Scientific Papers. Series D. Animal Science. Vol. LXIV, No. 1, 2021
ISSN 2285-5750; ISSN CD-ROM 2285-5769; ISSN Online 2393-2260; ISSN-L 2285-5750

GENETIC DETERMINISM FOR THE MASTITIS RESISTANCE IN ROMANIAN PINZGAU

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Abstract

The Pinzgau breed in Romania (known as Pinzgau from Transylvania) is a very valuable genetic resource, and can be found mainly in the NW of the Carpathian Mountains, the Dornelor basin with the Bucovina High Hills (Obcinele Bucovinene), SW of Transylvania. In the absence of a coherent active conservation program, this resource may disappear at any time. In our opinion, the major vulnerability of the Pinzgau breed is the indiscriminate infusions with Red Holstein or Simmental, as a consequence of the lack of firm actions to preserve the genetic heritage. 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 252 milk yield and associated characters records, belonging to 63 females from Suceava County, which coming from 8 sire families, for 4 lactations were analyzed. In the absence of consistent data, the paternal origin of females was established after ear tags. 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 for mastitis resistance of Romanian Pinzgau within active conservation program.

Key words*: genetic parameters, Romanian Pinzgau, somatic cells count.*

INTRODUCTION

The Pinzgau breed is also called Pinzgauer after its region of origin (Pinzgau, near Salzburg, Austria) and is an alpine breed. The breed emerged in the 19th century from the local alpine breeds and was developed in three directions: traction, milk and meat. Its use as traction animals has played an important role in the history of the breed, contributing to the increase in size, the development of muscles and exceptional walking skills. Pinzgau traction oxen were famous in the lowlands of Austria, Bavaria, and neighboring countries.

Around 1820, Pinzgau specimens were exported to countries such as Romania, Yugoslavia, the Czech Republic and Slovakia, and later to over 25 countries around the world.

In last decades, even in the birthplace, the number of specimens of the breed declined drastically due to changes in "fashion" and intensive agriculture, which caused the race to be in danger. Pinzgau, only Austrian indigenous breed, worldwide famous, should receive special attention through the establishment of national park and through the use of race to achieve its organic productions.

In Romania, the Pinzgau breed is treated as an independent breed. In Romania there are flocks that are made up of the descendants of Pinzgau cattle brought on the territory of the country during the Habsburg Empire.

The breeding area of the Pinzgau cattle breed in Romania is quite large, covering a part of the north west of the Carpathian chain, the Dornelor basin with the Bucovina High Hills (Obcinele Bucovinene), the south west of Transylvania and not only.

There were about 35000 Pinzgau cattle at the national level.

In Romania, Red Pinzgau breed formed after absorption crosses made between local breeds of cattle (Grey Steppe and Mocăniţa) and Pizgau of Austria, since the second half of the nineteenth century, and black Pinzgau named "Cow of Dorna" by crossing local cattle with various mountain improved breeds (Pinzgauer, Mölltal, Zillertal, Dux-Zillertal, Dutch, Brown, etc.).

The Pinzgau breed is exploited today in two directions: for milk production (quantitatively lower than the Austrian and German Simmental, but close in terms of quality) and for the special quality of the meat. It is very well adapted to severe environmental conditions, suitable for extensive exploitation. These are the main reasons why the breed should be kept in a form of active conservation.

The Transylvanian (Romanian) Pinzgau breed from is in real danger of being absorbed by the Simmental super-breed, of which Bălţata Românească (Romanian Spotted) is also a part.

Kladlecik et al. (2004) state that the Pinzgau breed has reached an endangered status, a consequence of the sharp decrease in numbers over time. According to Draganescu (2003), Transylvanian Pinzgau breed from seems to be only vulnerable. As long as there is a very low chance that the situation will change in the growing areas, the breed has all the chances to be preserved in the next 15-20 years. However, the author states that during all this period it is mandatory to build an efficient conservation program.

As is known, one of the major steps in the design of the breeding or active conservation 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 (Grosu, 2005; Popa, 2009).

It is known that the quality of milk can be affected by the number of somatic cells. These can provoke some change in the milk constituents. 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.

Mastitis is an inflammation of the mammary gland, being a pathology that relatively frequently affects dairy cows, causing, in addition to issues related to the ethics of cow exploitation, numerous and important economic losses.

From this point of view, the selection of dairy cows for mastitis resistance should be included in the breeding program, but the difficulty of this action lies in the weak genetic determinism of this trait (Urioste et al., 2010; Koeck et al., 2012).

