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

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ABSTRACT: The objective of this study was to estimate heritabilities and genetic correlations of lactational and daily somatic cell scores with descriptive and linear type traits in Polish Holstein-Friesian cows. Data were: test-day somatic cell scores and conformation evaluations of 24 599 primiparous cows, daughters of 802 sires. Cows calved from 2006 to 2007. The lactational somatic cell score was calculated as the average of four test-day somatic cell scores at least. The daily somatic cell score was the test-day somatic cell score closest to the date of type evaluation. A multi-trait animal model was used to estimate genetic parameters. (Co)variance components were estimated by a Bayesian algorithm via Gibbs sampling. The heritability of lactational somatic cell score was 0.20 and it was much higher than that of daily somatic cell score (0.13). Heritabilities of type traits were high to moderate for height at rump (0.46), size (0.39), overall conformation score (0.30), two linear rump traits (0.28–0.29) and three linear teat traits (0.26–0.29). The genetic correlation between lactational and daily somatic cell scores was 0.84. In many cases, daily somatic cell score showed higher genetic correlations with type traits than lactational somatic cell score. Descriptive udder and feet and legs scores were genetically correlated negatively with both lactational (–0.22 and –0.20) and daily somatic cell scores (–0.28 and –0.33). Somatic cell traits were genetically correlated positively with rump angle (0.21 and 0.19) and negatively with fore udder height (–0.26 and –0.29), udder depth (–0.23 and –0.17) and central ligament (–0.14 and –0.16). Due to higher heritability, direct selection for lower lactational somatic cell score would be more effective than selection for lower daily somatic cell score. The magnitude of obtained heritabilities and the favourable genetic correlations indicate that the selection utilizing some type traits could improve the resistance to mastitis.

Keywords: conformation traits; somatic cell score; dairy cattle; genetic parameters

The high level of genetic improvement of milk production has caused a decline in functional traits. Udder diseases – mainly mastitis – impose increasing costs on milk producers and could ultimately lead to involuntary culling. Direct selection for mastitis is practised only in Nordic countries (Denmark, Finland, Norway and Sweden) where the incidence of mastitis is registered in a national database (Interbull, 2010). In most countries the incidence of mastitis has not been recorded routinely, so the indirect selection for somatic cell score (SCS) is a commonly used alternative solution to improve resistance to this disease. SCS usually has a higher heritability than clinical mastitis (CM), and these two traits are highly correlated genetically. To improve udder health, other functional traits, especially conformation traits and longevity, genetically related to SCS, are also used as selection criteria (Charfeddine et al., 1997; Nash et al., 2000; Šafus et al., 2005).

An increased somatic cell count (SCC) in milk is mainly caused by the presence of mastitis-causing bacteria in the udder, so SCC can be used for monitoring the udder health and for selection to reduce the incidence of mastitis (Harmon, 1994; Ødegård et al., 2003). Although the genetic correlation between SCS and CM is positive and relatively high (around 0.70), these two traits cannot be considered as an expression of the same trait (Rupp and Boichard, 1999; Samoré et al., 2008). However, the results of some studies indicate that selection for lower SCS decreases the prevalence of mastitis (Rupp and Boichard, 1999; Nash et al., 2000). Ødegård et al. (2003) concluded that both traits (SCS and CM) were capable of changing the incidence of clinical mastitis in the second-crop daughters but that direct selection using CM data was more efficient. They suggested that combining the two traits in selection would increase the efficiency of selection for udder health.

On the other hand, somatic cells in milk constitute a natural defence mechanism of the mammary gland. Suriyasathaporn et al. (2000) found out that too low SCC is associated with an increased risk of clinical mastitis. Ødegård et al. (2003) also reported that selection for the lowest possible SCC may reduce cows' ability to respond to infection and suggested defining an optimum for SCC. In contrast, Rupp and Boichard (1999) and Nash et al. (2002) did not find any indication that cows with low SCC were at a higher risk of subsequent infections or that their natural defence was weakened.

In Poland, a multi-trait animal model based on test-day somatic cell score (SCS) in each of the first three lactations has been implemented recently (Interbull, 2010). Estimated breeding values for lactational somatic cell score (LSCS) were calculated on the basis of test-day SCS, then averaged over three lactations and directly included in the total index. In other countries both SCS and type traits are included in selection subindexes. Some of the type traits are genetically correlated with SCS, and the magnitude of heritabilities and genetic correlations enable to evaluate the correlated response in udder health (Charfeddine et al., 1997).

