$ G
SAT	-0.56	0.34	-0.31	0.95	0.60	-0.04	-0.12	0.19	0.00	-0.15	-0.10	-0.08
MONO	-0.48	0.33	-0.20	0.86	0.64	-0.03	-0.08	0.14	0.08	-0.10	-0.08	0.01
dUNSAT	-0.01	-0.04	0.05	-0.02	0.12	0.06	-0.11	0.03	0.04	0.01	-0.10	0.09
dMONO	0.26	0.07	0.26	-0.21	-0.07	0.05	0.07	-0.18	0.19	0.07	0.06	0.16

* Individual traits represent official EBVs computed during routine genetic evaluations or provided by INTERBULL. For more details please refer to <http://www.elinfo.be>. FFERT = female fertility, SCS = somatic cell score, LONG = longevity, V $\u20ac$ L = subindex 'milk', V $\u20ac$ T = subindex 'type', V $\u20ac$ F = subindex 'functionality', V $\u20ac$ G = global index.