Over time, selection for mastitis resistance has been used both directly and indirectly (de Haas et al., 2002; Odegard et al., 2002).

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 (Popa, 2009) i.e. milking hygiene. For clarification, studies on the genetic structure of the population associated with this character, become binding. In this regard, research has shown that direct selection for mastitis resistance is totally inefficient, a consequence of the very weak genetic determinism of this pathology (heritability between 0.02 and 0.05) and the difficulty in measuring character (Mrode & Swanson, 1996; Rupp & Boichard, 1999). On the other hand, the inclusion of udder health in the selection criteria of dairy cows becomes mandatory to compensate for the negative effect of selection for milk quantity on health, longevity and reproduction (Oltenacu & Broom, 2010).

A number of studies have shown that the inclusion of somatic cell counts in dairy cows breeding programs for indirect selection for mastitis resistance was superior compared to those that included only the milk yield, a superiority quantified by their overall economic value (Rogers, 1993; Colleau & Bihan-Duval, 1995). The issue is supported by genetic correlations between somatic cell number and milk quantity, ranging from 0.13 to 0.22 (Rupp & Boichard, 1999; Carlen et al., 2004).

Indirect selection for mastitis resistance uses as a selection criterion a character that has a higher genetic determinism than the manifestation of the disease itself, namely the number of somatic cells (Rupp & Boichard, 1999).

In the case of indirect selection, there must be a close genetic correlation between the primary and the secondary character in order for it to have the expected effect. Research has shown a genetic correlation between 0.7 and 0.8 between the number of somatic cells and the appearance of mastitis in its clinical form, and selection to decrease the number of somatic cells should increase resistance to mastitis (Shook & Schutz, 1994; Rupp & Boichard, 1999; Kadarmideen & Pryce, 2001).

In general, research on the genetic determinism of somatic cell numbers has shown a low heritability, with heritability values of the average number of somatic cells per lactation ranging from 0.05 to 0.17 (Odegard et al., 2002; Carlen et al., 2004).

We note that in many countries, the selection for udder health is made not only on the number of somatic cells, but also on a variant of this character obtained by logarithmic (logarithmic transformation) in order to normalize the distribution, the new feature called somatic cells score (Guzzo et al., 2018).

In this context, the objective of this study was to estimate genetic determinism for Transylvanian (Romanian) Pinzgau milk somatic cells count, using a methodology that gives the maximum accuracy in conditions of the existence an inconsistent data.

MATERIALS AND METHODS

In order to estimate genetic parameter values, data collected by authors from cows from individual households, with known and identifiable origin, were used. To analyze parameters in dynamic were included in the analysis only females presenting records to an equal number of lactations.

A total 252 milk yield and associated characters records, belonging to 63 females from Suceava County, which coming from 8 sire families, for 4 lactations were analyzed. In the absence of consistent data, the paternal origin of females was established after eartags.

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

RESULTS AND DISCUSSIONS

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

Table 1. Descriptive statistics for somatic cells count

Spec.	UM	n	$\overline{X} \pm s_{\overline{X}}$	s	v%
Lactation 1	no/ml	63	389606 ± 19279.1180	153076.1974	39.29
Lactation 2	no/ml	63	309416 ± 13062.4991	103716.2432	33.52
Lactation 3	no/ml	63	286753 ± 15291.0857	121411.2202	42.34
Lactation 4	no/ml	63	375242 ± 19348.1202	153624.0748	40.94

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

However, although the values obtained for the number of somatic cells are in the standard for cow's milk, they suggest the existence of conditions for the maintenance of cows that would need to be improved.

Being a local population of cows, from individual households, so small farms, the housing of cows is debatable in terms of meeting the welfare conditions. Especially on rainy days, most likely, the mud is taken to the stable, and the resting area of the animals becomes unsuitable. These conditions certainly affect the health status of cows. Improper housing conditions will increase the chance of developing diseases in the mammary gland, creating the opportunity for the development of infections. To all this is added a poor milking hygiene.

As a result, it becomes imperative to improve farm management, in order to maintain well-being (clean, dry stables with a comfortable rest area, with the possibility of easy removal of manure) and ensure impeccable milking hygiene. Improving environmental conditions, in addition to animal welfare issues, will result in a reduction in its variation and, as a result, the share of additive variance in the total phenotypic variance will increase and heritability will be higher, ensuring the premises of efficient selection.

