Genetic relationship of conformation traits with average somatic cell score at 150 and 305 days in milk in Holstein cows of Iran

M. Dadpasand,[1] M. J. Zamiri, H. Atashi, and A. Akhlaghi
Department of Animal Science, College of Agriculture, Shiraz University, Shiraz, Iran 71441-65186

ABSTRACT

Genetic, environmental, and phenotypic correlations among average somatic cell score (SCS) at different stages of lactation and conformation traits were estimated. Data consisted of the lactational average of SCS at 150 (SCS_{150}) and 305 (SCS_{305}) d in milk and 19 conformation traits recorded on 57,154 primiparous Holstein cows, that calved from 1996 to 2009 in 119 herds in Iran. Variance components were estimated using the restricted maximum likelihood procedure based on multiple-trait animal models. Udder depth (-0.32), fore udder attachment (-0.22), and udder width (0.34) showed moderate genetic correlation with SCS_{150}. Heart girth (0.17), body depth (0.14), chest width (0.26), and angularity (0.19), showed modest genetic correlation with SCS_{150}. The estimated heritabilities for SCS_{150} and SCS_{305} were 0.06 and 0.08, respectively. The heritability of the conformation traits ranged from 0.09 to 0.29. Genetic and environmental correlations between SCS_{150} and SCS_{305} were very high (means ± SE; 0.99 ± 0.01 and 0.89 ± 0.01, respectively), which indicates that recording SCS over a shorter period of lactation is an alternative approach for involving many herds in SCS data collection. The low heritability of SCS indicated that indirect selection for some of udder and body traits might be helpful to reduce the SCS. Additionally, selection for udder traits may help reduce SCS in developing countries where SCS data are sparsely recorded.

Key words: somatic cell score, conformation trait, genetic correlation

INTRODUCTION

Mastitis is the most costly and challenging disease in the dairy industry worldwide. Due to some critical limitations, including low heritability and lack of precise data, direct selection for improving the resistance to mastitis is not feasible in many countries. However, Nordic countries have implemented selection programs based on direct data of mastitis (Heringstad et al., 2000). Somatic cell score is often used as an indirect selection criterion for reducing the incidence or severity of mastitis (de Haas et al., 2008; Bloemhof et al., 2009; Windig et al., 2010; Koeck et al., 2012). Higher heritability and strong genetic relationship with resistance to mastitis have made SCS a good indicator of mammary health. Not only does SCS affect milk yield, content, and quality (Miller et al., 2004; Dürr et al., 2008; Rekik et al., 2008; Halasa et al., 2009), but it is also associated with decreased fertility and longevity (Samoré et al., 2004; Sewalem et al., 2006; Pinedo et al., 2009). In addition to a selection criterion for mastitis and udder health, SCS is a determinant of milk price penalty in Iran.

Although SCS is routinely recorded in dairy cattle breeding programs in many countries, in some systems or areas such recording is not regularly practiced. Several studies suggested that selection for some of the conformation traits, especially the udder traits, might help to reduce the SCS of milk and susceptibility to mastitis (Němcová et al., 2007; Bloemhof et al., 2009; Ptak et al., 2011).

The relationship between type traits and SCS is not consistent across populations and breeds. In Brown Swiss and Red and White cows, an extremely large size or high scores of dairy form was associated with high SCS, but this was not the case in Holstein cows (de Haas et al., 2007). These differences might be partly related to the structure of data, trait definition, and applied model.

In spite of discrepancies found among the various estimates, the strong genetic correlations of SCS with udder depth, rear udder width, and fore attachment were more consistent across breeds and populations (Rupp and Boichard, 1999; Samoré and Groen, 2006; Ptak et al., 2011). Previous studies on Italian Brown Swiss (Samoré et al., 2010) and French Holstein (Rupp and Boichard, 1999) cows revealed a negative genetic correlation between udder depth and SCS (-0.46 and -0.40, respectively). Recently, Ptak et al. (2009, 2011) suggested that the Polish Holstein cows with deep and wide udders had a higher SCS than the cows with an optimum score for these traits.