The objective of this study was to examine the possibility of using conformation traits in indirect selection to decrease SCS and consequently the frequency of mastitis in Polish Holstein-Friesian cattle. The magnitude of heritabilities and genetic correlations between LSCS or DSCS and type traits would allow to choose a combination of traits that could be used to construct an effective health index.

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. Each cow was scored for type between 15 and 180 days in milk (DIM), once during lactation. The date of type evaluation for a cow was matched with the closest test-day milk record of a cow, and SCC on that test-day was chosen. The ave-rage number of days between the date of type evaluation and the closest test-day was 12 (SD = 15.98). The scoring of conformation traits was performed at 100 DIM (SD = 41.55) on average, and for DSCS at 112 DIM (SD = 52.38). Somatic cell score (SCS) was obtained as a logarithmic transformation of SCC, i.e. SCS = $\log_2$(SCC/100 000) + 3 (Ali and Shook, 1980). Lactational somatic cell scores (LSCS) were calculated as the average of four test-day SCS at least. The conformation traits included five descriptive traits, height at rump, and sixteen linearly scored traits (Table 1).

Cows, daughters of 802 sires, calved for the first time in 2006 and 2007 at the age of 18–48 months. Limitations for age of calving were the same as in the routine evaluation system. Firstly, a restriction of a minimum of 10 daughters per sire was imposed; secondly, herd-year-season subclasses were restricted to a minimum of 10 contemporaries. After the second restriction, half-sib groups numbering less than 10 cows might occur. The distance between the date of test and the date of the 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 was as follows:

$$Y_{ijkl} = a_i + \text{HTD}_j + s_k + m_l + \beta X_i + \varepsilon_{ijkl}$$

where:

Y_{ijkl} = daily somatic cell score (DSCS) for i-th cow calved in j-th herd-test-date (HTD) subclass, recorded by l-th method and scored for conformation in k-th lactation stage at age X_i

a_i　　= random additive genetic effect (with 87 777 levels)

HTD_j = fixed herd-test-date effect (with 2495 levels)

m_l　　= method of milk recording (with 3 levels)

s_k　　= lactation stage effect (with 11 levels)

X_i　　= age at calving (18–48 months)

β　　= linear regression of Y on age at calving

ε_{ijkl}　= residual

The linear model for each of 22 type traits was as follows:

$$Y_{ijk} = a_i + \text{HYS}_j + s_k + \beta X_i + \varepsilon_{ijk}$$

where:

Y_{ijk}　= conformation score for i-th cow calved in j-th herd-year-season (HYS), scored for conformation in k-th lactation stage at age X_i

HYS_j = fixed herd-year-season effect (with 1285 le-vels)

$a, s, X, \beta, \varepsilon$ = as in the model for DSCS

The LSCS were analysed using a linear model with the same effects as DSCS except for the fixed effect of HTD which was replaced by the HYS effect.

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. The classifier effect was not included in the model because cows in the same herd were always scored by the same classifier. 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 (SD) and ranges for all analysed traits are shown in Table 1. The mean of lactational somatic cell score (LSCS) was slightly higher and less variable than that of daily SCS (DSCS). Among the descriptive type traits, the largest standard deviations were calculated for traits with the lowest (udder) and highest (size) means. For most linear conformation traits the average scores were close to the assumed intermediate optimum. The extreme values of linear type traits (1–2 or 9) corresponding to biological extremes

occurred rarely (less than 3% of the records), except central ligament, for which values 1 or 2 were observed in 4.7% of the records.

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, heritability of udder traits ranged from 0.18 (central ligament) to 0.27 (rear udder height and udder depth). Heritabilities obtained for 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). 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. The genetic correlation lower than 1 meant that DSCS and LSCS were not the expression of the same trait, but this correlation was high enough to believe that some genes affected both DSCS and LSCS. Selection for decreased DSCS would also lower the average somatic cell score (LSCS) in lactation.