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 4 lactations, are presented in Table 2.

Table 2. Heritability values for somatic cells count

Spec.	Lactation 1	Lactation 2	Lactation 3	Lactation 4
	$h^2 \pm S_{h^2}$	$h^2 \pm S_{h^2}$	$h^2 \pm S_{h^2}$	$h^2 \pm S_{h^2}$
Somatic cells count	0.065 ± 0.205	0.084 ± 0.250	0.172 ± 0.184	0.106 ± 0.290

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 4 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 errors on production recording.

Heritability coefficient values for somatic cells count found in present paper are similar to those reported by other authors. Heritability for somatic cells count varied between 0,05 and 0,29 (Coffey et al., 1985; Kennedy et al., 1982; Monardes et al., 1985; Monardes et al., 1985; Mrode & Swanson, 1996; Mrode et al., 1998). Jattawa et al. (2012) found a heritability value for somatic cells count of 0.12 and although the heritability was low, authors suggest that the trait could be improved by selection, but in conjunction with improvements in farm management.

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, at first side, it appears advisable that the female selection for somatic cells count in order to improve mastitis resistance should not be done. Even if the value of the heritability of the somatic cell number is small, still the economic importance of this character, seen through the prism of the economic losses generated by mastitis, claims the need to improve it through selection. Certainly, we expect the response of the population to the selection to be small.

As a result of this state of affairs, two solutions can be discussed: on the one hand, the selection of females to focus on other traits associated with milk production, and for the resistance to mastitis, respectively for the decrease of the number of somatic cells, to improve the hygiene conditions in the farms, and on the other hand the selection for the number of somatic cells to be included in the breeding program, but along with improvements in farm management, respectively in hygiene and maintenance conditions. Opting for the second variant, taking into account the genetic determinism of the character, there is the chance to reduce the environmental variation, increase the value of heritability and thus make the selection more efficient. However, the issue is difficult to implement in the case of a local population, respectively at the level of small breeders. Improvements are also needed in performance control to obtain consistent data.

Genetic correlation between characters is another important aspect of establishing the selection objective within breeding or active conservation program. The genetic correlation values for the somatic cells count with other milk production traits, for 4 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
Somatic cells count x				
- Milk yield	0.088	-0.122	0.068	0.060
- Fat yield	0.276	-0.181	-0.148	-0.220
- Protein yield	0.188	-0.200	0.229	0.198

The results presented in Table 3 show that the somatic cells count is weakly and negatively correlated with milk yield in the second lactation and very weakly and positively in the other analysed lactations.

The values of genetic correlations differ from those reported by other authors (Rupp & Boichard, 1999; Carlen et al., 2004) who communicate values of this parameter between 0.15 and 0.22. The small values of genetic correlations found in this paper are determined by the genetic structure of the population, but can also be attributed to a sample error caused by the small data set.

The negative genetic correlation recorded in the second lactation between the number of somatic cells and the milk yield seems to be convenient for the selection of females. Thus, this negative value indicates that cows with high production would tend to have a low number of somatic cells, so with a low chance of mastitis, which is beneficial if maintained regardless of the degree of lactation, which does not happen.

Negative genetic correlations between somatic cells counts and fat yield suggest that selection for the latter should lead to fewer somatic cells. Thus, with the exception of the first lactation, a simultaneous selection made in the logic of increasing the amount of fat and decreasing the number of somatic cells could have a favorable effect on the overall economic efficiency of the breeding program, which would translate into an increase in farmers' incomes, provided that the results are confirmed on large, consistent data sets.

Also, a smaller amount of protein could lead to a smaller number of somatic cells. Similar results were reported by Schutz et al. (1990). On the other hand, according to market demands, selection for a larger amount of protein would lead to increase the number of somatic cells and, very likely, the incidence of mastitis. This situation requires improvement of the environment conditions, especially hygiene of milking, because the amount of protein in milk is an important character which directly affects the quantity and quality of cheese.

CONCLUSIONS

The somatic cells count, as a component of cattle milk quality, at Transylvanian (Romanian) Pinzgau analysed females, 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.

As a result, resistance to mastitis, quantified by the number of somatic cells, could be included in the breeding program, but without being mandatory, at least in a first phase. Ensuring proper maintenance conditions, even imposing a minimum standard of well-being in individual households, would have the effect of reducing environmental variation and increasing the value of heritability, which would streamline selection for udder health.

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