Ptak et al. (2009) found no genetic or phenotypic relationship between SCS and suspensory ligament, teat placement, or teat length. However, a genetic correlation of 0.22 was found between teat length and SCS in Italian Brown Swiss cattle (Samoré et al., 2010). In Dutch Holstein cows, the genetic correlation of average SCS over 3 lactations with udder depth and fore udder attachment were 0.35 and 0.30, respectively, whereas a low value (−0.15) was reported for teat length (Bloemhof et al., 2009). Additionally, some studies have showed a moderate (−0.30 to −0.36) genetic correlation between some of the body traits and SCS (DeGroot et al., 2002; de Haas et al., 2007).

The Iranian Holstein population was expanded following introduction of purebred pregnant heifers from the United States, Canada, and Europe during the 1970s and early 1980s. The Animal Breeding Centre (**ABC**, Karaj, Iran), a governmental organization located 30 km west of Tehran (the capital of Iran), is the official organization of livestock improvement. About 80 young bulls were annually entered into the progeny-testing program, from which 12 to 20 bulls are selected as proven sires. Although about 1,500 dairy farms (≈200,000 cows) participate in milk recording, only 200 herds (≈0.25% of population) contribute to collect the SCS data. Type classification is performed on approximately 300 herds by the trained technicians of ABC according to the guidelines of the International Committee for Animal Recording (ICAR, 2011), with slight modification. Several conformation traits are evaluated on a scale of 1 to 9 and others are measured in centimeters (M. B. Sayadnejad, ABC, personal communication). Artificial insemination is used in almost all herds and 60 to 80% of semen is usually from US- and Canadian-proven sires. The herds used in this study were among the purebred Holsteins that were under official performance and pedigree recording and managed under conditions similar to most other developed countries. The average milk production for Iranian Holsteins is currently about 8,000 kg per lactation (Ghavi Hossein-Zadeh et al., 2008).

The objective of the present study was to estimate the genetic, environmental, and phenotypic relationships between the average SCS at 150 (**SCS$_{150}$**) and 305 (**SCS$_{305}$**) DIM and the conformation traits in Holstein cattle of Iran. Due to costs of collecting the SCS data and lack of necessary infrastructure, SCS data were only available for herds in relatively more developed areas exploiting a higher level of management. The possibility of recording SCS data only for a short period during lactation (i.e., in the first 150 DIM) was investigated to eventually reduce the costs of SCS data recording and, therefore, to expand the SCS recording in the country by increasing both the number of herds and cows involved. Average SCS over the 150 d was, therefore, considered as an alternative to the 305-d average, by comparing genetic and environmental correlations of conformation traits with 2 SCS traits. Genetic and environmental correlations of SCS$_{150}$ with SCS$_{305}$ were also considered.

MATERIALS AND METHODS

Data

Conformation scores and SCS records of 57,154 first-lactation Iranian Holstein dairy cows, which calved during 1996 to 2009, were obtained from the database of the ABC. The data were from 119 registered Holstein herds, having both conformation and SCC records. The data from herds with at least 20 observations on each trait were used. The records associated with ambiguous calving dates, incorrect evaluation dates, and age at first calving outside 20 to 38 mo were not included in the analysis. Only the sires with a minimum of 10 daughters in at least 5 herds were considered for the parameter estimation. The pedigree file included animals in the data file and 3 generations of their ancestors. The descriptive statistics of the data are in Table 1. Test-day SCC were first log transformed to SCS based on the following equation and then averaged along 5 to 150 and 5 to 350 DIM:

$$SCS = \ln(SCC/100{,}000) + 3.$$

Because of the dilution effect of milk yield on SCC (Green et al., 2006), weighted means of SCS were calculated based on the following formula (Raffrenato et al., 2003), taking into account the milk yield corresponding to SCC for each test day:

$$WSCS = \frac{\sum_{i=1}^{n}(m_i SCS_i)}{\sum_{i=1}^{n} m_i},$$

where *WSCS* is the weighted average of SCS$_{150}$ or SCS$_{305}$, SCS_i is the monthly SCS, and m_i is the test-day milk production of the ith month of recording. The observations between 5 to 305 d of lactation were used. A minimum of 3 and 4 test-day records were required to calculate SCS$_{150}$ and SCS$_{305}$, respectively. The average (±SD) interval between test-day records was 30.81 ± 3.77. The frequencies of observations for 2 SCS traits are shown in Table 2. For SCS$_{150}$, 88.7% of cows had full test-day records (5 records) and for SCS$_{305}$, 81.4% of cows had at least 6 records.