Genetic correlations of conformation traits with LSCS ranged from –0.26 to 0.21, and with DSCS from –0.33 to 0.19. In many cases DSCS showed a closer genetic relationship with type traits than LSCS. Out of 22 type traits, 8 showed a genetic correlation with DSCS higher than 0.15 (ignoring the sign) and 5 of them had similar correlations also with LSCS. These results indicate that good characteristics of feet and legs, udder, fore udder attachment and udder depth were associated with higher genetic merit for both DSCS and LSCS. Additionally, final score and central ligament were favourably associated with DSCS but the correlations of these traits with LSCS were slightly lower than 0.15. Correlations for 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) indicated that cows with tight fore udder attachment, shallow udders and strong central ligament had both lower DSCS and lower LSCS, and potentially a lower risk of mastitis incidence. In two cases (fore udder attachment and central ligament) there was a stronger genetic relationship with DSCS while the relationship with LSCS was closer for udder depth.

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

Trait	Mean	SD	Minimum	Maximum
LSCS	3.71	1.38	0.057	10.168
DSCS	3.49	2.03	−3.644	11.119
Size	82.08	4.03	51	89
Overall conformation score	79.82	3.39	58	89
Feet and legs	79.18	3.56	50	89
Udder	77.88	4.62	50	88
Final score	79.08	3.26	58	88
Height at rump	142.40	3.97	122	159
Body depth	6.11	1.18	1	9
Chest width	5.49	1.18	1	9
Rump angle	5.25	1.12	1	9
Rump width	5.46	1.21	1	9
Rear legs – side view	5.37	1.04	1	9
Foot angle	5.27	1.29	1	9
Rear legs – rear view	5.39	1.34	1	9
Fore udder height	5.59	1.28	1	9
Rear udder height	5.43	1.17	1	9
Central ligament	5.49	1.51	1	9
Udder depth	5.64	1.46	1	9
Udder width	5.49	1.22	1	9
Rear teat placement	5.76	1.48	1	9
Fore teat placement	5.05	1.28	1	9
Teat length	4.69	1.17	1	9
Dairy character	6.10	1.13	1	9

Correlations between rump angle and SCS measures (0.21 with LSCS, 0.19 with DSCS) or between rear legs – side view and SCS measures (0.04 with LSCS, 0.14 with DSCS) were difficult to interpret as an optimum (i.e. the most desired value of a trait) for these two type traits was in the middle of the scale. When selected towards the optimum, these correlations seemed to be unfavourable for cows with high pins or straight rear legs (low type scores) and favourable for cows with low pins or sickled legs (high type scores).

Height at rump showed a low correlation with LSCS (0.11) and DSCS (0.09). Very low correlations were estimated between rear legs – rear view and both SCS measures (−0.02 and −0.08) but they tended to be favourable. Foot angle, rear teat placement and teat length showed no correlation with LSCS and DSCS.

DISCUSSION

Heritability of daily SCS (0.13) was lower than that of lactational SCS (0.20). This is in accordance with other studies in which the heritability of LSCS was higher than that of single tests (Liu et al., 2001; Koivula et al., 2004). In the literature, most estimates of heritability for lactation average SCS (LSCS) ranged from 0.07 to 0.27 (Monardes et al., 1990; Rupp and Boichard, 1999; Berry et al., 2004; 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 and fairly stable throughout the remainder of lactation (De Roos et al., 2003; Muir et al., 2007; Ptak et al., 2007). The DSCS used in this paper were recorded on the test date next to the date of type evaluation, i.e. usually in the middle part of lactation, so DSCS heritability estimates were low.

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

Trait	h^2	Genetic correlation with	
		LSCS[a]	DSCS[a]
LSCS	0.20 ± 0.034	–	0.84
DSCS	0.13 ± 0.029	0.84	–
Size	0.39 ± 0.052	0.11	0.07
Overall conformation score	0.30 ± 0.035	0.04	−0.08
Feet and legs	0.11 ± 0.019	−0.20	−0.33
Udder	0.14 ± 0.024	−0.22	−0.28
Final score	0.20 ± 0.032	−0.12	−0.22
Height at rump	0.46 ± 0.059	0.11	0.09
Body depth	0.18 ± 0.031	−0.10	−0.14
Chest width	0.17 ± 0.023	−0.01	0.04
Rump angle	0.29 ± 0.045	0.21	0.19
Rump width	0.28 ± 0.041	0.13	0.17
Rear legs – side view	0.11 ± 0.025	0.04	0.14
Foot angle	0.07 ± 0.017	0.03	0.00
Rear legs – rear view	0.09 ± 0.022	−0.02	−0.08
Fore udder height	0.19 ± 0.034	−0.26	−0.29
Rear udder height	0.27 ± 0.038	0.02	−0.05
Central ligament	0.18 ± 0.033	−0.14	−0.16
Udder depth	0.27 ± 0.042	−0.23	−0.17
Udder width	0.20 ± 0.033	0.08	−0.03
Rear teat placement	0.26 ± 0.040	−0.02	−0.01
Fore teat placement	0.28 ± 0.036	−0.03	−0.11
Teat length	0.29 ± 0.038	0.00	0.02
Dairy character	0.27 ± 0.036	0.05	−0.04

