

## HERITABILITY ESTIMATES FOR SAMPLE TEST-DAY SOMATIC CELL SCORE AND MILK TRAITS FOR HUNGARIAN HOLSTEIN-FRIESIAN CROSSBREDS

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### SUMMARY

Sample test day (STD) of somatic cell score (SCS) and milk production traits were analysed. Data included records of Hungarian Native Breed (HNB), Holstein-Friesian (HF) and their crossbreds. Hungarian Holstein-Friesian crossbreds were <25%HF, ≥25-<50%HF, ≥50-<75%HF and ≥75%HF. The total number of lactation records were 348108 of 130335 cows, daughters of 2124 sires in the first three parities. All records of the studied traits were analysed by Multi-Trait Derivative Free REML animal model. The highest  $h^2$  of SCS was obtained for genetic groups of <25% and ≥25-<50%HF inheritance. Crossbreds of ≥75%HF genes showed a greater genetic variation in milk yield than the other groups.  $h^2$  estimates for SCS in the 1<sup>st</sup> parity were similar in different genetic groups.  $h^2$ 's of fat (F%) decreased with increasing HF%, while  $h^2$ 's of lactose (Lc%) increased.  $h^2$ 's for F% in low %HF groups were smaller than in high %HF in all parities.  $h^2$ 's of protein (P%) in different genetic group decreased with parity.

*Keywords: Somatic cell, milk production, heritability, Holstein, crossbred*

### INTRODUCTION

Efficient milk production is the principle goal for dairy cattle enterprises and most of breeding programs. Disturbances in health of dairy herds are expensive and hardly acceptable for economic management or for ethical reasons. Crossbreds in most countries play an important role for covering their dairy needs. In different European countries milk somatic cell count has been considered as an accurate indicator of udder health and as a useful criterion for selection decisions (Coffey *et al.*, 1986). Elevates of somatic cell in milk are mostly associated with mastitis incidence and milk yield declines, even at relatively low levels of SCC (Kennedy *et al.*, 1982; Monardes and Hayes, 1985).

The objective of the present study was to examine the effect of introducing Holstein Friesian genes in the Hungarian native breed on the inheritance of somatic cell score and milk production traits in different parities using sample test days measures.

### MATERIALS AND METHODS

Sample test-day (STD) observations for six genetic groups are shown in Table (1). Data included records of Hungarian Native Breed (HNB), Holstein-Friesian (HF) and their crossbreds. Hungarian Holstein-Friesian crossbreds were <25%HF, ≥25-<50%HF, ≥50-<75%HF, and ≥75%HF. Records included in the present study had at least 220 days of production with at least five subsequent monthly sample observations. Data were of the first three parities of cows calving from June 1990 to December 1994. Sample day observations were ignored if any sample day measure on the studied traits was missing. Records with missing two consecutive sample test day observations were also ignored. Variations due to age at calving within parity were adjusted according to (Zhang *et al.*, 1994).

Sample test day observations were daily milk yield (DY<sub>K</sub>), fat (F%), protein (P%), and lactose (Lc%) percentages, somatic cell count (SCC) measure as thousand per ml of milk. SCC was transformed to SCS with the base 2 log scale as  $SCS = \log_2[(SCC/100)+3]$ , a method accepted by the National Co-operative Dairy Herd Improvement Program of the USA as a standard recording form for SCC (Rogers *et al.*, 1991).

STD records were classified by parity (the first three parities only) for four genetic groups and two purebreds (Table 1). Least Squares means were estimated for somatic cell count (Table 1), and heritabilities computed for SCS.

