SUMMARY

Of the doctoral thesis entitled:

RESEARCH ON THE GENETIC IMPROVEMENT OF SHEEP FOR SOME TRAITS OF ECONOMIC IMPORTANCE

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<u>CUVINTE-CHEIE</u>: traits, breeding value, BLUP methodology, heritability, genetic correlations

In this doctoral thesis, a population from the Milk-Palas Line was analyzed with the aim of optimizing the selection criteria for improving milk production and prolificacy. Four traits were analyzed, three related to milk production (the amount of milk , the amount of milk fat, the amount of milk protein) and one related to reproductive traits, namely prolificacy expressed by the number of lambs per ewe at calving.

The study was conducted on 485 ewes, with performances in their first lactation, belonging to 170 paternal half-sib families, with an average family size of 2.85 daughters per sire.

The doctoral thesis is structured into two parts, the first part consisting of three chapters and the second part consisting of seven chapters.

The first chapter provides general information about the importance of sheep breeding globally and in the context of Romania.

The economic value of traits involved in sheep breeding is presented in the second chapter. Both milk production value and prolificacy are essential aspects in sheep breeding as they can significantly contribute to increasing breeders' income and improving profitability in the sheep industry.

The third chapter analyzes sources of information, genetic parameters, and selection methods used in the genetic improvement of sheep for economically important

traits. Understanding genetic parameters, using efficient selection methods, and reliable sources of information are crucial for improving economically important traits in sheep breeding programs. This chapter delves into these aspects to elucidate their significance in sheep breeding programs.

Optimizing sheep genetic improvement programs requires a comprehensive understanding of genetic parameters, adept selection methods and reliable sources of information. By using these tools effectively, breeders can accelerate genetic progress, increase the economic viability of their flocks and contribute to the sustainable development of the sheep industry.

The second part of the thesis presents the personal research, in which the purpose of the doctoral thesis, the biological material and the working methodology for achieving the objectives, the results obtained and their interpretation, the general conclusions and recommendations are highlighted.

Chapter IV – the purpose and objectives of the research and material and methods. In this chapter, the statistical methods used, the parameters and the measurements performed to achieve the proposed objectives are described. Several statistical procedures were used for the biometric analysis of the observation data, among which we specify:

a) Vital statistics of the population (Mean, error of the mean, variance, standard deviation, coefficient of variability), for the presentation of the phenotypic structure of the investigated population,

b) The BLUP (Best Linear Unbiased Prediction) methodology for estimating the genetic parameters of the traits in the breeding objective and predicting the breeding value for the selection candidates,

c) The method of standardized distances, for estimating the economic values of the characters in the improvement objective,

d) BLP (Selection Indices) method to optimize the selection criterion.

In the fifth chapter, the phenotypic characterization of the population is presented for the characters analyzed at the beginning of the improvement program, an aspect that involves the estimation of the level (mean) and dispersion parameters (variance, standard deviation, coefficient of variability) of the original population.

Chapter VI is devoted to the problem of estimating genetic parameters for milk production and prolificacy in sheep. Knowledge of genetic parameters (heritability, genetic correlations) is the essential element for making decisions regarding the improvement of animal populations. Based on the causal components of the additive genetic variance and the environmental variance, the heritabilities of the four analyzed traits were estimated, it is observed that all four characters have an intermediate genetic determinism.

In this context, there is a substantial positive genetic correlation between milk quantity and milk fat quantity. This suggests that genes coordinating milk production growth act in the same direction for increasing milk fat quantity. The genetic correlation between milk quantity and milk protein quantity is positive but lies halfway between milk quantity and milk fat quantity.

There is a positive genetic association between milk production and prolificacy, indicating that genes associated with increased milk production may also be associated with higher prolificacy.

The genetic correlation between milk fat and milk protein quantity is positive, but it is intermediate. The genetic correlation between milk protein quantity and prolificacy is weakly positive.

Chapter VII presents the economic values of milk production and prolificacy in sheep. Results show that, in the analyzed population, the order of importance of traits in selection is as follows: prolificacy, milk quantity, fat quantity, protein quantity.

The eighth chapter includes a study on optimizing the selection criterion for improving milk production and prolificacy in sheep. It's noteworthy that the number of traits in the aggregate genotype structure may differ from the number of traits in the selection index structure, as the selection criterion optimization proceeds. For example, the aggregate genotype (selection objective) may include two traits (the amount of milk and prolificacy), while the selection criterion (index) may include three or more traits (e.g., the amount of milk, fat content and prolificacy, etc.). In the end, the variant with the highest selection accuracy was chosen and ensured the greatest genetic progress for the two considered traits (the amount of milk and prolificacy).

Chapter nine addresses the prediction of breeding value for milk production and prolificacy. Knowing the genetic breeding value in sheep milk production is essential for improving average farm performance and obtaining superior quality dairy products.

In this context, the BLUP methodology was applied in two operational variants:

1) Genetic evaluation of selection candidates based on the animal model, separately, for each analyzed trait.

2) Genetic evaluation of selection candidates based on the animal model, simultaneously, for all analyzed traits.

Finally, in chapter ten, the conclusions and recommendations obtained from the study are presented. Within the respective population, four traits were analyzed, namely, three traits of milk production (amount of milk milked, amount of fat, amount of protein) and one trait of reproduction (prolificity). A great phenotypic variability was noted for all three traits, which means that the herd analyzed has a high potential for artificial selection. The average prolificacy of the population is 1.3 with a variability of 31%.

The genetic determinism of the traits is intermediate. Regarding the interdependence of the traits, the results have shown high correlation values. Concerning the optimization of the selection criterion, which maximizes the total progress per generation, five selection index variants were devised for combinations of 2, 3, and four traits. The rank correlation between the two calculation variants was 99%. It is recommended to use the BLUP methodology, where traits are analyzed separately.

In conclusion, based on the obtained results, the following conclusions have been formulated:

-To maximize genetic progress within the Milk-Palas Line sheep population, the breeding objective (aggregate genotype - H) should include two fundamental traits: the amount of milk and prolificacy.

-The selection criterion, which maximizes genetic progress in the aggregate genotype, should include three traits: the amount of milk, the amount of fat, and prolificacy.

-For the genetic evaluation of selection candidates in sheep populations, especially in numerous ones, it is recommended that breeding values be estimated using the BLUP methodology, in the single-trait variant, where each trait is analyzed independently. This is particularly important in cases of computational facilities with limited potential (reduced capacity to solve large systems of equations).

In conclusion, this doctoral thesis significantly contributes to understanding and optimizing the genetic improvement of sheep, with a special focus on the Milk-Palas Line. The obtained results provide the necessary framework for developing efficient selection and breeding strategies aimed at maximizing milk production and prolificacy among sheep populations.

This thesis serves as a starting point for future research in the field of sheep breeding, emphasizing the importance of continuing studies in this area to meet the requirements and challenges of sheep farming sustainable and efficient way.