[a]standard deviations of all estimated genetic correlations were in range between 0.0132 and 0.0438

Heritability for DSCS (0.13) was higher than h^2 estimated by Liu et al. (2001), Dal Zotto et al. (2007), Negussie et al. (2008), and Yazgan et al. (2010), similar to estimates given by Muir et al. (2004) and Ptak et al. (2007), and lower than heritabilities reported by Jamrozik et al. (1998), de Roos et al. (2003) or Samoré et al. (2008). LSCS had a heritability estimate (0.20) slightly higher than the estimate by Rupp and Boichard (1999) (0.17) and Lund et al. (1994) (0.18) but these authors used test-day SCS from the first 180 days of lactation for calculating LSCS. Charfeddine et al. (1997), Kadarmideen (2004), and Ptak et al. (2009a) obtained lower h^2 for LSCS (0.13–0.14); Berry et al. (2004) reported even much lower h^2 (0.07) but they did not impose any restrictions on the number of SCS tests per lactation used for calculating LSCS. DeGroot et al. (2002) obtained relatively high heritability for

LSCS (0.38) but their data were restricted to one dairy research herd and were preadjusted for age, season of calving and length of lactation before analysis. The differences between h^2 estimates may be attributable mainly to differences among the models used for statistical analyses, the population sizes in the studies, restrictions imposed on data, and the definitions of the analysed traits (Rupp and Boichard, 1999).

For most conformation traits the heritabilities were consistent with those reported by Berry et al. (2004) in the population of Irish Holstein cows. Heritabilities of linear type traits were higher than estimates reported by Dal Zotto et al. (2007) and Zavadilová et al. (2009), and similar to or lower than heritabilities obtained by Boettcher et al. (1998), DeGroot et al. (2002) or De Haas et al. (2007). Estimates of udder and teat trait heritabilities were

very close to those reported by Rupp and Boichard (1999), except h^2 for fore udder attachment (0.18). All heritabilities were also consistent with previous estimates obtained for the Polish Holstein-Friesian population (Żarnecki et al., 2003), except final score (0.30), rear udder height (0.20) and fore teat placement (0.21). In most cases the estimated heritabilities were slightly higher than those used in routine evaluation (Interbull, 2010). There were two traits for which the differences between current and previous estimates of heritability were large: height at rump (0.46 and 0.63) and dairy character (0.27 and 0.37). De Haas et al. (2007) also obtained high heritability of 0.69 for height at rump.

Genetic correlations between type traits and DSCS or LSCS were moderate or low, and in most cases higher for DSCS than for LSCS. The results for genetic relationships between lactational SCS and conformation traits are in agreement with those from other authors (Boettcher 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., 2009b).

Generally, LSCS and leg traits were not genetically correlated in Polish Holstein-Friesian cattle, whereas DeGroot et al. (2002) obtained favourable close genetic relationships between those traits (–0.61 for rear legs – rear view and rear legs – side view; –0.48 for foot angle), and Berry et al. (2004) only for foot angle (–0.53). Rear legs – side view showed a positive genetic correlation with DSCS (0.14), indicating that sickled legs were associated with a high somatic cell count in milk. Rogers et al. (1995) reported the same value for the rear legs – side view correlation (0.14), but with LSCS in that paper. Kadarmideen (2004) also obtained a positive genetic relationship for rear legs – side view (0.10) with lactational SCS for Swiss Holstein cattle. A much higher genetic correlation between rear legs – side view and LSCS (0.69) was estimated by Berry et al. (2004) for Irish Holstein cows. All those findings indicated that cows with genetically straighter rear legs had a chance of having fewer somatic cells in milk.