**Table 1. Least squares means in different genetic groups for somatic cell counts and milk traits**

Genetic group	SCC*10 <sup>3</sup>	F%	P%	Lc%	DY
<i>Overall</i>					
NHB	97±47	5.1±.14	5.1±.14	6.4±1.1	9.3±1.4
<25% HF	114±23	4.7±.07	4.7±.14	5.2±1.1	11.4±1.9
≥25-<50% HF	278±47	4.7±.07	4.2±.10	4.9±1.0	15.2±2.1
≥50-<75% HF	372±48	4.2±.08	3.7±.10	4.1±.80	18.4±2.1
≥75% HF	415±64	4.0±.10	3.4±.08	3.6±.77	19.7±2.8
HF	541±91	4.0±.10	3.5±.08	3.2±.96	24.4±2.9
<i>1<sup>st</sup> Parity</i>					
NHB	77±18	6.1±.13	4.2±.09	7.7±1.4	9.5±1.0
<25% HF	83±23	4.8±.10	3.9±.08	6.1±1.2	10.1±1.1
≥25-<50% HF	170±47	4.5±.09	3.5±.08	5.7±1.1	14.7±1.7
≥50-<75% HF	297±65	4.1±.09	3.3±.08	4.7±.80	16.9±1.9
≥75% HF	326±65	3.9±.07	3.0±.07	4.3±.80	18.9±2.5
HF	453±112	3.7±.08	3.1±.04	3.9±.80	19.2±2.9
<i>2<sup>nd</sup> Parity</i>					
NHB	89±27	4.8±.90	5.0±.13	6.8±1.7	9.8±1.1
<25% HF	116±23	4.9±.04	4.9±.14	5.4±1.7	10.7±1.7
≥25-<50% HF	293±49	4.3±.05	4.3±.11	5.0±1.4	15.7±1.7
≥50-<75% HF	361±69	3.7±.11	3.7±.12	4.1±1.1	18.9±2.8
≥75% HF	419±72	3.7±.11	3.2±.12	3.5±.97	21.3±2.9
HF	491±97	3.4±.10	3.3±.12	3.1±.97	22.5±3.4
<i>3<sup>rd</sup> Parity</i>					
NHB	125±43	4.3±.90	6.0±.14	4.9±1.1	10.1±1.7
<25% HF	143±43	4.3±.02	5.2±.14	4.3±1.0	11.5±2.1
≥25-<50% HF	391±76	3.5±.04	5.0±.15	4.1±.99	17.3±2.4
≥50-<75% HF	461±71	3.3±.07	4.5±.11	3.6±.91	21.8±2.7
≥75% HF	513±119	3.0±.07	4.0±.11	3.0±.87	23.2±3.1
HF	679±134	3.2±.08	4.1±.09	2.3±.77	28.8±3.3

NHB: native Hungarian Breed, HF: Holstein Friesian, SCC: Somatic cell count, F%: Fat percentage, P%: Protein percentage, Lc%: Lactose percentage, DY: Daily milk yield.

The statistical animal model was used to explore variation due to the fixed effects of genetic groups, and random effects of sires. Sire half-sib sisters covariances were estimated applying animal mixed model {AMM} analysis of variance.

The general mathematical model used was

$$Y_{ijklmn} = \mu + G_i + S_{ji} + C_{kji} + P_l + STG_{ml} + \epsilon_{ijklmn}$$

Where:-

$Y_{ijklmn}$ : is the SCC (log<sub>2</sub> transformed), sample test day of F%, P%, Lc%, and DY<sub>kg</sub>

$\mu$ : Population mean,  $G_i$ : fixed effect of  $i$ th genetic groups,  $i = 1$  to 6 (classified according to the percentage of Holstein Friesian (HF) genes when crossed with the native Hungarian breed {HNB}),  $S_{ji}$  is the effect of  $j$ th sire nested within  $i$ th genetic group assumed to be randomly distributed around zero with variance  $A\sigma^2_s$ , where  $A$  is the numerator relationship matrix between sires,  $C_{kji}$ : random effect of  $k$ th cow nested within  $j$ th sire and within  $i$ th genetic group,  $P_l$ : fixed effect of  $l$ th order of lactation ( $l = 1, 2, 3$  parity),  $STG_{ml}$ : is the effect of  $m$ th lactation stage within  $l$ th parity,  $\epsilon_{ijklmn}$ : is the residual randomly distributed around 0 with variance  $I\sigma^2_e$ , where  $I$  is the identity matrix.

Separate analyses of variances were also applied for each genetic group and for each parity to obtain heritability estimate for all investigated traits.

Variance and covariance components required for the estimation of  $h^2$  for SCS, DY, F%, P% and Lc% were computed applying multi-traits derivative free restricted maximum likelihood procedure (MT-DF-REML), Boldman (1997).

