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GENETIC ANALYSIS OF SOMATIC CELL COUNT IN IRANIAN HOLSTEIN CATTLE

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ABSTRACT

Using monthly test day records, the genetic parameters of Iranian Holstein cattle studied. Data included 278230 test-day SCS trait records from 65320 cows and 2210 sires. An animal random regression model was employed in the analysis, using restricted maximum likelihood method. The model consisted of herd-test-date, interaction between year-season of calving, days in milk (linear and quadratic) and dam age (linear and quadratic) as fixed effects, and random regression coefficients for additive genetic and permanent environmental effects. The mean of SCS was 4.26 (±0.15), and the differences of SCS in different provinces was significant ($p \leq 0.05$). The range of Heritability estimates of SCS were 0.01 to 0.37. The genetic correlation of SCS between adjacent test-day records were low and decreased as the interval between tests increased.

Keywords: Random Regression Model, Somatic Cell Score, Legendre Polynomial

INTRODUCTION

The number of somatic cells (SCC) can be an indicator of incidence of both clinical and subclinical infections. The Somatic cells in the milk consist of Neutrophils, Macrophages, Lymphocytes, Eosinophils, and various epithelial cells from the mammary gland **[10].** The Cells in milk from a healthy udder are mainly from mammary gland epithelium and only 8% are leukocytes and less than 1% are macrophages **[10].** The distribution of SCC in cow milk samples is positively skewed (the mean is greater than the median) and there is a strong heterogeneity of variance among groups or herds **[1].** The Conventional statistical methods usually assume normal distribution and homogeneity of variance of data. Therefore, to make the distribution of SCS normal, mostly the SCC values are transformed to logarithmic basis and called SCS. The formula widely used is: **[1, 3]**

$SCS = \log_2 (SCC / 100) + 3$ …….**(1)**

The objective of the present study was to estimate the variation and distribution of SCS in different provinces of the country and the genetic parameters of SCS in different test days (TD) of the first lactation Iranian Holstein cows.

MATERIAL AND METHODS

The data of SCS in different test days of Holstein dairy cows were provided by the animal breeding center of Iran. The information of the cows for which the first test day was more than 60 days after parturition and TD intervals less than 15 days were discarded. The information of animals being of 5 to 300 days in milk, having at least one known parent, calving age of 18 to 45 months during years 2001 to 2014 were used for this study **(Table 1)**. The significant fixed effects on SCS determined using the GLM procedure of SAS **[9].** The genetic parameters of SCS estimated using random regression animal model by restricted maximum likelihood method (REML) **[6].** The order of Legendre polynomial for additive genetic (AG) and permanent environmental (PE) effects, selected to be cubic and quadratic respectively **[4].** Homogeneous residual variance was assumed throughout the lactation. The use of random regression (RR) model makes it possible to study changes in TD records over time and a better understanding of lactation genetics **[6].** A Single-trait model with Legendre polynomials for describing trait curve in the population used to fit data. The Legendre polynomials were defined for the range of -1 to +1 and the days in SCS values transformed using the formula 2 **[6] :**

$d_t^* = -1 + 2 (d_t + d_{min}) / (d_{max} - d_{min})$..**(2)**

Where d_{min} and d_{max} are the minimum and maximum values for the days in SCS variable in

data. For the *t*-th standardized days in milk (d_t^*), the *k*-th polynomial is given as **[6]:**

$$\phi(d_t^*)_k = \frac{1}{2^k}\sqrt{\frac{2k+1}{2}}\left(\sum_{m=0}^{k}(-1)^m\binom{k}{m}\binom{2k+1}{r}(d_t^*)^{r-2m}\right)$$

. ……..**(3)**

The model equation for the analysis of data can be expressed as **[6]:**

$$Y_{tijk} = F_i + \sum_{k=0}^{n} \emptyset jtk\ \beta_k + u_j + pe_j + e_{tijk}$$

