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GENETIC PARAMETERS OF DAILY SOMATIC CELL SCORE AND SOME CONFORMATION TRAITS IN POLISH HOLSTEIN CATTLE*

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Abstract

The objective of this paper was to estimate genetic parameters of daily SCS and nine conformation traits. A total of 21,957 first parity cows with records containing test day SCS, two descriptive and seven linearly scored conformation traits were included. Test day SCS were matched with the closest date of type evaluation. Genetic parameters were estimated using a multi-trait animal model and the Bayesian method. The linear model contained random additive genetic effect, fixed effects of herd-year-season-classifier (HYSC), lactation stage, and fixed linear regression on age at calving for all type traits. SCS was analysed based on a linear model containing the same effects as above with the exception of fixed effect of HYSC, which was replaced by herd-year-season effect (HYS). All estimates of heritabilities were low to moderate (0.06–0.33). The highest genetic correlations were between SCS and two descriptive traits: overall udder score (–0.28) and feet and legs (–0.37). Among linearly scored traits, rear legs – rear view (0.25) and udder support (–0.19) showed the strongest association with SCS. These conformation traits can be used as auxiliary traits in indirect selection for improvement of udder health.

Key words: somatic cell score, type traits, genetic parameters

Improvement of milk yield is the main goal in most breeding programmes. However, it is well documented that selection only for milk production traits leads to a decrease in cow health and reproduction performance (Dematawewa and Berger, 1998; Negussie et al., 2008). Mastitis is one of the most frequent production oriented cow diseases but in many countries, including Poland, incidence of mastitis is not registered therefore selection for this trait is not feasible. As the indicator of mastitis

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Somatic Cell Count (SCC) in milk is used. Heritabilities of clinical mastitis reported in literature are usually very low and vary from 0.02 (Negussie et al., 2008) to 0.05 (Lund et al., 1999); heritability of the Somatic Cell Score (SCS – log transformed SCC) ranges from 0.06 (Dal Zotto et al., 2007) to 0.13 (De Haas et al., 2008). The genetic correlations between SCS and mastitis estimated by other authors are close to 0.7 (Rupp and Boichard, 1999; Negussie et al., 2008), therefore SCS is included in most selection indexes (Miglior et al., 2005) as a tool for indirect selection against mastitis.

Some type traits are moderately heritable and at the same time show favourable genetic relationships to both production and functional traits (Dechow et al., 2002; Żarnecki et al., 2003; De Haas et al., 2007). Moreover, conformation may be evaluated earlier than other traits. Genetic correlations between SCS and conformation were investigated by several authors (Rogers et al., 1995; Rogers et al., 1998; Chrystal et al., 1999; Němcowá et al., 2007). The largest correlations were obtained for fore udder attachment, udder depth, teat length, teat placement, and dairy form. Earlier available evaluations of type traits may be used for indirect selection for mastitis. Rogers (1993) analysed efficiency of the selection indexes based on SCS, milk yield and several type traits and found that udder depth, teat placement together with foot angle had substantial impact on reducing undesirable response in mastitis.

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

Material and methods

Data consisted of 21,957 records with test day somatic cell counts (SCC) and nine conformation traits of Polish Holstein-Friesian primiparous cows. The conformation traits included two descriptive traits: feet and legs and overall udder score, and seven linearly scored traits: rump angle and width, rear legs – side and rear view, foot angle, central ligament, teat length. Test day SCC were matched with the closest date of type evaluation. SCC were log-transformed to somatic cell score (SCS) (Ali and Shook, 1980).

Cows were daughters of 561 sires. They calved in 2006 and 2007, in 700 herds, at age of 18–48 months. Restrictions of a minimum 10 cows per herd and sires with at least 20 daughters were imposed. The distance between date of test and date of type evaluation had to be less than 60 days.

Days in milk (15 to 180 days for type traits and 5 to 213 days for SCS) were divided into 11 stages for type traits and 9 stages for SCS. In case of conformation traits stages were defined as 15-day intervals whereas for SCS: first 3 lactation stages as 10-day intervals and 6 later – as 30-day intervals. Two seasons of calving were created: April-September and October-March.

