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Short communication

GENETIC PARAMETERS FOR SOMATIC CELL COUNT, LOGSCC AND SOMATIC CELL SCORE OF BREEDS: IMPROVED VALACHIAN, TSIGAI, LACAUNE AND THEIR CROSSES

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In the last few years there has been increasing emphasis on reducing milk somatic cell count to improve the milk quality in dairy ruminants. Genetic parameters for somatic cell count (SCC), LOGSCC and somatic cell score (SCS) were estimated. About 1193 measurements were included in the analysis for each character of 358 ewes of 9 genotypes. Nine breeds and genotypes were included in these experiments: purebred Improved Valachian (IV), Tsigai (T), Lacaune (LC) ewes, and IV and T crosses with a genetic portion of Lacaune and East Friesian (EF) – 25 %, 50 % and 75 %. Primary data were processed using restricted maximum likelihood (REML) methodology and the multi-trait animal model, using programs REMLF90 and VCE 4.0. Heritability coefficients for somatic cell count were low: h^2=0.03, for LOGSCC h^2= 0.08 and for somatic cell score h^2=0.06. Somatic cell score can be considered for inclusion in a breeding program aimed at reducing somatic cell count and frequency of clinical mastitis in dairy sheep.

Key words: ewes, genetic and phenotypic correlations, heritability, somatic cell count, somatic cell score

INTRODUCTION

In the last few years, dairy sheep farming has become more important thanks to genetic selection and to better feeding conditions [1], which have led to higher milk yields, improved milk composition and type traits [2].

In the recent years several traits were linked to functional longevity: udder morphology [3-6], milk flow traits [7-9] and somatic cell count [10-15] are taking on a more important role within these breeding programs [16]. On an international level, improving the health of livestock is of dramatically increasing interest to the dairy industry and consumers [17]. The SCC in milk is a reliable parameter to indirectly diagnose the

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health status of mammary glands [18-22] and is, therefore, an effective tool to control mammary disorders such as mastitis.

The use of SCC as an indicator of the health status for cow milk is widely known. The values of normal cow milk are inappropriate to evaluate and interpret goat milk due to the presence of many cytoplasmatic particles resulting from apocrine milk secretion in goat udders, while the process in cow udders is merocrine [23]. Indeed, milk SCC mainly reflects the number of neutrophils that migrate from the blood to the mammary gland in response to infection [24]. In several dairy sheep breeds, somatic cell count in bulk milk has been used as an indicator of animal welfare, hygiene and prevalence of mastitis [25,26]. Somatic cell count is also included in the parameters considered for the determination of milk price in several European countries [27]. Mastitis is one of the major diseases which leads to significant economic losses mainly due to discarded milk, decreased milk production, quality, early culling, and increased health care costs in dairy ewes [28-37], cows [38-42] and goats [43-47]. Studies on the genetic resistance to mastitis have increased recently, showing the economic importance of this trait [48]. Selection for improved resistance to mastitis can be done directly, by selecting against mastitis itself, or indirectly by selecting for a trait correlated with mastitis [49]. However, genetic evaluation of mastitis is particularly difficult because of the low heritability and the categorical nature of the trait [42]. Somatic cell count has been promoted as an indirect method of predicting mammary infections [50] and as a selection criterion to improve subclinical mastitis resistance [51,52]. Somatic cell count has been widely promoted as an indirect method of predicting mammary infections and as a selection criterion to improve mastitis resistance [21,53]. Somatic cell count is a continuous variable, so in order to use it as a diagnostic tool a decision threshold (or cut-off value) needs to be defined to discriminate between uninfected and infected sheep. In sheep there is no universally accepted threshold [54]. A genetic improvement program for milk yield and composition in dairy sheep is an important component toward the development of a viable industry. One of the traits to be improved in dairy sheep is the somatic cell count of milk [13], as an indicator of mastitis and as a trait which influences milk quality. Nevertheless, breeding programs for mastitis resistance have been implemented throughout the world in dairy sheep [55] and dairy cattle [13,56] using indirect predictor traits such as clinical mastitis and SCS. Somatic cell count is currently recorded in several milk recording schemes in dairy sheep [57].