……**(4)**

Where y_{tijk} is the test day somatic cell score record, F_i represent fixed effects in the model (including herd-test date, year-season of calving), days in milk and age of dam as covariate, β_k are fixed regression coefficients to describe the curve of traits for the whole population, u_j and pe_j refer to the *j*-th animal additive genetic and permanent environmental effects, respectively, $\emptyset_{jtk}$ is the *k*-th Legendre polynomial for the standardized time *t* of milking (days in milk), *n* is the order of Legendre Polynomials for fitting traits curve for the population and e_{tijk} is the random residual effect describing the unknown effects on traits. The days in milk were partitioned into 10 equal period of about 30 days and an independent residual variance structure was assumed. In matrix notation, the model is as:

$$y = Xb + Qu + Zp + e \quad \text{……}\textbf{(5)}$$

Where *y* is the vector of test day SCS, *b* is a vector of solution for fixed effects and regression coefficients of SCS on days in milk, *u* and *p* are vectors of animal additive genetic and permanent environmental effects, respectively. The matrices *X*, *Q* and *Z* are incidence matrices relating effects to the observations. The co-variance structure was assumed as:

$$\text{var}\begin{bmatrix} u \\ p \\ e \end{bmatrix} = \begin{bmatrix} G & 0 & 0 \\ 0 & P & 0 \\ 0 & 0 & R \end{bmatrix} \quad \textbf{……(6)}$$

Where $G = A\ \sigma^2_a$, $P = I\ \sigma^2_p$ and R is a diagonal matrix containing the 10 constant variances of residuals and A is the numerator relationship matrix among animals, σ^2_a and σ^2_p are the variances for additive genetic and permanent environmental effects respectively and I denotes an identity matrix. Genetic analysis was done using WOMBAT software with REML procedure for estimation of co-variance components **[7].**

RESULTS AND DISCUSSION

Since during lactation, cows with mastitis are possible, to get breast infections in the time of drying and SCS will be high in excess. By continuing to milk production in the months after birth, SCS than the volume of milk production decreases. The average differences of SCS in different provinces was high ($p \leq 0.05$). The highest average of SCS was

in province No. 5 **(Table 2)**. Since all cows are of the same race, high differences in average of SCS among the provinces, indicate the effect of environmental and management. The Permanent environmental variance on the first, second, ninth and tenth of test day was maxim um and on the other test days was minimum. This trend is consistent with the with the other reports **[2; 5; 8].** Heritability SCS in the first and last month was the lowest rates and was moderate in the other months. This trend is consistent with the other reports **[2; 5; 8].** Genetic and phenotypic correlations between test day records were low and with increasing distance between the test days records the amount decreased.

CONCLUSION

It is recommended that to use cows's sperms that have less SCS. To reduce mastitis in progeny testing of bulls, calves should be selected as productive that the SCS's average in their milk is lower in their daughters.

ACKNOLEDGMENTS

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Table 1: Description of the data set

Test day records	**278230**
Mean of SCS ± (S.D.)	**4.2 ± (0.002)**
Cows with record	**65320**
Number of sires	**2210**
Number of herds	**82**
Average test-day records per cow ± (S.D.)	**5.0 ± (0.15)**
Number of animals in pedigree file	**74860**

SCS: Somatic Cell Score and SD: Standard Deviation.

Table 2: Average test day records of SCS into separate the different provinces of Iran

Province	Total SCS
1	5.85^{b}
2	5.81^{cb}
3	5.89^{b}
4	5.04^{cd}
5	7.22^{a}
6	5.31^{cb}
7	4.37^{d}
8	6.14^{b}
9	6.09^{b}
10	6.13^{b}
11	5.77^{cb}
12	5.53^{cb}

SCS: Somatic Cell Score.

Table 3: Additive Genetic (below the diagonal) and Phenotypic (above the diagonal) Correlation Coefficients for SCS In Different Test Days

TD	30	60	90	120	150	180	210	240	270	300
30		0.2	0.15	0.1	0.11	0.09	0.05	0.04	0.02	0.03
60	0.42		0.21	0.16	0.15	0.11	0.08	0.09	0.04	0.03
90	0.39	0.52		0.1	0.1	0.08	0.07	0.05	0.03	0.04
120	0.09	0.13	0.14		0.11	0.09	0.06	0.03	0.02	0.02
150	0.1	0.11	0.11	0.12		0.14	0.07	0.07	0.04	0.01
180	0.06	0.08	0.09	0.11	0.17		0.15	0.1	0.1	0.06
210	0.07	0.06	0.06	0.03	0.1	0.17		0.18	0.15	0.08
240	0.06	0.07	0.07	0.06	0.03	0.1	0.17		0.14	0.09
270	0.11	0.11	0.11	0.02	0.06	0.05	0.09	0.16		0.12
300	0.15	0.18	0.15	0.05	0.07	0.03	0.03	0.07	0.18	

