ASSOCIATION BETWEEN MILK PRODUCTION TRAITS AND SOMATIC CELL SCORES OF HUNGARIAN HOLSTEIN-FRIESIAN CROSSBREDS USING MULTI-TRAIT ANIMAL MODEL

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SUMMARY

Genetic and phenotypic correlations were estimated for means of $\log_2$ SCC (somatic cell scores: SCS) with milk production traits of sample test-day. Data of SCS and milk production traits for six genetic groups, Holstein-Friesian (HF), Hungarian Native Breed (NHB) and four of their crossbreds were used. Multi trait animal model was used for the estimation of genetic and phenotypic (co)variances. All estimates of correlations, genetic (R_g) and phenotypic (R_p), between SCS and milk production traits were negative except with protein percentage. Sample test-day estimates (STD) of R_g between SCS and each of daily milk yield (DY), fat (F%), protein (P%) and lactose (Lc%) percentages were $-.13\pm.07$, $-.13\pm.08$, $.11\pm.04$, $-.11\pm.08$, respectively. STD R_p estimates were higher than R_g's for SCS with DY and P%. STD R_g with F% decreased with parity. The highest estimate of STD R_g between SCS and DY was -0.25 for HF in the 4th lactation. STD R_g of SCS with milk composition ranged from .08 to .20 and $-.10$ to $-.25$ for HF *vs.* .01 to .13 and $-.07$ to $-.32$ for NHB. It could be concluded that, relationship of SCS with milk production differs among purebreds and their crossbreds according to percentage of crossing.

Keywords: Somatic cell, correlations, milk, Hungarian-Holstein Friesian

INTRODUCTION

Despite a reduction in the incidence of clinical and subclinical mastitis over the past 25 years in some developed countries (Booth, 1995), mastitis remains one of the most costly health problems of dairy cattle and a major source of economic loss to dairy farms. Young *et al.* (1960) reported that an average value of 0.89 for the genetic correlation between SCC and clinical mastitis while a value of 0.83 was obtained by Afifi (1968). Therefore, developing efficient dairy cattle industry depends to a great extent on the evaluation of association between mastitis expressed as its correlated trait (SCC) and milk production traits. Phenotypic correlations between SCC and milk yield tended to be more negative in older lactations than in early lactations ranging from $-.12$ to $-.24$ (Banos and Shook, 1990).

The aim of the present study is to investigate the genetic association of test-day measures between SCS and milk production traits in six genetic groups of Holstein- Friesian (HF) and Native Hungarian Breed (NHB).

MATERIALS AND METHODS

A total of 458348 lactation records from 172065 cows daughters of 873 sires in the first four parities were used. Sample test-day somatic cell count (SCC) and milk production traits for 14329 Holstein Friesian (HF) cows, 13021 Native Hungarian Breeds (NHB) and 144715 of their crossbred cows calving between 1993 to 1997 were provided by the local associations in Hungary. Crossbred groups involved in the present study were classified according to percentage of HF inheritance into: <25% HF genes, $\geq$25-<50% HF genes, $\geq$50-<75% HF genes and $\geq$75% HF genes. The data set involved measurements of at least 5 months and maximum observations were not more than 14 months for all studied traits. Traits involved in the data set were the actual test-day somatic cell score (SCS), daily milk yield (DY), fat (F%), protein (P%), and lactose (Lc%) percentages. Measurements of somatic cell count were adjusted for calendar month of test, stage of lactation and test day milk (Zhang *et al.*, 1994; Charfeddine *et al.*, 1997). Cows were not required to have a 2nd lactation to be included in the 1st lactation analysis. All cows included in the 2nd parity analysis might have not a usable first lactation data but calved successively in the 2nd parity at not more than 50 months of age. Genetic and phenotypic correlations among the various SCS means and milk production traits were estimated using an animal model of MTDFREML package (Boldman, 1997) that includes both animals with records and genetically related animals with no records, $y=XB+Zu+e$. Where y is an $n*1$ vector (augmented to $t*1$ with the additional of a t-n null vector when evaluating animals without records) of observations on

the trait of interest; X is an $n * p$ incidence matrix; Z is a $t * t$ matrix equal to an $n * n$ identity matrix relating observations to the animals that made them and augmented by null rows and vectors for animals that are to be evaluated but have no records; B is a $p * 1$ vector of known fixed effects (farm, parity, age of calving within parity); u is a $t * 1$ vector of random breeding values, which can be partitioned into u_1, and $n * 1$ vector representing animals having records and u_2, a $(t-n) * 1$ vector for related animals with no records; and e is an $n * 1$ vector of random errors.

