IJAS Iranian Journal of Applied Animal Science

Estimation of Genetic Parameters and Genetic Trends of Somatic Cell Score in Iranian Holstein Cows Using Test-Day Records

Research Article

K. Kheirabadi[1*] and S. Alijani[2]

[1] Department of Animal Science, Ramin Agricultural and Natural Resources University, Mollasani, Ahvaz, Iran
[2] Department of Animal Science, University of Tabriz, Tabriz, Iran

Received on: 28 Nov 2013
Revised on: 17 Jan 2014
Accepted on: 30 Jan 2014
Online Published on: Dec 2014

*Correspondence E-mail: kheirabadi89@ms.tabrizu.ac.ir

Online version is available on: www.ijas.ir

ABSTRACT

The aim of the present study was to estimate the genetic parameters and genetic trends of somatic cell score (SCS) in the first 3 lactations of Iranian Holstein cows by random regression (RR) animal model by using Restricted Maximum Likelihood (REML) method. The data set used in this analysis included observations of 340318 test-day records of 41526 cows in 288 herds; 89969 test-day of 11750 cows in 127 herds and 20010 test-day of 2461 cows in 60 herds in the first-, second- and third-parity, respectively, during the period from 2002 to 2010. Fixed effects considered were: year of calving, age-season of calving (by applying a fixed regression for each subclass of this effect) and herd-test date. Estimates of additive genetic variances for all parities, with only small changes, show a similar trend. Heritability estimates for first parity (0.03 to 0.07) were lower than those for second (0.07 to 0.11) and third (0.08 to 0.17) parities. Genetic correlations between daily SCS within parity were high for adjacent tests and low between the beginning and the end of lactation and decreased with increase parity number. Genetic correlations between parities were higher than 0.70 but environmental correlations between parities were in range of 0.22 to 0.51. Genetic correlations between parity demonstrate that genes that control SCS in parities are same and selection animal for SCS in first parity would have affected SCS in other parity. The genetic trend for SCS was favorable until 1995 and unfavorable since then. The relatively high level of SCS and positive genetic trends (0.431 to 0.701 cells/mL/year) would suggest that genetic improvement of SCS is at unacceptable level in Iran.

KEY WORDS genetic parameters, genetic trend, random regression, somatic cell score.

INTRODUCTION

Mastitis is one of the major diseases in dairy industry which causes serious economic loss. The losses are associated with increased costs of replacement, veterinary treatments, labor, and reduce milk yield, and lower milk quality premium (Luttinen and Juga, 1997; Mrode and Swanson, 2003). Strategies to control mastitis include preventive health care, hygiene, veterinary remedies, and genetic selection (Weller *et al*. 1992; Norman *et al*. 2000). Breeding and selection for increased resistance to mastitis can be performed by either clinical mastitis records as direct information or via on traits that are genetically correlated to mastitis as indirect information; or a combination of both (Heringstad *et al*. 2000; Ødegard *et al*. 2003; Luhar *et al*. 2006). In many countries, especially in the developing countries, information concerning clinical mastitis is not collected by genetic improvement center or veterinarians, thus direct selection to reduce mastitis incidence is not often possible. Increasingly, research indicates a positive relationship between milk somatic cell count (SCC) and mastitis (Heringstad *et al*. 2000; Carlén *et al*. 2004). Owing to the higher heritability of SCC and its high genetic correlation with clinical mastitis, it can be used as an indirect se-

lection tool for reducing mastitis (Heringstad *et al*. 2000; Mrode and Swanson, 2003). On the other, hand direct mastitis diagnosis is more expensive whereas SCC can be recorded at low cost in routine milk recording. However SCC which are recorded through dairy herd improvement testing, because of better statistical properties, often transformed into logarithmic scale (referred to somatic cell score (SCS)) (Schutz, 1994; Luttinen and Juga, 1997). Whereas mastitis incidence increases with age and parity of cows (Thompson *et al*. 1983; Reents *et al*. 1995; Carlén *et al*. 2004), therefore apposite selection against mastitis would ideally include information on SCC from first and later lactations, which could be achieved by considering records from multiple lactations as a distinct trait. Additionally, analyzing data from different parities as separate traits will account for selection and culling on correlated traits both within and between lactations (Jamrozik *et al.* 1998).

Genetic trends are critical tool to evaluate the effects of the genetic improvement program (Intaratham *et al*. 2008; Ghavi Hossein-Zadeh, 2011). Moreover annual trends for economic traits should be monitored over time to check the validity of the predictions made and to investigate direction of genetic change and whether the selection strategies implemented could reach a selection limit or have unexpected other effects (Intaratham *et al*. 2008). In Iran, the majority studies on dairy cows are on milk yield traits and usually during the first lactation. Although few investigations have been carried out on Iranian Holstein cows in regard to the estimation of genetic parameters (Bakhtiarizadeh *et al*. 2009; Cheraghi *et al*. 2012) and genetic trend of SCS (Abdini *et al*. 2012) but there were scare estimate of genetic parameters and genetic trend for SCS by multi-lactation random regression model (ML-RRM). Therefore, the aim of this study was to estimate the genetic parameters and genetic trend of SCS in the first 3 lactations by a random regression (RR) animal model using Restricted Maximum Likelihood (REML) method. This study was a first step toward an Iranian genetic evaluation system based on ML-RRM.

MATERIALS AND METHODS

Data

Monthly test-day (TD) records of SCC of first three parities of Iranian Holstein cows from 2002 to 2010 provided by the Animal Breeding Center of Iran were used in this study. Cows with third parity records had to have their first and second parities in the data set. Likewise, second lactation cows had first lactation records. The records of cows were deleted if their ages at first, second, and third calving were out of the range of 660-1020, 1000-1420, and 1390-1840 days, respectively.

