Adjustment Factors and Genetic Evaluation for Somatic Cell Score and Relationships with Other Traits of Canadian Holsteins

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ABSTRACT

Test day SCC records were obtained from the Ontario DHI and converted to somatic cell score using a logarithmic transformation. Adjustment factors for stage of lactation and calendar month were obtained for first and later lactations. Effects of stage of lactation were significant and followed a systematic pattern. Seasonal effects were small. Sire estimated breeding values for lactation mean adjusted test day somatic cell scores were obtained from an animal model based on first, later, and all lactations, assuming a heritability of .11 and repeatability of .27. Mean accuracy of estimated breeding values for sires with at least 30 daughters was .64 for first lactation, .76 for second to fifth, and .86 for all lactations. Genetic trends for somatic cell score were not significant. The correlation of breeding values estimated from first lactations with estimates based on later lactations was .62 for sires with at least 50 daughters, which resulted in an approximate genetic correlation of .72. Correlations of sire estimated breeding values for somatic cell score from first lactation with estimated breeding values for milk, fat, protein, fat percentage, protein percentage, and milking speed were .12, .05, .11, −.09, −.02, and .20. Correlations between sire estimated breeding values for somatic cell score and type traits were generally small, but favorable with mammary system, −.13, and fore udder, −.16, and unfavorable with dairy character, .24. Somatic cell score should be considered as an auxiliary trait in dairy cattle breeding programs.

(**Key words**: mastitis, somatic cell count, environmental effects, genetic evaluation)

Abbreviation key: **EBV** = estimated breeding value, **LSCS** = lactation average SCS, **SCS** = somatic cell score.

INTRODUCTION

Mastitis is recognized as one of the most costly diseases of the dairy industry. The National Mastitis Council (Arlington, VA) has estimated mastitis costs to be approximately $225 (US)/yr per cow. In Canada, the estimate was $140 to $300 (Canadian)/yr per cow (7).

Interest in genetic aspects of mastitis has a history of nearly 50 yr in the scientific literature. Direct selection for reduced mastitis incidence is not possible in the US and Canada because mastitis incidence is not recorded consistently. Even with a complete clinical mastitis recording system, subclinical mastitis would be ignored. Development of SCC testing in milk recording programs has opened opportunities for the indirect measurement of mastitis incidence and the practical genetic improvement of mastitis resistance. Advantages of SCC over other mastitis indicator traits have been summarized by Shook (24) and Shook and Schutz (25). In addition, some type traits, especially those associated with udder health, have been suggested as indirect measures to select for mastitis resistance along with SCC (14, 19, 22, 23, 26, 29).

Individual test day SCC are influenced by systematic environmental effects, such as stage of lactation, lactation number, and season (1, 2, 6, 9, 21). Adjustment factors for these effects can be derived and used to summarize in-

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dividual test day SCC observations into a lactation measure of SCC for use in genetic evaluation (14). Wiggans and Shook (28) reported on adjustment of SCC for stage of lactation. Sire evaluations for SCC were reported by Boettcher et al. (3) and Hansen (9); evaluations were computed based on a sire model. A lactation measure of unadjusted mean test day SCC from first lactation was analyzed.

Objectives of this study were 1) to obtain adjustment factors for stage of lactation and season for test-day records of SCC to develop lactation measures of SCC for genetic evaluation; 2) to establish a genetic evaluation system for SCC using an animal model; and 3) to determine relationships of sire genetic evaluations for SCC with production traits, milking speed, and type traits.

MATERIAL AND METHODS

Data

A total of 2,607,864 test day SCC records was obtained from the Ontario Dairy Herd Improvement Corporation from lactations of Holstein cows that were initiated between 1985 and 1990. Records were edited on the following requirements: at least 5 test day records per lactation; first test within the first 60 d of lactation; exclusion of tests beyond 305 d of lactation and for sixth and later lactations; valid pedigree, birth date, and calving date; and age at first calving within 18 to 36 mo. After editing, records on 92,579 cows with a total of 1,227,561 test day observations remained. These cows were from 3497 herds by 3777 sires and out of 76,708 dams.

