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Estimation of the genetic parameters for Somatic Cell Scores in the first lactation of Romanian Black and White cattle

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ABSTRACT

The aim of study was the estimation of the genetic parameters of somatic cell score of Romanian Black and White cattle population. Test-day records of somatic cell count (SCC) of 305 days lactation were from Romanian Black and White cattle population from experimental farm of our institute. The mean of somatic cell count of milk in the first lactation of Romanian Black and White cows was 291966.89. The genetic parameters were estimates with random regression test-day animal model. The heritability for somatic cell score (SCS) ranged from 0.0473 to 0.147. The breeding values for the best cows for somatic cell score were between -35.566 and -191.358. The genetic correlations between somatic cell count milk records test-day were positive. The phenotypic and genetic correlations between somatic cell count and milk yield were negative.

Keywords: breeding value, animal model, heritability, cows, somatic cell count

INTRODUCTION

Romanian Black and White is a dairy cattle breed. In Romania, the breed has a high milk production. In Romania, in the breeding program of Romanian Black and White cattle breed the main objective is the increase of milk yield and the milk quality. The somatic cell count is a trait which is included in the breeding program of Romanian Black and White cattle breed.

In Romania, Ilie et al, (2021) realized genome-wide association studies for milk somatic cell score in Romanian dairy cattle.

The goals of breeding programs included health and functional traits, selection for improved milk yield traits and SCC reduction can be improved by genomic selection by identifying potential candidate genes associated with these traits (Meredith et al. 2012).

In dairy breeding programs, selection for udder health has an important role. SCC is considered an important trait for udder health (Alam et al., 2015). Erdem and Okuyucu (2019) showed that hygienic status of cows is important to ensure high quality cow's milk. For this reason, the cows must be kept clean and healthy in order to obtain high quality milk. Kaskous (2021) reported that the milk quality depends on the milking technology and routine. Sebastiano et al. (2020) reported that as test year increased, SCC decreased, the mammary gland health improved and the quality of the milk was better. The genetic evaluation of this trait is based on SCS (Ali and Shook, 1980). The breeding for milk quality traits included SCC is important because consumer demands healthy products.

The factors that influenced the somatic cells count are: milk productivity, cow health, management and environment (Alhussien and Dang, 2018).

Different authors (Rupp and Boichard, 1999, Nash et al. 2000) have shown that lower SCC in milk reduced the incidence of mastitis.

Many authors (Rzewuska et al. 2011, Kheirabadi, 2018, Padilha et al. 2019, Atashi and Hostens, 2021) used the random regression model to estimate the genetic parameters for somatic cell count. Padilha et al. (2019) used random regression model to estimate the genetic parameters for 305-day in milk yield, SCS and lactation persistence in Holstein cows.

The aim of this study was to estimate the genetic parameters of somatic cell score of Romanian Black and White cattle herd using a random regression test-day model.

MATERIALS AND METHODS

The samples were collected monthly from 30 cows in first lactation from Romanian Black and White breed and the somatic cell counts were determined.

The 151 records from 30 cows Romanian Black and White at the first calving (2014-2015) from experimental farm of our institute were used in this study. The fixed effects are represented by milk test-day and regression coefficients. The levels of milk test-day fixed effect are 10 (ten). The levels of fixed regression coefficients are 5 (five). The pedigree consists of 78 animals, 25 dams, 23 sire and 30 cows with performances. Inbreeding is 1.04% in this herd.

Statistical analysis. Random regression test-day animal model used for analysis of data was: (Grosu et al., 2013, 2019)

$$y_{tijk} = TD_i + \sum_{m=0}^{3}(\beta_m \cdot z_{tm}) + \sum_{m=0}^{3}(\alpha_{jm} \cdot z_{tm}) + \sum_{m=0}^{3}(\gamma_{jm} \cdot z_{tm}) + e_{tijk} \quad [1]$$

y_{tijk} = test day (TD) somatic cell count milk record;
TD_i = the data of milk recording (the fixed effect);
β_m= fixed regression coefficient (the fixed effect)
α_{jm} = random regression coefficients of the additive genetic value;
γ_{jm}=random regression coefficients of the permanent environmental effect;
Z_{tm}=Legendre Polynomials at time"***t***";
e_{tijk}=residual effect.

