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GENETIC DETERMINISM ESTIMATE FOR THE MASTITIS RESISTANCE IN ROMANIAN BUFFALO

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Abstract

The Romanian Buffalo is one of the most important genetic resources for milk and meat production, but the sharp decline in the livestock and in the absence of adequate financial support, it can disappear at any time.In this respect, it is very important to develop efficient breeding programs or active conservation (according to risk status) to improve population for characters associated with these productions.

The objective of this study was to estimate genetic parameters for milk somatic cells count, character that significantly affect the health of animals and milk constituents that gives its quality. Also, this character could allow a selection of individuals in the direction of resistance to mastitis. A total 609 milk yield and associated characters records, belonging to 87 females, which coming from 11 sire families, for 7 lactations were analyzed. The method used for genetic parameters estimates was REML.

Study has revealed the existence of a poor genetic determinism for somatic cell count and a high variability of character analyzed according to number of lactation. The results indicate that environmental factors have a greater contribution to the phenotypic manifestation of character. So, the number of somatic cells must be exclusively an indicator of milk hygiene and not included in selection objective of buffaloes (resistance to mastitis).

Key words: buffaloes, genetic parameters, somatic cells count

INTRODUCTION

In Romania, the buffalo entered with the invasion of the Huns and Avars in the Carpatho-Danubian area. It found the good pedo-climatic conditions and so, in our country, has developed a buffalo population which had its own evolutionary path as a result of reproductive isolation [12]. The Romanian Buffalo is one of the most important genetic resources for milk and meat production.

Compared with cows, buffalo milk has quality parameters with higher values. Regarding total number of germs and somatic cells count, the buffalo milk fall in grade A (under 100000) and somatic cell count falls within European standards for cow and buffalo milk [12].

In this respect, it is very important to develop efficient breeding programs to improve population for characters associated with milk production.

As is known, one of the major steps in the design of the breeding program is to determine with maximum accuracy the population genetic structure. Many of the decisions to be taken in animal breeding, in relation to the choice of breeding system and selection methods, depend on the values of genetic parameters. The accuracy of the genetic parameter estimation depends on the amount and quality of the primary data and the statistical model selection [4, 6].

It is known that the quality of milk can be affected by the number of somatic cells. These can provokes some change in the milk constiuents. Also, the somatic cells count is a tool for assessment milk health by diagnosing of sub-clinic mastitis and can be a trait that allows the selection of individuals for genetic resistance to this disease.

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In general, resistance to disease has a weak genetic determinism, being strongly influenced by environmental factors. As a result, the characters on the viability and resistance to disease are difficult to improved, giving preference to environmental conditions improving [6] i.e. milking hygiene. For clarification, studies on the genetic structure of the population associated with this character, become binding.

There are a number of studies showing estimates of genetic parameter values related to buffalo milk yield [1, 3, 7, 8, 9, 10] and milk quality parameters [1, 7, 9, 10], but there are few studies reported genetic determinism for somatic cells count [1, 2].

The objective of this study was to estimate genetic determinism for buffalo milk somatic cells count, using a methodology that gives the maximum accuracy in conditions of the existence an inconsistent data. The work is part of a larger study, some results were published in 2014.

MATERIAL AND METHODS

In order to estimate genetic parameter values, were used the data resulting following control milk production in females belonging Şercaia Research and Development Station. To analyze parameters in dynamic were included in the analysis only animals presenting records to an equal number of lactations.

A total 609 milk yield and associated characters records, belonging to 87 females, which coming from 11 sire families, for 7 lactations were analyzed.

In control milk production, records with length greater than 270 days were truncated at this point, as suggested by Tonhati et al, 2008 [11] and Aspilcueta-Borquis et al, 2010 [1].

The method used for genetic parameters estimates was REML developed by Sir Ronald Fisher (1925) and perfected by Patterson and Thompson in 1971 [5].

RESULTS AND DISCUSSIONS

The results on the average performance of milk somatic cells count are presented in Table 1.

The data presented in Tables 1 shows that the average values of milk somatic cells count are characteristic of a buffaloes population, with a large variability, within standards for buffalo milk quality, and that trait can has a good response to selection. The values of the descriptive statistics indicate the existence of a population that can constitute object of a breeding program, with a sufficiently large field for action of artificial selection.