Table 1. Descriptive statistics for SCS and conformation traits

Trait[1]	No. of records	Mean	SD	Minimum	Maximum
SCS_{150}	33,591	2.53	1.00	0.28	6.98
SCS_{305}	38,661	2.62	0.95	0.43	6.80
Fore udder attachment[2]	27,158	6.77	1.33	1	9
Rear udder height (cm)	27,203	25.55	2.43	12	65
Rear udder width (cm)	27,189	16.23	2.11	7	33
Udder depth[2]	27,185	5.94	1.02	1	9
Udder cleft[2]	27,192	6.32	1.70	1	9
Front teat placement[2]	27,189	4.95	0.88	1	8
Rear teat placement[2]	27,194	6.10	1.10	1	9
Teat length (cm)	27,166	4.60	0.86	1	10
Heart girth (cm)	27,192	191.93	6.45	164	230
Stature (cm)	27,198	140.11	2.70	121	160
Body depth	27,110	5.61	0.98	1	9
Loin[2]	27,159	6.52	1.09	2	9
Angularity[2]	27,178	6.67	0.77	1	9
Chest width[2]	27,192	5.40	0.99	1	9
Rump length (cm)	27,180	51.40	1.98	40	62
Pin width (cm)	27,165	19.81	1.44	14	35
Rump angle[2,3] (cm)	27,189	2.28	1.45	−5	10
Foot angle[2]	27,178	6.67	0.77	1	9
Rear legs side view	27,159	6.52	1.09	2	9

[1]SCS_{150} = SCS at 150 DIM; SCS305 = SCS at 305 DIM.

[2]Evaluated subjectively on a scale from 1 to 9.

[3]Measured based on the relative position of pin to hip bones.

Models

Variance components were estimated using the restricted maximum likelihood (REML) procedure based on multiple-trait animal models through the VCE6 Package (Kovac et al., 2008). Different sets of 4-trait analyses were performed based on the category of type traits (i.e., udder, feet and legs, body, and rump traits). An analysis of data with a generalized linear model was used to identify significant fixed effects with SAS software (SAS Institute, 1999).

The following 4-trait animal model was used for the analyses:

$$
\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \\ \mathbf{y}_3 \\ \mathbf{y}_4 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{X}_3 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{X}_4 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \\ \mathbf{b}_3 \\ \mathbf{b}_4 \end{bmatrix}
$$
$$
+ \begin{bmatrix} \mathbf{Z}_1 & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{Z}_3 & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{Z}_4 \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{a}_3 \\ \mathbf{a}_4 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \end{bmatrix},
$$

where $\mathbf{y}_1$ to $\mathbf{y}_4$ are vectors of observations of SCS or conformation traits in each set of multiple trait analysis, $\mathbf{X}_1$ to $\mathbf{X}_4$ are design matrices relating the fixed effects in $\mathbf{b}_1$–$\mathbf{b}_4$ (vectors of fixed effects) to $\mathbf{y}_1$–$\mathbf{y}_4$, $\mathbf{Z}_1$ to

$\mathbf{Z}_4$ are design matrices relating the random effect of animals to $\mathbf{a}_1$ to $\mathbf{a}_4$ (vectors of animal additive genetic effects), and e_1 to e_4 are random residuals. The vectors of fixed effects were as follows:

$$
\mathbf{b}_{\textbf{Conformation}} = \begin{bmatrix} hys \\ E \\ \alpha_{Age} \\ \beta_{Age} \\ \lambda_{DIM} \end{bmatrix} \quad \text{and} \quad \mathbf{b}_{\textbf{SCS}} = \begin{bmatrix} hys \\ \alpha_{Age} \end{bmatrix},
$$

where $\mathbf{b}_{\textbf{Conformation}}$ and $\mathbf{b}_{\textbf{SCS}}$ are the vectors of fixed effects for conformation and SCS, respectively; *hys* is the effect of herd-year-season of calving or classification

Table 2. Relative frequency (%) of test-day records for each SCS[1]

Number of test-day records	SCS_{150}	SCS_{305}
3	5.38	—
4	5.93	8.00
5	88.69	10.62
6	—	12.12
7	—	13.87
8	—	14.68
9	—	13.10
10	—	27.71

[1]SCS_{150} = SCS at 150 DIM; SCS305 = SCS at 305 DIM.