Records obtained before 5 or after 305 days in milk (DIM) were also discarded. Data in first lactation were included only those animals which their first TD was taken at or before d 60 and last TD was taken at or after d 250 and about other lactations it was d 90 and d 180, respectively. From there correlations of yields depend on the interval between tests (Haile-Mariam *et al*. 2001), thus in any interval between consecutive TD records that was less than 15 days the second one was omitted. A minimum of 5, 3 and 3 TD records, respectively, in first, second and third parity was required for a cow observation to be included in the analysis. In the present study, herds with fewer than 10 cows per herd × year of calving were removed. All records belonging to the cows whose sires had less than 10 daughters were also omitted. The SCS were calculated from SCC (Ali and Shook, 1980) as:

$$SCS = \log_2 (SCC/10^5) + 3$$

After editing the data, 340318; 89969 and 20010 TD records collected from 41526; 11750 and 2461 first-, second- and third-lactation cows, which were the offspring of 744; 350 and 106 sires, respectively. Four seasons (spring, summer, fall and winter) and three subclasses for age at calving for first lactation (<800 days, 800-900 and >900 days), three classes for the second lactation (<1200 days, 1200-1350 and >1350 days) and three classes for the third lactation (<1580 days, 1580-1760 and >1760 days) were defined. Descriptive statistics of the dataset are presented in Table 1. Pedigree information was obtained from the database center of National Breeding Center of Iran (during the period from 1981 to 2010). The final pedigree contained in total 1097459 entries, which were the offspring of 12608 sires.

Model

The equation model analyzed can be written in scalar notation as:

$$y_{ijklmo} = \mu_o + yc_{ok} + htd_{ol} + \sum_{n=0}^{3} \beta_{omn} \chi_{on} + \sum_{n=0}^{2} \alpha_{oijn} \Phi_{aojn} + \sum_{n=0}^{3} \omega_{oijn} \Phi_{pojn} + e_{ijklmo}$$

Where:

y_{ijklmo}: SCS from the j^{th} cow, made on day i, in k^{th} year of calving, within L^{th} herd-test date, belonging to subclass m of age-season of calving in the o^{th} parity.

μ: mean for the o^{th} parity.

yc_{ok}: fixed effect of k^{th} year of calving in the o^{th} parity.

Htd_{Ol}: fixed effect of L^{th} herd-test date belonging to o^{th} parity.

β_{omn}: n^{th} fixed regression coefficients specific to the subclass m nested within o^{th} parity.

$\boldsymbol{X}_{on}$: n^{th} order orthogonal polynomial corresponding to age

season of calving in the o^{th} parity.
α_{oijn} and ω_{oijn}: n^{th} random regression coefficient for the SCS record of cow j, made on day i, in the o^{th} parity associated with the animal genetic (AG) and permanent environmental (PE) effects, respectively.
$\boldsymbol{\Phi}_{aojn}$ and $\boldsymbol{\Phi}_{pojn}$: n^{th} orders orthogonal polynomial corresponding to TD record from the j^{th} cow, based on the function used for the AG and PE effects in o^{th} parity, respectively.
e_{ijklmo}: random residual.

Residual error variance was assumed to be constant throughout all lactations. Legendre polynomial functions, due to the low correlations between parameters than other functions (Kirkpatrick *et al*. 1990) were chosen for modeled TD records.

The matrix notation of the model was:

Y= Xb + Za + Wp + e

Where:
Y: a vector of TD records.
b: a vector of the fixed effects.
a and p: vectors of random regression coefficients for animal and PE effects, respectively.
e: a vector of residual effects.
X, Z and W: incidence matrices relating observations to various effects. The following (co) variance structure was assumed:

$$var\begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 & 0 \\ 0 & P \otimes I & 0 \\ 0 & 0 & E \otimes I \end{bmatrix}$$

Where:
G, P and E: are 9×9, 12×12 and 3×3 (co) variance matrices for AG, PE and residual effects, respectively.
A: numerator relationship matrix between all animals.
I: identity matrix.
$\otimes$: Kronecker product.

Variance and covariance for curve parameters were estimated by using the REMLF90 software (Misztal *et al*. 2002).

Convergence was assumed when the difference between the -2log values of the likelihood functions obtained in consecutive iterations was smaller than 10^{-9}. Heritabilities and genetic correlations were calculated according to the formula given by Jakobsen *et al*. (2002).

Genetic trends

Understanding the concept and knowing the breeding value of animals for economically important traits in first and later lactations help considerably in deciding which cows to cull. These estimates are useful in making and management decisions, since they help us make the best possible guess at how well the cow will do next year if we know how well she did this year. The predictions of breeding values or genetic merits were used to estimate genetic trends. The estimated breeding values (EBVs) of animal j for day i was calculated by:

$$EBV_{ij} = Z'_{ai}\hat{\alpha}_j$$

Let α_j represent the 3 by 1 vector of the estimates of AG random regression coefficients specific to the animal j, and Z_{ai} represent as a vector of Legendre polynomial coefficients evaluated at day i, that is:

$$\hat{\alpha}_j = \begin{bmatrix} \hat{\alpha}_{j0} \\ \hat{\alpha}_{j1} \\ \hat{\alpha}_{j2} \end{bmatrix} \qquad Z_{ai} = \begin{bmatrix} \phi_{0i} \\ \phi_{1i} \\ \phi_{2i} \end{bmatrix}$$

Therefore, the EBV of animal j for completed lactation was obtained by:

$$EBV_{j305d} = Z'_{a305d}\hat{\alpha}_j$$

For estimating genetic trends, a cow's estimated genetic merit was used only in the year of birth and a sire's estimated transmitting ability was used only in the year of a daughter's first calving (Hintz and Van Vleck, 1978). Transmitting ability was defined as one-half of AG value. So, breeding value of sires was obtained from the weighted average of sires transmitting abilities for each year on year.

