Use of Interbull Traits as Indicators for Only Locally Evaluated Traits as Milk Quality Traits

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Introduction

Combination, or better integration, of a priori know breeding values for indicator traits is an important topic especially for small genetic evaluation systems, additional or novel traits with very little depth of data. Interest in the topic of combining breeding values from separate sources has been shown by a certain number of papers (e.g., Weigel *et al.*, 1998, VanRaden, 2001). Generally the idea was in this context to combine breeding values. Similarly other methods were based on approximate multi-trait models using preadjusted data (e.g., Tarres *et al.*, 2005) where the basic idea was to combine adjusted data. However there seems to be no direct and formalized method to integrate breeding values of indicator traits directly into genetic evaluations of other related and economically important traits.

Currently existing methodologies to integrate information are not the best option in the context of milk quality traits. There are several reasons for this fact. First regular multi-trait methods are locally optimal and appropriate, however as most selection is done outside of our region these methods will not rank foreign young bulls, nor integrate information from proven sires for indicator traits. Methods proposed to integrate breeding values a posteriori of evaluations (Van Raden, 2001) can adapted as used in our system for genetic evaluations of type traits by first predicting missing type traits and then combining information. However all these strategies are by definition approximations and a direct integration would be better. The objective of this paper was to present such a strategy allowing indicator trait breeding values (e.g., provided from INTERBULL evaluations) to be used to improve evaluations of other traits that are only locally evaluated. The methodology presented will then be used in the context of milk quality traits, however it will probably also used in the context of type traits.

Materials and Methods

Milk Quality Traits

Currently there is no cattle selection program in Walloon Region of Belgium that is considering the fatty acid profile of milk fat. However the interest of dairy industry for differentiated products is increasing and selective collection of milk has started. These farms are on a special feeding scheme, however adapted official performance recording is missing.

Recent advances were made in determination of fatty acids contents using Mid-Infrared Spectrometry (Soyeurt *et al.*, 2006). Based on already collected data and added historical, production only, data for the cows on the farms records were extracted. Heritabilities and genetic correlations were estimated using the available data for saturated and monounsaturated fat, major fatty acids in milk (C12:0, C14:0, C16:0, C16:1 9-cis, C18:0, C18:1 and C18:2 9-cis,12-cis) and the ratio of fatty acids which reflected the importance of the delta-9 desaturase activity (C14:1 9-cis/C14:0; C16:1 9-cis/C16:0 and C18:1/C18:0) using a multi-trait mixed-model and EM-REML. The results reported here were extracted from Soyeurt (2006). The model used was a repeatability model with fixed herd-test-day-class of lactation number (1,2 or 3+), fixed class of stage of lactation (15 days)-class of lactation number (1,2 or 3+) and fixed age class-class of lactation (1,2 or 3+) effects and random across and among lactation permanent environmental effects and an additive genetic effect.

Integration of Indicator Traits

Milk quality traits are potentially highly related. Therefore a natural choice is to use a multi-trait model. Also the number of quality and indicator traits that should potentially be evaluated together is very high. Therefore a natural choice was to use a multi-trait canonical transformation extended to multiple diagonalization model (MT-CT-MD) allowing missing values. Such evaluation programs exist nowadays, as MTJAAM (Gengler, 1998) and can be adapted. The requirement was therefore to develop a method that integrates into this type of modelling. It should allow integrating solutions for indicator traits and adjusting reliabilities for their contribution. Development of the software is under way, we will give in the present study only the basic algorithms and the theoretically achievable reliabilities from indicator traits.

Results and Discussion

Strategy for the Integration of Indicator Traits

Let $\mathbf{s}$ be a vector of breeding values of all traits for a given animal and $\mathbf{s}_t$ a vector of transformed breeding values where $\mathbf{T}$ is the transformation matrix. The relationship between both vectors of breeding values can be given as $\mathbf{s}_t = \mathbf{T}\mathbf{s}$ and $\mathbf{s} = \mathbf{W}\mathbf{s}_t$ where $\mathbf{W} = \mathbf{T}^{-1}$. The vector of transformed solutions can also be written and decomposed in an alternative way:

$$\mathbf{s}_t = \mathbf{T}\mathbf{s} = \mathbf{T}_v\mathbf{s}_v + \mathbf{T}_f\mathbf{s}_f \qquad [1]$$

where f designates indicator traits for which breeding values on the original scales are considered known and fixed and v designates local traits for which breeding values are estimated and considered unknown and variable. To simplify representation traits will be considered ordered.