Statistical Models

Adjustment of Test Day Observations. Additive adjustment factors for calendar month of test and stage of lactation were obtained within lactation. The following fixed model was used.

$$\mathbf{y} = \mathbf{Wh} + \mathbf{Xc} + \mathbf{V}_1\mathbf{t} + \mathbf{V}_2\mathbf{m} + \mathbf{e},$$

where $\mathbf{y}$ = vector of test day SCC transformed on a $\log_2$ basis (1) to somatic cell scores (**SCS**), $\mathbf{h}$ = vector of herd-year of calving effects, $\mathbf{c}$ = vector of cow effects within herd-year, $\mathbf{t}$ = vector of stage of lactation effects, $\mathbf{m}$ = vector of calendar month effects, and $\mathbf{e}$ = vector of random residual effects. $\mathbf{W}$, $\mathbf{X}$, $\mathbf{V}_1$ and $\mathbf{V}_2$ are design matrices. Also,

$$E(\mathbf{y}) = \mathbf{Wh} + \mathbf{Xc} + \mathbf{V}_1\mathbf{t} + \mathbf{V}_2\mathbf{m}$$

and

$$V(\mathbf{y}) = \mathbf{I}\sigma_e^2,$$

where σ_e^2 is the residual variance. Stage of lactation was assigned based on 10-d intervals for the first three stages, starting from the date of calving. Subsequent stages were based on 30-d intervals, except for the last stage, which had 35 d.

Least squares solutions for calendar month and stage of lactation were used as additive correction factors for preadjustment of test day records. Adjusted test day records were then averaged to produce lactation measures of SCS (**LSCS**) for genetic evaluation.

Genetic Evaluation. A total of 65,695 lactation measures (LSCS) for first lactation, 96,982 for the second to fifth lactations, and 162,677 for the first to fifth lactations were used in three separate genetic evaluations. Analysis involved 2646, 3047, and 3688 sires for first, second to fifth, and all lactations and 65,695, 47,005, and 91,392 cows for first, second to fifth, and all lactations.

The following animal model was used for genetic evaluation:

$$\mathbf{y} = \mathbf{Wh} + \mathbf{Xl} + \mathbf{Va} + \mathbf{Zg} + \mathbf{Zp} + \boldsymbol{\epsilon},$$

where $\mathbf{y}$ = vector of LSCS, $\mathbf{h}$ = vector of fixed herd-year effects, $\mathbf{l}$ = vector of fixed lactation effects (omitted for analysis of first lactation only), $\mathbf{a}$ = vector of fixed age at calving effects, $\mathbf{g}$ = vector of random animal additive genetic effects, $\mathbf{p}$ = vector of random permanent environmental effects, and $\boldsymbol{\epsilon}$ = vector of random residuals. $\mathbf{W}$, $\mathbf{X}$, $\mathbf{V}$, and $\mathbf{Z}$ are design matrices. Also,

$$E(\mathbf{y}) = \mathbf{Wh} + \mathbf{Xl} + \mathbf{Va}$$

and

$$V(\mathbf{y}) = \mathbf{ZAZ}'\sigma_g^2 + \mathbf{ZZ}'\sigma_p^2 + \mathbf{I}\sigma_\epsilon^2,$$

where σ_g^2 is additive genetic variance, σ_p^2 is permanent environmental variance, and σ_ϵ^2 is

residual variance. **A** is the numerator relationship matrix. All relationships obtained from pedigree information present in the data were used. Unknown ancestors were assigned to a common unrelated base population. Parameters used were obtained from the literature (15, 16, 27): heritability = .11, and repeatability = .27. For each data file (first lactation, second to fifth lactations, and all lactations), the mean EBV over all animals evaluated was set to zero.

The computer program PEST (8) was used to obtain estimated breeding values (**EBV**) for LSCS. Accuracy of EBV was not provided by PEST. Therefore, EBV were calculated by a modification of the method of Meyer (12), based on Chesnais (1990, personal communication), to accommodate multiple lactations with an animal model.

Pearson correlations were computed between sire LSCS EBV based on first lactation records and EBV based on later lactations for sires with at least 30, 50, or 100 first lactation daughters. From these correlations, approximate genetic correlations between LSCS from first and later lactations were derived using the procedure of Cassell et al. (4):

$$\text{EBV correlation} = \left[r_g\left(\frac{3+n}{n}\right) + \frac{4e^2}{nh_1h_2}\right]\sqrt{R_1R_2}$$

where r_g = genetic correlation (to be estimated); n = number of first lactation daughters; h_1^2 and h_2^2 = heritability of LSCS from first and later lactations (assumed = .11); e^2 = environmental correlation between first and later lactation LSCS on same cow (= .27 – $h_1r_gh_2$, where .27 is the assumed repeatability of LSCS); and R_1 and R_2 are the mean reliabilities of sire EBV for first and later lactations, respectively. The formula of Cassell et al. (4) is strictly valid only if daughters with records for later lactations are a subset of daughters with first lactation records, which was not entirely the case in the current study. However, resulting biases in the estimate of the genetic correlation are expected to be small, especially when the number of first lactation daughters is large.