RESULTS AND DISCUSSION

Fixed effects

Figure 1 show that fitted lactation curves for SCS resembled inverted lactation curves for milk yield. The trend for first parity differed from curves for second and third parities, which increased more slowly after the minimum during the second month of lactation. SCS increase with increase parity number.

Over the period considered in the current study, SCS showed a vividly increase. For instance, the year of calving solution for 2002 was 2.87 and that for the last year (2010) was 3.32 in the first parity. Also the average fixed regression coefficient (intercept) of TD records on age-season of calving was 0.16, 0.28 and -0.28 for 1st, 2nd, and 3rd parity, respectively.

Table 1 Structure and description of the data set used in the first three lactations

Item	First lactation	Second lactation	Third lactation
Monthly test day records (TD)	340318	89969	20010
SCS (S.D.)	2.36 (1.96)	2.91 (2.08)	3.34 (2.14)
Cows (no.)	41526	11750	2461
Sires (no.)	744	350	106
HTD (no.)	9703	3756	1435
Average number of daughters per bull	55.8	33.6	23.2
Average number of TD records per cow	8.2	7.7	8.1
Average number of TD records per HTD classes	35.1	24	13.9

SCS: somatic cell score and HTD: herd-test date.

Variances and heritability

With a few exceptions for third parity, the estimates of daily AG variances showed a plain trajectory with only small changes over time during parities (Figure 2).

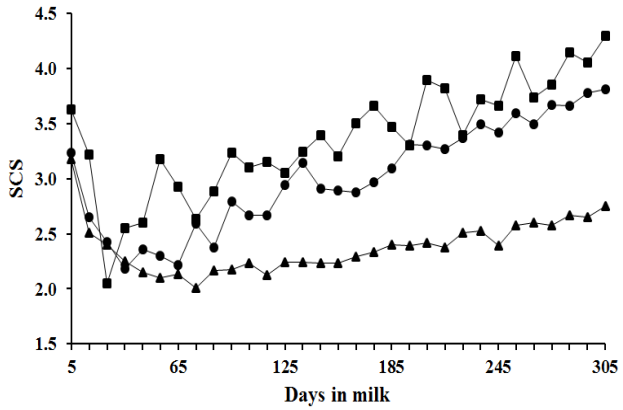

Figure 1 Effect of stage of lactation on SCS in parities 1 (▲), 2 (●), and 3 (■)

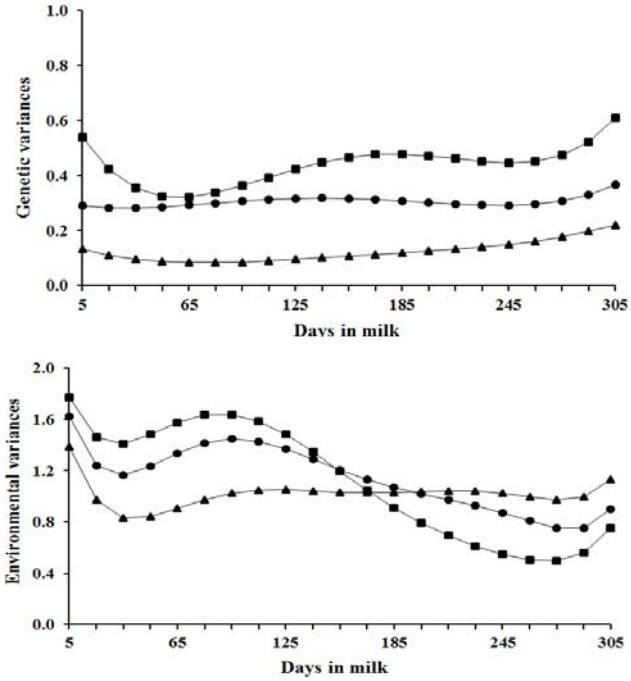

Figure 2 Additive genetic and PE variances for SCS in the first three parities [parities 1 (▲), 2 (●) and 3 (■)]

In general, the estimates were low at the peak of the lactation and rise to the maximum at the end test (DIM 305; 0.22 to 0.61).

In the inner part of the lactation, they remained relatively constant in the second parity and increased with DIM in the first and third parity, whereas the increase was strongest in third parity. However AG variances increased from first to third lactation. In contrast a marked variation of the PE variances with parity number was found (see Figure 2). Generally, most of the curves estimated rise at the edge. These growths were particularly high for the beginning of daily PE variances.

As expected, the PE variance was consistently higher than the AG variance for all three parities. In the inner part of the lactation, they remained relatively constant in the first parity and decreased with DIM in the second and third parity (around 170 DIM at the end), whereas the decrease was strangest in third parity. Figure 3 displays the trend of the daily heritability (h_i^2) in all three parities for different stages of lactation.

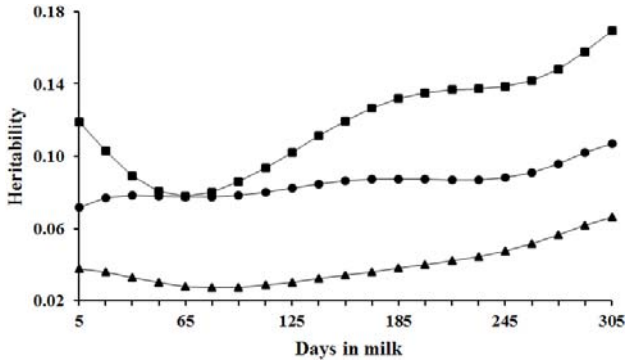

Figure 3 Daily heritabilities for SCS in the first three parities [parities 1 (▲), 2 (●) and 3 (■)]

These results indicate h_i^2 in the first stage of lactation (30 to 80 DIM) slightly decreased and then subsequently increased with DIM in the first two parities and were highest in end of the lactation (DIM 305; 0.07 to 0.11). Heritability of daily SCS tended to be more uniform over DIM in the second parity compared with daily heritability in the first parity.

