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Heritabilities and genetic correlations of lactational and daily somatic cell score with conformation traits in Polish Holstein cattle

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Introduction

Large genetic improvement of milk production has caused a decline in many functional traits. One of the most important is udder health. Udder diseases – mainly mastitis – impose increasing costs on milk producers and could ultimately lead to involuntary culling. In many countries the incidence of mastitis is not routinely recorded and direct selection for udder health is not possible, so other selection criteria are needed. Possible indirect selection criteria include somatic cell score (SCS) and some conformation traits, especially udder traits (Charfeddine et al., 1997). The results of previous studies indicate that selection for decreased SCS reduces the incidence of mastitis (Rupp and Boichard, 1999, Nash et al., 2000). Also, the genetic correlation between SCS and clinical mastitis is positive and moderate to high (0.36-0.98) (Rupp and Boichard, 1999); in most countries SCS is used for indirect selection against mastitis (Miglior et al., 2005).

In Poland, a multi-trait animal model based on lactational SCS (LSCS), calculated as means of test-day SCS in each of the first three lactations, is used for genetic evaluation. Estimated breeding values for LSCS are directly included in the total index, whereas in other countries both SCS and conformation traits are included in selection subindexes. Some of the type traits are genetically correlated with SCS, and the magnitude of heritabilities and genetic correlations allow evaluation of the correlated response in udder health (Charfeddine et al., 1997).

In the near future the lactational model of SCS genetic evaluation will be replaced by the test-day model; therefore, the objective of this study was to estimate heritabilities and genetic correlations for lactational (LSCS) and daily somatic cell scores (DSCS) with descriptive and linear type traits of Polish Holstein-Friesian cows.

Material and Methods

Data were obtained from the Polish Federation of Cattle Breeders and Dairy Farmers and consisted of test-day somatic cell scores (DSCS), lactational somatic cell scores (LSCS) and 22 conformation traits of 24,599 Polish Holstein-Friesian primiparous cows. Test-day somatic cell scores (DSCS) were matched with the closest date of type evaluation. Lactational somatic cell scores (LSCS) were calculated as the average of at least four test-day SCS. The conformation traits included five descriptive traits, height at rump, and sixteen linearly scored traits (Table 1).

Cows calved for the first time in 2006 and 2007 at the age of 18-48 months. They were daughters of 802 sires. Restrictions of a minimum 10 daughters per sire and 10 cows per herd were imposed. The distance between date of test and date of type evaluation had to be less than 50 days.

(Co)variance components for all 24 traits (DSCS, LSCS and 22 type traits) were estimated using the multi-trait Gibbs Sampling algorithm and the BLUPF90 computing package (Misztal, 1999). The linear model used for DSCS contained random additive genetic animal effect, fixed effects of herd-test date (HTD), milk recording method and lactation stage, and fixed linear regression on age at calving. The LSCS were analyzed based on the linear model with the same effects as above except for the fixed effect of HTD, which was replaced by herd-year-season-classifier effect (HYSC). The model for each type trait included HYSC and lactation stage as fixed effects, fixed linear regression on age at calving, and random additive genetic animal effect. There were 2,495 HTD subclasses, 1,285 HYSC subclasses, 11 lactation stages, and 3 milk recording methods. Two seasons of calving were defined: April to September and October to March. Days in milk (15 to 180 days for type traits) were divided into 11 lactation stages as 15-day intervals. There were 87,777 animals included in the analysis. The number of generated samples of (co)variance components was equal to 100,000, with the first 10,000 samples discarded as the burn-in period. (Co)variance components were calculated as an average of 18,000 samples (every fifth sample of 90,000).

Results

Means with standard deviations and ranges for all analyzed traits are shown in Table 1. Mean lactational somatic cell score (LSCS) was 3.71 and was slightly higher and less variable than daily SCS (DSCS). The DSCS ranged from -3.64 to 11.12 (mean 3.49). Average height at rump was 142.4 (minimum 122, maximum 159). The means of descriptive traits were 77.88 for udder, close to 79.0 for final score and feet and legs, 79.82 for overall conformation score and 82.08 for size, with the highest standard deviations for udder and size. Average linear type scores were from 4.69 for teat length to 6.1 for body depth and dairy character. For all linear type traits the standard deviations ranged from 1.04 to 1.51.