Pearson correlations of sire EBV for LSCS with production and conformation traits and milking speed were also calculated. The EBV for production and type traits were obtained from Agriculture Canada and the Holstein Association of Canada (July 1991).

RESULTS AND DISCUSSION

Adjustment Factors

Figure 1 shows the effect of stage of lactation on SCS by lactation. Trends for lactations 2 to 5 were very similar. Thus, only two sets of adjustment factors were necessary, one for first lactation and one for second and later lactations. Similar results were reported by Banos and Shook (2) and Wiggans and Shook (28), who showed lactation curves of SCS that resembled inverted milk yield curves.

Adjustment factors for calendar month were not systematic and small (ranging from –.06 to .05 for first lactation and from –.06 to .06 for second to fifth lactation). Interactions between stage of lactation and calendar test month were tested, were significant, but resulted in only minor modifications to the adjustment factors presented. Kennedy et al. (10) indicated that lowest SCC occurred during spring, regardless of geographical location. However, seasonal effects were small in the current study and in the study by Wiggans and Shook (28).

Additive adjustment factors for SCS were used to obtain lactation measures of SCS for genetic evaluation. In a future study, data from other provinces will be analyzed to verify or to update adjustment factors for stage and season obtained.

Genetic Evaluation

Figure 2 shows the frequency distribution of EBV for LSCS based on all lactations for 378 bulls with at least 55% reliability (accuracy squared) and daughters in at least 10 herds. Mean and standard deviation for EBV and reliabilities of these sires were .005 ± .31 and .72 ± .14. The EBV approximately followed a normal distribution. The range of sire EBV for LSCS indicates that daughters of highest LSCS sires had a one-unit higher LSCS than daughters of low LSCS sires, or double the raw SCC. This result agrees with that of Boettcher et al. (3), who reported a range of 1.06 in sire predicted transmitting abilities, which are half the EBV. Table 1

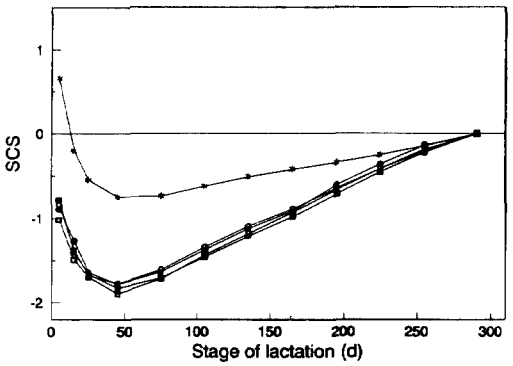

Figure 1. Effects of stage of lactation on test day somatic cell score (SCS) by lactation: 1 (*), 2 (○), 3 (□), 4 (●), and 5 (■).

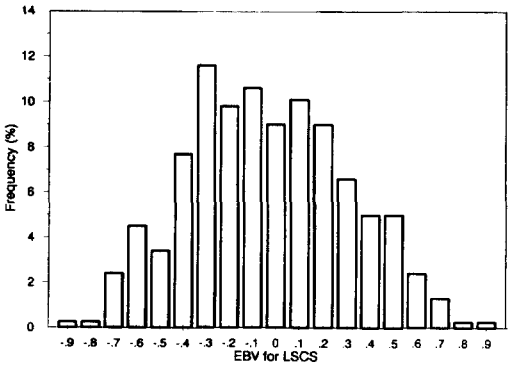

Figure 2. Frequency distribution of sire estimated breeding values (EBV) for lactation somatic cell score (LSCS) based on all lactations for 378 bulls with at least 55% reliability.

shows means and standard deviations of EBV by number of progeny for first, second to fifth, and all lactations. As the number of progeny increased, the standard deviation of EBV increased, as expected, because of increased accuracy of prediction. Mean reliabilities for bulls with at least 30 daughters were .64 ± .18 for first lactation, .76 ± .15 for second to fifth lactations, and .86 ± .14 for all lactations. Table 2 gives means and standard deviations for EBV of cows based on first lactation LSCS by year of first calving. Virtually no genetic trend was detectable.

The EBV based on second to fifth lactation could be biased if culling for mastitis (and high LSCS) occurred during first lactation. Similarly, EBV based on all lactations could be biased because cows were not required to have a first lactation record present in the current study. Culling biases could also influence EBV from any lactation because of the requirement of at least 5 test day SCC observations per lactation. As a result, short records from cows culled for mastitis were excluded. Although this requirement is needed to obtain unbiased adjustment factors for stage of lactation for SCS, lactation records with fewer test days are recommended for inclusion in a routine genetic evaluation of LSCS. Records would then need to be weighted, depending on the number of

TABLE 1. Means and standard deviations of sire estimated breeding values for lactation somatic cell score by number of progeny and lactation.

