

Genetic Analysis and Genetic Evaluation for Somatic Cell Score in French Dairy Cattle

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Abstract

A lactation measure of somatic cell count was defined by a weighted average of test-day somatic cell scores adjusted for the number of days in milk. Genetic parameters were obtained by REML in Holstein, Montbéliarde, and Normande breeds. Heritability estimates of lactation somatic cell score were close to 0.15 and rather homogeneous across breeds and parities. The genetic standard deviation of somatic cell score increased with parity. The genetic correlations across parities was high (>0.8), except between parities 1 and 3 in Holsteins (0.75). The genetic correlations between somatic cell score and production traits were antagonistic, whereas the phenotypic correlation was opposite in sign.

As a result, a genetic evaluation was implemented for somatic cell score, based on a single trait repeatability animal model applied to the first three lactations. No clear genetic trend was observed over the last five years, except in Montbéliarde breed. In Holsteins, significant bull proof correlations were found with milking speed, udder depth, and udder balance.

1. Introduction

In France, dairy selection was oriented toward fat and protein yields and type in the 70's. Gradually, with the quota system, fat has been removed from the breeding objective. Little attention, however, has been given to functional traits other than udder shape. Negative genetic trends are expected for mastitis resistance, somatic cell count (SCC), and female fertility, as an indirect response to dairy selection, although the influence of type selection remains unclear. In 1995, it was decided to improve the recording system of functional traits and to implement new genetic evaluations as quickly as possible.

SCC is an economically important trait, because it affects the price of the milk and it is genetically highly correlated (>0.7) with mastitis resistance. The economic weight of one genetic standard deviation of SCC (including mastitis resistance) under French conditions is about one fifth of the corresponding value for protein yield (Colleau and Le Bilan-Duval, 1995). In this paper, we report the results of a genetic analysis of somatic cell score and the characteristics of the new national

evaluation for this trait, to be released in July 1997, in addition to a sire evaluation on functional longevity.

2. Definition of the trait

SCC have been measured monthly in France on a routine basis since 1984. Unfortunately, they have only been collected for genetic purpose since April 1995. Presently, the national data base situation is the following: 20, 28, and 50% individual test-days measured in 1991, 1992, and 1993, respectively, have SCC information, whereas the information is quasi-exhaustive for data collected after 1994.

As SCC have a highly skewed distribution, somatic cell scores (SCS) were defined in the classical way through a logarithmic transformation :

$$SCS = \log_2(SCC/100000) + 3$$

where SCC is the somatic cell number per ml

When applying such a transformation, it is postulated that the genetic determinism of the trait

is always the same throughout its range of variation and that all factors of variation affect SCC multiplicatively. Clearly, this assumption requires further investigations.

Test-day models are presently considered as ‘state-of-the-art’ methods to analyze such repeated correlated data (Reents et al, 1995). However, because of the large amount of data (17 million test-days per year in Holsteins) and the difficulty of properly modelling their variance-covariance structure, a lactation model has been preferred as a first step, whereas a full test-day model is still projected as a second step.

Three lactation criteria were compared : the raw average SCS (=SCS1), and two weighted averages of adjusted SCS. Adjustment factors for days in milk at each test-day were estimated within parity from a large test-day sample of lactations with an average SCS lower than 4, as in Wiggans and Shook (1987). Because these lactations are likely to be unaffected by mastitis, adjustment factors should mainly reflect the dilution effect of days in milk. It

is believed that these adjustments could replace projection factors for in-progress lactations and could, to some extent, accommodate for a lack of strict periodicity in the recording design. Adjusted test-day SCS were then averaged with two different weights depending on days in milk and parity. SCS2 weights were the squared correlation R^2 between test-day SCS and the average of the other SCS, as in Wiggans and Shook (1987). SCS3 weights were defined by the R/σ ratio, with R defined as above and σ being the SCS standard deviation for a given number of days in milk. This ratio is analogous to a regression coefficient. For SCS2 as well as SCS3, weights were maximal in the middle of the lactation but the differences were more pronounced for SCS2 than for SCS3.

The behavior of these criteria were compared by simulating 120 and 200-day in-progress lactations. Basic statistics of completed and in-progress lactations are presented in table 1. Adjustments and weights improved the prediction efficiency to a limited extent.

Table 1. Comparison of completed and in-progress lactations (80,987 first lactations).