(1,287 levels); E is the effect of type evaluator (52 levels); α_{Age} and β_{Age} are the linear and quadratic regression coefficients of age at calving (a linear covariate defined in days), respectively; and λ_{DIM} is the linear regression coefficient effect of stage (defined in days) of lactation at the time of type classification. The minimum number of observations for each hys was 5 records. Four season of calving were defined (April–June, July–September, October–December, and January–March).

RESULTS AND DISCUSSION

Estimated Heritabilities

Table 3 shows the estimated heritabilities of SCS and type traits. The estimated heritabilities for SCS_{150} and SCS_{305} were 0.06 and 0.08, respectively, which are in close agreement with the estimate of Safdari Shahroudi et al. (2010). Mostert et al. (2004) also reported very low heritability (0.04 to 0.07) for SCS in lactations 1 to 3 of South African Holstein and Jersey cows. However, in a more recent study, the estimated heritability of SCS in the South African Holstein cows was between 0.17 and 0.19 (Dube et al., 2008). The estimated heritability of SCS in the Polish Holstein cows was 0.07 (Ptak et al., 2009). Several studies have reported heritabilities of 0.09 to 0.32, depending on the SCS definitions and criteria (Muir et al., 2007; Bohmanova et al., 2009; Miglior et al., 2009). The estimates for conformation traits in most cases were in the range of values reported for the same population (Bakhtiari Zadeh et al., 2010; Safdari Shahroudi et al., 2010). Although for some traits, some differences existed between the estimates in the present study and those in the literature (Němcová et al., 2011).

Genetic Correlations

Udder Traits. Among the mammary traits, udder depth, fore udder attachment, and rear udder width showed a relatively strong genetic correlation with both SCS_{150} and SCS_{305} compared with other udder traits (Table 4). The correlation of udder width (means ± SE) with SCS_{150} (0.34 ± 0.08) was higher than with SCS_{305} (0.24 ± 0.05).Teat length and teat position had no relationship with SCS_{150} and SCS_{305}. In other populations, however, a moderate genetic correlation was found between the teat traits and SCS (Dube et al., 2008; Bloemhof et al., 2009). Several reports suggested an association between shorter and more closely placed teats and reduced SCS (Mrode et al., 1998; Němcová et al., 2007; Dube et al., 2008). DeGroot et al. (2002) reported a genetic correlation of −0.24 between SCS and teat length, and −0.19 between SCS and fore teat placement. However, the respective genetic correlations in Italian Brown Swiss were 0.22 and 0.01.

The genetic correlation of 0.12 between the rear udder height and SCS_{305} indicated a tendency for reduced SCS in cows with suitable udder height and attachment. Although wider rear udders are favored in many type-classification systems, rear udder width was unfavorably correlated with SCS in this study. In agreement with the previous studies (Němcová et al., 2007; Bloemhof et al., 2009; Ptak et al., 2009, 2011), udder depth, and fore udder attachment showed a relatively strong genetic correlation with SCS. A small positive genetic correlation (0.07) was reported between SCS and fore udder attachment in Italian Brown Swiss cattle (Samoré et al., 2010). However, in Italian (Samoré and Groen, 2006) and South African Holstein (Dube et al., 2008) cows, genetic correlations of SCS with fore udder attachment were −0.16 and −0.09, respectively. Part of these discrepancies might be related to the population, data, and model used, but the definition of the trait and the method of data transformation might also have contributed.

Body, Rump, Feet, and Leg Traits. Heart girth (0.17), body depth (0.14), chest width (0.26), and angularity (0.19), showed moderate genetic correlations with the SCS_{150} (Table 4). Other traits of this category had a very weak genetic relationship with both SCS_{150} and SCS_{305} (Table 4). In agreement with Mrode et al. (1998), the estimated genetic and nongenetic correlations between rump traits and SCS_{150} or SCS_{305} were close to zero (Table 4). On the other hand, Ptak et al.

Table 3. Estimated heritability (h^2) of SCS and conformation traits

Trait[1]	h^2	SE
SCS_{150}	0.06[2]	0.01
SCS_{305}	0.08[2]	0.01
Fore udder attachment	0.15	0.01
Rear udder height	0.10	0.01
Rear udder width	0.11	0.01
Udder depth	0.23	0.01
Udder cleft	0.13	0.01
Fore teat placement	0.13	0.01
Rear teat placement	0.18	0.01
Teat length	0.17	0.02
Heart girth	0.20	0.01
Stature	0.29	0.02
Body depth	0.11	0.01
Loin	0.09	0.01
Angularity	0.11	0.01
Chest width	0.12	0.01
Rump length	0.23	0.02
Rump width	0.26	0.02
Rump angle	0.19	0.02
Foot angle	0.12	0.01
Rear legs side view	0.09	0.01

[1]SCS_{150} = SCS at 150 DIM; SCS305 = SCS at 305 DIM.
[2]Average of 5 estimates.