Thus,

$$E\begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} XB \\ 0 \\ 0 \end{bmatrix}, \text{ and } V\begin{bmatrix} y \\ u \\ e \end{bmatrix} = \begin{bmatrix} V \dots \dots A\sigma^2{}_a \dots \dots I_n\sigma^2{}_e \\ A\sigma^2{}_a \dots \dots A\sigma^2{}_a \dots \dots 0 \\ I_n\sigma^2{}_e \dots \dots 0 \dots \dots \dots I_n\sigma^2{}_e \end{bmatrix}$$

where $V=A^{-1}\sigma^2{}_G+I_n\sigma^2 e$, A = additive genetic relationship matrix, $\sigma^2{}_G$= additive genetic variance and $\sigma^2 e$ = residual variance. SCC has been transformed to SCS with the base 2 log scale as $SCS=\log_2[3+(SCC/100)]$ accepted by the National Co-operative Dairy Herd Improvement Program of the USA as a standard recording form for SCC (Rogers et al., 1991).

RESULTS AND DISCUSSION

Table (1) shows estimates of R_g and R_p between all studied traits. R_g of SCS with milk traits were mostly negative. These results indicate that the increased somatic cells in milk yield are genetically associated with a slight decrease in milk yield, F% or Lc%. The highest relationships of SCS, either R_p or R_g, were obtained with DY. Results in Table (1) also show great differences between estimates of R_p and R_g of DY with F% and P%, while approximately similar values of R_p and R_g were obtained for the relationship of DY with SCS. Results of the present study were generally consistent with previous reports (Maijala and Hanna, 1974; Hargrove et al., 1981; De Jager and Kennedy, 1987). R_p of SCS with Lc% was much lower than the corresponding R_g, which may indicates that lactose genetically decreased under mastitic conditions. R_g for Lc% with each of P% and F% were high, and ranged from 0.50 to 0.53 (Table 1).

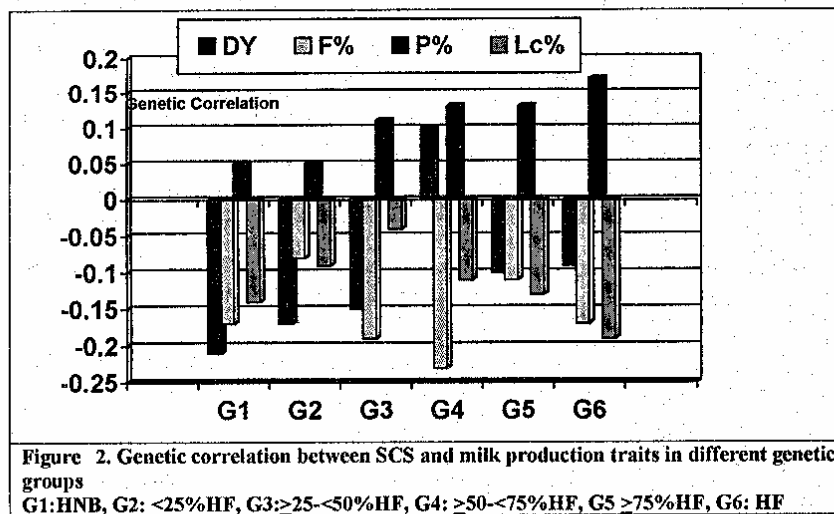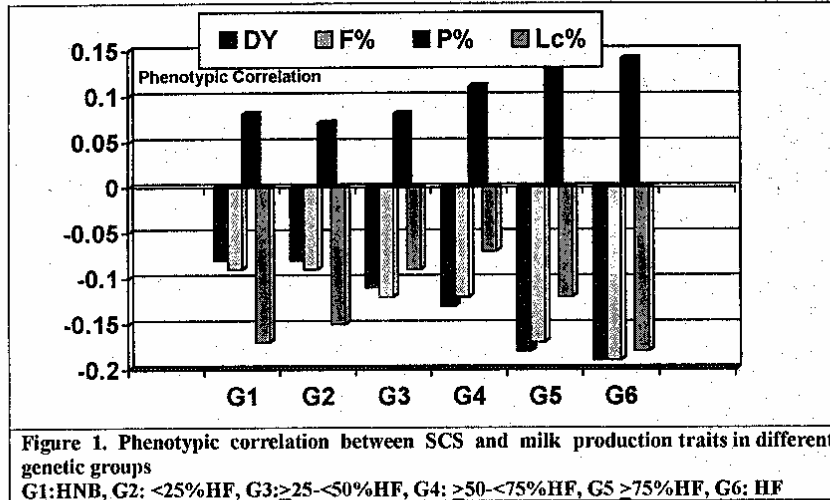Table 1. Sample test-day genetic (above) and phenotypic (below) correlations between different studied traits