## RESULTS AND DISCUSSION

Published Hungarian studies for estimating  $h^2$  of SCS in HF are very scarce. Estimates of  $h^2$ , sire additive and residual variance components for all traits are shown in Table (2). In general, STD of sire additive variance for all studied traits in HF herein, are higher than those reported by (Kennedy *et al.*, 1982 and Boettcher *et al.*, 1992) but a greater magnitude of STD estimates of sire additive and a reduced residual variance component than those reported by (Grossman *et al.*, 1986). STD analysis of SCS could possibly remove a considerable amount of its environmental variance components.  $h^2$  for milk SCS ranged from 0.14 to 0.37 in all genetic groups. These estimates are higher than that reported by Schutz *et al.* (1994). Seykora and McDaniel (1986) found that  $h^2$  of neutral SCC in the 1<sup>st</sup> parity was slightly higher than those for log transformation SCS while the opposite trend was reported by Schutz (1994).  $h^2$  of SCS increased with HF genes in different crosses except in  $\geq 75\%$ HF. HF had the lowest  $h^2$  of SCS and is less than NHB by 33%. There is association between  $h^2$  for SCS and both of DY and P% in NHB,  $<25\%$  HF and  $\geq 25\text{-}<50\%$ HF (Table 2). On the other hand,  $h^2$  for F% decreased with advancing HF inheritance. Therefore, selection against SCS, needs accurate study to consider the relationship between milk composition and SCS. This indicates that inclusion DY or/and P% in selection against SCS may prevent reduction in F%. Crossbreds with medium HF inheritance had the highest  $h^2$  of SCS ( $\geq 25\text{-}<50\%$ HF and  $\geq 50\text{-}<75\%$ HF). Similar results were obtained for P%. Shook *et al.* (1982) has shown that  $h^2$  of a lactational average of SCS is higher than that of a single test. In contrast, Emanuelson *et al.* (1988) found that lactational average of SCS was not very different from estimates based on single tests.  $h^2$  of DY (Table 2) decreased from  $\geq 25\text{-}<50\%$ HF toward NHB and then increased from  $\geq 50\text{-}<75\%$ HF toward HF. Changes in  $h^2$ 's for DY across HNB to  $\geq 25\text{-}<50\%$ HF and HF to  $\geq 50\text{-}<75\%$ HF are small and approximately similar.

Estimates of heritability for SCS and milk traits in the first three parities are shown in Figures 1-1, 1-2, 1-3.  $h^2$ 's of SCS in the 1<sup>st</sup> parity are within a narrow range among different genetic groups. This may reflect that, STD may reduce the amount of environmental variance as opposed to lactational estimates (Coffey *et al.*, 1985) as well as total phenotypic variance. On the other hand, differences in  $h^2$ 's for SCS among genetic groups increased in the 2<sup>nd</sup> and the 3<sup>rd</sup> parity. Kennedy *et al.* (1982) reported that STD observation of SCS had  $h^2$  ranging from 0.05 to 0.10 with a tendency to increase with cow age.  $h^2$ 's of SCS for HF and  $\geq 75\%$  HF declined sharply with increasing parity.

Replacing half or little more of NHB genes by HF genes causes increasing  $h^2$  for SCS. In general differences between  $h^2$ 's of SCS across parities were not small. This may be due to change amount of residual variance across parities. These results are in agreement with that reported by Coffey *et al.* (1986). They also concluded that SCS early and late in life may genetically constitute different traits. Differences in  $h^2$ 's for milk somatic cell among genetic groups indicate there is a real difference in the inheritance of resistance to mastitis not only across parities but also among different stages of lactation.  $h^2$ 's of DY (Fig.1-2) had strong linearly up-ward trend with advancing parity for  $\geq 25\text{-}<50\%$ HF &  $\geq 50\text{-}<75\%$ HF. While  $h^2$ 's of DY were linearly down ward for  $\geq 75\%$ HF and HF. Extremely antagonistic trend obtained between  $h^2$  of F% and DY.  $h^2$ 's of F% revealed up word trend with advancing parity for  $\geq 75\%$  HF vs. for  $<25\%$  HF.

$h^2$ 's of P% decreased with parity for all genetic groups. Differences of  $h^2$ 's for P% decreased with parity among NHB,  $<25\%$ HF, and  $\geq 25\text{-}<50\%$ HF.  $h^2$  for Lc% HF,  $\geq 50\text{-}<75\%$ HF and  $\geq 75\%$ HF were higher than the corresponding estimates of the other genetic groups in the 2<sup>nd</sup> and the 3<sup>rd</sup> parity. The genetic groups of high Holstein inheritance had rapid progressive change in  $h^2$ 's of Lc%. On the other hand the reduction rate was low in groups of low HF%. Monardes and Hays (1985) reported that, accumulation of the temporary environmental variance in each month of test day into one single residual was an important reason in increasing the residual components of variance with parity. Treating sample test day observations as multiple traits is an appropriate statistical solution for the analysis of variance. Genetic groups with high  $h^2$  estimates and wide range of additive variance for SCS are more appropriate in selection programs to reduce SCS and to improve mastitis resistance. Crossbreds with medium HF inheritance may be more appropriate genetic group for selection against SCS and consequent improves udder health. The current results indicate that, crossbreeding generated genetic variation in SCS among different grades of corssbreds that may be used to genetically improve that trait.