SCS: Somatic Cell Score and TD : Test Day

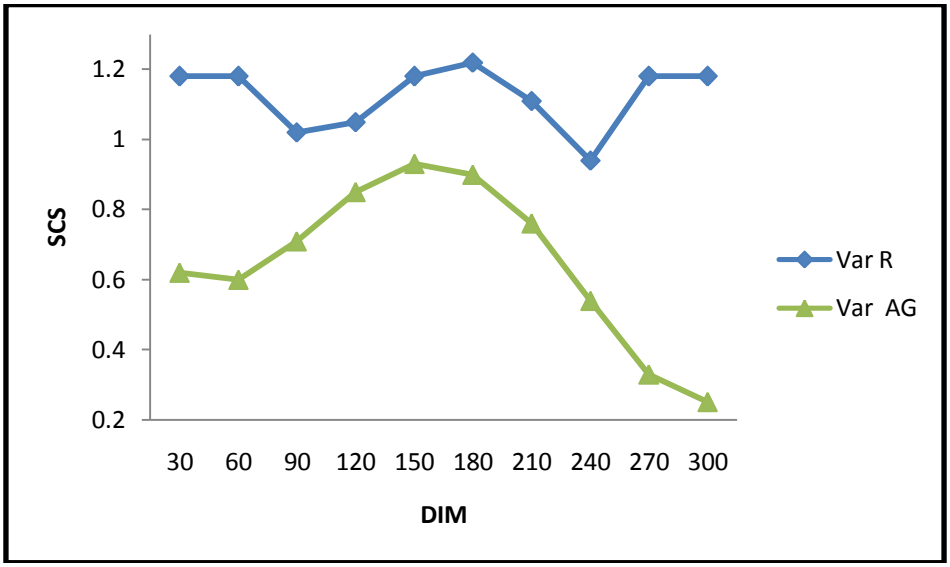

Figure 1: The Variation of Additive Genetic and Residual Variances SCS In Different Test Days
NOTE: SCS: Somatic Cell Score, DIM : Days in Milk, AG : Additive Genetic and R: Residual

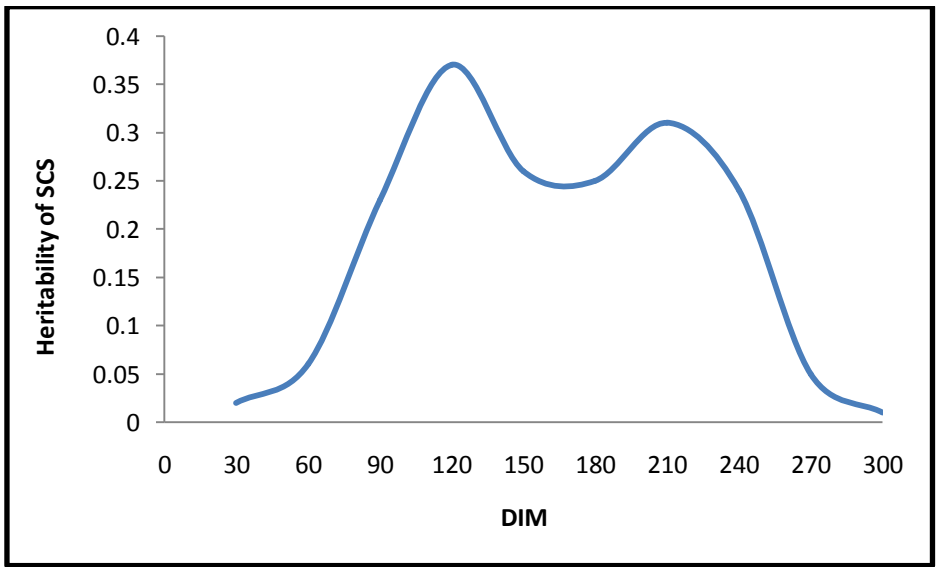

Figure 2: Variation of Heritability of SCS In Different Test Days
NOTE: SCS: Somatic Cell Score and DIM: Days in Milk