Heritability estimates in third parity showed a similar trend across the lactation as in the first and second lactation but were higher than in both first parities (DIM 305; 0.17). Similar to the first two parities, h_i^2 in third parity increased with DIM. However, h_i^2 in the middle part of this parity in order to agree with respective AG variances slightly decline then increased subsequently for the remaining part of the lactation. Large drops or increases in daily heritability were noted at 60, 180 and 305 DIM when the daily PE variances changed. Generally, for a given DIM h_i^2 increased with an increase in parity number. For instance, the average daily heritabilities for DIM 5 to 40 was 0.04 in parity 1, compared with 0.08 and 0.10 in parities 2 and 3, respectively. One exception to this general trend is that at the peak of the third parity, where decline close the value in second parity. In general heritabilities of daily yields were distinctly lower than that for completed lactations (Table 2) and varied from 0.03 to 0.07 for first lactation, 0.07 to 0.11 for second lactation, and 0.08 to 0.17 for third lactation (Table 3), which are medium values in comparison with other studies. As a consequence all variances for complete lactation increased with parity number (Table 2). However the rate of increase from second to third parity was small. A disproportionate increase in residual variance was found as lactation number increased. Consequently, heritability estimates increased, especially from the first to the second parity.

Genetic and permanent environmental correlations

Within lactation correlations: Genetic and PE correlations between TD at different stages of lactation are presented in Table 3. Generally, the highest genetic correlation (close to unity) was founded for consecutive DIM, while the lowest was between SCS at DIM early and late lactation. The genetic correlations were particularly high within the first parity than other parity, even when DIM were far apart. For instance, the genetic correlation between DIM 5 and 305 was 0.59 in first parity, compared with 0.39 and 0.20 in second and third parities, respectively. With the exception of third parity, the genetic correlations within parity were higher than the respective PE correlations. As a consequence, genetic correlations between early and late lactation decreased with parity number. In contrast, this trend for PE effect increased with parity number. For instance, the genetic correlation between DIM 75 and DIM 285 is 0.78 for first parity, 0.57 for second parity, and 0.42 for third parity (Table 3). These values for permanent effect are 0.52, 0.63 and 0.74, respectively.

Across lactation correlations: Table 4 presents the AG and PE covariances and correlations of average daily SCS between different lactations for all DIM. Both AG and PE covariances were the highest between adjacent parities, especially between second and third lactations. The PE covariances for SCS between any two lactations were higher than the respective AG covariances. In contrast the AG correlations for average daily SCS between lactations were relatively high and it was more than the respective PE correlations. The environmental correlation was the highest between the second and third parity (0.51) and the lowest between the first and third parity (0.22). The estimates of genetic and PE correlations for SCS among different DIM between different parities were also defined (presented in Table 3). In general, correlations were stronger for the AG components than for the PE effects. Both AG and PE correlations were the highest between adjacent lactations. Generally, rations between daily records across parities depend on the interval between tests and on whether they are registered at the same stage of lactation or not. Daily tests close to each other in time are relatively more correlated than tests far apart in time, e.g. the genetic correlation between lactation 1 DIM 25 and lactation 2 DIM 305 is 0.23, while that between lactation 1 DIM 305 and lactation 2 DIM 25 is 0.66; respective estimates were 0.06 and 0.21 for PE effect. In addition, observed the middle stages of lactation are more highly correlated between lactations than the two end of lactation.

For instance, the highest genetic correlation (0.88) observed between parity 1 DIM 185 and parity 2 DIM 140. As can be seen in the Table (3), the environmental correlations between parities 1 and 2, and 1 and 3 varied from low (0.38) to very low (0.06).

Estimates of genetic correlations for SCS on the same DIM among first three parities show a similar trend with the lowest estimates at the peripheries of lactation (Figure 4). With the exception of some low values at the beginning of lactation, the estimates of genetic correlations in parities 1 and 3 and parities 2 and 3 were of medium size, varying from 0.45 to 0.81, but those between parities 1 and 2 were high, varying from 0.76 to 0.87. The daily PE correlations among lactations were near 0.4 for adjacent and 0.2 for nonadjacent lactations (Figure 4). Considering parities 1 and 2, the correlations were lowest in the early stage of lactation and increased with an increase in DIM. The correlations were lowest around 190-250 DIM for parities 1 and 3 and increased towards the end of lactation. Generally both genetic and environmental correlations showed more variability between parities 2 and 3. The lowest relation was found out between the first and third parity, whereas the strongest relation was found out between the second and third parity.

Genetic trends

Changes in average estimated breeding values (EBVs) of cows for 305-day SCS in first 3 parities according birth year of them during 1984 to 2008 are illustrated in Figure 5.

Table 2 Genetic, permanent environmental, and residual variances and heritabilities for cumulative 305-d SCS

Trait or variable	Parity		
	1st	2nd	3rd
AG variance	9266.01	23439.34	27977.55
PE variance	66470.15	77210.22	79006.12
Residual variance	593.87	647.45	671.23
Heritability	0.12	0.23	0.26

SCS: somatic cell score; AG: additive genetic and PE: permanent environmental.