Table 2. Sample test-day (STD) estimates of sire ( $\sigma^2_s$ ), residual variance ( $\sigma^2_r$ ) component, heritability ( $h^2$ ) and standard error (SE) for somatic cell scores (SCS) and milk production traits

Genetic group	SCS			DY			F%		
	$\sigma^2_s$	$\sigma^2_r$	$h^2 \pm SE$	$\sigma^2_s$	$\sigma^2_r$	$h^2 \pm SE$	$\sigma^2_s$	$\sigma^2_r$	$h^2 \pm SE$
NHB	9871	197890	.21 $\pm$ .19	18.55	389.550	.20 $\pm$ .13	2.11	24.921	.37 $\pm$ .14
<25% HF	12314	182162	.29 $\pm$ .20	22.30	447.062	.21 $\pm$ .07	2.01	27.135	.32 $\pm$ .14
>25-<50% HF	17189	203016	.37 $\pm$ .11	28.19	479.230	.25 $\pm$ .09	1.78	26.331	.29 $\pm$ .15
>50-<75% HF	14921	201433	.32 $\pm$ .12	26.01	459.510	.24 $\pm$ .17	1.50	26.500	.24 $\pm$ .10
$\geq$ 75% HF	8814	216202	.17 $\pm$ .19	32.11	490.824	.28 $\pm$ .22	1.33	23.497	.24 $\pm$ .10
HF	10470	309612	.14 $\pm$ .07	33.18	507.180	.28 $\pm$ .07	1.21	25.410	.20 $\pm$ .10
		P%			Lc%				
NHB	4.77	56.338	.37 $\pm$ .12	12.28	246.185	.21 $\pm$ .09			
<25% HF	4.12	44.315	.41 $\pm$ .12	9.01	172.828	.22 $\pm$ .07			
>25-<50% HF	5.31	52.510	.45 $\pm$ .20	10.31	189.614	.23 $\pm$ .05			
>50-<75% HF	6.13	63.153	.43 $\pm$ .18	22.37	235.418	.42 $\pm$ .19			
$\geq$ 75% HF	4.37	77.203	.24 $\pm$ .18	26.97	272.151	.44 $\pm$ .22			
HF	3.94	82.740	.20 $\pm$ .11	29.91	295.777	.45 $\pm$ .17			

NHB: native Hungarian Breed, HF: Holstein Friesian, SCS: Somatic cell score, F%: Fat percentage, P%: Protein percentage

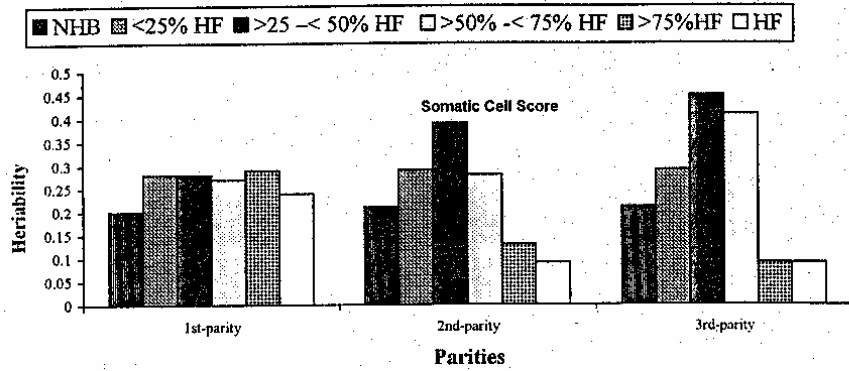


Figure 1-1 Sample test day heritability estimates for somatic cell score per parity in the six genetic groups of Holstein X Hungarian crossbred.

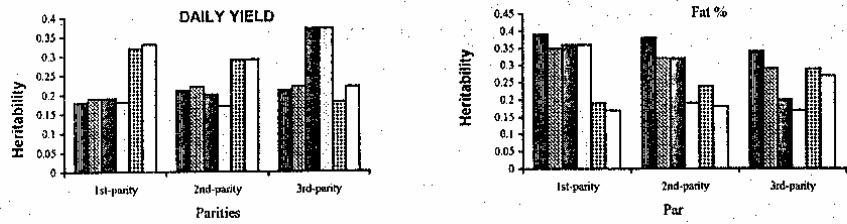


Figure 1-2 Sample test day heritability estimates for daily milk yield and fat % per parity in the six genetic groups of Holstein X Hungarian crossbred.

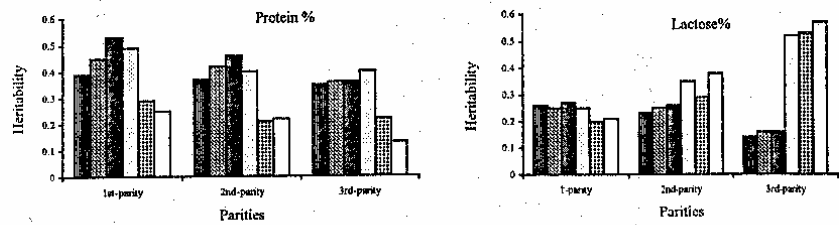


Figure 1-3 Sample test day heritability estimates for protein and lactose percentage per parity in the six genetic groups of Holstein X Hungarian crossbred.

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