The aim of the present study is to find out the genetic characteristics of selected parameters which characterize the milk quality of ewes. There is no published research on genetic parameters for milk quality traits of Improved Valachian and Tsigai sheep. Implementation of SCC in breeding programs requires the knowledge of the relationships between these major health traits.

MATERIAL AND METHODS

Nine different sheep genotypes were included in this experiment to determine the milk quality of ewes which belong to the following populations:

Improved Valachian (IV), n = 214; IV x East Friesian (25%), n = 66; IV x East Friesian (50%), n = 78; IV x East Friesian (75%), n = 72; Tsigai (T), n = 277; Tsigai x East Friesian (25 %), n = 18; Tsigai x East Friesian (50%), n = 163; Tsigai x East Friesian (75%), n = 47; Lacaune (LC), n = 258

Three-breeding crosses with 25%, 50% and 75% of the genetic proportion of both specialized dairy breeds: Lacaune (LC) and East-Friesian (EF) formed during the entire period were significantly less from the assessed population (about 5%). For the estimation of covariance components and genetic parameters determining udder health status of sheep were used from our own database. Estimation of covariance components followed by calculation of genetic parameters was conducted using restricted maximum likelihood (REML) methodology and the multi-trait animal model, using the REMLF90 and VCE 4.0 programs [58]. The estimation of covariance was based on a multiple trait animal model including the 7 traits described. Due to the fact that the somatic cell count did not follow a normal distribution it was transformed logarithmically into somatic cell score (SCS) according to the formula [59]:

$$\text{Somatic cell score} = \log2 (\text{SCC} / 100.000) + 3$$

Genetic parameters were determined separately for somatic cell count, LOGSCC and somatic cell score using untransformed data: 1193 measurements were taken during the seven year long experimental process from 358 ewes, out of which 209 of them were purebred and 149 crossbreed. Some ewes were included in the experiment for one or more years. It follows that at least some of them could perform up to 8 control milk measurements. Somatic cell count (SCC) was determined in the accredited Central Laboratory for Milk Analyses, Breeding services of the Slovak Republic in Zilina, Slovakia using the apparatus Bentley 500. In addition to genetic correlations, Pearson phenotype correlations were determined also. For the calculation of the same data sets were used as for the calculation of genetic correlations. Phenotypic correlations were calculated using CORR procedure in mathematical-statistical program package [60].

For the estimation of covariance and genetic parameters of all of the above parameters, the following model was used:

$$y_{ijklmno} = m + Y_i + LS_j + GEN_k + P_l + b^*DIM_{ijklm} + a_m + tp_n + e_{ijklmno},$$

where:

$y_{ijklmno}$ = is the vector of observations for the investigated characteristics (see above for details); Y_i = year (fixed effect with 5 to 7 levels; depending on the analysed indicator 2002–2008); LS_j = lactation stage (fixed effect with 4 levels; from 40th to 99th lactation day, from 100th to 129th lactation day, from 130th to 159th lactation day and from 160th

to 210th lactation day); GEN_k = genotype (breed group, fixed effect with 9 levels; see above for characterization); P_l = parity (fixed effect with 3 levels; first, second, third and over parity); a_m = is the additive genetic effect of ewes; DIM_{ijklm} = days in milk (covariate; 40 to 210 days in milk); tp_n is the permanent environmental effect of ewes; $e_{ijklmno}$ is the random error.

