

## **RELATIONSHIP BETWEEN SOMATIC CELL SCORE AND UDDER CONFORMATION TRAITS IN POLISH HOLSTEIN-FRIESIAN COWS\***

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### **Abstract**

Somatic cell score (SCS) has been recognized as an indicator of the presence of mastitis. The purpose of this study was to estimate genetic relationships between SCS and udder traits. Data were lactational SCS (LSCS) calculated as the average of a minimum of 5 test-day SCS of 26,727 first-parity cows, sired by 295 bulls. The following udder type traits were included: udder score, fore udder attachment, rear udder height, central ligament, udder depth, rear udder width, fore teat placement and teat length. The multi-trait REML model consisted of fixed effects of herd-year-season-classifier, stage of lactation and linear regression on calving age, and random additive genetic and residual effects. Heritabilities estimated for LSCS and udder traits were low to moderate, ranging from 0.12 to 0.31. Genetic correlations between LSCS and udder traits were very low with the exception of genetic correlations between LSCS and udder depth (–0.17) and between LSCS and rear udder width (0.20), which suggested that shallower and narrower udders are associated with lower SCS.

**Key words:** dairy cattle, somatic cell score, udder type traits, genetic parameters

The large increase in milk production observed in the last decades has been accompanied by an adverse response in fertility, health and longevity. One of the most important udder health traits is mastitis, indirectly measured by SCS (Boettcher et al., 1998).

Beaudeau et al. (2000) reported that at least half of all cullings of dairy cows were health-related, with mastitis being one of the most frequent reasons. In Poland in recent years the proportions of cows culled due to mastitis was about 10% (Żarnecki, unpublished data).

Both positive and negative (favourable) genetic correlations between milk production and SCS have been reported in the literature (Charfeddine et al., 1997; Rupp

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and Boichard, 1999). Low heritabilities of SCS have prompted a search for udder conformation traits that could improve the effectiveness of selection for increased mastitis resistance. Generally, genetic correlations between SCS and udder conformation traits have been favourable, allowing those traits to be included in selection indexes (Boettcher et al., 1998; Rogers et al., 1998).

The objective of this study was to estimate genetic relationships between lactational SCS and udder conformation traits in the Polish Holstein-Friesian population.

### Material and methods

Data were first-parity somatic cell counts (SCC) and eight udder conformation traits of 26,727 Polish Holstein-Friesian cows that calved for the first time from 1998 through 2006. Cows were daughters of 295 sires. The following restrictions on data were imposed: 1) a minimum of 20 cows per herd-year subclass, 2) sires with at least 30 daughters, and 3) cows with at least five test-day records.

The conformation scores included descriptive evaluations of overall udder conformation, and seven linearly scored traits (fore udder attachment, rear udder height, central ligament, udder depth and width, fore teat placement, teat length). The daily somatic cell counts (SCC) were log-transformed to somatic cell scores according to the formula:  $SCS = \log_2 (SCC/100,000) + 3$ , and adjusted for calendar month and lactation stage. Then the lactational somatic cell scores (LSCS) were obtained as arithmetic means of daily SCS. Means with standard deviations of all traits are presented in Table 1. Overall udder values were between 50 and 88, all other type traits—between 1 and 9, and LSCS—from -0.30 to 9.21.

Table 1. Means and standard deviations (SD) of the udder conformation traits and LSCS (N = 26,727)

No.	Trait*	$\bar{x}$	SD	min	max
1.	Udder score (50–100 scale)	77.04	4.50	50.00	88.00
2.	Fore udder attachment (1–9 scale)	5.76	1.20	1.00	9.00
3.	Rear udder height (1–9 scale)	5.55	1.13	1.00	9.00
4.	Central ligament (1–9 scale)	5.59	1.43	1.00	9.00
5.	Udder depth (1–9 scale)	5.69	1.39	1.00	9.00
6.	Rear udder width (1–9 scale)	5.61	1.15	1.00	9.00
7.	Fore teat placement (1–9 scale)	5.03	1.19	1.00	9.00
8.	Teat length (1–9 scale)	4.65	1.13	1.00	9.00
9.	Lactational somatic cell score (LSCS)	3.46	1.31	-0.30	9.21

\*Description of type traits in Żarnecki et al. (2000).