The order of Legendre polynomials was 3.
y =$X_1b+X_2\beta+Z_1\alpha+Z_2\gamma+e$ (2)
where: y = vector of TD somatic cell count record;
X_1= matrix for fixed effect;
b = vector of fixed effect for test-day;
X_2 = covariates matrix for fixed effect;
β = fixed regression coefficients;
Z_1= covariates matrix for all cows
α = random regression coefficients of the additive genetic value;
Z_2 = covariates matrix for performance cows;
γ = random regression coefficients of the permanent environmental effect;
e = vector of residual effects

The Mixed Model Equations (MME) are:

$$\begin{bmatrix} X_1'\cdot X_1 & X_1'\cdot X_2 & X_1'\cdot Z_1 & X_1'\cdot Z_2 \\ X_2'\cdot X_1 & X_2'\cdot X_2 & X_2'\cdot Z_1 & X_2'\cdot Z_2 \\ Z_1'\cdot X_1 & Z_1'\cdot X_2 & Z_1'\cdot Z_1 + (A^{-1}\otimes G^{-1})\cdot\sigma_e^2 & Z_1'\cdot Z_2 \\ Z_2'\cdot X_1 & Z_2'\cdot X_2 & Z_2'\cdot Z_1 & Z_2'\cdot Z_2 + (I\otimes P^{-1})\cdot\sigma_e^2 \end{bmatrix} \cdot \begin{bmatrix} \tilde{b} \\ \tilde{\beta} \\ \hat{\alpha} \\ \hat{\gamma} \end{bmatrix} = \begin{bmatrix} X_1'\cdot y \\ X_2'\cdot y \\ Z_1'\cdot y \\ Z_2'\cdot y \end{bmatrix}$$

$$V=\begin{bmatrix} A\otimes G & 0 & 0 \\ 0 & I\otimes P & 0 \\ 0 & 0 & I\sigma_e^2 \end{bmatrix}$$

Var (a) =$A\otimes G$;
Var (a) = additive variance;
Where $\otimes$ is Kronecker product function;
Var (p) = $I\otimes P$;
Var (p) = environmental variance;

G and P are the matrices of genetic and permanent environmental variances and covariances between random regression coefficients.

I = represents the identity matrix

σ_e^2= residual variance for lactation

$$h_t^2 = \frac{g_{tt}}{(g_{tt} + p_{tt} + \sigma_e^2)}$$

where:

h_t^2= heritability for somatic cell score milk

g_{tt}= genetic variance for somatic cell score

$g_{tt} = z_t' * G * z_t$

$p_{tt} = z_t' * P * z_t$

p_{tt}= permanent environmental variance for somatic cell score milk

z_t= co(variables) related to a specific test day l measured during days in milk t;

σ_e^2= residual variance;

$$r_{g\,t't} = \frac{g_{t't}}{\sqrt{g_{t't'} * g_{tt}}}$$

where:

$r_{g\,t't}$= genetic correlations between test-day t` and t somatic cell score;

$g_{t't}$= genetic covariances between two test days during days in milk;

$g_{t't} = z_{t'}' * G * z_t$

$z_{t'}'$= transpose of z;

The somatic cell score was calculated:

SCS=3+$\log_2$(SCC/100000) (Wiggans ans Shook, 1987, Guzzo et al., 2018)

RESULTS AND DISCUSSION

The average SCC and SCS and mean error due to different month of lactation are presented in table 1. The somatic cell count trait in the genetic evaluation is log transformed as SCS (somatic cell score) because it is not normally distributed (Guzzo et al., 2018). Alhussien and Dang (2018) observed that SCC was highest shortly after calving, declined rapidly between days 25 and 45 and then increased throughout the rest of lactation. Caraviello et al., (2005) divided Holstein herds in five categories in function of lactation average SCC: herds with low lactation average SCC (111 to 279 thousand cells/ml), low-medium (279 to 305 thousand), medium (305 to 329 thousand), medium-high (329 to 358 thousand) and high (35 to 540 thousand). Alam et al. (2015) obtained the lactation mean of somatic cell score 3.507 and 4.322 in Holstein cows from Korea.