Heritabilities and genetic correlations are presented in Table 2. Heritabilities estimated for lactational (LSCS) and daily (DSCS) somatic cell scores were 0.20 and 0.13, respectively. Among five descriptive type traits the most heritable were size (0.39) and overall conformation score (0.30); heritability estimated for feet and legs was the lowest (0.11). Comparing linearly scored traits, height at rump had the highest heritability (0.46). Heritability of rump traits and teat traits were moderate and similar (0.29 and 0.28 for rump angle and rump width, 0.26 and 0.28 for rear and fore teat placement, 0.29 for teat length). Heritabilities obtained for udder traits ranged from 0.18 (central ligament) to 0.27 (rear udder height and udder depth). Among linearly scored type traits the least heritable were leg traits: foot angle (0.07), rear legs – rear view (0.09) and rear legs – side view (0.11).

The genetic correlation between two measures of somatic cell score (LSCS and DSCS) was 0.84. Genetic correlations of conformation traits with LSCS ranged from -0.26 to 0.21, and with DSCS from -0.33 to 0.19. Generally, DSCS showed a higher genetic relationship with type traits than LSCS. Among descriptive traits the highest negative correlations were for feet and legs (-0.20 with LSCS, -0.33 with DSCS) and for udder (-0.22 with LSCS, -0.28 with DSCS). The relationships of the remaining descriptive traits and both SCS measures were much lower. Height at rump showed a low correlation with LSCS (0.11) and DSCS (0.09). Among linear type traits, correlations were moderate for rump angle (0.21 with LSCS, 0.19 with DSCS), fore udder attachment (-0.26 with LSCS, -0.29 with DSCS), udder depth (-0.23 with LSCS, -0.17 with DSCS) and central ligament (-0.14 with LSCS, -0.16 with DSCS). Correlations were very low between both SCS measures and leg traits (-0.08 to 0.04) as well as between LSCS (or DSCS) and the remaining udder traits (-0.03 to -0.02).

Discussion

Estimates of heritabilities of LSCS, DSCS and all conformation traits except height at rump were low to moderate (from 0.07 for foot angle to 0.39 for size). Height at rump showed much higher heritability (h^2=0.46) than the other type traits. Heritability of daily SCS (0.13) was lower than that of lactational SCS (0.20). This is in accord with other studies in which the heritability of LSCS was higher than that of single tests (Koivula et al., 2004, Liu et al., 2001). In the literature most estimates of LSCS heritabilities have ranged from 0.10 to 0.27 (Rupp and Boichard, 1999, Monardes et al., 1990, Mark and Sullivan, 2005), whereas DSCS heritabilities were within a wider interval (0.05-0.30), often with the highest values at the peripheries of lactation (Muir et al., 2007, Ptak et al., 2007). DSCS was usually recorded in the middle part of lactation, that is, at the test date next to the date of type evaluation, so DSCS heritability estimates were rather low or moderate.

Heritability for DSCS (0.13) was higher than h^2 estimated by Dal Zotto et al. (2007), Negussie et al. (2008) and Liu et al. (2001), similar to estimates given by Ptak et al. (2007), and lower than heritabilities reported by de Roos et al. (2003) or Jamrozik et al. (1998). Heritability for LSCS estimated in this study (0.20) was slightly higher than estimated by Rupp and Boichard (1999) (0.17). Kadarmideen (2004) and Charfeddine et al. (1997) obtained lower h^2 for LSCS (0.13-0.14). The differences between h^2 estimates may be attributable mainly to differences between the models used for statistical analyses, the population sizes in the studies, and the definitions of the analyzed traits (Rupp and Boichard 1999).