The multi-trait Bayesian method via Gibbs Sampling was applied for (co)variance components estimation for all 10 traits (Misztal, 1999). The linear model containing random additive genetic effect, fixed effects of herd-year-season-classifier (HYSC), lactation stage, and fixed linear regression on age at calving was used for all type traits. There were 1,785 HYSC subclasses, 11 lactation stages and 52,005 animals included in the analysis. The SCS were analysed based on the linear model with the same effects as above except the fixed effect of HYSC which was replaced by herd-year-season effect (HYS). There were 1,762 HYS and 9 lactation stages for SCS. The number of generated samples of (co)variance components was equal to 100,000. The first 5,000 samples were discarded as the burn-in period.

Results

Descriptive characteristics of the data are shown in Table 1. Mean calving age of cows was 26 months. The SCS ranged from –3.6 to 11.4 with the mean value of 3.51. The means of descriptive traits were 79.15 for feet and legs and 78.01 for overall udder score with higher standard deviation for the latter. Average linear type scores were from 4.69 for rear legs – rear view and teat length to 5.51 for central ligament. For most of linear type traits standard deviations ranged from 1.03 to 1.49 except for rear legs – rear view which had standard deviation of 2.20.

Table 1. Means and standard deviations (SD) of age at calving, SCS and type traits

Trait	$\bar{x}$	SD
1. Age at calving	26.27	3.17
2. SCS	3.51	2.05
3. Feet and legs	79.15	3.32
4. Overall udder score	78.01	4.29
5. Rump angle	5.27	1.11
6. Rump width	5.46	1.19
7. Rear legs – side view	5.36	1.03
8. Foot angle	5.24	1.26
9. Rear legs – rear view	4.69	2.20
10. Central ligament	5.51	1.49
11. Teat length	4.69	1.15

Estimated genetic parameters are presented in Table 2. Heritability of SCS (0.07) was lower than most published estimates of heritabilities for SCS because it was based on one single test day record per lactation. Heritabilities of descriptive conformation traits were similar (0.13 for feet and legs and 0.12 for overall udder score). Among linear type traits the least heritable were leg traits: foot angle (0.06), rear legs – rear view (0.08) and rear legs – side view (0.09). The highest heritabilities were obtained for teat length (0.33) and rump traits: rump angle (0.30) and rump width (0.29). Heritability of central ligament was 0.18.

Phenotypic correlations between SCS and conformation traits were small and often close to zero. Negative phenotypic relationships were found with central ligament

(–0.10) and overall udder score (–0.09). The largest negative genetic correlations occurred between SCS and descriptive conformation traits indicating that daughters of bulls with higher breeding value for feet and legs and overall udder have lower SCS. Leg traits showed lower genetic correlations with SCS than descriptive traits. The most positively correlated were rear legs – side view (0.24) whereas correlations with foot angle (–0.13) and rear legs – rear view (–0.10) were smaller and negative. Among udder linear traits central ligament was favourably (negatively) correlated with SCS (–0.18) and teat length was not correlated with SCS (0.01). Somatic cell score was positively correlated with rump width (0.12) and the correlation with rump angle was close to zero (0.03).

Table 2. Heritabilities (on diagonal) and genetic (above diagonal) and phenotypic (below diagonal) correlations among somatic cell score (SCS) and conformation traits

No.	Trait*	1.	2.	3.	4.	5.	6.	7.	8.	9.	10.
1.	SCS	**0.07**	–0.37	–0.28	0.03	0.12	0.24	–0.13	–0.10	–0.18	0.01
2.	Feet and legs	–0.03	**0.13**	0.67	0.09	0.24	–0.61	0.64	0.57	0.38	0.04
3.	Overall udder	–0.09	0.36	**0.12**	–0.07	0.37	–0.34	0.26	0.49	0.54	–0.01
4.	Rump angle	0.02	–0.04	–0.08	**0.30**	0.05	–0.20	0.04	0.05	–0.06	0.00
5.	Rump width	0.00	0.13	0.07	0.07	**0.29**	–0.08	0.32	0.26	0.19	–0.04
6.	Rear legs – side view	0.02	–0.36	–0.12	–0.04	–0.03	**0.09**	–0.36	–0.49	–0.19	–0.04
7.	Foot angle	0.00	0.42	0.12	–0.03	0.12	–0.14	**0.06**	0.25	0.15	–0.01
8.	Rear legs – rear view	0.00	0.43	0.19	–0.04	0.09	–0.22	0.24	**0.08**	0.18	0.01
9.	Central ligament	–0.10	0.14	0.39	–0.07	0.02	–0.02	0.05	0.05	**0.18**	0.09
10.	Teat length	–0.03	0.05	0.06	–0.02	0.03	–0.03	0.04	0.03	0.05	**0.33**