Table 1. Mean and error mean of SCC and SCS test day records

Test day	Somatic cell count (SCC) (thousand)	Somatic cell score (SCS)
1	233,6±186,7	2.720±0.91
2	314,4±205,0	3.001±1.14
3	102,3±36,6	2.213±0.542
4	209,8±75,0	3.056±0.376
5	275,6±69,1	3.482±0.429
6	352,3±144,4	3.070±0.502
7	314,2±132,5	2.711±0.596
8	302,2±109,3	3.638±0.351
9	309,1±783,8	3.672±0.410
10	393,4±116,6	3.871±0.490
Mean	291,9±36,0	3.250±0.160

Koç (2008) obtained the mean SCC in milk per herd in Holstein-Friesian cows from Turkey was between 296483 and 688811 cells/ml. This author showed that in different countries considered 400000 cells/ml the maximum limit for SCC in milk.

Cinar et al. (2015) reported the average SCC in Holstein from Turkey 246700 cell/ml in Holstein cows. These authors constated that high SCC affect negatively the milk yield and milk quality.

This trait is currently included in Italian Holstein cattle breeding programs in Italy (Bobbo et al. 2017, Sandri et al., 2015).

In table 2 gives the heritability for daily somatic cell score. In our study heritability ranged between 0.0473 to 0.1471. Our results are similar with the heritability in another studies.

Table 2. Heritability for somatic cell score

Days in milk	Heritability
5	0.0473
35	0.0548
65	0.0629
95	0.0688
125	0.0714
155	0.0715
185	0.0711
215	0.0743
245	0.0861
275	0.1120
305	0.1471

The lowest heritability values were observed at the first three test day and increased afterwards. Higher heritability observed at the end of lactation.

Similarly, Mrode and Swanson (2003) and Koivula et al (2005) found that the heritability of SCS increased toward the end of lactation. Mrode and Swanson (2003) observed that the heritability for SCS was 0.07. The heritability values for SCS obtained by Costa et al. (2015) were between 0.06 and 0.14 in Holstein cows. Padilha et al. (2019) obtained the heritability for SCS in Holstein cows was 0.14.

In our country, Bugeac (2014) reported heritability for somatic cell count 0.16 for Holstein population. The heritability was between 0.05 to 0.29 (Schutz et al., 1990) or 0.06 to 0.13 (Ptak et al., 2009). Different authors have published heritability for lactation mean SCS between 0.10 and 0.27 (Monardes et al., 1990, Mrode and Swanson, 1996, Rupp and Boichard, 1999, Mark and Sullivan, 2005). Rupp and Boichard (2003) review that lactation averages of SCS obtained shows heritability around 0.15. In Austrian Fleckvieh cows had a heritability 0.09 to 0.13 for SCC in five lactations (Koeck et al., 2010). The heritability reported by Kadarmideen (2004) and Charfeddine et al. (1997) are 0.13 to 0.14. Similar results were obtained by Carlen et al., (2004) in Swedish Holstein. Rzewuska et al., (2011) obtained heritability 0.11 for SCS in the first lactation in Holstein cows. The heritability from our study was in agreement with the heritability of SCS for Holstein in first lactation 0.09 (Rents et al., 1995). Dube et al. (2008) obtained the heritability for SCS 0.19 in the first lactation for South African Holstein cows higher than the heritability from our study. The same value of heritability 0.19 for somatic cell score was obtained by Romano et al. (2020) 0.19 for somatic cell score in Holstein from Brasil. Atashi and Hostens (2021) reported for Holstein cows in the first lactation from Iran that the heritability across lactation ranged between 0.11 to 0.20, the mean heritability was 0.18. Ptak et al. (2007) obtained the similarly values for heritability for SCS for Polish Black and White cattle in the first lactation was from 0.11 to 0.20. Mostert et al. (2004) reported the heritability for SCS 0.19 for the Holstein. Table 3 shows the breeding value for the best 10 cows.

Table 3. The breeding value of the best Romanian Black and White cows for somatic cell score test day

No.	Breeding value
1	-191.358
2	-180.349
3	-167.262
4	-124.732
5	-102.398
6	-92.831
7	-87.517
8	-40.309
9	-39.144
10	-35.566

The best cows are the cows with the lowest number of somatic cells counts. The breeding values for the best Romanian Black and White cows ranged from -35.566 to -191.358 for somatic cell score. The genetic correlations between selected days in milk (DIM) of somatic cell score daily records in our study were positive (Table 4). Test-day analyses of SCC showed that the genetic correlation between SCS early in lactation were higher and decreased between SCS in early in lactation and SCS late in lactations.

