

Implementing a National Routine Genetic Evaluation for Milk Fat Compositions as First Step Towards Genomic Predictions

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Abstract

Currently the Walloon Region of Belgium is one of the first regions in the World where mid-infrared (MIR) spectral data is recorded in routine for nearly all cows under milk recording. Based on this data, in some herds collected since 2007, saturated (SFA) and monounsaturated fatty acid (MUFA) contents in milk are predicted for each test-day. Together with correlated traits as milk, fat and protein yields, estimated breeding values (EBV) are now computed in routine for SFA and MUFA starting in June 2012. A total of 499 821, 392 255, 277 465 fatty acid records were available in first, second and third lactation for this run. A restricted selection index, called NQI (nutritional quality index) was developed that puts a negative weight on SFA, a positive weight on MUFA and restricts changes in milk and fat yields to zero. By using this index for a constant fat content, milk fat will be selected to be less saturated with a high contribution from MUFA. Based on this system a single-step genomic evaluation is under development including the introduction of MACE breeding values for correlated traits. The final step is to offer for owners of genotyped animals, a service to provide them with genomically enhanced NQI. Similar systems are under development in Wallonia for other novel traits (e.g., methane emissions) based on the ability to predict them from MIR spectral data.

Key words: milk fat composition, genetic evaluation, genomic predictions

Introduction

Currently 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. Genetic variability of milk fatty acid composition is now well established (e.g., Bastin *et al.*, 2011). Based on recent advances made in determination of content of fatty acids (FA) using Mid-Infrared Spectrometry (MIR) (e.g., Soyeurt *et al.*, 2011), and under the condition that this type of data is available, a genetic evaluation for milk fat compositions has become feasible. By extension such a system is then also a first steps towards a genomic evaluation system.

The objective of this report was to describe the current status toward the development and the implementation of a genetic and also

genomic evaluation system for milk fat compositions in the Walloon Region of Belgium and to show some perspectives, also for other novel traits, that can be predicted from MIR data.

Materials and Methods

Fatty acids and milk recording data

Spectral data from regular milk recording is currently available for nearly all cows and test-day records in the Walloon Region of Belgium, recorded in some herds since 2007. For this study spectral records up to December 2011 were used (1 801 597 records). Moreover, a total of 25 256 171 standard test-day records for milk, fat and protein recorded since 1975 were also available. Only records from first, second and third lactations were

used that passed some basic validations (e.g., ICAR limits). For genetic evaluations, fat and protein content (PFAT, PPROT) were 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 is currently represented by saturated (SFA) and monounsaturated (MUFA) fat content in milk, two traits that can be predicted from MIR data with a very high accuracy. The newest equations available developed by Soyeurt *et al.* (2011) were used.

Model and variance component estimation

The model used was the multi-lactation multi-trait test-day random regression (ML-MT-TD-RRM) standard model used for genetic evaluation of production traits in the Walloon Region of Belgium but extended to five traits. (Co)variance components were obtained using results from previous studies (e.g., Bastin *et al.*, 2011) and the components those currently used in the Walloon genetic evaluation. (Co)variances had to be banded using the procedure proposed by Jorjani *et al.* (2003) keeping the (co)variances also used in the routine production trait evaluation constant.

Computations

Computations were done using the standard genetic evaluation software used in the Walloon Region of Belgium which allows elimination of outliers (Mayeres *et al.*, 2003). 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 only filters. EBVs were expressed as deviations from the average of a base population of cows born in 2005 with FA records. Reliabilities (REL) were computed using the Effective Daughter Contribution

(EDC) method used for our routine INTERBULL computations. As from the beginning the objective was to develop a genomic evaluation using external information for correlated traits using the same data and model as for the routine evaluation simplified the next steps to implement this.

Expression of results

Expression of results as traits of interest should follow the definition of breeding goals. Currently for milk fat composition there is no global consensus about the traits that could have a place in breeding goals. However, it is clear that these traits should express current trends in milk pricing (i.e., premium for lower SFA) linked to nutritional quality and potential human health issues (i.e., higher MUFA). Also they should have no deleterious effects on other important traits, especially milk yield and fat content. In our previous studies EBVs for milk fat composition were reported as deviations from expected values. This method has two major disadvantages. First it creates two residual traits similar to residual feed intake with all the related issues (i.e., interpretation). Second it is based on two traits, which complicates the interpretation and potential selection decisions. Therefore, it was decided that in this study a restricted selection index, called NQI (nutritional quality index) was developed that will be used in routine implementation. This index puts a negative weight on SFA, a positive weight on MUFA, both relative ‘economic’ weights (“a” values) being put for the moment to be equal in absolute value. Index weights (“b” values) were computed restricting changes in milk and fat yields to zero. By using this index expected genetic progress would be, for a constant fat content, that milk fat will be selected to be less saturated (less SFA) with a high contribution from MUFA. Using equal weightings was a preliminary choice and can be updated easily if additional information about the value of SFA

and MUFA become available. Final index weights were defined in order that the resulting index values were expressed in genetic standard-deviations. Reliabilities for NQI were defined and computed as proposed by Cole and VanRaden (2010).

