

Genetic Parameters of Butter Hardness Estimated by Test-Day Model

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Introduction

Currently many studies focused on the effects of fatty acids on human health. However, the fatty acids composition plays also a role in the hardness of butterfat. Historically the aim of the first researches on fatty acids studied this technological property. Coulter and Hill (1934) studied the variation of fatty acid contents among dairy breeds based on the estimation of the iodine value. These authors observed that the butterfat produced by Channel Island cows was firmer than the one produced by Holstein or Ayrshire cows. Recently, Bobe *et al.* (2003) showed that butter produced by cows with a more unsaturated fatty acid composition was more spreadable, softer, and less adhesive. The conclusion of these authors was that the phenotypic variation in milk fatty acids composition among cows fed the same diet was sufficient to produce butter with different textural properties. This variation could be partially genetic. Unfortunately, no studies were found on the individual genetic effect, probably, due to the large amount of money necessary for the reference chemical analyses to measure the fatty acid contents in milk. However, Soyeurt *et al.* (2006) showed the possibility to estimate the fatty acid contents by mid-infrared (MIR) spectrometry, a technology used routinely during the milk recording to predict the contents of major milk components like fat, protein, urea or lactose. Based on to the estimation of fatty acid contents by MIR spectrometry, the objective of this study was to estimate the genetic parameters of the hardness of butter and its relationship to milk yield, fat and protein contents using a multi-trait random regression test-day model. Results from this study are potentially useful to establish genetic evaluations for milk quality traits.

Materials and Methods

A total of 24,122 milk samples were collected between April 2005 and May 2007 in the Walloon dairy herd performance recording. All samples were analyzed by a MilkoScan FT6000 spectrometer and the generated spectra were recorded. Only Holstein cows ($\geq 85\%$ Holstein) in first lactation were studied, representing 3,853 spectral test day records from 1,099 cows in 87 herds.

Fatty Acids

Calibration equation established by Soyeurt *et al.* (2006) used a capillary column of 50m length. This column did not permit to isolate correctly fatty acids with long carbon chain. New calibration equations were therefore established. Reference values were measured by gas chromatography using a capillary column of 100m length from 114 milk samples. First, 48 samples were selected on 1,600 collected milk samples based on the spectral variability. Then 36 other samples were chosen based on the results of successive Principal Components Approach (PCA) during the routine milk spectral analysis. Finally, multivariate calibration equations were built using Partial Least Squares regression method (PLS) (Dardenne *et al.*, 2007).

Only the calibration equations which predicted the unsaturated (UNSAT) and saturated (SAT) fatty acid contents in milk were used. These equations showed a cross-validation coefficient of determination equal to 0.97 and 0.93, respectively. To represent the hardness of butter, the ratio SAT/UNSAT was calculated for all recorded spectra. Figure 1 illustrates the evolution of %FAT, %PROT and SAT/UNSAT within lactation.

Additional Milk Records

To take into account the milk history of animals and herds, the information about milk yield (MILK), fat content (%FAT) and percentage of protein (%PROT) were added to the data base. The final edited data file contained 57,759 first lactation test day records from 7,070 cows. Table 1 presents the descriptive statistics for all studied traits.

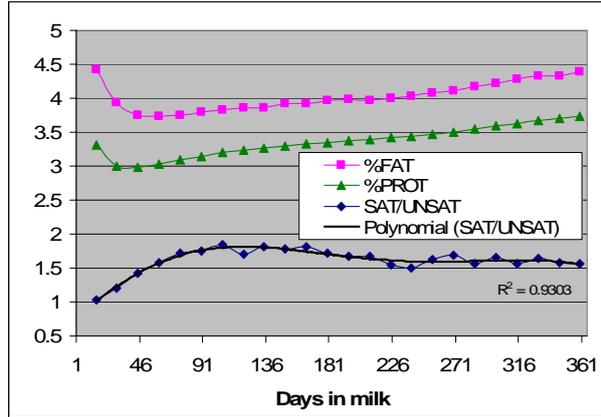


Figure 1. Evolution of %FAT, %PROT and SAT/UNSAT within class of 15 DIM.

Table 1. Descriptive statistics of test-day records.

Trait	N	Mean	SD
Milk (kg/day)	57,758	23.6	6.13
Fat (%)	57,758	3.99	0.68
Protein (%)	57,758	3.31	0.34
SAT/UNSAT	3,853	1.63	0.56

Estimation of (Co)Variance Components

Variance components were estimated by Bayesian methods as implemented by Misztal (2007) using a multi-trait random regression test-day model:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Q}(\mathbf{W}\mathbf{h} + \mathbf{Z}\mathbf{p} + \mathbf{Z}\mathbf{u}) + \mathbf{e}$$

where \mathbf{y} is the vector of observations (MILK, %FAT, %PROT and SAT/UNSAT); $\boldsymbol{\beta}$ is the vector of fixed effects (herd * test day, stage of lactation, age); \mathbf{Q} is the covariate matrix of

second-order Legendre polynomials; \mathbf{h} is the vector of random herd*date of calving effects; \mathbf{p} is the vector of random permanent environmental effects; \mathbf{u} is the vector of animal effects; \mathbf{X} , \mathbf{W} and \mathbf{Z} are incidence matrices; \mathbf{e} is the vector of random residual effects.