Table 4. Genetic correlations between somatic cell score daily records

DIM	5	35	65	95	125	155	185	215	245	275	305
5	1	0.97	0.94	0.92	0.91	0.91	0.90	0.86	0.76	0.62	0.49
35		1	0.99	0.98	0.97	0.96	0.92	0.85	0.70	0.52	0.37
65			1	0.99	0.99	0.97	0.93	0.83	0.67	0.47	0.31
95				1	0.99	0.98	0.94	0.84	0.68	0.47	0.31
125					1	0.99	0.96	0.87	0.72	0.52	0.36
155						1	0.98	0.92	0.79	0.61	0.45
185							1	0.97	0.88	0.73	0.59
215								1	0.96	0.86	0.76
245									1	0.96	0.90
275										1	0.98
305											1

In our study the genetic correlations between somatic cell score daily records were high and positive with values between 0.31 to 0.99. The genetic correlations were different among the stage of lactation. The genetic correlations were high in the middle of lactation when the distance between test day was low and were low between SCS at distant days in milk. Our results were in agreement with those obtained by Mrode and Swanson (2003).

Costa et al. (2015) reported that genetic correlations between adjacent DIM were very high (>0.83) but between DIM in the extremes of lactation were lower.

Rupp and Boichard (1999) noticed genetic correlation of 0.72 between clinical mastitis (CM) and SCS. Mrode and Swanson (1996) obtained genetic correlations across lactations for SCC 0.77, 0.76 and 0.87 between first three lactations. Another study reports genetic correlation around 0.7 to 0.9 between first and second parity, 0.7 to 0.8 between first and third parity, and 0.9 between second and third parity, Mrode and Swanson (2003).

Kadarmideen (2004) noticed genetic correlations of 0.13, 0.10 and 0.15 between lactation-mean SCS and milk, fat and protein yields in Swiss Holstein. Dechow et al. (2007) observed higher genetic correlation for milk, fat and protein yields with lactation average SCS (0.53) in Holstein, Carlen et al. (2004) noticed lower genetic correlations between production traits and SCS in Swedish Holstein cows. Koivula et al., 2005 obtained negative phenotypic correlation between SCC and milk traits in first lactation. Siatka et al (2019) observed that the increase SCC in milk in Polish Holstein Friesian influence cow's fertility. A cow with a good health had SCC egal or lower than 100000 cell/ml (Hillerton 1999). It is very important to have in herds cows with a good health.

The phenotypic and genetic correlations between somatic cell score and milk yield, protein percentage and fat percentage are presented in table 5. The average fat milk day percentage was 4.12 and average protein milk day percentage was 3.28.

Table 5. The phenotypic and genetic correlations between somatic cell score and milk yield, protein content and fat content

Somatic cell score	Milk yield	Protein percentage	Fat percentage
Phenotypic correlations	-0.128	0.234	-0.063
Genetic correlations	-0.138	0.620	0.0012

The phenotypic and genetic correlations between somatic cell count and milk yield were negative. The phenotypic and genotypic correlations between somatic cell score count protein percentage were positive. The phenotypic correlation between somatic cell score and fat percentage was negative and genetic correlation between two traits was positive.

Guo et al. (2010) reported highly significant negative correlation coefficient between somatic cell score (SCS) and milk and protein yield -0.084, -0,037 and positive correlation coefficient between SCS and fat yield 0.041 in Holstein breed. Milk yields losses due to increases SCC were very high and fat and protein yield decreased with varying SCC observed Guo et al. (2010).

Cinar et al. (2005) reported negative correlation between somatic cell counts and milk yield and lactose and positive correlation with total solids, milk fat and protein in Holstein breed. Cinar et al. (2005) observed that high SCS negatively affects milk and milk composition and quality, when SCC increased, the milk yield decreased. Wei et al. (2021) observed a moderate and negative correlation between somatic cell score and milk lactose percentage.

Padilha et al. (2019) reported genetic correlation between 305 days milk yield and SCS up to 305 days was -0.47.

CONCLUSIONS

The monthly test day of somatic cell count is necessary to indicate the health status of cows.

Importance of low SCS it can also be seen in higher milk yield and lower management cost too.

The heritability for somatic cell score was low ranged between 0.047 to 0.1471, this trait can be improved by the selection of genetically correlated traits.

The genetic correlation between somatic cell score daily records were high and positive with values ranged from 0.31 to 0.99. The phenotypic and genetic correlations between somatic cell count and milk yield were negative.

Somatic cell count is a trait that has influenced the quality and milk yield, it is recommended to use this trait as management tool for mastitis resistance.

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