Table 4. Genetic, environmental, and phenotypic correlations (means ± SE) between SCS at 150 DIM (SCS$_{150}$), SCS at 305 DIM (SCS$_{305}$), and linear conformation traits[1]

Trait[2]	SCS$_{150}$			SCS$_{305}$		
	r_G	r_E	r_P	r_G	r_E	r_P
FUA	−0.22 ± 0.08	−0.03	−0.05	−0.21 ± 0.06	−0.06	−0.08
RUH	0.10 ± 0.07	0.05[3]	0.05	0.12 ± 0.06	0.02	0.02
RUW	0.34 ± 0.08	0.00	0.03	0.24 ± 0.05	0.00	0.02
UD	−0.32 ± 0.07	−0.06	−0.09	−0.29 ± 0.05	−0.08	−0.10
UC	−0.05 ± 0.09	0.06	−0.06	−0.02 ± 0.07	−0.06	−0.06
FTP	0.01 ± 0.09	−0.05	−0.04	−0.01 ± 0.01	−0.05	−0.04
RTP	0.01 ± 0.07	−0.06	−0.05	−0.01 ± 0.01	−0.06	−0.06
TL	0.00 ± 0.04	0.02	−0.02	−0.03 ± 0.01	0.02	0.01
HG	0.17 ± 0.08	−0.02	0.00	0.07 ± 0.02	0.00	0.01
STA	0.04 ± 0.08	−0.01	0.00	0.01 ± 0.02	0.00	0.00
BD	0.14 ± 0.07	−0.01	0.00	0.07 ± 0.03	0.00	0.01
Loin	0.08 ± 0.05	−0.02	−0.02	0.11 ± 0.07	0.00	0.01
ANG	0.19 ± 0.07	0.00	−0.02	0.12 ± 0.07	0.01	0.01
CW	0.26 ± 0.08	−0.02	0.00	0.11 ± 0.07	0.00	0.01
RL	0.06 ± 0.03	−0.01	0.00	−0.01 ± 0.03	0.00	0.00
RW	0.05 ± 0.05	0.00	0.01	0.00 ± 0.02	0.02	0.02
RA	−0.06 ± 0.06	0.03	0.02	0.06 ± 0.04	0.01	0.01
FA	0.11 ± 0.08	−0.01	0.02	0.12 ± 0.07	0.00	0.01
RLSV	0.01 ± 0.05	0.01	0.00	0.06 ± 0.04	−0.02	0.02

[1]r_G, r_E, and r_P = genetic, environmental, and phenotypic correlations, respectively.

[2]FUA = fore udder attachment; RUH = rear udder height; RUW = rear udder width; UD = udder depth; UC = udder cleft; FTP = fore teat placement; RTP = rear teat placement; TL = teat length; HG = heart girth; STA = stature; BD = body depth; ANG = angularity; CW = chest width; RL = rump length; RW = rump width; RA = rump angle; FA = foot angle; RLSV = rear legs side view.

[3]Standard errors of the environmental and phenotypic correlations were in the range of 0.01 to 0.02.

(2011) reported genetic correlations of 0.21 and 0.13 between the SCS and rump angle and width, respectively. The corresponding correlations for Italian Brown Swiss cows were −0.08 and 0.15, respectively (Samoré et al., 2010).

Feet and leg traits were less correlated with either SCS$_{150}$ or SCS$_{305}$, which is consistent with the findings of Ptak et al. (2011) in Polish Holstein cows. However, in an experimental herd of Holstein cows at the University of Nebraska (Lincoln), strong genetic relationships of −0.61, −0.61, and −0.48 were reported between SCS and the rear legs, rear and side view, and foot angle, respectively (DeGroot et al., 2002). The genetic and phenotypic correlation (mean ± SE) between the corrected and uncorrected SCS was 0.99 ± 0.01. Also, the estimated genetic and environmental correlations between SCS$_{150}$ and SCS$_{305}$ was 0.99 ± 0.01 and 0.89 ± 0.01, respectively, implying that average SCS in 150 or 305 DIM could be genetically regarded as the same trait. It shows that recording of SCS for shorter periods (i.e., the first 150 DIM), but in a larger number of cows and herds would be informative enough to be applied in breeding programs, providing a cost-effective alternative to collecting SCS for the whole lactation. Due to inconsistency of data collection, less than 50% of herds had both SCS and conformation data. Completeness of data on both traits might result in more accurate estimates.