	Trait	Mean	Stand dev	Correlation with completed lactations (x1000)		
				SCS1	SCS2	SCS3
Complete	SCS1	2.61	1.05	1000		
	SCS2	2.64	1.08	992	1000	
	SCS3	2.65	1.06	996	997	1000
120-day	SCS1	2.37	1.15	871	826	842
	SCS2	2.64	1.17	883	857	867
	SCS3	2.63	1.16	882	849	862
200-day	SCS1	2.46	1.09	968	951	975
	SCS2	2.65	1.11	968	969	970
	SCS3	2.64	1.10	975	965	968

3. REML estimation of genetic parameters

Two different analyses were carried out. **The first one** was limited to first lactation data only. The two primary goals were to compare the three SCS criteria and to obtain very accurate estimates of genetic parameters. A very large data set was used

from the three main French dairy breeds : Holstein, Normande, and Montbéliarde. Because only 4 years of data were available, with few dam-daughters pairs with performance, a sire model was used, with a limited loss of information compared to an animal model. The analyzed traits were milk, fat, and protein yields, in addition to SCS1, SCS2, and

SCS3. For each trait, the model was the same and included the fixed effects of herd x year, year x month of calving, age at calving, group of sires, and the random effect of sire. Two-generation relationships between bulls were accounted for. All sampling sires born after 1987 and had at least 20 daughters with cell information. Service bulls were

required to have at least 200 hundred daughters (1000 in Holstein). Service bulls were considered as fixed effects. In practice, a canonical transformation as well as a tridiagonalization of the coefficient matrix dramatically reduced the computing requirements. Data are presented in Table 2.

Table 2. Characteristics of the data sets.

	Montbéliarde	Normande	Holstein
# females	236 628	256 265	1 429 410
# sampling bulls	473	526	2330
# service bulls	100	80	171

Heritability estimates are presented in Table 3. They are very similar across breeds and, surprisingly, slightly higher for the unadjusted and unweighted SCS mean (SCS1). However, differences were very small. Genetic correlations across SCS traits were very high. The lowest

correlation was 0.982 between SCS1 and SCS2, whereas SCS2 and SCS3 were virtually the same trait (0.998). The genetic standard deviation was close to 0.4 SCS unit for the three traits, and was slightly higher (0.44) in Holstein.

Table 3. Heritability estimates of SCS traits in first lactation.

	Montbéliarde	Normande	Holstein
SCS1	0.142	0.150	0.144
SCS2	0.136	0.143	0.141
SCS3	0.138	0.145	0.143

Genetic and phenotypic correlations with production traits are presented in Table 4. As is usually found in the literature, the genetic correlations were positive, reflecting an antagonism between production and mastitis resistance,

whereas the phenotypic correlations were negative, reflecting an unfavorable effect of mastitis on production. This genetic opposition was higher for protein than for fat.

Table 4. Genetic (R_g) and phenotypic (R_p) correlations between production and SCS3 (x100).

	Montbéliarde		Normande		Holstein	
	R_g	R_p	R_g	R_p	R_g	R_p
Milk	17	-8	17	-10	10	-13
Fat	18	-8	13	-9	9	-13
Protein	20	-6	17	-6	15	-12

The goal of the **second analysis** was to study the genetic determinism of SCS across lactations. This study was restricted to SCS3 and to females who first calved in 1993-94, *ie* might have a second and a third lactation within the time period covered by the data set. The Holstein data set was partitioned into 4 subpopulations according to the geographical area and the predominant AI stud operating within this area. Only bulls belonging to this AI stud were considered. The same edit criteria as in the first

analysis were applied. The VCE (Groeneveld, 1996) REML package was used. Each service sire was considered as fixed, defining one group effect for all daughters of each such bull. Four traits were analyzed : SCS3 within each parity, and milk yield in first lactation. The model included the effects of herd x year, month effect, group of sire, and sire. The model for milk yield also included the effect of age at calving. The characteristics of the data sets are presented in Table 5.

Table 5. Characteristics of the data sets.

	Females	Sampling bulls	Service bulls
Montbéliarde	97 429	196	40
Normande	106 627	225	46
Holstein 1	159 619	286	40
Holstein 2	231 891	348	54
Holstein 3	57 928	219	17
Holstein 4	147 467	240	53
Holstein total	596 905	1093	164

Heritability estimates are presented in Table 6. Some variations appeared across parities in Montbéliarde and Normande breeds but these data sets were of limited size. On the other hand, the estimates were quite stable in Holsteins. Genetic

standard deviations are presented in Table 7. They tended to increase with parity, reflecting the increase in phenotypic variability and the relative stability in heritability.

Table 6. Heritability estimates of SCS3 in the first 3 parities.

	Montbéliarde	Normande	Holstein (*)
Parity 1	0.128	0.134	0.163
Parity 2	0.108	0.140	0.145
Parity 3	0.094	0.180	0.151

(*)estimates pooled over 4 data sets

Table 7. Genetic standard deviations estimates of SCS3 in the first 3 parities.