	DY	F%	P%	Lc%	SCS
DY		-0.59±0.10	-0.62±0.18	-0.29±0.14	-0.13±0.07
F%	-0.27±0.07		0.66±0.19	0.50±0.14	-0.13±0.08
P%	-0.33±0.18	0.38±0.14		0.52±0.12	0.11±0.04
Lc%	-0.09±0.10	0.53±0.24	0.51±0.12		-0.11±0.08
SCS	-0.15±0.07	-0.09±0.11	0.12+.07	-0.01±0.08	

DY: Daily milk yield, F%: Fat percentage, P%: Protein percentage, Lc%: Lactose percentage, SCS: Somatic cell score.

Corrlations of SCS with milk traits within genetic groups

Phenotypic correlations (R_p) of SCS with milk traits are represented in Figure (1). R_p's were high for crossbred of high HF inheritance than NHB and crossbred of low HF inheritance. Results in Figure (1), show that R_p of SCS with DY and F% changed across different genetic groups. Increasing R_p of SCS with F% was lower than of SCS with DY in HNB, <25%HF and ≥25-<50%HF. On the other hand, R_p's of SCS with DY and F% were similar in HF. R_p estimates (Figure 1) of SCS with P% were positive and increased progressively with increasing HF inheritance, while this estimate for NHB was higher than for <25%HF. Results in Figure (1) show that STD may constitute a statistical model which reveal real association of SCS with each of F% and DY especially for HF and crossbreds with high HF inheritance. Genetic correlations (R_g) between SCS and milk traits in different genetic groups are shown in Figure (2). R_g estimates of SCS with P% were less than 0.05 for NHB and <25%HF. Moreover, no notable change in R_g of SCS with P% among NHB with <25%HF, ≥50-<75%HF and ≥75%HF was observed. Changing rate of R_g for SCS with P% from crossbred of low to medium HF inheritance crossbred (≥25-<50%, ≥50-<75%) was greater than the corresponding change rate from medium inheritance crossbreds to HF. Medium HF inheritance crossbreds had higher for only Rg estimate of SCS with F%. In general these results reflect the increasing trend of relationships with increasing HF inheritance. Estimates of R_g

for SCS with DY, F%, and Lc% declined with HF genes except in $\geq$50-<75%HF, where positive R_g was observed for DY (0.1). Notable reduction of R_g for SCS with Lc% was shown in $\geq$25-<50%HF.

Figure 1. Phenotypic correlation between SCS and milk production traits in different genetic groups
G1:HNB, G2: <25%HF, G3:$\geq$25-<50%HF, G4: $\geq$50-<75%HF, G5 $\geq$75%HF, G6: HF

Figure 2. Genetic correlation between SCS and milk production traits in different genetic groups
G1:HNB, G2: <25%HF, G3:$\geq$25-<50%HF, G4: $\geq$50-<75%HF, G5 $\geq$75%HF, G6: HF

Correlations of SCS with milk traits within parity

Genetic and phenotypic correlations between milk traits and SCS in the first four parities are presented in Table (2). R_g's for SCS with DY were negative and increased from 2nd to the 4th parity. R_g and R_p of SCS with F% decreased with parity. Downward trend was shown for R_p of SCS with DY. These results are in agreement with other reports (De Jager and Kennedy, 1987; Charfeddin, 1997). On the other hand, some studies indicated that the genetic correlations of MY with SCS within the early lactations were positive and ranged from 0.12 to 0.48 (Kennedy *et al.*, 1982; Monardes *et al.*, 1985; and Banos and Shook, 1990). The highest R_g estimates in the present study were -.16, -14, .13 and -.13 in the 4th, 2nd, 2nd, 1st parities for DY, F%, P% and Lc%, respectively. These results indicate that, expected correlated response in milk production through selection against SCS will be more efficient if P% is genetically restricted in selection index. Schutz *et al.* (1990) found genetic correlations between SCS

and MY ranging from -0.15 to -0.28 in different lactation and suggested that mastitis, as indicated by SCS, is more common during early lactations of cows of sires that transmit higher milk yield, perhaps because of the stress from high productivity of milk. The highest R_p estimates were presented mainly in the 1st and 4th parities and differences between these estimates were very small.