In a similar fashion one can rewrite $\mathbf{s} = \mathbf{W}\mathbf{s}_t$ as:

$$\mathbf{s} = \begin{bmatrix} \mathbf{s}_v \\ \mathbf{s}_f \end{bmatrix} = \mathbf{W}\mathbf{s}_t = \begin{bmatrix} \mathbf{W}_v \\ \mathbf{W}_f \end{bmatrix}\mathbf{s}_t \qquad [2]$$

By substituting by $\mathbf{W}_f\mathbf{s}_t$ we can also write that $\mathbf{T}_f\mathbf{s}_f = \mathbf{T}_f\mathbf{W}_f\mathbf{s}_t$. Using this equivalence we can subtract from current estimates of $\mathbf{s}_t$ (transformed scale) the contributions from fixed traits estimated from current solutions and add the contribution to canonical traits from a priori considered known breeding values for these fixed traits.

$$\hat{\mathbf{s}}_t = \hat{\mathbf{s}}_t - \mathbf{T}_f\mathbf{W}_f\hat{\mathbf{s}}_t + \mathbf{T}_f\mathbf{s}_f \qquad [3]$$

Based on [3] the following equations to update estimates at round n based on a priori considered known breeding values and previous (round n-1) estimates, can be developed:

$$\hat{\mathbf{s}}_t^n = \left[\mathbf{I} - \mathbf{T}_f\mathbf{W}_f\right]\hat{\mathbf{s}}_t^{n-1} + \mathbf{T}_f\mathbf{s}_f \qquad [4]$$

Reliabilities of breeding values can also be adjusted using the updating equations given in [4]. The strategy used in our implementation was the one presented by Gengler and Misztal (1995) where Prediction Error Variance (**PEV**) were computed on a transformed scale and final reliabilities obtained by backtransformation of PEV. Equations [4] can be adapted to reflect relationships between diagonal elements of PEVs as shown in equations [5].

$$\begin{aligned} \mathrm{diag}\left(\mathrm{PEV}\left(\hat{\mathbf{s}}_t^{\,*}\right)\right) = & \\ \left[\mathbf{I} - \mathbf{T}_f\mathbf{W}_f\right]\mathrm{diag}\left(\mathrm{PEV}(\hat{\mathbf{s}}_t)\right)\left[\mathbf{I} - \mathbf{T}_f\mathbf{W}_f\right]' + & \\ \mathbf{T}_f\mathrm{diag}\left(\mathrm{PEV}(\mathbf{s}_f)\right)\mathbf{T}_f' & \end{aligned} \qquad [5]$$

where $\mathrm{PEV}\left(\hat{\mathbf{s}}_t^{\,*}\right)$ are the PEV for adjusted transformed solutions and $\mathrm{PEV}(\hat{\mathbf{s}}_t)$ are the PEV of transformed solutions from local data. Equations [5] are in line with the original estimation methods used to obtain PEV for transformed traits (Misztal and Wiggans, 1988; Gengler and Misztal, 1996). However in order to adjust for parent contributions the adjustment of PEVs has to be done iterating for those.

Solutions and reliabilities for original traits are obtained by backtransformation. One can show that backtransformation of [4] guaranties obtaining of fixed solutions.

In order to demonstrate the improvement of reliabilities, maximum theoretical achievable reliabilities from correlated indicator traits only were obtained using formula [5] and standard selection index theory. PEV were computed locally on a transformed scale and adjusted, then backtransformed to the original scales using an optimal and perfect diagonalization of genetic and phenotypic (co)variances.

Genetic Parameters for Milk Quality Traits and Search of Indicator Traits

Table 1 contains first heritability estimates for certain milk quality traits. The values obtained are very encouraging showing that several traits had a very acceptable heritability. Most differences seem to be linked to the metabolically pathways distinguishing fatty acids that are more feed related (lower heritabilities) from those that are less related to feeding.

Table 1. Heritabilities of milk, fatty acids and fatty acid ratios.

Trait	Heritability
Milk	0.21
Fat (%)	0.31
Protein (%)	0.28
Saturated fat (%)	0.35
Mono unsaturated fat (%)	0.16
C12:0 (%)	0.30
C14:0 (%)	0.32
C16:0 (%)	0.36
C16:1 9-cis (%)	0.25
C18:0 (%)	0.30
C18:1 9-cis (%)	0.12
C18:2 9-cis, 12-cis (%)	0.22
C14:1/C14:0	0.14
C16:1/C16:0	0.11
C18:1/C18:0	0.17

Potential indicator traits for milk quality traits are milk, fat and protein. Some preliminary computations showed the interest to used content instead of yield for fat and protein. Table 2 gives correlations among milk, fat, protein, saturated and monounsaturated fat content. Genetic correlations among milk, fat and protein content

show the expected behaviour. Interesting was that the correlations among fat, saturated and monounsaturated fat were not all high and quiet different showing some potential for differentiated selection. For example with a correlation of 0.62 one can imagine improving monounsaturated fatty acids independently from saturated ones. At the same time monounsaturated fatty acids are less related to overall fat than saturated.