	Montbéliarde	Normande	Holstein (*)
Parity 1	0.40	0.40	0.44
Parity 2	0.39	0.45	0.46
Parity 3	0.39	0.53	0.50

(*)estimates pooled over 4 data sets

Genetic and phenotypic correlations are presented in table 8. Phenotypic correlations were highest between parities 2 and 3 (0.4) and lowest between parities 1 and 3 (0.3). Genetic correlations were usually higher than 0.8. However, in Holstein, a relatively low value was estimated between parities 1 and 3. Estimates were lower than 0.75 in 3 out of 4 data sets. The genetic antagonism with first lactation milk yield usually increased with parity, for instance up to 0.28 in Holstein.

The main conclusion of this analysis in French dairy breeds are in good agreement with the

literature data (see the recent review of Mrode and Swanson, 1996). SCS has a heritability close to 0.15, which is rather stable across parities. Its genetic variability increased with parity, in parallel with the phenotypic variability. SCS could be (at least in a first approach) considered as one single trait, as genetic correlations across parities were usually higher than 0.8. This correlation was higher for consecutive parities, and seemed to drop more rapidly in Holstein than in the other breeds. The repeatability was close to 0.35, was highest for parities 2 and 3, and lowest between 1 and 3.

Table 8. Genetic and phenotypic correlations between SCS3 in different parities (x100).

Parities	Montbéliarde		Normande		Holstein (*)	
	R _g	R _p	R _g	R _p	R _g	R _p
1-2	85	34	83	36	89	36
1-3	91	28	82	31	69	30
2-3	99	40	100	49	88	43

(*)estimates pooled over 4 data sets

4. Genetic evaluation

Trait SCS3 was chosen for genetic evaluation. This evaluation included all lactations in parity 1 to 3 started after September 1st 1990 and with at least one test-day with SCC information. Presence of data from the first lactation was not required. A single trait repeatability model was assumed with heritability 0.15 and repeatability 0.35. Data were preadjusted to homogenize the genetic variances across parities. Within the analysis, data were affected by weights depending on the number of

test-days with SCC information, and therefore reflecting the accuracy of the lactation measure. As the heritability appeared to be similar in the three parities, the weights did not depend on parity. The same model was applied as for the dairy evaluation, with the fixed effects of herd x year, age at calving, month of calving, days dry, and groups of unknown parents, and the random effects of breeding value and permanent environmental effect. Age, month and days dry effects were defined within parity, year, and region. Table 9 presents the available data for the first evaluation test.

Table 9. Data sets for the first evaluation test.

	Montbéliarde	Normande	Holstein
Females with data	504 230	604 715	3 496 376
Records	893 943	1 028 594	6 150 059

Evaluations were expressed in genetic standard deviation, *ie* with a range from -3 to +3, on a rolling base defined by AI bulls born in year (n-7) to (n-10), *ie* in 1987-1990 for the 1997 release, and with a change of sign, in order that positive proofs correspond to fewer cells. As for dairy traits, the reliability of bull proofs was computed on daughter information only.

With data spanning only a few years, it is difficult to draw general conclusions on genetic trends. Most bulls born after 1986 have a quite accurate SCS evaluation. Average SCS bull proofs by birth year show a clear decrease in Montbéliarde breed (-0.25 genetic standard deviation in 5 years) and no clear trend in Normande and Holstein breeds (Table 10).

As shown in Table 11, SCS bull evaluations were basically independent of production proofs (milk, fat, protein, fat and protein contents) in

Montbéliarde breed, whereas slightly negative correlations were found in the Holstein and Normande breeds between production and SCS. In Holsteins, the correlation between bull proofs of AI bulls for SCS and **milking speed, udder depth**, udder balance, rear udder height and udder composite reached -0.33, 0.28, 0.20, 0.14 and 0.23, respectively. In contrast, low correlations were found with teat length (0.05), teat placement (0.09), udder cleft (0.09), front teat distance (0.09) and teat distance side view (0.11). Continuous efforts to improve udder traits may explain why the genetic response for SCS was lower than predicted by the genetic trend on production traits. SCS also appeared to be a major component of functional longevity. For this reason, a guideline is presently being developed proposing the optimal use of type, SCS, and functional longevity evaluations.

Table 10. Average SCS bull proofs by birth year (in genetic standard deviation ; a decrease means more cells).

	Montbéliarde	Normande	Holstein
86	0.21	0.00	0.19
87	0.16	0.06	0.16
88	0.00	-0.03	0.02
89	-0.04	-0.15	-0.15
90	-0.03	0.10	-0.04
91	-0.05	0.08	0.08

Table 11. Bull proof correlations between SCS and production traits (x100).

	Montbéliarde	Normande	Holstein
Nr bulls (*)	526	540	2592
Milk	1	-10	-4
Fat	1	-5	2
Protein	0	-9	-8
Fat %	0	8	6
Protein %	-3	3	-5
INEL (**)	-1	-8	-9

(*) French AI bulls born from 1987 to 1990, reliability of SCS proof > 60%

(**) INEL = Protein (kg) + 30 Protein %

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