Type trait heritabilities ranged from 0.07 (foot angle) to 0.46 (height at rump). For most traits the heritabilities were consistent with previous estimates obtained for the Polish Holstein-Friesian population (Zarnecki et al., 2003) and were slightly higher than those used in routine evaluation (www.izoo.krakow.pl). There were large differences between current and previous estimates of heritability for two traits: height at rump (0.46 and 0.63) and dairy character (0.27 and 0.37). These heritabilities were higher than estimates reported by Dal Zotto et al. (2007) and Charfeddine et al. (1997), and similar to or slightly lower than heritabilities obtained by DeGroot et al. (2002) or Boetcher et al. (1998).

Genetic correlations between DSCS, LSCS and type traits were moderate or low, and in most cases higher between DSCS and type traits than between LSCS and conformation traits. The results for genetic relationships between lactational SCS and conformation traits are in agreement with those from other authors (Boetcher et al., 1998, Kadarmideen, 2004). However, there is a paucity of literature concerning genetic parameters of daily SCS together with type traits (Dal Zotto et al., 2007, Ptak et al., 2008).

Generally LSCS and leg traits were not genetically correlated in Polish Holstein-Friesians, whereas DeGroot et al. (2002) obtained strong favorable genetic relationships between those traits (-0.61 for rear legs – rear view and rear legs – side view; -0.48 for foot angle). Rear legs – side view showed an unfavorable genetic correlation with DSCS (0.14), indicating that sickled legs are associated with a high somatic cell count in milk. Rogers et al. (1995) reported the same undesirable value for a rear legs – side view correlation (0.14), but with LSCS in that work. Kadarmideen (2004) also obtained a positive (unfavorable) genetic relationship for rear legs – side view (0.10) with lactational SCS for Swiss Holsteins.

Some udder traits were favorably genetically correlated with both LSCS and DSCS (udder depth: -0.23 with LSCS and -0.17 with DSCS; fore udder attachment: -0.26 with LSCS and -0.29 with DSCS), in agreement with Mrode et al. (1998) and Kadamideen (2004) who reported significant correlations of LSCS with udder depth (-0.19 and -0.12, respectively), and of the same magnitude with fore udder attachment. DeGroot et al. (2002) also found strong relationships of LSCS with udder depth (-0.20) and fore udder attachment (-0.24). All these findings indicate that cows with tight and deep udders have lower SCS and are less susceptible to udder infections. A negative genetic correlation of LSCS and DSCS with central ligament (-0.14 and -0.16, respectively) was confirmed by DeGroot et al. (2002) and Charfeddine et al. (1997).

Three type traits related to teat (rear teat placement, fore teat placement, teat length) showed very low or negligible genetic correlations with both LSCS and DSCS, with one exception: a negative correlation between DSCS and fore teat placement (-0.11). Similar estimates of generally no genetic correlations between LSCS and teat traits were reported by Kadarmideen (2004) and Boetcher et al. (1998). DeGroot et al. (2002) found much stronger negative relationships of LSCS with fore teat placement (-0.19) and teat length (-0.24), concluding that closer teats would be favorable for reducing SCS. On the other hand, Charfeddine et al. (1997) obtained a positive genetic correlation between LSCS and teat length (0.14).

Conclusions

Heritability of LSCS was higher than heritability of DSCS, and DSCS was more genetically correlated with conformation traits than LSCS was. Relationships were moderate and favorable between SCS measures and 3 linear udder traits: fore udder attachment, udder depth and central ligament. Among other linear traits only rump angle was substantially correlated with both DSCS and LSCS. Correlations of the remaining linear type traits with DSCS as well as with LSCS were negligible. Relatively large correlations were found between DSCS and two descriptive traits: udder and feet and legs; they were considerably higher than those of LSCS with udder and feet and leg traits.

The magnitude of genetic parameters suggests that two descriptive traits (udder and feet and legs) and some linear udder traits (fore udder attachment, central ligament and udder depth) could be included in an udder health subindex. Replacing LSCS with DSCS in routine evaluation will not affect the possibility of using the above-mentioned type traits for indirect selection for udder health.

