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Relationship between somatic cell score and udder conformation traits in Polish Holstein-Friesian cows

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Introduction

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. Both positive and negative (favourable) genetic correlations between milk production and SCS have been reported in the literature. 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.

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 share of cows culled due to mastitis was about 10%.

The objective of this study was to estimate genetic relationships between 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, daughters of 295 sires. Restrictions of a minimum 20 cows per herd-year subclass and sires with at least 30 daughters were imposed.

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: $\mathrm{SCS} = \log_2(\mathrm{SCC}/100{,}000) + 3$, and adjusted for calendar month and lactation stage. Then the lactational somatic cell scores (LSCS) were obtained as arithmetic means of SCS only for cows with at least five daily SCS.

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 animal 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 and Discussion

Heritabilities and genetic and phenotypic correlations are shown in Table 1. Heritabilities estimated for LSCS and udder traits were low to moderate: LSCS 0.14, overall udder 0.12, udder width 0.15, central ligament 0.16, fore udder attachment 0.18, fore teat placement 0.20, rear udder height 0.21, udder depth 0.28, and teat length 0.31. Heritability for LSCS was in agreement with previously reported estimates (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 data file size and the model for statistical analysis were also important. In most cases, heritabilities for udder type traits 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).

Genetic correlations between LSCS and udder traits were very low in most cases (Table 1). The exceptions were between LSCS and udder depth (-0.17) and between SCS and rear 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 a much stronger correlation between LSCS and udder depth (-0.40 and -0.25). Central ligament, teat placement and teat length were not genetically correlated with LSCS (r_g=0.02), although Charfeddine et al. (1997) obtained favourable correlations between LSCS and these udder traits (-0.12 with central ligament, -0.12 with teat placement, 0.14 with teat length).

Almost all phenotypic correlations between LSCS and type traits were negative and negligible (Table 1). The only remarkable correlation was between LSCS and udder depth (-0.11), which indicated that cows with shallower udders had lower SCS. These results agree with other reports (Charfeddine et al., 1997; Rogers et al., 1991).

These and other findings suggest that genetic evaluations for SCS and some udder conformation traits (udder depth for instance) can be a useful tool to improve genetic resistance to mastitis in dairy populations if used properly in selection indexes.

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Table 1. Heritabilities (on diagonal) and 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	**0.12**	0.71	0.75	0.46	0.62	0.64	0.54	-0.31	0.06
2.	Fore udder attachment	0.42	**0.18**	0.31	0.27	0.73	0.17	0.49	-0.13	-0.08
3.	Rear udder height	0.39	0.19	**0.21**	0.38	0.38	0.76	0.31	-0.19	0.07
4.	Central ligament	0.32	0.17	0.26	**0.16**	0.38	0.26	0.36	-0.03	0.02
5.	Udder depth	0.26	0.41	0.19	0.27	**0.28**	-0.01	0.32	-0.13	-0.17
6.	Udder width	0.41	0.12	0.47	0.19	-0.09	**0.15**	0.36	-0.24	0.20
7.	Fore teat placement	0.23	0.21	0.10	0.15	0.17	0.10	**0.20**	-0.38	0.02
8.	Teat length	0.02	0.01	0.01	0.03	-0.04	0.03	-0.09	**0.31**	0.02
9.	LSCS	-0.08	-0.07	-0.03	-0.09	-0.11	0.01	-0.02	-0.01	**0.14**

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