Additive adjustment factors for each calendar month and lactation stage were computed based on a linear model including fixed effects of herd-year, calendar month and lactation stage (SAS/STAT, 1990). Lactations (5 to 305 days) were divided into 12 lactation stages consisting of 30-day intervals except for the first, second and third stages (10 days) and the last stage (35 days).

The multi-trait REML method was applied for (co)variance components estimation (Misztal and Perez-Enciso, 1993). The linear model included random additive genetic effect, fixed effects of herd-year-season-classifier (HYSC) and lactation stage, and fixed regression on age at calving. There were 1,506 HYSC subclasses, 12 lactation stages and 60,183 animals included in the analysis.

## Results

Heritabilities and genetic and phenotypic correlations are shown in Table 2. Estimates of heritabilities were 0.14 for LSCS, 0.12 for overall udder, 0.15 for udder width, 0.16 for central ligament, 0.18 for fore udder attachment, 0.20 for fore teat placement, 0.21 for rear udder height, 0.28 for udder depth, and 0.31 for teat length.

Genetic correlations between LSCS and udder traits in most cases were very low (Table 2). The exceptions were correlations between LSCS and udder depth ( $-0.17$ ) and between SCS and udder width (0.20). Central ligament, teat placement and teat length were not genetically correlated with LSCS (0.02).

Table 2. Heritabilities (on the diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations among udder conformation traits and lactational somatic cell score (LSCS)

No.	Trait	1.	2.	3.	4.	5.	6.	7.	8.	9.
1.	Overall udder	<b>0.12</b>	0.71	0.75	0.46	0.62	0.64	0.54	-0.31	0.06
2.	Fore udder attachment	0.42	<b>0.18</b>	0.31	0.27	0.73	0.17	0.49	-0.13	-0.08
3.	Rear udder height	0.39	0.19	<b>0.21</b>	0.38	0.38	0.76	0.31	-0.19	0.07
4.	Central ligament	0.32	0.17	0.26	<b>0.16</b>	0.38	0.26	0.36	-0.03	0.02
5.	Udder depth	0.26	0.41	0.19	0.27	<b>0.28</b>	-0.01	0.32	-0.13	-0.17
6.	Udder width	0.41	0.12	0.47	0.19	-0.09	<b>0.15</b>	0.36	-0.24	0.20
7.	Fore teat placement	0.23	0.21	0.10	0.15	0.17	0.10	<b>0.20</b>	-0.38	0.02
8.	Teat length	0.02	0.01	0.01	0.03	-0.04	0.03	-0.09	<b>0.31</b>	0.02
9.	LSCS	-0.08	-0.07	-0.03	-0.09	-0.11	0.01	-0.02	-0.01	<b>0.14</b>

Teat length was negatively and moderately correlated with all other type traits ( $-0.13$  to  $-0.38$ ) except central ligament ( $-0.03$ ). Central ligament is used by the Interbull Centre for validation because this trait is similarly defined in all countries participating in the international evaluation. Genetic correlations between central ligament and other udder traits were all positive and ranged from 0.26 (with udder width) to 0.46 (with overall udder). The only descriptive trait (overall udder) showed high genetic correlations with all linearly scored udder traits; the highest were with rear udder height (0.75) and fore udder attachment (0.71). The correlation between overall udder and teat length was negative ( $-0.31$ ), showing that cows with shorter teats obtained higher descriptive scores.

Almost all phenotypic correlations between LSCS and type traits were negative and negligible (Table 2). The only remarkable correlation was between LSCS and udder depth ( $-0.11$ ), which indicated that cows with shallower udders had lower SCS. Phenotypic correlations between overall udder and linearly scored traits were positive

(from 0.23 to 0.42). Correlations between teat length and all udder traits (including overall udder) were close to zero. In most cases the phenotypic correlations between other analysed linearly scored traits (udder width and depth, fore udder attachment, rear udder height, central ligament, fore teat placement) were positive and moderate (0.10 to 0.47).