	Lactation 1			Lactations 2 to 5			Lactations 1 to 5		
Progeny	Sires	$\bar{X}$	SD	Sires	$\bar{X}$	SD	Sires	$\bar{X}$	SD
(no.)	(no.)			(no.)			(no.)		
1	868	.0034	.060	712	.0012	.056	1290	.0006	.081
2–5	767	.0028	.098	1157	−.0004	.093	1157	.0070	.130
6–10	325	.0070	.152	383	.0096	.143	383	.0102	.189
11–30	466	.0137	.228	446	.0038	.200	553	.0036	.274
31–50	103	−.0062	.285	168	−.0253	.297	142	.0198	.318
51–100	41	−.0596	.270	78	.0079	.321	66	.0209	.370
101–200	25	.0556	.363	35	.0188	.382	32	−.0809	.381
201–500	22	.0647	.335	33	−.0053	.421	30	.0725	.342
>500	29	−.1271	.372	35	−.0006	.362	35	−.0298	.380
Total	2646	.0037	.155	3047	.0009	.158	3688	.0048	.180

TABLE 2. Means and standard deviations of cow estimated breeding values for lactation somatic cell score for first lactation by year of calving.

Calving year	Cows	$\bar{X}$	SD
1985	2400	−.0116	.145
1986	8770	−.0190	.157
1987	12,172	−.0169	.183
1988	19,980	−.0302	.196
1989	15,207	−.0284	.203
1990	6894	−.0327	.200
Total	65,494	−.0254	.190

tests included in the LSCS, which is similar to procedures used for production traits when records are incomplete.

In the current study, only limited pedigree information was used, and unknown parents were assigned to a common phantom group. Given the limited selection for SCC in the past, this likely did not affect EBV. However, consideration of complete pedigree information and assignment of unknown parents to phantom groups by path of selection, country of origin, and birth year is recommended for routine genetic evaluation for LSCS.

Relationship Between LSCS EBV Based on Different Lactations

Table 3 shows Pearson correlations for sire EBV based on lactation 1 versus 2 to 5. With relatively high accuracy (.73 to .86) of EBV, correlations of EBV from different lactations were moderately high (.57 to .67) and increased with more progeny. Correlations between EBV would be estimates of genetic correlations if accuracy of EBV is unity. With lower accuracy, correlations between EBV are biased estimates of genetic correlations because of environmental effects and environmental correlations. Table 3 also gives approximate genetic correlations for SCS between first and second to fifth lactations, based on the method of Cassell et al. (4). Estimated genetic correlations of .72 to .74 are in general agreement with those of earlier reports (2, 16) and indicate that LSCS is not the same genetic trait for first versus later lactations. As a result, using all lactation records in a repeatability model is not entirely appropriate. However, using all lactation records increases accuracy of EBV, which is important in view of the relatively low heritability of SCS and the number of cows that are recorded for SCC. An ideal solution would be to analyze LSCS from first and later lactations simultaneously with a multiple-trait procedure, allowing for a less than unit genetic correlation. However, given the computational complexities of such a procedure and the moderately high genetic correlation, analysis using a repeatability model provides a suitable alternative.

Relationships of EBV for LSCS with Other Traits

Correlations between EBV for LSCS and production traits, milking speed, and type traits

TABLE 3. Correlations between estimated breeding values (EBV) for lactation somatic cell score of sires based on minimum numbers of first and later (second through fifth lactation) records of their daughters in each data file and resulting approximate genetic correlations.

		Progeny		
Lactation		>30	>50	>100
First	Sires, no.	142	93	63
	Daughters per sire, no.	336	476	658
	Reliability, $\bar{X}$ (SD)	.73 (.18)	.82 (.13)	.89 (.08)
Later	Sires, no.	142	93	63
	Daughters per sire, no.	306	442	645
	Reliability, $\bar{X}$ (SD)	.79 (.14)	.87 (.09)	.92 (.06)
Correlation between EBV from first and second to fifth lactations		.58	.62	.67
Approximate genetic correlation[1]		.74	.72	.73

[1]Approximate genetic correlation between lactation somatic cell score from first and later lactations, following work of Cassell et al. (4).

TABLE 4. Pearson correlations of sire estimated breeding values for yield, type, and milking speed with estimated breeding values for lactation somatic cell score (LSCS), based on different lactations, for sires with at least 50 daughter records for LSCS.