Table 3 Genetic correlations (above diagonal), heritability estimates (diagonal) and environmental correlations (below diagonal) on selected days for SCS in the first three lactations

Parity		1st					2nd					3rd				
	DIM	25	75	140	185	285	25	75	140	185	285	25	75	140	185	285
1st	25	**0.04**	0.89	0.67	0.60	0.64	0.69	0.63	0.53	0.47	0.29	0.30	0.38	0.35	0.33	0.24
	75	0.72	**0.03**	0.93	0.88	0.78	0.82	0.82	0.76	0.72	0.46	0.45	0.63	0.60	0.57	0.38
	140	0.48	0.90	**0.03**	0.99	0.83	0.80	0.87	0.86	0.84	0.58	0.50	0.73	0.72	0.69	0.46
	185	0.40	0.73	0.94	**0.04**	0.89	0.78	0.86	0.88	0.87	0.63	0.49	0.73	0.74	0.71	0.47
	285	0.34	0.52	0.70	0.81	**0.06**	0.70	0.78	0.81	0.82	0.66	0.37	0.59	0.61	0.60	0.43
2nd	25	0.19	0.21	0.24	0.27	0.25	**0.08**	0.95	0.84	0.78	0.50	0.67	0.73	0.60	0.54	0.38
	75	0.14	0.24	0.28	0.30	0.35	0.77	**0.08**	0.97	0.91	0.57	0.66	0.81	0.72	0.67	0.46
	140	0.14	0.23	0.27	0.29	0.35	0.57	0.92	**0.08**	0.98	0.68	0.60	0.81	0.77	0.73	0.52
	185	0.16	0.21	0.25	0.28	0.33	0.46	0.76	0.94	**0.09**	0.78	0.54	0.78	0.77	0.75	0.56
	285	0.11	0.21	0.26	0.28	0.38	0.34	0.63	0.80	0.88	**0.10**	0.28	0.49	0.56	0.59	0.55
3rd	25	0.23	0.27	0.19	0.14	0.15	0.44	0.29	0.31	0.39	0.50	**0.10**	0.79	0.43	0.31	0.24
	75	0.13	0.18	0.18	0.16	0.22	0.34	0.34	0.37	0.40	0.43	0.82	**0.08**	0.89	0.80	0.42
	140	0.06	0.17	0.18	0.16	0.21	0.21	0.35	0.44	0.48	0.47	0.65	0.95	**0.11**	0.98	0.56
	185	0.06	0.21	0.20	0.15	0.20	0.13	0.35	0.51	0.59	0.57	0.59	0.86	0.97	**0.13**	0.68
	285	0.15	0.23	0.21	0.17	0.23	0.06	0.27	0.45	0.55	0.59	0.61	0.74	0.77	0.81	**0.15**

Table 4 Genetic and permanent environmental covariances and correlations between parities for average daily SCS in the first three lactations

Genetic parameters	Parity 1 and 2	Parity 1 and 3	Parity 2 and 3
AG covariance	25341	22550	41477
PE covariance	48607	31619	79692
AG correlation	0.86	0.70	0.81
PE correlation	0.34	0.22	0.51

SCS: somatic cell score; AG: additive genetic and PE: permanent environmental.

Estimates of genetic gains per year were not uniform. The increases and decreases in the graph are apparently due to the effect of specific widely used bulls that were either strongly positive or negative for this trait. In general, for the first two decades this process was acceptable and appropriate. Considering first parity, as shown in this plot, average of the genetic values efforts to achieve above zero has been successful in three points (1985, 1990 and 1995). After each success, the genetic value for SCS has experienced a failure and decreased again.

The rates of decrease in these points are different. In the first two points breeding values decreased again below zero. In finally the genetic value for SCS forever reached above zero in 1995 and has risen about 10 in 2002. However, it decreased continuously after 2002 until 2008. The genetic trends of all three studied parities were calculated using regression of means of breeding values over the years (Table 5). The rate of genetic changes in first three lactations was positive and ranged from (0.701 to 0.431) per period decreasing trend in SCS.

EBVs will be used to identify genetic difference among bulls in order to identify sires that regularly have daughters more liable to mastitis. In the other side most progress in selection for lower SCC will come through sires of cows (Schutz, 1994), hence in this study BVs of 5 super bulls as well 5 worst bulls for completed lactation were estimated (Table 6).

Within parity

Averages of SCS in primiparous cows were 2.36 (±1.96), and 2.91 (±2.08) and 3.34 (±2.14) in the multiparous (refers second and third parity, respectively) cows (Table 1).

Those levels were in the range of SCS values usually reported in dairy cattles in 2 French (Boichard and Rupp, 1997), and Italian (Samoré *et al*. 2008) dairy cattle populations.

Larger values are reported in various dairy cattle. For instance, average values of SCS in Czech multiparous Holstein and Czech multiparous Fleckvieh (Zavadilová *et al*. 2011) were 3.4 to 4.13 and 3.16 to 4.01, respectively.

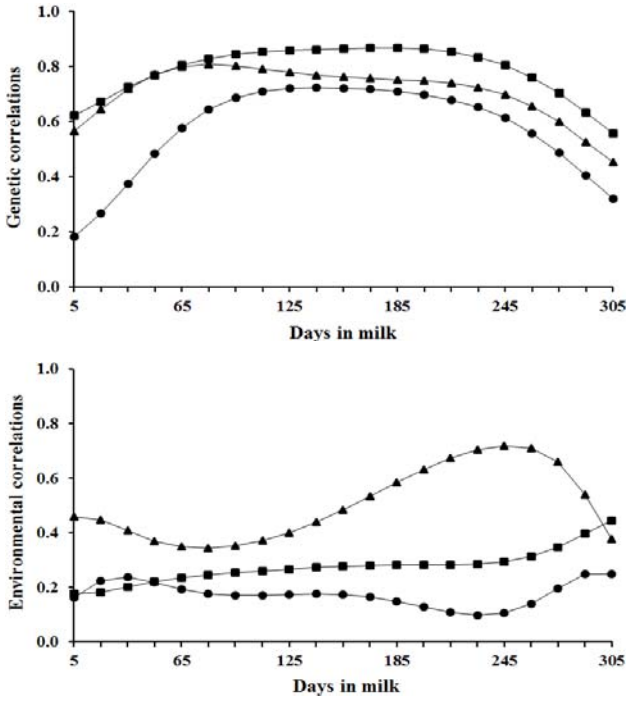

Figure 4 Genetic and PE correlations between SCS of parities 1 and 2 (■), 1 and 3 (●) and 2 and 3 (▲) for same DIM

As can be seen in the Figure 1, the observed increase in SCS with parity which was in agreement with that observed for Canadian (Jamrozik *et al*. 2010) and Polish (Rzewuska *et al*. 2011) dairy cattle populations. The increase in the SCS with parity and age is attributed to the fact that multiparous cows have a greater opportunity for exposure to mastitis-causing pathogens (Emanuelson *et al*. 1993; Rajala-Schultz *et al*. 1999).