## Discussion

Heritability for LSCS (0.14) was in agreement with previously reported estimates (Boettcher et al., 1998; Charfeddine et al., 1997; Rogers et al., 1991; Rupp and Boichard, 1999). Differences in estimates could be attributed partly to differences in definitions of lactational SCS, although size of data file and the model for statistical analysis were also important. In most cases the heritabilities for udder type traits (Table 2) were slightly greater than previous estimates (Żarnecki et al., 2000), very similar to those reported by Rupp and Boichard (1999), and markedly higher than those estimated by Charfeddine et al. (1997).

As shown in Table 2, genetic correlations between LSCS and udder type traits were low with the exception of the genetic correlation between LSCS and udder depth ( $-0.17$ ) and between SCS and udder width (0.20), suggesting that shallower and narrower udders are associated with lower SCS. Rupp and Boichard (1999) and Charfeddine et al. (1997) found much stronger correlations between LSCS and udder depth ( $-0.40$  and  $-0.25$ ).

The genetic correlations between LSCS and three udder traits (central ligament, teat placement, teat length) suggested that these traits were not genetically correlated, although Charfeddine et al. (1997) obtained moderate correlations between LSCS and those udder traits ( $-0.12$  with central ligament,  $-0.12$  with teat placement, 0.14 with teat length), showing that stronger central ligament, closer teat placement and longer teats may be favourable. Rupp and Boichard (1999) reported an undesirable correlation between LSCS and teat placement (0.14) and a slightly higher correlation between LSCS and teat length than that shown in Table 2 (0.08); the genetic correlations between LSCS and udder type traits reported in the literature are inconsistent and vary in magnitude and sign.

Among the phenotypic correlations between LSCS and udder traits, the only remarkable correlation was between LSCS and udder depth ( $-0.11$ ), which indicated that cows with shallower udders had lower SCS. This result agrees with other reports (Charfeddine et al., 1997; Rogers et al., 1991).

Our and other authors' findings show that most of the genetic correlations between LSCS and udder conformation traits are low except for udder depth and udder width. The correlations between LSCS and these two udder traits are of moderate magnitude, and therefore can be included in a selection index aimed at improving genetic resistance to mastitis in dairy populations.

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**Zależność między zawartością komórek somatycznych a cechami budowy wymienia w populacji krów rasy polskiej holsztyńsko-fryzyjskiej**

STRESZCZENIE

Zawartość komórek somatycznych (SCS) jest uważana za wskaźnik występowania mastitis. Celem badań było oszacowanie genetycznych zależności pomiędzy SCS a cechami budowy wymienia. Dane stanowiły laktacyjne zawartości komórek somatycznych (LSCS), które obliczono jako średnie z co najmniej 5 dziennych próbnych udojów, pochodzących z pierwszych laktacji 26 727 krów-córek 295 buhajów. W badaniach uwzględniono następujące cechy budowy wymienia: ogólną ocenę, zawieszenie przednie, zawieszenie tylne, więzadło środkowe, położenie, szerokość, a także ustawienie strzyków przednich i długość strzyków. Do obliczeń zastosowano metodę REML opartą na wielocechowym modelu liniowym, zawierającym stałe efekty podklasy stado-rok-sezon-klasyfikator, faz laktacji i regresję liniową na wiek ocielania. Ponadto w modelu uwzględniono losowy genetyczny efekt addytywny i błąd losowy.

Odziedziczalności oszacowane dla LSCS były niskie lub umiarkowane i wahały się od 0,12 do 0,31. Korelacje genetyczne między LSCS i cechami budowy wymienia były bardzo niskie, z wyjątkiem korelacji między laktacyjną zawartością komórek somatycznych (LSCS) i położeniem wymienia (–0,17) oraz zawieszeniem tylnym wymienia (0,20), co wskazuje, że płytsze i węższe wymiona są związane z mniejszą liczbą komórek somatycznych w mleku.