	LSCS for lactations		
	1	2 to 5	1 to 5
Sires, no.	123	117	164
Milk yield	.12	.11	.05
Fat yield	.05	−.02	−.02
Fat percentage	−.09	−.16	−.10
Protein yield	.11	.12	.04
Protein percentage	−.02	.00	−.02
Milking speed	.20	.02	.11
Final class	−.08	−.06	−.09
General appearance	−.09	−.06	−.09
Dairy character	.24	.24	.18
Capacity	−.05	.07	−.01
Rump	−.09	−.05	−.01
Feet and legs	.05	.00	−.00
Mammary system	−.13	−.10	−.13
Fore udder	−.16	−.13	−.15
Rear udder	−.06	−.03	−.07
Size	−.00	.10	.02
Stature	−.03	.08	−.01
Style	−.04	−.01	−.03
Head	.04	.06	.01
Chest floor	−.05	.09	.00
Loin strength	−.14	−.19	−.09
Rump width	−.05	.05	−.03
Pin setting	−.12	−.02	.05
Foot	−.02	.01	−.03
Bone quality	.14	.02	.06
Set rear legs	.04	−.03	.00
Udder texture	.08	.02	−.01
Fore udder attachment	−.13	−.14	−.13
Rear attachment height	−.01	−.03	−.03
Median suspensory ligament	−.04	.00	−.06

are in Table 4. Because of less than unit reliabilities, these correlations tend to be closer to zero than the genetic correlations between the corresponding traits. When the same daughters are included in both EBV, correlations would be further biased because of environmental correlations. The direction of the latter bias depends on the size of the environmental correlation relative to the genetic correlation. Table 4 shows modest unfavorable correlations between sire EBV (for sires with at least 50 daughters) for milk yield and LSCS of .12 for first lactation and .11 for second to fifth lactations. Correlations for protein yield were similar. Correlations with fat yield were lower. Several studies have reported positive genetic correlations between SCC and milk yield for first lactation data that ranged from .09 to .82 (6, 11, 15, 21, 23). Monardes and Hayes (15) reported positive genetic correlations of .31 to .58 between milk yield from first lactation and SCC during subsequent lactations. However, Coffey et al. (5) found a negative correlation between sire EBV for SCC and daughter mean daily milk yield.

Pearson correlations between sire EBV for LSCS and type traits are in Table 4. Of 24 type traits investigated, most correlations with LSCS were unimportant and small. The largest correlation was with dairy character (.24, unfavorable). Others were with mammary system (−.13, favorable), fore udder (−.16, favorable), and rear udder (−.06, favorable). These results, that desirable udder conformation tends to be associated with lower SCC, agree in general with those of earlier reports (14, 19, 20, 23, 26), but dairy character, which is highly related to milk yield, has an unfavorable relationship with SCC. Young et al. (29) first found that udder height was genetically negatively correlated (i.e., favorably) with scores for clinical mastitis, bacterial infection, and leukocyte count (−.48 to −.28). Seykora and McDaniel (22, 23) found that the genetic correlation between udder height and SCC was near negative unity. Rogers et al. (19) suggested selection for higher, more tightly attached udders and closer teat placement should reduce or slow the increase in SCC from selection for increased milk yield. Udder conformation traits have been suggested as traits for indirect selection for lower mastitis (14, 19, 23, 26, 29). Type traits and SCC are currently both recorded systematically on a large portion of the dairy population.

Pearson correlation coefficients between sire EBV for LSCS and milking speed (from first lactation) were .20 (unfavorable) for LSCS EBV from first lactation, .02 for LSCS EBV from second to fifth lactations, and .11 for LSCS EBV from all lactations (Table 4). Little literature information is available on the relationship between milking speed and SCC. Seykora and McDaniel (22) reported a genetic correlation between the percentage of 2-min milk and LSCS of .18 and a phenotypic correlation of .10. However, the regression of mastitis infection cases on either rate or time of milking did not support the idea that faster

milking is associated with more mastitis (13). More studies are needed on this aspect.

Finally, although few studies have been reported in the literature, the genetic correlation between SCC and mastitis has generally been reported as moderately high. Adjusted lactation SCS provides an overall measure of mastitis susceptibility. Genetic evaluation of SCS is possible and results in estimated genetic differences between sires. The EBV for LSCS can be a useful tool to reduce mastitis incidence in dairy populations, if used properly, preferably as part of a total merit index (18). Current genetic evaluations for conformation traits can also be used to help to reduce mastitis incidence by genetic means (18).

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