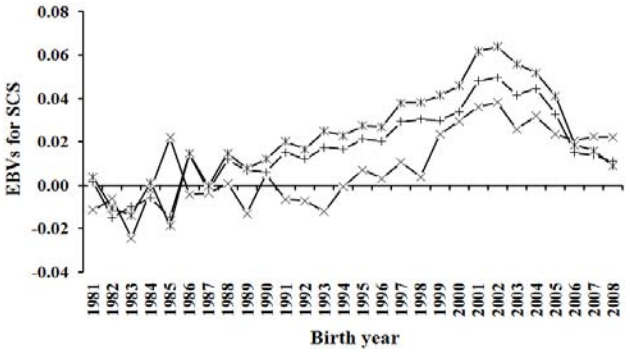

Figure 5 Average estimated breeding values for 305-day SCS in the first three parities [parities 1 (×), 2 (+) and 3 (∗)]

Genetic and PE variances were calculated for each day along lactation trajectory from the estimated (co) variance function coefficients (Figure 2). For first parity, genetic variances ranged from 0.08 to 0.18 for most of the lactation but approached 0.22 at the end of lactation.

For later parity, genetic variances were within 0.28 to 0.37 throughout the second lactation and within 0.32 to 0.61 throughout the third lactation. In general, the trends and values in the AG and PE variance estimates throughout lactation obtained in this study are same to trends found by Zavadilová *et al*. (2011).

Table 5 Estimation of linear regression coefficients of animal estimated breeding values (EBV) for cumulative 305-d SCS

Parity	Intercept±SE	L[a]±SE	Mean of EBV
1st	-49.59*±2.52	0.701*±0.031	6.31
2nd	-27.91*±3.81	0.474*±0.048	9.87
3rd	-21.77*±3.76	0.431*±0.047	12.59

[a]: linear regression coefficients (genetic trends).
SCS: somatic cell score.
SE: standard error.
* (P<0.05).

Table 6 Estimated breeding value (EBV) for SCC of five superior and worst sires according to their EBVs for 305-day milk yield with more than 50 daughters

Best sire number	EBVs for 305-d	Worst sire number	EBVs for 305-d
128524	-190.53	125323	291.67
107666	-176.39	800441	219.13
800348	-149.30	125687	218.53
601146	-145.38	601318	216.72
800221	-140.57	601325	207.39

SCS: somatic cell score.

Similarly to our result, who reported all variances increased with increasing parity. These patterns were also comparable with those obtained for UK Holstein-Friesian cows (Mrode and Swanson, 2003). For Iranian Holsteins, PE variances until 100 DIM showed higher values for higher parity numbers on the same DIM. These results supports previous the hypothesis, that variation in SCC after calving is largely influenced by differences in environmental factors (Miller *et al*. 1991) especially for later parities. Vividly the estimations of heritability of test day (TD) records were not constant throughout the lactation. Assesses of hi^2 for SCS used worldwide in national genetic evaluation programs differ across countries and evaluation systems: from 0.11 to 0.43 for the lactation models, and from 0.06 to 0.35 for TD models (Interbull, 2008). Based on the results in Figure 3, heritability estimates along the lactation trajectory showed shapes similar to the genetic variation but were less extreme at the beginning of the trajectory because of higher PE variances. As, for all parity there was a tendency towards higher heritability estimates in end lactation.

The higher values of hi^2 at the end of lactation were due to an increase in respective AG variances but also, in some cases, due to decreasing PE variances with DIM. However, the shape of heritability curve obtained in this study was previously observed in 2 Netherlands (De Roos *et al*. 2003) and Polish (Rzewuska *et al*. 2011) Holstein populations.

As a consequence, heritability tended to increase as lactation numbers increased, which supports previous results (de Roos *et al*. 2003; Samoré *et al*. 2008; Rzewuska *et al*. 2011) but is in contrast to results published for UK (Mrode and Swanson, 2003) and Swedish (Carlén *et al*. 2004) dairy cattles. A higher heritability for 3rd parity might be due to an increased frequency of clinical and subclinical mastitis during that lactation (Reents *et al*. 1995).

The ranges of daily heritabilities in the first parity (0.03 to 0.07) were similar to the results obtained with a TD model (Abdini *et al*. 2012; Cheraghi *et al*. 2012) on the same population used for this study. The results were also comparable with those observed on other populations (Mrode and Swanson, 2003; Ødegard *et al*. 2003). Ranges of heritabilities calculated for a completed lactation SCS of first three parities varied considerably among previous studies. For instance, much higher and very low estimates of heritability can be found in literature for Canadian (Miglior *et al*. 2007) and North Carolina Holstein populations (De Groot *et al*. 2007), respectively.

Our results, which were in the range from 0.12 to 0.26, are in good agreement with De Roos *et al*. (2003), Mrode and Swanson (2003), Muir *et al*. (2007) and Samoré *et al*. (2008). However, these values were larger than those reported for Canadian (Reents *et al*. 1995) and Czech (Zavadilová *et al*. 2011) Holstein dairy cows, especially for third parity. However, the estimates of Miglior *et al*. (2007) for the second and third parity (0.27 and 0.34) of Canadian Holsteins seem to be extremely large. These differences may be explained by differences in populations, statistical and estimation models.