Stage of lactation was divided in 24 classes of 15 DIM. Test-day records with DIM less than 4 and greater than 366 were deleted. Age at test day was defined as number of months from birth. There were 3 classes of age (less than 29 mo, 29-32 mo, 33 mo and older).

Priors of (co)variances were estimated by REML (Misztal, 2007) using 4 single trait models including the same effects as those mentioned previously. Residuals were considered independent. Posterior means of (co)variance components were calculated using 40,000 samples after a burn-in of 60,000 samples.

Average daily heritability values were defined as a ratio of average genetic variance to the average sum of genetic, herd*date of calving, permanent environment and residual variances for each DIM from 1 to 365. Methodology to estimate heritability values for each trait expressed on 305-d lactation yield basis was inspired by Wood *et al.* (2003) and can be resumed by this expression:

$$\frac{\mathbf{t}'\mathbf{G}_0\mathbf{t}}{\mathbf{t}'\mathbf{H}_0\mathbf{t} + \mathbf{t}'\mathbf{P}_0\mathbf{t} + \mathbf{t}'\mathbf{G}_0\mathbf{t} + \sum_1^{305} \sigma_{\text{residual}}^2}$$

where \mathbf{t} is the vector corresponding to the sum of Legendre polynomials for each DIM from 1 to 305 for every trait, \mathbf{H}_0 , \mathbf{P}_0 et \mathbf{G}_0 are the elementary (co)variance matrices among random regression coefficients.

Genetic and phenotypic correlations among lactation yields were the ratio of the sum of covariance between two traits and the sum of squares of variances products estimated for each DIM from 1 to 305.

Results and Discussion

Table 2. Heritability estimates on lactation and average daily heritability values calculated for all studied traits.

Trait	Lactation heritability	Average daily heritability
Milk (kg/day)	0.28	0.24
Fat (%)	0.61	0.35
Protein (%)	0.65	0.44
SAT/UNSAT	0.22	0.11

Lactation heritability of MILK (Table 2) was lower than that currently used for Holstein cows in Belgium (0.48) (Interbull, 2007). Lactation heritability for %PROT and %FAT (Table 2) were higher than those obtained by Welper and Freeman (1992) and Schutz *et al.* (1990). Average daily heritability values for %FAT and %PROT presented in Table 2 were lower than those observed for the first lactation of Holstein cows by Miglior *et al.* (2007). As in the present study, these authors have observed a difference in the heritability values of %PROT and %FAT, even if this difference was smaller than those shown in Table 2. Heritability estimate for lactation SAT/UNSAT was moderate compared to the other traits and was higher than the average daily heritability observed for this same trait.

Phenotypic and genetic correlations among studied traits were resumed in Table 3. Genetic correlations between MILK and %FAT was similar to that observed by Miglior *et al.* (2007) but not in agreement with the results obtained by Schutz *et al.* (1990) and Welper and Freeman (1992). Phenotypic correlation between these two traits was in agreement with the results shown by Schutz *et al.* (1990) but higher than those observed by Miglior *et al.* (2007) and Welper and Freeman (1992).

Table 3. Phenotypic (above the diagonal) and genetic correlations (below the diagonal) among lactation yields for the studied traits.

Trait	Milk	Fat	Prot.	S/U
Milk (kg/day)		-0.42	-0.65	0.05
Fat (%)	-0.50		0.60	0.39
Protein (%)	-0.42	0.56		0.28
SAT/UNSAT	-0.71	0.87	0.58	

Genetic correlation between MILK and %PROT was in agreement with Welper and Freeman (1992) and lower than that observed by Schutz *et al.* (1990). Phenotypic correlation between these two traits was higher than that observed by Schutz *et al.* (1990) and Welper and Freeman (1992). Genetic and phenotypic correlations between MILK and PROT were lower than those observed by Miglior *et al.* (2007) and Welper and Freeman (1992).

Genetic correlation between %FAT and %PROT was in agreement to that obtained by Miglior *et al.* (2007) and Welper and Freeman (1992) but smaller than the one estimated by Schutz *et al.* (1990). Phenotypic correlation between these 2 traits was equal to that obtained by Schutz *et al.* (1990) and was higher than the one observed Miglior *et al.* (2007) and Welper and Freeman (1992).

Phenotypic correlation between MILK and SAT/UNSAT was close to 0 suggesting no dilution effect due to the increase of milk production. However %FAT and %PROT showed this effect because all phenotypic correlations among MILK, %PROT and %FAT were negative. On the other hand, genetic correlation between MILK and SAT/UNSAT was largely negative.