Table 2. Sample test-day genetic and phenotypic correlations between somatic cell score and milk production traits per parity

Parity	R_g				R_p			
	DY	F%	P%	Lc%	DY	F%	P%	Lc%
1st	.10±.11	.13±.04	.10±.04	-.13±.07	-.14±.07	-.11±.03	.07±.01	-.12±.09
2nd	-.12±.07	-.14±.07	.13±.01	-.08±.01	-.11±.08	-.11±.07	.07±.05	-.08±.08
3rd	-.14±.01	-.10±.03	.12±.09	-.12±.02	-.12±.01	-.09±.01	.11±.03	-.11±.07
4th	-.16±.07	-.08±.11	.08±.11	-.04±.01	-.20±.11	-.07±.09	.12±.09	-.07±.04

DY: Daily milk yield, F%: Fat percentage, P%: Protein percentage, Lc%: Lactose percentage
R_g :Genetic correlations , R_p :Phenotypic correlations

Correlations between SCS and milk traits within genetic groups within parities

Estimates of R_p and R_g of SCS with milk traits in different genetic groups within parities are presented in Table (3).

SCS with DY: Estimates were negative in all parities except in the 1st parity where positive. R_g's in the 1st parity corresponded to negative R_p's for each genetic group. The highest R_p (>-0.20) was obtained for HF, <25%, and NHB in the 4th, (2nd &3rd), and 1st parity, respectively. In General the highest genetic correlation estimates of SCS with milk yield were mostly obtained in the 4th parity for HF and NHB. While crossbreeds showed moderate estimates in deferent parities. This may suggest that SCS in the early and late parities may be genetically considered different traits, implying that selection in the early lactations could be more effective to reduce SCS and increase mastitis resistance. Estimates of R_p decreased with HF inheritance. Small differences among R_g's within the 1st parity with advancing percentage of HF inheritance were observed compared with those in other parities. Differences between estimates among different genetic groups may reflect true genetic differences across all genetic groups used in the present study.

SCS with F%: R_g of SCS with F% within different parities in various genetic groups were mostly lower than the corresponding estimates with DY. However, this result is more obvious in the <25%HF genetic group. The highest R_g of SCS with F% was -0.27 found in the 3rd & 4th parity (Table 3). Differences between the highest R_g of SCS with DY and SCS with F% were small. Moderate values of genetic correlations among milk constituents may lead to the conclusion that measures of sample test day could be used as a reliable prediction indicator of the production in cases one or more component of milk production traits are missed in monthly observations.

SCS with P%: All estimates of phenotypic and genetic correlations were low to moderate and positive. Genetic correlations ranged from .01 to .20, while phenotypic correlations ranged from .02 to .22 and were nearly in agreement with previous works (Maijala and Hanna, 1974; Hargrove et al., 1981; De Jager and Kennedy, 1987). R_g estimates of SCS with P% were very small (.01 to .09) across different genetic groups in the 1st parity. While R_p of SCS with P% in the 4th parity were very low except for HF and ≥75%HF. The highest R_p for medium HF inheritance crossbreds (≥25-<50%, ≥50-<75%HF) ranged from 0.15 to 0.19 in the 2nd and 3rd parity. The highest R_p for NHB and <25%HF ranged from 0.10 to 0.13 in the 1st and 2nd parity. Estimates of R_p in HF and >75%HF increased with advancing order of lactation while changing rate was approximately similar across parities. Changes of R_p among various parities for HF were much greater than the corresponding changes across genetic groups in the 1st parity. Generally, negative relationship of SCS with F% and positive association of SCS with P% may suggest that sires that transmit higher SCS can also transmit the inheritance of milk with lower F% and higher P%.

SCS with Lc%: Estimates of correlations between Lc% and SCS were in general negative. Among all studied groups the highest R_g's were -0.30, -0.27, and -0.21, obtained in the 3rd, 4th and 2nd parity for HF, respectively. These estimates were the highest correlations obtained for various relationships of SCS with milk production traits. This may indicate that a notable decline in Lc% in milk will occur under mastitic conditions in HF cows. R_g and R_p of SCS with Lc% were mostly higher than the corresponding estimates for SCS with F% of HF. These results may suggest that correlated responses to single trait selection against SCS might result in remarkable improvement in Lc%. Phenotypic

Table 3. Sample test day genetic and phenotypic correlations between somatic cell score and milk production for each genetic group within parity