RESULTS AND DISCUSSION

Table 1 shows the effect of genotype on absolute SCC and transformed somatic cell count in ewes' milk. As expected, there was a high variability especially in the somatic cells count. This indicator ranged from 5,000 to nearly 23 million. Previous reports [61], describe ewes with a healthy udder to have on average SCC in milk less than 500,000 cells per ml, and SCC exceeds the level of 1 million cells / 1 ml in milk from udders with subclinical or clinical inflammation. Maximum values found in SCC clearly point to the fact that in the experiment were also involved sheep with mastitis without obvious clinical signs. Table 1 and Figure 1 show that the highest average of SCC was found in purebred ewes LC (1063719 ± 126848). The second highest value (948196± 227060) of this indicator, was found in hybrids IV x EF (EF 50%), and average of SCC (257394 ± 247537) was observed in hybrids IV x EF (EF 25%). Genotype had a highly significant effect on the somatic cell count (SCC) at $P < 0.01$, decadal logarithm of the somatic cell count (LOGSCC) and somatic cell score (SCS) were both at $P<0.001$ [15]. The highest average of LOGSCC (5.42 ± 0.041) was found in pure-bred ewes LC and hybrids TS x EF (EF 25%) with a value at 5.36 ± 0.154, while the lowest average value was found in pure-bred ewes Tsigai (5.07 ± 0.040). Even for the somatic cell score (SCS), we found the highest average for Lacaune pure-bred ewes (2.80 ± 0.072) and hybrids TS x EF (EF 25%) at 2.71 ± 0.270. The lowest average SCS was detected in the milk of hybrids IV x EF (EF 25%) at 2.26 ± 0.140.

Table 2 shows the coefficients of heritability (on diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) characterizing the udder health status of ewes. Heritability coefficients calculated using a 7 character were low and ranged: for somatic cell count: $h^2 = 0.03$, for LOGSCC: $h^2= 0.08$ and for somatic cell score: $h^2= 0.06$. Heritability coefficients in this study have a relatively low value for the rate udder health status, but are still of value for an efficient selection. Genetic studies of SCC in several dairy ewes are more recent and less frequent than in dairy goats and cattle. The available genetic studies are mainly limited to the Churra [10, 12, 62] and Lacaune [63-65]. Results based on repeatability test- day models for SCS, indicated heritability estimates ranging from 0.04 for the Churra breed [10] to 0.16 for the East Friesian breed [66]. Other studies reported higher heritability estimates for the average SCS during lactation, from 0.11 to 0.18 [2,64,67]. The low heritability of SCS will result in a slow response to selection for resistance to mastitis.

Table 1. Effect of genotype on absolute (SCC) and transformed somatic cell count in ewes' milk

Source of variation		Indicator		
Genotype	**N of measure-ments**	**SCC**	**LOGSCC**	**SCS**
IV	**214**	**573323 ± 137736**	**5.13 ± 0.04**	**2.38 ± 0.08**
IV x EF (25%)	66	257394 ± 247537	5.10 ± 0.08	2.26 ± 0.14
IV x EF (50%)	78	948196 ± 227060	5.24 ± 0.07	2.58 ± 0.13
IV x EF (75%)	72	532088 ± 233498	5.30 ± 0.08	2.59 ± 0.13
TS	**277**	**440753 ± 124073**	**5.07 ± 0.04**	**2.30 ± 0.07**
TS x EF (25%)	18	693923 ± 475273	5.36 ± 0.15	2.71 ± 0.27
TS x EF (50%)	163	307138 ± 156925	5.12 ± 0.05	2.29 ± 0.09
TS x EF (75%)	47	519412 ± 299651	5.18 ± 0.10	2.42 ± 0.17
LC	**258**	**1063719 ± 126848**	**5.42 ± 0.04**	**2.80 ± 0.07**
Significant differences		100:300++; 125:150+; 125:300++; 150:200,250+; 175:300+; 200:300+++; 250:300+++;	100:175+; 100:300+++; 125:300+++; 150:200+; 150:300+; 175:200++; 175:250+; 200:300+++; 250:300+++; 275:300+;	100:300+++; 125:300+++; 150:200,250+; 175:200,250+; 200:300+++; 250:300+++; 275:300+;