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References

Boettcher P.J., Dekkers J.C.M., Kolstad B.W. 1998. Development of an udder health index for sire selection based on somatic cell score, udder conformation, and milking speed. J Dairy Sci. 81: 1157-1168

Charfeddine N., Alenda R., Carabaño M.J. 1997. Relationships between somatic cell score and longevity, production and type traits in Spanish Holstein-Friesian cows. In: Proceedings of 48th Annual Meeting of EAAP, Vienna (Austria), 7pp

Dal Zotto R., De Marchi M., Dalvit C., Cassandro M., Gallo L., Carnier P., Bittante G. 2007. Heritabilities and genetic correlations of body conformation score and calving interval with yield, somatic cell score, and linear type traits in Brown Swiss cattle. J. Dairy Sci. 90: 5737-5743

DeGroot B.J., Keown J.F., Van Vleck L.D., Marotz E.L. 2002. Genetic parameters and responses of linear type, yield traits, and somatic cell score to divergent selection for predicted transmitting ability for type in Holsteins. J. Dairy Sci. 85: 1578-1585

De Ross A.P.W., Harbers A.G.F., de Jong G. 2003. Genetic parameters of test-day somatic cell score estimated with a random regression model. In: Proceedings of the Interbull Meeting. Rome (Italy). Interbull Bull. 31, pp. 97-101

Jamrozik J., Schaeffer L.R., Grignola F. 1998. Genetic parameters for production traits and somatic cell score of Canadian Holstein with multiple trait random regression model. In: Proceedings of 6th World Congr. Gen. Appl. Livest. Prod., Armidale (Australia), 23: 303-306

Kadarmideen H.N. 2004. Genetic correlations among body condition score, somatic cell score, milk production, fertility and conformation traits in dairy cows. Animal Science 79: 191-201

Koivula M., Negussie E., Mäntysaari E.A., 2004. Genetic parameters for test-day somatic cell count at different lactation stages of Finnish dairy cattle. Livest. Prod. Sci. 90, 145-157

Liu Z., Reinhardt F., Reents R. 2001. Parameter estimates of a random regression test day model for first three lactation somatic cell scores. In: Proceedings of the Interbull Technical Workshop, Verden (Germany), Interbull Bull. 26: 61-65

Mark T. and Sullivan P.G. 2005. Multiple-trait-multiple-country genetic evaluations for udder health. Interbull Bull. 33: 8-15

Miglior F., Muir B. L., Van Doormaal B. J. 2005. Selection indices in Holstein cattle of various countries. J. Dairy Sci. 88: 1255-1263

Misztal I. 1999. Complex models, more data: simpler programming? In: Proceedings of the Interbull Technical Workshop, Tuusula (Finland), Interbull Bull. 20: 32-41

Monardes H.G., Cue R.I., Hayes J.F. 1990. Correlations between udder conformation traits and somatic cell count in Canadian Holstein cows. J. Dairy Sci. 73: 1337-1342

Mrode R.A., Swanson G.J.T., Winters M.S. 1998. Genetic parameters and evaluations for somatic cell counts and its relationship with prodution and type traits in some dairy breeds in the United Kingdom. Animal Science 66: 569-576

Muir B.L., Kistemaker G., Jamrozik J., Canavesi F. 2007. Genetic parameters for a multiple-trait multiple-lactation random regression test-day model in Italian Holsteins. J. Dairy Sci. 90: 1564-1574

Nash D.L., Rogers G.W., Cooper J.B., Hargrove G.I., Keown J.F., Hansen L.B. 2000. Heritability of clinical mastitis incidence and relationships with sire transmitting abilities for somatic cell score, udder type traits, productive life, and protein yield. J. Dairy Sci. 83: 2350-2360

Negussie E., Stradén I., Mäntysaari E.A. 2008. Genetic association of clinical mastitis with test-day somatic cell score and milk yield during first lactation of Finnish Ayrshire cows. J. Dairy Sci. 91: 1189-1197

Ptak E., Brzozowski P., Jagusiak W., Zdziarski K. 2007. Genetic parameters for somatic cell score for Polish Black and White cattle estimated with a random regression model. J. Anim. and Feed Sci. 16: 357-369