Parity	Genetic correlations R_g						Phenotypic correlations R_p					
	HNB	<25%HF	≥25-50%HF	≥50-75%HF	≥75%HF	HF	HNB	<25%HF	≥25-<50 %HF	≥50-<75% HF	≥75%H F	HF
Daily milk Kg												
1st	.13±.08	.14±.10	.14±.12	.14±.09	.11±.04	.08±.01	-.22±.07	-.20±.09	-.20±.11	.15±.11	-.14±.18	-.11±.01
2nd	-.13±.07	-.13±.07	-.17±.18	.18±.04	-.14±.02	-.15±.11	-.20±.10	-.21±.07	-.19±.04	-.17±.02	-.14±.07	-.13±.11
3rd	-.09±.07	-.11±.01	-.11±.04	-.08±.03	-.08±.07	-.14±.17	-.20±.12	-.24±.09	-.18±.09	-.11±.01	-.15±.03	-.17±.11
4th	-.22±.11	-.17±.07	-.10±.02	-.12±.06	-.18±.11	-.25±.10	-.18±.09	-.14±.08	-.13±.07	-.13±.11	-.16±.07	-.24±.11
Fat %												
1st	-.22±.12	-.10±.12	-.20±.18	-.11±.07	.05±.11	-.10±.02	-.04±.02	-.05±.03	-.08±.09	-.09±.03	-.11±.03	-.13±.06
2nd	-.19±.11	-.11±.05	-.22±.10	-.13±.06	.06±.02	-.12±.08	-.04±.01	-.06±.03	-.08±.03	-.12±.07	-.12±.09	-.19±.10
3rd	-.11±.03	-.08±.09	-.11±.09	-.27±.07	-.11±.02	-.19±.07	-.09±.03	-.11±.06	-.11±.07	-.04±.03	-.15±.08	-.22±.11
4th	.08±.02	.06±.03	-.10±.03	-.27±.11	-.15±.06	-.23±.12	-.13±.05	-.13±.06	-.14±.05	-.15±.10	-.19±.06	-.17±.03
Protein %												
1st	.01±.01	.03±.02	.09±.11	.05±.06	.08±.09	.08±.07	.12±.19	.11±.04	.04±.06	.08±.06	.11±.06	.12±.05
2nd	.03±.01	.03±.01	.11±.05	.09±.03	.20±.12	.15±.10	.13±.07	.10±.06	.15±.02	.18±.08	.12±.08	.15±.03
3rd	.09±.02	.05±.01	.13±.06	.12±.07	.19±.11	.13±.12	.09±.01	.03±.07	.17±.02	.19±.09	.17±.09	.19±.07
4th	.11±.03	.12±.10	.04±.01	.17±.09	.09±.02	.07±.15	.02±.04	.02±.07	.05±.02	.07±.05	.19±.04	.22±.04
Lactose %												
1st	.07±.01	.09±.11	.01±.12	-.12±.01	-.11±.01	-.10±.03	-.18±.10	-.13±.12	-.11±.09	-.05±.09	-.07±.02	-.09±.01
2nd	-.07±.01	-.08±.03	-.03±.01	-.13±.01	-.11±.02	a.21±.06	-.17±.20	-.12±.12	-.08±.07	-.09±.01	-.07±.03	-.12±.07
3rd	-.09±.11	-.09±.02	-.07±.12	-.15±.02	-.12±.06	-.30±.07	-.19±.11	-.12±.09	-.07±.02	-.11±.03	-.12±.09	-.18±.01
4th	-.15±.12	-.11±.09	-.03±.03	-.09±.03	-.08±.06	-.27±.06	-.22±.14	-.19±.11	-.13±.02	-.13±.02	-.15±.07	-.19±.01

R_g: Genetic correlations, R_p: Phenotypic correlations
HNB: Hungarian Native Breed, HF: Holstein Friesian

correlation estimates of SCS for NHB were generally higher than those for HF across parities. The lowest R_p between Lc% and SCS was –0.05 obtained for $\geq$50-<75%HF in the 1st parity.

CONCLUSION

R_g's of SCS with milk traits were generally negative and low. Therefore, increase in SCC is not accompanied genetically with a great decrease in DY, F% or Lc%. The highest R_p's of SCS with milk production were obtained in the 1st and 4th parities. Therefore analysis of separate parities may be more appropriate than using the pooled analysis of STD. R_g for SCS with DY progressively negative increased in later parities. The negative genetic relationship between SCS and F% and positive between SCS and P% may suggest that sires transmit higher SCS can also transmit lower F% and higher P%. R_g and R_p of SCS with Lc% were mostly higher than the corresponding estimates for SCS with F% of HF. These results may suggest that correlated responses to single trait selection against SCS might result in remarkable improvement in Lc%.

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