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

Phenotypic and genetic correlations among conformation traits ranged from –0.61 to 0.67 and were of similar magnitude to estimates published by other authors. The highest genetic correlation occurred between two descriptive traits (0.67). Both feet and legs and overall udder score were also highly correlated with central ligament and leg traits. Very low correlations were estimated between rump traits (0.05) as well as between teat length and other type traits (–0.04 to 0.09).

Discussion

All estimates of heritabilities were low to moderate (0.06–0.33). Heritability for daily SCS (0.07) was lower than earlier estimates of h^2 for this trait in Polish HF population (0.08–0.22) (Ptak et al., 2007) and similar to those estimated by Dal Zotto et al. (2007), Negussie et al. (2008), Liu et al. (2001) and Mrode and Swanson (2003). Some authors have reported higher heritabilities for SCS than 0.07 (De Roos et al., 2003; Jamrozik et al., 1998) but they used all test day SCS available during lactations and RRM as the model of (co)variances estimation.

Heritabilities for type traits were consistent with those reported by Żarnecki et al. (2003) for the Polish Holstein population. They were also in the range of the values estimated by Charfeddine et al. (1997), Dal Zotto et al. (2007) and DeGroot et al. (2002).

Genetic correlations between SCS and type traits obtained in this paper in general were lower than estimates published by DeGroot et al. (2002) and different (opposite sign) from those presented by Charfeddine et al. (1997). SCS showed large and favourable genetic correlations with feet and legs (–0.37) and overall udder score (–0.28), indicating that bulls with high breeding value for these traits will have daughters with smaller SCS. Much lower genetic correlations between SCS and two descriptive type traits (–0.05 for feet and legs and –0.10 for overall udder score) were presented by Kadarmideen (2004). The correlation between SCS and feet and legs obtained by Charfeddine et al. (1997) showed opposite direction of the relationship (0.11).

Negative genetic correlation between central ligament and SCS (–0.18) is similar to the estimate published by DeGroot et al. (2002) (–0.20) and indicates that cows – daughters of bulls with higher breeding value for central ligament have lower SCS. On the other hand, in the population of Polish Holstein cattle teat length showed much smaller correlation with SCS (0.01) than values published by Charfeddine et al. (1997) and DeGroot et al. (2002) (0.14 and –0.24, respectively) and is rather not suitable for indirect selection for SCS. Correlations between leg traits and SCS (0.24 for rear legs – side view, –0.10 for rear legs – rear view and –0.13 for foot angle) suggested that higher SCS is determined for cows with sickled, toe out legs and lower heels. Kadarmideen (2004) obtained smaller and also positive correlation between SCS and rear legs – side view (0.10). Opposite (negative) correlations between SCS and rear legs – side view were estimated by DeGroot et al. (2002) and Charfeddine et al. (1997) (–0.61 and –0.15, respectively). Genetic correlations for other leg traits, presented by DeGroot et al. (2002) were higher than ours and negative (–0.48 for foot angle and –0.61 for rear legs – rear view).

Rump traits were less correlated with SCS than leg traits. Positive correlation of rump width (0.12) indicates that cows with narrow rump have lower SCS. This estimate was lower than presented by DeGroot et al. (2002) but higher than that reported by Mrode et al. (1998).

All these findings suggest that genetic evaluations for SCS and descriptive and some linear conformation traits (central ligament and leg traits for instance) can be a useful tool to reduce mastitis incidence in dairy cows.

References

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

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), 7 pp.

Chrystal M.A., Seykora A.J., Hansen L.B. (1999). Heritabilities of teat end shape and teat diameter and their relationships with somatic cell score. J. Dairy Sci., 82: 2017–2022.

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.