As can be seen in the Table 3, trends of genetic correlations were different and showed more instability in third than in first and second parities, which could be due to the smaller number of data in the later part of the third lactation. As a consequence, the genetic correlations decreased with parity number. The above facts are consistent with those published by Zavadilová *et al*. (2011). Also the genetic correlations within lactations for selected DIM were similar in range to the results of Haile-Mariam *et al*. (2001).

Between parities

In agreement with our results for Iranian Holstein, most authors found that genetic correlations between adjacent lactations were greater than the genetic correlation between the first and third parity. As a consequence the largest genetic correlation (0.86) estimates was observed between the first and second lactation yield, whereas the smallest correlations (0.70) was found between the first and third lactations, which was consistent with those published by Boichard and Rupp (1997). Although, higher genetic correlation effect was observed between second and third parity for Holstein data in the Czech (Zavadilová *et al*. 2011) and Holstein-Friesian data in the Australian (Haile-Mariam *et al*. 2001), but similarly to our results the highest genetic correlations for three Australian (Haile-Mariam *et al*. 2001), Polish (Rzewuska *et al*. 2011) and Czech (Zavadilová *et al*. 2011) dairy cattle populations were for middle stage of lactation. In general, correlations computed for completed lactations SCS across three parities were stronger for the AG components than for the PE effects. This pattern was also reported by Haile-Mariam *et al*. (2001), Mrode and Swanson (2003) and Zavadilová *et al*. (2011).

Genetic trend

The genetic level of SCS favorable until 1995 and since then trend has been positive (i.e., economically negative). Genetic trends were positive and significant ($P<0.01$) for all three lactation. Positive genetic trend for SCS are likely the result of major emphasis on milk yield and neglecting udder health in sire selection at the level of farms during past years. This condition could cause a correlated response for SCS as the result of selection for milk because of the probably positive correlation between milk yield and SCS (Carlén *et al*. 2004). The positive genetic trend in SCS (shown in Figure 5 and Table 5) is undesirable and provides future justification for including SCS in the national economic selection index. Similar report was given by Harris and Winkelman (2004) in New Zealand breed. Jattawa *et al*. (2012) estimated genetic trend of 49.02 for SCC in the Thai dairy cattle. De Ponte Bouwer *et al*. (2013) reported the genetic trend of 0.86 for SCS. Abdini *et al*. (2012) reported no significant genetic trend was observed for SCS of primiparous Iranian Holstein cows. This report is in contrast with the results of present study. This discrepancy is probably due to the difference between models and years of procurement records for these studies.

CONCLUSION

In countries such as Iran, where there is a lack of national complete recorded data on diseases such as mastitis, SCC become very important as a genetic monitor for reducing mastitis incidence in addition to management initiatives. The positive trend in SCS observed over the period covered in the current study is unpromising since it indicates that Iranian farmers are taking inappropriate measures to reduce SCC. Results of this investigation showed that genetic improvement of performance traits (referred to SCC) is at an unacceptable level in Holstein cattle of Iran, where the majority of studies in dairy cows did on milk yield traits and it was only focused on first parity. This emphasizes the need for including udder health traits in the breeding and man-

agement goals. However, the magnitude and trend of the last heritability (referred to third parity) may be suggested that improvement in SCC of Iranian Holsteins could be achieved by basing selection on yield potential of animals in end of this period.

ACKNOWLEDGEMENT

The authors are grateful to the Animal Breeding Center of Iran for providing the data used in the present study. We also express our appreciation to L. Zavadilová for many helpful suggestions during development of this investigation.

REFERENCES

Abdini A., Farhangfar H., Shojaian K., Naeemipour H., Bashtani M. and Mohammad Nazari B. (2012). Estimation of genetic parameters and trend for somatic cell score trait in Iranian Holsteins using a random regression test day model. *Iranian J. Anim. Sci*. **2,** 193-200.

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

Bakhtiarizadeh M.R., Moradi Shahrebabak M. and Pakdel A. (2009). Genetic relationships between linear type traits, somatic cell score and longevity in Holstein cows of Iran. *Iranian Anim. Sci. J.* **84,** 29-38.

Boichard D. and Rupp R. (1997). Genetic analysis and genetic evaluation for somatic cell score in French dairy cattle. Pp. 54-60 in Proc. Int. workshop genet. improv. func. trait. cattle health. Uppsala, Sweden.

Carlén E., Strandberg E. and Roth A. (2004). Genetic parameters for clinical mastitis, somatic cell score and production in the first three lactations of Swedish Holstein cows. *J. Dairy Sci*. **87,** 3062-3070.

Cheraghi S., Kheirabadi K., Alijani S., Moghaddam G. and Rafat S.A. (2012). Estimate of genetic parameters of somatic cell score of Holstein cows. *Anim. Sci*. **5,** 29-30.

De Groot B., Keown J.F., Van Vleck L.D. and Kachman S.D. (2007). Estimates of genetic parameters for Holstein cows for test-day yield traits with a random regression cubic spline model. *Gen. Mol. Res*. **6,** 434-444.

De Ponte Bouwer P., Mostert B.E. and Visser C. (2013). Genetic parameters for production traits and somatic cell score of the SA dairy Swiss population. *South African J. Anim. Sci*. **43,** 113-122.

De Roos A.P.W., Harbers A.G.F. and De Jong G. (2003). Genetic parameters of test-day somatic cell score estimated with a random regression model. *Int. Bull*. **31,** 97-101.

