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Study Regarding the Genetic Relationship between Broodmares from the Reproductive Nucleus of a Native Horse Breed

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ABSTRACT

Background: In this study we present a part of the genetic history of a native horse breed. Genetic analyzes are the basis of the development of strategies regarding the conservation of genetic resources and implicitly of inbreeding management plan. In this study we present another essential component of the inbreeding of a population, namely the inbreeding of broodmares themselves.

Method: The method that we used in this study is based on A matrix coefficients. The research was carried out during 2012-2021, at Lucina National stud farm. The material was represented by a sample of 73 broodmares from the reproductive nucleus of the breed, from 5 bloodlines, analyzed on 5 generation of ascendants. The research was performed in the profile laboratories of the Faculty of Engineering and Management in Animal Production (Animal Sciences) from Bucharest.

Results: The correlation between the breeding values of the reproductive active broodmares of Huþul from the Lucina stud, Suceava County, at the time of the analysis is 0.1875±0.0015. It was found the existence some differences between the values of the kinship coefficients of the mares born in different years, but the calculated value of the Fisher test (F= 1.3667NS) shows that the observed differences have no statistical significance.

Key words: Genetics, Genotype**,** Horse, Inbreeding, Phenotype, Relationship.

INTRODUCTION

Genetic analyzes are the basis of the development of strategies regarding the conservation of genetic resources and implicitly of inbreeding management plans (Maftei *et al*., 2011, 2022). It is imperatively necessary to start with the genetic analysis in order to elaborate the strategic inbreeding management plan. This situation applies not only to horses but also to other animal species.

As we have already shown, there are three important parameters when we spoke about genetic relationship of a population. These are the genetic relation sheep between mares themselves, stallions themselves and the most important of them the genetic relationship between stallions and mares (Falconer and Mackay, 1997) cited by Maftei *et al*., 2022).

In the case of broodmares this component has its own importance due to the mating system adopted since 1856: intrafamilial selection and interfamilial crossing. An important characteristic of the horse population is the existence of overlapping generations. This situation had two important roles, concerning the evolution of population for genetic variability and the generation interval, increasing both of them (Metzger *et al.,* 2015, Maftei, 2022). Due to the conditions created for artificial selection, the effect of selection is influenced in the opposite direction, the selection difference increases and the annual response to selection decreases over time (Popa in 2009, cited by Maftei 2011, 2022).

In 2012, Maftei M. *et al*, showed that, at the level of this population of horses, there was no significant trend in the genetic similarity of the population with any male ancestor. In other words, in the population analyzed by us, we did not want to increase the genetic similarity of the population with outstanding breeders. The non-existence of this tendency and the maintenance of relatively small differences between breeders is a beneficial issue as inbreeding was avoided and normal evolution of the population was ensured. Of course, a special role was played by the observance of the mating matching system, specific to the studs, to avoid inbreeding.

Marginean *et al*. (2005, 2012) and Maftei *et al*. (2012, 2022) shows that the kinship between individuals directly influences the increase of homozygosity.

MATERIALS AND METHODS

The biological is represented by an entire number of broodmares from the reproductive nucleus (N=73), from 5 bloodlines, analyzed on 5 generations. This research was performed in the laboratories of the University of Agronomic

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Sciences and Veterinary Medicine, Faculty of Engineering and Management of Animal Production (Animal Sciences) from Bucharest. The method that we used in this study is based on A matrix coefficients (Grosu, 1997, Popa, 2009). The numerator relationship matrix describes the genetic relationships between individuals of a population. Its inverse is used for the prediction of breeding values, as outlined by Henderson (cited by Popa, 2009). The Fisher test was used and applied, to highlight the existence of differences. The research took place, theoretically, between 2012 and 2021, but due to the complexity of the study, we must specify that they continue at this time as well.

RESULTS AND DISCUSSION

From the analysis of the data presented, it can be found that there are some differences between the values of the kinship coefficients of the mares born in different years, but the calculated value of the Fisher test (F= 1.3667) shows that the observed differences have no statistical significance (basically, the significance of the differences was tested observed between the averages of different years).

Also, genetic diversity or, more correctly, the cumulative action of improvement factors, can be highlighted by determining the genetic relationship coefficients between groups of broodmares born in different years. In the present case, this action does not make sense, since the previously calculated Fisher test statistic did not highlight the existence of significant differences and, as a result, statistically significant differences between groups of mares are improbable (with no chance of occurring) born in different years.

In order to highlight the genetic diversity, the broodmares were grouped by year of birth (those considered

Table 1: The genetic relationship between broodmares grouped by year of birth.

Year of birth (code)	Number of mares	Number of combinations	Average kinship
A	1	0	1.0000
B	4	6	0.1796
C	3	3	0.1015
D	5	10	0.1906
E	2	1	0.1651
F	3	3	0.1625
G	2	1	0.1407
H	3	3	0.1550
I	3	3	0.1182
J	4	6	0.1364
K	2	1	0.1659
L	3	3	0.2781
M	4	6	0.1849
N	1	0	1.0000
O	7	21	0.2122
P	14	91	0.2020
Q	14	91	0.1860

F = 1.3667^{NS}

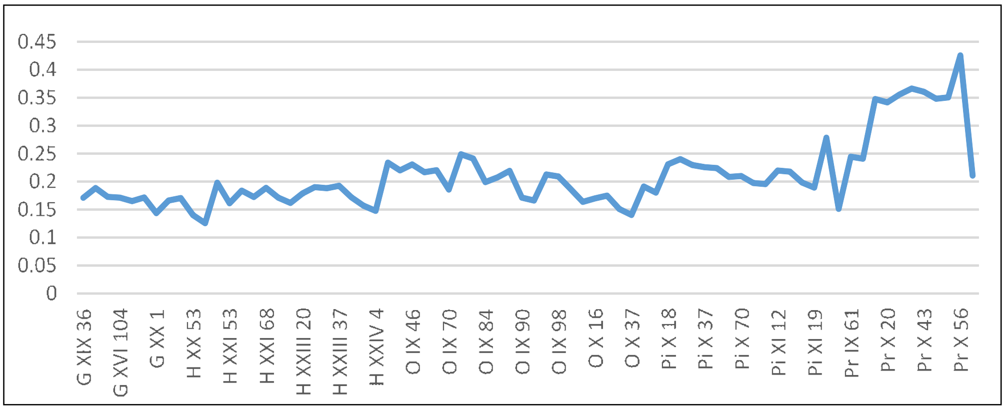

Fig 1: Graphic representation of genetic relationship between broodmares.

in the age structure) and the average relatedness of the groups of females born in different years was determined, values presented in Table 1.

CONCLUSION

The average genetic relationship, in the analyzed population, was 0.1941 or 19.41% (Maftei *et al*., 2022), means which a relatively low genetic variability. As is known, a kinship more distant than 12.5% (as in the case of first cousins) when the relationship is more distant from first cousins (12.5%), the proportion of heterozygotes tends to be a constant as a limit (not zero). This will allow the population to remain in a state of equilibrium, but only as long as the selection and mating system is respected, taking into account the principles of matching pairs (Wright, 1921, cited by Drãgãnescu, 1979).

The corelations between the improvement values of the mares' active reproduction in the population of Huþul from the Lucina stud, at the time of the analysis, is 0.1875±0.0015. The situation is graphically represented in Fig 1.

We strongly recommend: keeping the system of intrafamilial selection and interfamilial crossing, ensuring an optimal size of the reproductive nucleus and achieving a balanced age structure.

Conflict of interest: None.

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