Some udder traits were favourably 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). These results were in agreement with Boettcher et al. (1998), Mrode et al. (1998) and Kadamideen (2004), who reported significant correlations of LSCS with udder depth (–0.26, –0.19 and –0.12, respectively), and of a similar magnitude

with fore udder attachment. DeGroot et al. (2002) also found close relationships of LSCS with udder depth (–0.20) and fore udder attachment (–0.24), whereas Berry et al. (2004) obtained a similar correlation only for fore udder attachment (–0.25) and a much weaker genetic relationship for udder depth (–0.07). Lower SCS for more tightly attached, shallower and higher rear udders were observed by Němcová et al. (2007) in Czech Holstein cows. All these findings indicate that cows with tight and deep udders have lower SCS and they 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 Charfeddine et al. (1997) and DeGroot et al. (2002).

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 Boettcher et al. (1998) and Kadarmideen (2004). DeGroot et al. (2002) found much closer negative relationships of LSCS with fore teat placement (–0.19) and teat length (–0.24), concluding that closer teats would be favourable for reducing SCS. On the other hand, Charfeddine et al. (1997) and Berry et al. (2004) obtained a positive genetic correlation between LSCS and teat length (0.14 and 0.31, respectively). The increased SCS in cows with longer teats might be attributable to a higher risk of injury to longer teats from milking, handling and housing (Berry et al., 2004).

Very low correlations with LSCS and DSCS were calculated for overall conformation score, chest width, rear udder height, udder width and dairy character. The relationship between dairy character and mastitis incidence was addressed in some previous studies. Hansen et al. (2002) and Lassen et al. (2003) estimated moderate genetic correlations between these two traits in Danish Holstein cattle and concluded that breeding for less expressed dairy character will increase resistance to mastitis. We had no data on CM, but assuming that SCS is a good indicator of mastitis, no such a tendency as in Danish Holsteins was observed in the Polish population.

CONCLUSION

Direct selection for mastitis resistance is not usually feasible because of difficulties in its recording

and low heritability. The most common breeding practice is to use indirect measures of mastitis such as LSCS or DSCS. Selection for lower LSCS could be more effective than selection for lower DSCS because of its higher heritability. The genetic improvement of udder health can also be achieved by indirect selection for conformation traits genetically correlated with LSCS or DSCS. For both SCS measures, moderate and favourable genetic correlations with type traits such as rump angle, fore udder attachment, udder depth and central ligament were found out. Relatively high correlations were obtained between both LSCS and DSCS and two descriptive traits: udder and feet and legs. Selection for those traits would result in a similar correlated response in both SCS measures.

The magnitude of genetic parameters suggests that two descriptive traits (udder and feet and legs) and some linear udder traits (udder depth, fore udder attachment and central ligament) could be included in an udder health index.

REFERENCES

Ali A.K.A., Shook G.E. (1980): An optimum transformation for somatic cell concentration in milk. Journal of Dairy Science, 63, 487–490.

Berry D.P., Buckley F., Dillon P., Evans R.D., Veerkamp R.F. (2004): Genetic relationships among linear type traits, milk yield, body weight, fertility and somatic cell count in primiparous dairy cows. Irish Journal of Agricultural and Food Research, 43, 161–176.

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. Journal of Dairy Science, 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: Proc. 48th Annu. Mtg. European Association for Animal Production (EAAP). Vienna, Austria, 7 pp.

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. Journal of Dairy Science, 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. Journal of Dairy Science, 85, 1578–1585.

De Haas Y., Janss L.L.G., Kadarmideen H.N. (2007): Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds. Journal of Animal Breeding and Genetics, 124, 12–19.

DeRoss 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: Proc. Interbull Mtg. Rome, Italy. Interbull Bulletin, 31, 97–101.

Hansen M., Lund M.S., Sorensen M.K., Christensen L.G. (2002): Genetic parameters of dairy character, protein yield, clinical mastitis, and other diseases in the Danish Holstein cattle. Journal of Dairy Science, 85, 445–452.

Harmon R.J. (1994): Physiology of mastitis and factors affecting somatic cell counts. Journal of Dairy Science, 77, 2103–2112.