Table 2. Genetic correlations among milk and major milk components

	Component (%)			
Trait	Fat	Protein	Sat.	Mono.
Milk	-0.23	-0.40	-0.19	-0.11
Fat (%)		0.57	0.97	0.74
Protein (%)			0.54	0.31
Saturated (%)				0.62

Complexity of fatty acid profiles makes it very difficult to consider them all easily. Literature cited by Soyeurt (2006) has shown interest in product/substrat ratios as indications for activity of delta-9 desaturase an important enzyme in the synthesis of unsaturated fatty acids.

Table 3. Genetic correlations among milk and ratios as indicators of delta-9 desaturase activity.

	Delta-9 desaturase indicator ratios		
Trait	C14:1/C14:0	C16:1/C16:0	C18:1/C18:0
Milk	0.01	0.16	0.02
Fat (%)	-0.47	-0.58	-0.79
Protein (%)	-0.08	-0.40	-0.40
C14:1/C14:0		0.84	0.72
C16:1/C16:0			0.77

Table 3 gives genetic correlation on delta-9 desaturase activity related fatty acid ratios and milk yield, fat and protein content. Even if the three ratios are different traits they are highly related and show more negative correlations to fat than to protein content. These large differences are in line with results for monounsaturated fatty acids, a product of delta-9 desaturase activity. For the rest of this study we will solely focus of these three traits.

Table 4. Data available for genetic evaluation of milk quality traits.

	Yield	Milk quality
Time frame	1975-2006	2005-2006
Animals with TD records	~ 800,000	1,524
TD records	~ 19,500,000	4,574
INTERBULL sires with EBV	~ 80,000	N/A
INTERBULL sires with daughters in the evaluations	~ 4,800	N/A

Available Data

Table 4 summarizes currently available data. Experimental data has been collected from March 2005 to March 2006 except for July and August from 25 farms for 1,524 cows and 4,574 test-day records. There is potential to extend this data collection scheme automating data acquisition in an experimental phase to around 50,000 cows and annually 500,000 test-day records. However even in this case the available data will be dwarfed compared to the more than 19,500,000 test-day records and the more than 31 years of time frame. This has implication on modelling.

Experimental Genetic Evaluation System

Even if a local interest exists in milk quality traits any genetic evaluation for such traits will be low cost, capitalizing on existing data collection and evaluation schemes and focusing also on management. Milk quality data will be added to currently existing milk records and pedigree information. In this context the use of a multi-trait-canonical transformation animal model (MT-CT-AM) similar to the one used for type traits in the Walloon Region is an optimal compromise between quality of evaluation and cost-efficiency. The genetic evaluation strategy could be summarized like this:

1. Regular local routine-run for production traits using a random-regression multi-trait multi-lactation test-day model.

2. INTERBULL routine-run.
3. Integration of INTERBULL results regular local routine-run using classical methods.
4. Milk quality evaluation run with a multi-trait-canonical transformation animal model without integration of INTERBULL EBV
5. Restart of run 4, integrating breeding values from run 2 using the strategy described in this study.

The adapted MTJAAM (Gengler, 1998) program used has also the feature that reliabilities are estimated directly in the programs. EBV and Producting Abilities (EBV + Permanent environment) will be reported to allow producers to manage individually milk quality traits for cows (adjusting feeding etc.) and to eventually select cows and sires on milk quality

Improvement of Reliabilities

Table 5 shows the theoretically maximum reliability that can be achieved from only correlated indicator traits under the hypothesis that no additional direct information was available and a perfect diagonalization of the genetic and phenotypic (co)variance matrices was used.

Table 5. Evolution of maximum expected reliability for certain milk quality traits from sole correlated trait information for a given indicator trait reliability (same reliability for all indicator traits).

Indicator	C14:1/C14:0	C16:1/C16:0	C18:1/C18:0
0.1	0.087	0.091	0.097
0.2	0.175	0.183	0.194
0.3	0.262	0.274	0.292
0.4	0.349	0.365	0.389
0.5	0.437	0.456	0.486
0.6	0.524	0.548	0.583
0.7	0.612	0.639	0.681
0.8	0.699	0.730	0.778
0.9	0.786	0.822	0.875

In practice these high values will not be obtained. However the assumption that no direct information is available is also not necessarily true as locally observed milk quality traits records can contribute through parents.

Conclusion

This paper shows the potential for selection in milk quality traits especially ratios expressing delta-9 desaturase activity. The heritabilties and genetic correlations shown are preliminary, however they are so promising that research for the development of an experimental genetic evaluation system is underway. This study showed the theoretical development needed to integrate INTERBULL traits as indicators for only locally evaluated traits as milk quality traits. The software developed is likely to be used also in the regular genetic evaluation system in order to replace the current methods.

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