Emanuelson U., Oltenacu P.A. and Gröhn Y.T. (1993). Nonlinear mixed model analyses of five production disorders of dairy cattle. *J. Dairy Sci*. **76,** 2765-2772.

Ghavi Hossein-Zadeh N. (2011). Genetic and phenotypic trends for age at first calving and milk yield and compositions in Holstein dairy cows. *Arch. Tierz*. **4,** 338-347.

Haile Mariam M., Goddard M. and Bowman P. (2001). Estimates of genetic parameters for daily somatic cell count of Australian dairy cattle. *J. Dairy Sci*. **84,** 1255-1264.

Harris B.L. and Winkelman A.M. (2004). Test-day model for national genetic evaluation of somatic cell count in New Zealand. *Int. Bull*. **32,** 101-104.

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

Hintz R. and Van VLeck L. (1978). Estimation of genetic trends from cow and sire evaluations. *J. Dairy Sci*. **61,** 607-613.

Intaratham W., Koonawootrittriron S., Sopannarath P., Graser H.U. and Tumwasorn S. (2008). Genetic parameters and annual trends for birth and weaning weights of a Northeastern Thai indigenous cattle line. *Asian-Australas J. Anim. Sci*. **21,** 478-483.

Interbull. (2008). Description of national genetic evaluation systems for dairy cattle traits as applied in different Interbull member countries. http://wwwinterbull.slu.se/national_ges_info2/framesidaages.htm. Accessed Jun. 2008.

Jakobsen J.H., Madsen P., Jensen J., Pedersen J., Christensen L.G. and Sorensen D.A. (2002). Genetic parameters for milk production and persistency for Danish Holsteins estimated in random regression models using REML. *J. Dairy Sci*. **85,** 1607-1616.

Jamrozik J., Bohmanova J. and Schaeffer L. (2010). Relationships between milk yield and somatic cell score in Canadian Holsteins from simultaneous and recursive random regression models. *J. Dairy Sci*. **93,** 1216-1233.

Jamrozik J., Schaeffer L.R. and Grignola F. (1998). Genetic parameters for production traits and somatic cell score of Canadian Holsteins with multiple trait random regression model. Pp. 303-306 in Proc. 6th World Cong., Genet. Appl. Livest. Prod. Armidale Australia.

Jattawa D., Koonawootrittriron S., Elzo M.A. and Suwanasopee T. (2012). Somatic cells count and its genetic association with milk yield in dairy cattle raised under Thai tropical environmental conditions. *Asian-Australas J. Anim. Sci*. **25,** 1216-1222.

Kirkpatrick M., Lofsvold D. and Bulmer M. (1990). Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics*. **124,** 979-993.

Luhar R., Patel R.K. and Singh K.M. (2006). Studies on the possible association of ß-lactoglobulin genotype with mastitis in dairy cows. *Indian J. Dairy Sci*. **59,** 155-158.

Luttinen A. and Juga J. (1997). Genetic relationships between milk yield, somatic cell count, mastitis, milkability and leakage in finnish dairy cattle population. *Int. Bull*. **15,** 78-83.

Miglior F., Sewalem A., Jamrozik J., Bohmanova J., Lefebvre D. and Moore R. (2007). Genetic analysis of milk urea nitrogen and lactose and their relationships with other production traits in Canadian Holstein cattle. *J. Dairy Sci*. **90,** 2468-2479.

Miller R., Paape M. and Fulton L. (1991). Variation in milk somatic cells of heifers at first calving. *J. Dairy Sci*. **74,** 3782-3790.

Misztal I., Tsuruta S., Strabel T., Auvray B., Druet T. and Lee D.H. (2002). BLUPF90 and related programs (BGF90). Pp.

28-32 in Proc. 7th World Congr., Genet. Appl. Livest. Prod., Montpellier, France.

Mrode R.A. and 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.

Muir B.L., Kistemaker G., Jamrozik J. and 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.

Norman H.D., Miller R.H., Wright J.R. and Wiggans G.R. (2000). Herd and state means for somatic cell count from dairy herd improvement. *J. Dairy Sci*. **83,** 2782-2788.

Ødegard J., Jensen J., Klemetsdal G., Madsen P. and Heringstad B. (2003). Genetic analysis of somatic cell score in Norwegian cattle using random regression test-day models. *J. Dairy Sci*. **86,** 4103-4114.

Rajala-Schultz P.J., Gröhn Y.T., McCulloch C.E. and Guard C.L. (1999). Effects of clinical mastitis on milk yield in dairy cows. *J. Dairy Sci*. **82,** 1213-1220.

Reents R., Jamrozik J., Schaeffer L.R. and Dekkers J.C.M. (1995). Estimation of genetic parameters for test day records of somatic cell score. *J. Dairy Sci*. **78,** 2847-2857.

Rzewuska K., Jamrozik J., Zarnecki A. and Strabel T. (2011). Genetic parameters of test-day somatic cell scores for the first three lactations of Polish Holstein-Friesian cattle. *Czech J. Anim. Sci*. **56,** 381-389.

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

Schutz M. (1994). Genetic evaluation of somatic cell scores for United States dairy cattle. *J. Dairy Sci*. **77,** 2113-2129.

Thompson J., Pollak E. and Pelissier C. (1983). Interrelationships of parturition problems, production of subsequent lactation, reproduction, and age at first calving. *J. Dairy Sci*. **66,** 1119-1127.

Weller J.I., Saran A. and Zeliger Y. (1992). Genetic and environmental relationships among somatic cell count, bacterial infection, and clinical mastitis. *J. Dairy Sci*. **75,** 2532-2540.

Zavadilová L., Wolf J., Štípková M., Nemcová E. and Jamrozik J. (2011). Genetic parameters for somatic cell score in the first three lactations of Czech Holstein and Fleckvieh breeds using a random regression model. *Czech J. Anim. Sci*. **56,** 251-260.