+++ P<0.001; ++P<0.01; +P<0.05; ns: non-significant effect

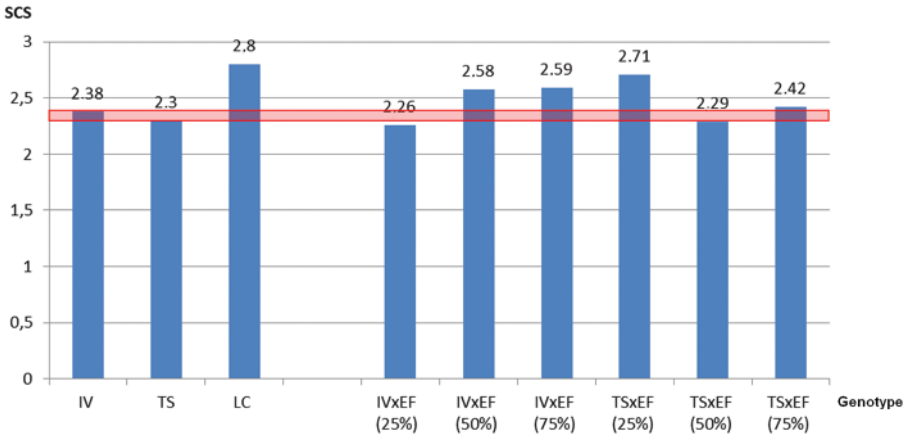

Figure 1. Effect of genotype on somatic cell score in ewes – compare differences between purebreds and crossbreeds

Maletić et al. [68] monitored the distribution of lactoferrin gene genotypes and its connection to milk quality and occurrence of mammary gland diseases in Holstein-

Friesian cows. In the study they included two genotypes of cows. There was no statistically significant difference in the number of somatic cells in milk samples between the examined genotypes of cows. Of the factors affecting SCC a comment should be made on the vaccination of ruminants against mastitis. In the study of Magaš et al. [69] the number of somatic cells in milk samples was higher in vaccinated cows. Regarding the somatic cell count in Alpine breed goat's milk [70] the positive effect on reduction was determined when a dietary supplement was added. The mentioned effects persisted after the supplement was withdrawn. However, our results show that the selection against subclinical mastitis can also contribute to success if we select for somatic cell count (indicator of udder health).

Table 2. Heritability coefficients (on diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations for the udder health status of ewes

Indicators	SCC	LOGSCC	SCS
Somatic cell count (SCC)	**0.03**	1	1
LOGSCC	0.64	**0.08**	1
Somatic cell score (SCS)	0.82	0.93	**0.06**

The genetic parameters for SCS for ewes estimated in this study are in agreement with results from other studies. The heritability for SCS is moderate, and little progress can be made toward decreasing the somatic cell score. These results show that genetic improvement can be achieved in SCC by including SCS in the selection index.

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GENETSKI PARAMETRI ZA BROJ SOMATSKIH ĆELIJA, LOGSCC I SKOR SOMATSKIH ĆELIJA KOD RASA: POBOLJŠANA VLAŠKA, CIGAJA, LAKON I NJIHOVIH MELEZA

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U poslednjih nekoliko godina postoji povećano interesovanje za smanjenje broja somatskih ćelija u mleku u cilju poboljšanja kvaliteta mleka kod preživara. Procenjivani su genetski parametri za broj somatskih ćelija (SCC), LOGSCC i skorovi somatskih ćelija (SCS). Obuhvaćeno je oko 1193 merenja u okviru analiza svakog od parametra i to kod 358 ovaca, u okviru 9 genotipova. Devet pasmina i genotipova obuhvaćeni su ovim ispitivanjem i to: čistokrvna poboljšana vlaška ovca (IV), cigaja (T), lakon (LC) ovce kao i ovce dobijene ukrštanjem IV i T sa genetskim primesama lakona i istočno-frizijske ovce – 25%, 50% i 75%. Preliminarni rezultati su obrađivani upotrebom restriktivne maksimalne verovatnoće (REML) primenom REMLF90 i VCE 4.0 programa. Nasledni koeficijenti za broj somatskih ćelija bili su niski: h2=0.03, za LOGSCC h2=0.08 i za skor somatskih ćelija h2=0.06. Skor somatskih ćelija može da se uzme u obzir prilikom pravljenja programa ukrštanja, a u cilju redukcije broja somatskih ćelija i učestalosti klinički izraženih mastitisa kod muznih ovaca.