Results & Discussion

Table 1 gives descriptive statistics about the available and used data (after some edits for each trait). A total of around 16 million test-day records were used from 908 894 cows. Out of these cows, 134 886 had also at least one test-day records for a detailed milk fat composition trait (SFA or MUFA).

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

Trait*	N	Mean	SD
First lactation			
MILK (kg)	7 019 473	17.2	6.92
FAT (kg)	7 017 143	0.69	0.29
PROT (kg)	6 997 697	0.57	0.22
PFAT(%)	7 017 143	4.02	0.71
PPROT(%)	6 997 697	3.33	0.39
SFA(%)	499 488	2.78	0.54
MUFA(%)	499 808	1.16	0.27
Second lactation			
MILK (kg)	5 253 380	19.5	8.66
FAT (kg)	5 251 831	0.78	0.36
PROT (kg)	5 244 437	0.65	0.27
PFAT(%)	5 251 831	4.04	0.75
PPROT(%)	5 244 437	3.41	0.42
SFA(%)	391 952	2.91	0.58
MUFA(%)	392 252	1.14	0.26
Third lactation			
MILK (kg)	3 756 721	20.8	9.24
FAT (kg)	3 755 555	0.83	0.39
PROT (kg)	3 750 253	0.69	0.29
PFAT(%)	3 755 555	4.04	0.76
PPROT(%)	3 750 253	3.39	0.43
SFA(%)	277 252	2.9	0.59
MUFA(%)	277 460	1.14	0.28

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

Results in Table 1 show that phenotypic variation of FA traits was large, indicating that there was significant variation in these traits.

Standardized weights (“b” values) obtained from the restricted selection index computations and used to compute NQI were 0.479, -0.425, -0.934 and 0.934 for MILK, FAT, SFA and MUFA.

Table 2. Genetic correlations among yields, major milk fat components and the NQI

Trait	Trait*				
	FAT	PROT	SFA	MUFA	NQI
MILK	0.91	0.97	-0.28	-0.38	0.00
FAT		0.93	0.00	-0.01	0.00
PROT			-0.22	-0.23	0.05
SFA				0.40	-0.69
MUFA					0.38

* FAT = fat yield, PROT = protein yield, SFA = saturated fatty acid content in milk, MUFA = monounsaturated fatty acid content in milk, NQI = nutritional quality index.

As used genetic parameters were obtained through bending the genetic correlations reported in Table 2 and expressed on a lactation basis where slightly different to those reported earlier, however the relative relationships between MILK, FAT, PROT and the new traits were conserved. Table 2 gives also details on the correlation between NQI and the original traits. Here the strong negative association between this index and SFA and moderate correlation with MUFA must be stressed.

Corresponding heritabilities on a lactation basis were 0.37, 0.43, 0.41, 0.71, 0.64 and 0.56 for MILK, FAT, PROT, SFA, MUFA and NQI respectively. As expected the results for MILK, FAT and PROT were those used for the routine evaluations, the results for SFA and MUFA were similar to those expected for FA contents in milk. The high heritability for NQI suggests that selecting for this index should result in a favorable response of the index, decreasing SFA and increasing MUFA (Table 2) without affecting MILK and FAT.

By restricting the reported sires to those that have at least REL of 0.50 for both FA traits and having at least 1 daughter in 1 herd with FA records, a total of 1196 bulls remained. Other bulls achieved also very large REL but only through correlated traits. More details on EBV and associated REL are in Table 3. Distribution of estimated NQI values were close to normal (Figure 1).

Table 3. Mean and SD of EBV for MFA; MUFA and index values for NQI with their associated REL for sires with a minimum REL of at least 0.50 for FA traits and at least 1 daughters in 1 herds with FA records.