Ptak E., Jagusiak W., Zarnecki A. 2008. Relationship between test day somatic cell score and conformation traits in Polish Holstein cattle. In: Proceedings of 59th Annual Meeting of EAAP, Vilnius (Lithuania), 4pp

Rogers G.W., Hargrove G.L., Copper J.B. 1995. Correlations among somatic cell scores of milk within and across lactations and linear type traits of Jerseys. J. Dairy Sci. 78: 914-920

Rupp R. and Boichard D. 1999. Genetic parameters for clinical mastitis, somatic cell score, production, udder type traits, and milking ease in first lactation Holsteins. J. Dairy Sci. 82: 2198-2204

Zarnecki A., Morek-Kopeć M., Jagusiak W. 2003. Genetic parameters of linearly scored conformation traits of Polish Black-and-White cows. J. Anim. and Feed Sci. 12: 689-696

Table 1. Means, standard deviations (SD) and ranges for lactational somatic cell score (LSCS), daily somatic cell score (DSCS) and conformation traits

No.	Trait	Mean	SD	Minimum	Maximum
1.	LSCS	3.71	1.38	0.057	10.168
2.	DSCS	3.49	2.03	-3.644	11.119
3.	Size	82.08	4.03	51	89
4.	Overall conformation score	79.82	3.39	58	89
5.	Feet and legs	79.18	3.56	50	89
6.	Udder	77.88	4.62	50	88
7.	Final score	79.08	3.26	58	88
8.	Height at rump	142.40	3.97	122	159
9.	Body depth	6.11	1.18	1	9
10.	Chest width	5.49	1.18	1	9
11.	Rump angle	5.25	1.12	1	9
12.	Rump width	5.46	1.21	1	9
13.	Rear legs - side view	5.37	1.04	1	9
14.	Foot angle	5.27	1.29	1	9
15.	Rear legs - rear view	5.39	1.34	1	9
16.	Fore udder height	5.59	1.28	1	9
17.	Rear udder height	5.43	1.17	1	9
18.	Central ligament	5.49	1.51	1	9
19.	Udder depth	5.64	1.46	1	9
20.	Udder width	5.49	1.22	1	9
21.	Rear teat placement	5.76	1.48	1	9
22.	Fore teat placement	5.05	1.28	1	9
23.	Teat length	4.69	1.17	1	9
24.	Dairy character	6.10	1.13	1	9

Table 2. Heritabilities of type traits, lactational (LSCS) and daily (DSCS) somatic cell score and genetic correlations of LSCS and DSCS with conformation traits

No.	Trait	h^2	Genetic correlation with	
			LSCS	DSCS
1.	LSCS	0.20	-	0.84
2.	DSCS	0.13	0.84	-
3.	Size	0.39	0.11	0.07
4.	Overall conformation score	0.30	0.04	-0.08
5.	Feet and legs	0.11	-0.20	-0.33
6.	Udder	0.14	-0.22	-0.28
7.	Final score	0.20	-0.12	-0.22
8.	Height at rump	0.46	0.11	0.09
9.	Body depth	0.18	-0.10	-0.14
10.	Chest width	0.17	-0.01	0.04
11.	Rump angle	0.29	0.21	0.19
12.	Rump width	0.28	0.13	0.17
13.	Rear legs - side view	0.11	0.04	0.14
14.	Foot angle	0.07	0.03	0.00
15.	Rear legs - rear view	0.09	-0.02	-0.08
16.	Fore udder height	0.19	-0.26	-0.29
17.	Rear udder height	0.27	0.02	-0.05
18.	Central ligament	0.18	-0.14	-0.16
19.	Udder depth	0.27	-0.23	-0.17
20.	Udder width	0.20	0.08	-0.03
21.	Rear teat placement	0.26	-0.02	-0.01
22.	Fore teat placement	0.28	-0.03	-0.11
23.	Teat length	0.29	0.00	0.02
24.	Dairy character	0.27	0.05	-0.04