CONCLUSIONS

The present study showed that selection for traits such as fore udder attachment, udder width, and udder depth might be beneficial to reduce SCS and, in turn, mastitis incidence. However, due to moderate genetic correlations, highly correlated responses could not be expected. Body traits such as heart girth, body depth, chest width, and angularity showed moderate genetic correlations with SCS$_{150}$. In comparison with milk yield, few records are available for SCS and conformation traits in registered Holstein cows of Iran, which seems to be a common feature of the dairy industry in many developing countries. Due to a very strong genetic correlation between SCS$_{150}$ and SCS$_{305}$, SCS data collected in the first 150 DIM could be a good indicator to average SCS of the whole lactation Collecting SCS data over the first 150 DIM might be a suitable approach for including many cows and herds in SCS data collection.

REFERENCES

Bakhtiari Zadeh, M. R., M. Moradi Shahre Babak, A. Pakdel, and A. Moghimi. 2010. Genetic relationship between linear type traits, milk yield, and open days in Holstein cows of Iran. Iran. J. Anim. Sci. 40:13–19. (In Farsi with English abstract.)

Bloemhof, S., G. de Jong, and Y. de Haas. 2009. Genetic parameters for clinical mastitis in the first three lactations of Dutch Holstein cattle. Vet. Microbiol. 134:165–171.

Bohmanova, J., F. Miglior, and J. Jamrozik. 2009. Use of test-day records beyond three hundred five days for estimation of three hundred five-day breeding values for production traits and somatic cell score of Canadian Holsteins. J. Dairy Sci. 92:5314–5325.

de Haas, Y., L. L. G. Janss, and H. N. Kadarmideen. 2007. Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds. J. Anim. Breed. Genet. 124:12–19.

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

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

Dube, B., K. Dzama, and C. B. Banga. 2008. Genetic analysis of somatic cell score and udder type traits in South African Holstein cows. S. Afr. J. Anim. Sci. 38:1–11.

Dürr, J. W., R. I. Cue, H. G. Monardes, J. Moro-Méndez, and K. M. Wade. 2008. Milk losses associated with somatic cell counts per breed, parity and stage of lactation in Canadian dairy cattle. Livest. Sci. 117:225–232.

Ghavi Hossein-Zadeh, N., A. Nejati-Javaremi, S. R. Miraei-Ashtiani, and H. Kohram. 2008. An observational analysis of twin births, calf stillbirth, calf sex ratio, and abortion in Iranian Holsteins. J. Dairy Sci. 91:4198–4205.

Green, L. E., Y. H. Schukken, and M. J. Green. 2006. On distinguishing cause and consequence: Do high somatic cell counts lead to lower milk yield or does high milk yield lead to lower somatic cell count. Prev. Vet. Med. 76:74–89.

Halasa, T., M. Nielen, A. P. W. De Roos, R. Van Hoorne, G. de Jong, T. J. G. M. Lam, T. van Werven, and H. Hogeveen. 2009. Production loss due to new subclinical mastitis in Dutch dairy cows estimated with a test-day model. J. Dairy Sci. 92:599–606.

Heringstad, B., G. Klemetsdal, and J. Ruane. 2000. Selection for mastitis resistance in dairy cattle: A review with focus on the situation in Nordic countries. Livest. Prod. Sci. 64:95–106.

ICAR (International Committee for Animal Recording). 2011. Guidelines approved by the General Assembly held in Riga on June 2010. Section 5.1-Conformation recording of dairy cattle, 199–213. Accessed May 15, 2012. http://www.icar.org/Documents/Rules%20 and%20regulations/Guidelines/Guidelines_2011.pdf.

Koeck, A., F. Miglior, D. F. Kelton, and F. S. Schenkel. 2012. Alternative somatic cell count traits to improve mastitis resistance in Canadian Holsteins. J. Dairy Sci. 95:432–439.