Trait	EBV		REL	
	Mean	SD	Mean	SD
MFA(%)	-0.022	0.252	0.77	0.13
MUFA (%)	-0.008	0.066	0.71	0.14
NQI (std)	0.001	0.571	0.75	0.13

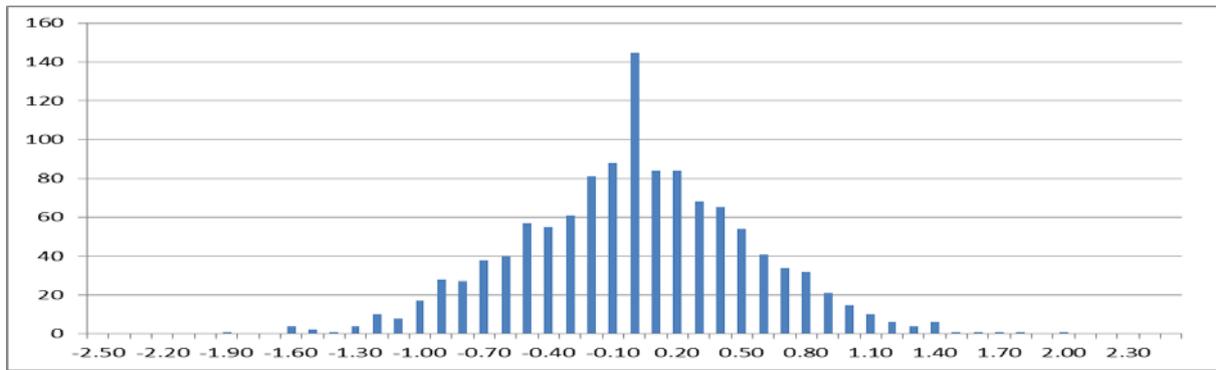


Figure 1. Distribution of 1196 sires among classes of NQI index values.

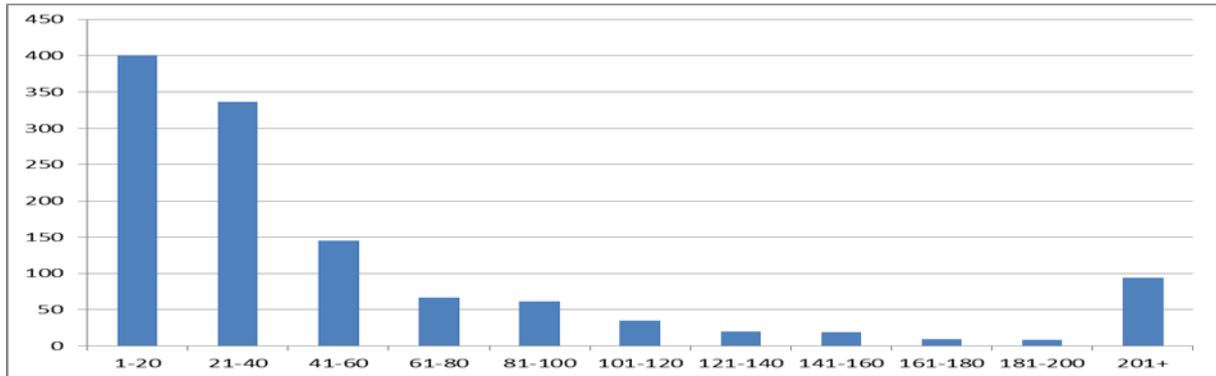


Figure 2. Distribution of 1196 sires among classes of number of daughters with FA records.

Figure 2 reports the distribution of the 1196 sires among classes of number of daughters with FA records. Many sires have rather small number of daughters, this was expected, but approximately 2/3 had over 20 daughters with 94 sires having more than 200 daughters. Among the sires with many daughters are several well-known sires of sons.

Conclusions and Perspectives

Given the current rate of MIR spectral data acquisition over 500 000 records are added

every year. Also if international sires are well used in our region they will get very reliable proofs for SFA, MUFA and NQI. This might be an opportunity for foreign AI centers by getting their bulls used in the Walloon Region. Research is ongoing to improve the models, the (co)variance components but also the available data. Recent research is focusing on adapted methods to integrate MACE EBV for MILK, FAT and PROT (e.g., Vandenplas and Gengler, 2012). Based on all this a single-step (Aguilar *et al.*, 2010) genomic evaluation system is under active development. This method is well suited for the ML-MT-TD-

RRM, also because in a single step all animal contribute (e.g., MACE EBV from non-genotyped ancestor). Given specific arrangements (e.g., providing genotypes) this could be the bases of a service to compute genomically enhanced NQI for owners of foreign animals.

One of the interesting features of MIR spectral data is that it can be used to predict other novel traits. Therefore similar systems are under development in Wallonia. E.g., first results show the feasibility to predict methane emissions from MIR (Dehareng *et al.*, 2012) and that there is genetic variation.

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