Interbull (2010): Description of National Genetic Evaluation Systems for dairy cattle traits as applied in different Interbull member countries. Available from http://www-interbull.slu.se/ national_ges_info2/ framesida-ges.htm

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: Proc. 6th World Congr. Genetics Applied to Livestock Production (WCGALP). 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. Livestock Production Science, 90, 145–157.

Lassen J., Hansen M., Sorensen M.K., Aamand G.P., Christensen L.G., Madsen P. (2003): Genetic relationship between body conformation score, dairy character, mastitis, and diseases other than mastitis in first-parity Danish Holstein cows. Journal of Dairy Science, 86, 3730–3735.

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

Lund M.S., Miglior F., Dekkers J.C.M., Burnside E.B. (1994): Genetic relationships between clinical mastitis, somatic cell count, and udder conformation in Danish Holsteins. Livestock Production Science, 39, 243–251.

Mark T., Sullivan P.G. (2005): Multiple-trait-multiple-country genetic evaluations for udder health. In: Proc. Interbull Mtg. Uppsala, Sweden. Interbull Bulletin, 33, 8–15.

Misztal I. (1999): Complex models, more data: simpler programming? In: Proc. Interbull Technical Workshop. Tuusula, Finland. Interbull Bulletin, 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. Journal of Dairy Science, 73, 1337–342.

Mrode R.A., Swanson G.J.T., Winters M.S. (1998): Genetic parameters and evaluations for somatic cell counts and its relationship with production 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. Journal of Dairy Science, 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. Journal of Dairy Science, 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. Journal of Dairy Science, 91, 1189–1197.

Němcová E., Štípková M., Zavadilová L., Bouška J., Vacek M. (2007): The relationship between somatic cell count, milk production and six linearly scored type traits in Holstein cows. Czech Journal of Animal Science, 52, 437–446.

Ødegård J., Klemetsdal G., Heringstad B. (2003): Genetic improvement of mastitis resistance: validation of somatic cell score and clinical mastitis as selection criteria. Journal of Dairy Science, 86, 4129–4136.

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. Journal of Animal and Feed Sciences, 16, 357–369.

Ptak E., Jagusiak W., Żarnecki A., Otwinowska-Mindur A. (2009a): Relationship between somatic cell score and udder conformation traits in Polish Holstein-Friesian cows. Annals of Animal Science, 9, 237–241.

Ptak E., Jagusiak W., Żarnecki A., Otwinowska-Mindur A. (2009b): Genetic parameters of daily somatic cell score and some conformation traits in Polish Holstein cattle. Annals of Animal Science, 9, 355–361.

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. Journal of Dairy Science, 78, 914–920.

Rupp R., Boichard D. (1999): Genetic parameters for clinical mastitis, somatic cell score, production, udder type traits, and milking ease in first lactation Holsteins. Journal of Dairy Science, 82, 2198–2204.

Šafus P., Štípková M., Stádník L., Přibyl J., Čermák V. (2005): Sub-indexes for bull of Holstein breed in the Czech Republic. Czech Journal of Animal Science, 50, 254–265.

Samoré A.B., Groen A.F., Boettcher P.J., Jamrozik J., Canavesi F., Bagnato A. (2008): Genetic correlation patterns between somatic cell score and protein yield in Italian Holstein-Friesian population. Journal of Dairy Science, 91, 4013–4021.

Suriyasathaporn W., Schukken Y.H., Nielen M., Brand A. (2000): Low somatic cell count: a risk factor for subsequent clinical mastitis in dairy herd. Journal of Dairy Science, 83, 1248–1255.

Yazgan K., Makulska J., Węglarz A., Ptak E., Gierdziewicz M. (2010): Genetic relationship between milk dry matter and Rother milk traits in extender lactations of Polish Holstein cows. Czech Journal of Animal Science, 55, 91–104.

Żarnecki A., Morek-Kopeć M., Jagusiak W. (2003): Genetic parameters of linearly scored conformation traits of Polish Black-and-White cows. Journal of Animal and Feed Sciences, 12, 689–696.

Zavadilová L., Němcová E., Štípková M., Bouška J. (2009): Relationships between longevity and conformation traits in Czech Fleckvieh cows. Czech Journal of Animal Science, 54, 387–394.

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