Table 1 Descriptive statistics for somatic cells count

Specification	UM	n	$\overline{X} \pm s_{\overline{X}}$	s	v%
Lactation 1	no/ml	87	387208 ± 17094.42	159490.97	41.19
Lactation 2	no/ml	87	295265 ± 12639.75	117928.84	39.94
Lactation 3	no/ml	87	324416 ± 12764.53	119093.11	36.71
Lactation 4	no/ml	87	356317 ± 16284.41	151933.57	42.64
Lactation 5	no/ml	87	345232 ± 14408.72	134433.34	38.94
Lactation 6	no/ml	87	369210 ± 13359.62	124645.30	33.76
Lactation 7	no/ml	87	285307 ± 12085.03	112753.33	39.52

Heritability is defined as the rate of additive genetic variance in the phenotypic variance. Estimates of heritability coefficients are considered very important as indicators of a breeding program effectiveness. Heritability coefficient values for the somatic cells count, for 7 lactations, are presented in Table 2.

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Table 2 Heritability values for somatic cells count

Specification	Lactation 1	Lactation 2	Lactation 3	Lactation 4	Lactation 5	Lactation 6	Lactation 7
	$h^2 \pm S_{h^2}$	$h^2 \pm S_{h^2}$	$h^2 \pm S_{h^2}$	$h^2 \pm S_{h^2}$	$h^2 \pm S_{h^2}$	$h^2 \pm S_{h^2}$	$h^2 \pm S_{h^2}$
Somatic cells count	0.17 ± 0.25	0.13 ± 0.48	0.07 ± 0.25	0.23 ± 0.38	0.10 ± 0.29	0.08 ± 0.44	0.18 ± 0.32

The analysis of data presented in Table 2 shows that the milk somatic cells count is a character that has a low genetic determinism, along the 7 lactations analyzed. The variation of heritability coefficient from one age to another can be explained by the existence of different polygenic complex that is involved in genetic determinism of somatic cells count, environmental conditions influence, errors due to sample size, or poor production recording.

Heritability coefficient values for somatic cells count found in present paper are similar to those reported by Aspilcueta-Borquis et al, 2010 [1], and Barros et al, 2014 [2].

The heritability values for somatic cells count found in present paper showed that exist some other factors (specified above) which were more important than additive factors. So, the buffalo female selection for somatic cells count in order to improve mastitis resistence should not be done. It appears advisable that the selection of female to be targeted towards other characters associated with milk production and for decreasing the number of somatic cells to be improved environmental conditions.

Genetic correlation between characters is another important aspect of establishing the selection objective. The genetic correlation values for the somatic cells count with other milk production traits, for 7 lactations, are presented in Table 3.

Table 3 Genotypical correlation estimates between somatic cells count and other traits

Specification	Lactation 1	Lactation 2	Lactation 3	Lactation 4	Lactation 5	Lactation 6	Lactation 7
Somatic cells count x							
- Milk yield	-0.12	-0.22	-0.16	-0.14	-0.09	-0.10	-0.15
- Fat yield	-0.32	-0.21	-0.19	-0.18	-0.15	-0.28	-0.36
- Protein yield	0.20	0.26	0.18	0.23	0.22	0.20	0.18

The results presented in Table 3 show that the somatic cells count is low and negative correlated with milk yield and fat yield, which means that the female selection for milk and fat yield, along with improving environmental condition, should determine a fewer somatic cells. A negative and lower correlation was reported by Aspilcueta-Borquis et al, 2010 [1]. At the same time, the results can be surprising because a drop in milk production could lead to an increase in the number of somatic cells. We believe that this issue would require further investigation using other methods of estimation. Perhaps an analysis of variability within the lactation would be appropriate.

Interesting is the value of genetic correlation between somatic cell count and protein yield. They suggest that selection for a larger amount of protein would lead to increase in the number of somatic cells and, very likely, the incidence of mastitis. This requires improvement of the environment conditions, especially hygiene of milking, because the amount of protein in milk is an important character which directly affects Mozzarrela index.

CONCLUSIONS

The somatic cells count, as a component of buffalo milk quality, has enough genetic variation for selection, but the low genetic determinism suggest that environmental factors have a greater contribution to the phenotypic manifestation of the trait. So, the number of somatic cells should be just an

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indicator of milk hygiene and not included in female selection objective. Because of genetic correlation values, it is advisable more accurate analysis, perhaps within lactation.

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