Kovac, M., E. Groeneveld, and A. García-Cortés. 2008. Accessed June 2, 2011. ftp://ftp.tzv.fal.de/pub/latest_vce/bin/vce-Windows-x86_32-gfortran-6.0.2.exe.

Miglior, F., W. Gong, Y. Wang, J. Kistemaker, A. Sewalem, and J. Jamrozik. 2009. Genetic parameters of production traits in Chinese Holsteins using a random regression test-day model. J. Dairy Sci. 92:4697–4706.

Miller, R. H., H. D. Norman, G. R. Wiggans, and J. R. Wright. 2004. Relationship of test-day somatic cell score with test-day and lactation milk yields. J. Dairy Sci. 87:2299–2306.

Mostert, B. E., C. Banga, E. Groeneveld, and F. H. J. Kanfer. 2004. Breeding value estimation for somatic cell score in South African dairy cattle. S. Afr. J. Anim. Sci. 34(Suppl. 2):32–34.

Mrode, R. A., G. J. T. Swanson, and M. S. Winters. 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. Anim. Sci. 66:569–576.

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

Němcová, E., M. Štípková, and L. Zavadilová. 2011. Genetic parameters for linear type traits in Czech Holstein cattle. Czech J. Anim. Sci. 56:157–162.

Němcová, E., M. Štípková, L. Zavadilová, J. Bouška, and M. Vacek. 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.

Pinedo, P. J., P. Melendez, A. Villagomez-Cortes, and C. A. Risco. 2009. Effect of high somatic cell counts on reproductive performance of Chilean dairy cattle. J. Dairy Sci. 92:1575–1580.

Ptak, E., W. Jagusiak, A. Żarnecki, and A. Otwinowska-Mindur. 2009. Relationship between somatic cell score and udder conformation traits in Polish Holstein-Friesian cows. Ann. Anim. Sci. 9:237–241.

Ptak, E., W. Jagusiak, A. Żarnecki, and A. Otwinowska-Mindur. 2011. Heritabilities and genetic correlations of lactational and daily somatic cell score with conformation traits in Polish Holstein cattle. Czech J. Anim. Sci. 56:205–212.

Raffrenato, E., R. W. Blake, P. A. Oltenacu, J. Carvalheira, and G. Licitra. 2003. Genotype by environmental interaction for yield and somatic cell score with alternative definitions. J. Dairy Sci. 86:2470–2479.

Rekik, B., N. Ajili, H. Belhani, A. Ben Gara, and H. Rouissi. 2008. Effect of somatic cell count on milk and protein yields and female fertility in Tunisian Holstein dairy cows. Livest. Sci. 116:309–317.

Rupp, R., and D. Boichard. 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.

Safdari Shahroudi, M., A. Pakdel, and S. R. Miraei Ashtiani. 2010. Estimation of genetic parameters, proposal of an udder health index and comparison of different selection strategies to include this trait in Iranian Holstein cows breeding programs. Iran. J. Anim. Sci. 41:381–390. (In Farsi with English abstract.)

Samoré, A. B., R. Rizzi, A. Rossoni, and A. Bagnato. 2010. Genetic parameters for functional longevity, type traits, somatic cell scores, milk flow and production in the Italian Brown Swiss. Ital. J. Anim. Sci. 9:145–151.

Samoré, A. B., M. del P. Schneider, F. Canavesi, A. Bagnato, and A. F. Groen. 2004. Relationship between somatic cell count and functional longevity assessed using survival analysis in Italian Holstein-Friesian cows. Livest. Prod. Sci. 80:211–220.

Samoré, A. B., and A. F. Groen. 2006. Proposal of an udder health genetic index for the Italian Holstein Friesian based on first lactation data. Ital. J. Anim. Sci. 5:359–370.

SAS Institute. 1999. SAS/STAT User's Guide. Version 8 ed. SAS Inst. Inc., Cary, NC.

Sewalem, A., F. Miglior, G. J. Kistemaker, and B. J. Van Doormaal. 2006. Analysis of the relationship between somatic cell score and functional longevity in Canadian dairy cattle. J. Dairy Sci. 89:3609–3614.

Windig, J. J., W. Ouweltjes, J. ten Napel, G. de Jong, R. F. Veerkamp, and Y. De Haas. 2010. Combining somatic cell count traits for optimal selection against mastitis. J. Dairy Sci. 93:1690–1701.