De Haas Y., Ouweltjes W., Napeldun J., Windig J.J., Jong de G. (2008). Alternative somatic cell count traits as mastitis indicators for genetic selection. J. Dairy Sci., 91: 2501–2511.

De Ross A.P.W., Harbers A.G.F., Jong de 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: 97–101.

Dechow C.D., Rogers G.W., Klei L., Lawlor T.J. (2003). Heritabilities and correlations among body conformation score, dairy form and selected linear type traits. J. Dairy Sci., 86: 2236–2242.

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.

Dematawewa C.M.B., Berger P.J. (1998). Genetic and phenotypic parameters for 305-day yield, fertility and survival in Holsteins. J. Dairy Sci., 81: 2700–2709.

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. Anim. Sci., 79: 191–201.

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.

Lund M.S., Jensen J., Peterson P.H. (1999). Estimation of genetic and phenotypic parameters for clinical mastitis, somatic cell production deviance, and protein yield in dairy cattle using Gibbs sampling. J. Dairy Sci., 82: 1045–1051.

Miglior F., Muir B.L., Van Doormaal B.J. (2005). Selection indices in Holstein cattle of various countries. J. Dairy Sci., 88: 1255-–263.

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

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. Anim. Sci., 66: 569–576.

Mrode R.A., Swanson G.J.T. (2003). Estimation of genetic parameters for somatic cell count in the first three lactations using random regression. Livest. Prod. Sci., 79: 239–247.

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.

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 J. Anim. Sci., 52: 437–446.

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. Feed Sci., 16: 357–369.

Rogers G.W. (1993). Index selection using milk yield, somatic cell score, udder depth, teat placement, and foot angle. J. Dairy Sci., 76: 664–670.

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.

Rogers G.W., Banos G., Sander Nelson U., Philipsson J. (1998). Genetic correlations among somatic cell scores, productive life, and type traits from the United States and udder health measures from Denmark and Sweden. J. Dairy Sci., 81: 1445–1453.

Rupp R., 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.

Żarnecki A., Jagusiak W., Trela J., Czaja H. (2000). Sire evaluation for type traits. National Research Institute of Animal Production and Central Animal Breeding Office, Krakow, 21: 63–70.
Żarnecki A., Morek-Kopeć M., Jagusiak W. (2003). Genetic parameters of linearly scored conformation traits of Polish Black-and-White cows. J. Anim. Feed Sci., 12: 689–696.

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Parametry genetyczne dziennej zawartości komórek somatycznych i niektórych cech pokroju polskiego bydła holsztyńsko-fryzyjskiego

STRESZCZENIE

Celem pracy było oszacowanie parametrów genetycznych dziennej zawartości komórek somatycznych w mleku (SCS) i dziewięciu cech pokroju. Materiał do obliczeń stanowiły następujące cechy: dzienna zawartość komórek somatycznych w pierwszej laktacji oraz dwie opisowe i siedem szczegółowych cech pokroju 21 957 krów. Wybrano dzienne SCS z próbnych udojów, które wykonano w terminie najbardziej zbliżonym do daty przeprowadzenia oceny pokroju. Parametry genetyczne oszacowano za pomocą metody Bayesa i wielocechowego modelu zwierzęcia. Model liniowy dla cech pokroju zawierał losowy, addytywny efekt genetyczny, stałe efekty podklasy stado-rok-sezon-klasyfikator (HYSC) i fazy laktacji, oraz stałą regresję liniową na wiek ocielenia. Do analizy SCS użyto modelu zawierającego te same efekty jak wyżej, z wyjątkiem efektu HYSC, który zastąpiono efektem podklasy stado-rok-sezon (HYS).

Wszystkie oszacowane odziedziczalności miały wartości małe lub średnie (0,06–0,33). Najwyższe korelacje genetyczne stwierdzono pomiędzy SCS i dwiema cechami opisowymi: oceną wymienia (–0,28) i oceną nóg i racic (–0,37). Spośród cech szczegółowych najsilniejszy związek z SCS wykazały postawa nóg tylnych-widok z tyłu (0,25) i więzadło środkowe wymienia (–0,19). Wymienione cechy pokroju mogą być pomocne w pośredniej selekcji mającej na celu poprawę stanu zdrowotności wymienia.