The hardness of butter seemed to be affected by the milk composition. Phenotypic correlations between MILK and %FAT or %PROT were all positive. As expected, the ratio SAT/UNSAT was more influenced by %FAT than by %PROT. Genetic correlations between these traits confirmed this observation.

Phenotypic correlations among studied traits seemed to be relatively stable within lactation (Figure 2), especially between %PROT and SAT/UNSAT. Phenotypic correlations between MILK and SAT/UNSAT within DIM increased linearly. Phenotypic correlations were negative until the middle of lactation and positive for the end of lactation. This observation explains why the correlation between MILK and SAT/UNSAT observed in Table 3 suggesting no dilution effect. Figure 2 suggests a slight dilution effect. Phenotypic correlations between %FAT and SAT/UNSAT within DIM were negative until less than the one third of lactation corresponding to the

strong decrease of %FAT in milk (Figure 2). Then the phenotypic correlations increased, became stable until more than two third of lactation and, then, tended to 0. The variation of %PROT in bovine milk did not seem to affect the ratio SAT/UNSAT. Phenotypic correlations between these two traits were stable within lactation.

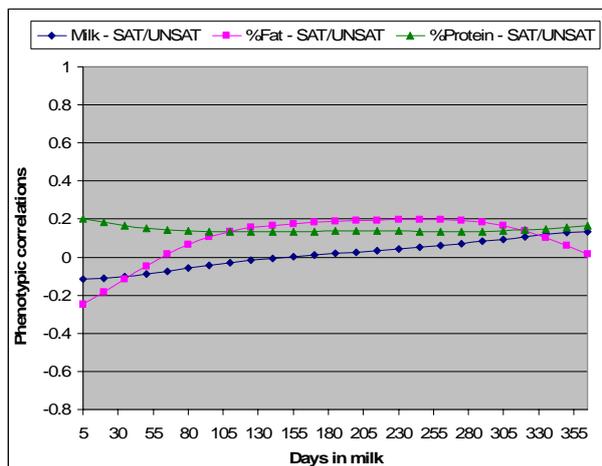


Figure 2. Phenotypic correlations among traits within DIM.

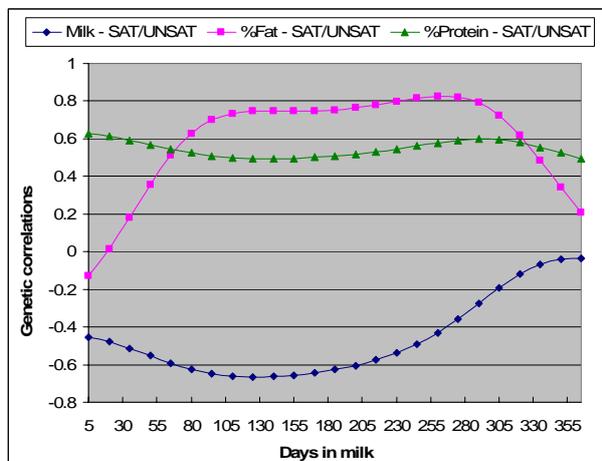


Figure 3. Genetic correlations among traits within DIM.

Genetic correlations between MILK and SAT/UNSAT were all negative (Figure 3). The highest negative genetic correlations were observed in the first third of lactation, where the milk production is higher. So, the hardness of butter seemed to be affected by the milk quantity produced by cows. Figure 3 shows a strong genetic link between %FAT and SAT/UNSAT. Values of genetic correlations between these traits were higher than phenotypic correlations (Figure 2). Genetic correlations between %PROT and

SAT/UNSAT were also higher than phenotypic correlations but more stable within lactation (Figure 3).

Conclusion

The hardness or spreadable properties of butter expressed as SAT/UNSAT ratio varied within lactation. This technological trait can be modeled using a multi-trait test-day random regression mixed model describing the trait specific lactation curves. Genetic variability of this trait seemed to exist. Lactation and average daily heritability estimates for SAT/UNSAT were 0.22 and 0.11, respectively. Based on genetic and phenotypic correlations within lactation between MILK and SAT/UNSAT, the hardness of butter seemed to be affected by the milk quantity produced by cows. As expected, phenotypic and especially genetic correlations within DIM showed a strong link between %FAT and SAT/UNSAT. %PROT seemed to influence less the spreadable property of butter. Genetic and phenotypic correlations within lactation between %PROT and SAT/UNSAT were stable through lactation.

From September 2007, it is planned to record all spectra generated during the Walloon milk recording for all cows. Consequently, additional data will be available and estimations of genetic parameters become more reliable.

Genetic correlation estimates indicate the important links between SAT/UNSAT and historical traits as MILK, %FAT and %PROT. Together with the availability of additional spectral data, the use of these historical traits would make future genetic evaluations for more detailed milk quality traits as butter hardness.

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