

RESEARCH ON COMPARISON OF BREEDING VALUE METHODS FOR SHEEP MILK PRODUCTION

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Abstract

The aim of this paper is to compare four methods for estimating the breeding value of sheep, for the milk production. The research was conducted at the National Institute of Research and Development for Biology and Animal Nutrition Balotesti, Ilfov. The biological material is represented by a flock of Palas Milk line, consisting of 805 animals: 344 downward, 121 rams and 340 sheep. The character analyzed was the amount of milk in the weaning lamb period to the end of the lactation. Lactation length was between 51 and 230 days. To estimate heritability (h^2) and breeding value, BLUP methodology applied to an animal model was used. The heritability value was estimated by the method of single factor analysis of variance, and was 0.73. By the animal model, the heritability was stabilized at 19 iterations, the value being 0.235. The breeding value was estimated in four ways: a) Performance (PP); b) Average performance of paternal half-sisters (PSS); c) LUSHIndex(IL); d) Individual Animal model (IAM). The best work option was comparatively analyzed through Spearman rank correlation and selection accuracy. The highest rank correlation was obtained with the combination IL –IAM, 0.82 respectively, due to the fact that the methods used commonly a high sources and amount of information. The opposite is the combination of IAM-PSS, where rank correlation is -0.0071. In terms of selection accuracy, the highest value was recorded for the IAM (0.52) and the lowest inbreeding value estimation based on PP (0.48), which indicates a superiority of IAM of 8.33%. In conclusion, to achieve a more precise evaluation of animal breeding, all available sources of information should be use in calculations. Also, the combination of these sources is recommended to be performed by using BLUP methodology, applied to an animal model.

Key words: animal breeding, sheep milk yield, animal model

INTRODUCTION

The new and modern conditions of sheep exploitation and the social requirements for milk need further improvement of sheep milk production based on better genetic selection criteria (Mrode, 2014). Success in this direction depends on the material used and on the applied method of breeding value estimation. The improvement of the evaluation methods means to know the level of precision of the implemented methods and their effectiveness. Identifying the best individuals on the genetic merit is the objective of all genetic evaluation (Grosu, 2003). The genetic progress is the criterion for selection of animals for breeding (Grosu et al., 1997). To achieve genetic progress of the sheep populations, those animals with the highest value for the required genetic traits economically important should be selected from the current generation

(Draganescu, 1979). Prediction accuracy represents a very important value for the estimation improvement; it depends on the genetic progress in the studied population (Popescu-Vifor, 1990). The purpose of this paper is a comparative analysis of the methods used to estimate the breeding value in sheep, within the context of a more accurate genetic evaluation of the selection candidates for the quantity of milk.

MATERIALS AND METHODS

Biologic material. A flock of Palas Milk Line, consisting of 781 animals, of which 344 offspring, 97 sires and 340 dams. From the 340 dams, 111 appear in the database with their milk production performance, while they also appearing in the position of daughters with associated performance. Therefore, in total, the number of sheep with performance is 455 (111

+ 344). The 455 sheep were born in the period 1991-1999, their performance being registered between 1993-2001. Since Palas Milk Line has been selected with priority for milk production, the trait of milk quantity obtained from the lambs weaning (2 months) to the end of lactation was used in the present study. Duration of lactation remaining from weaning the lambs to dry sheep was between 51 and 230 days.

The goals were achieved using a variety of statistical methods, from classical statistics and to BLUP methodology (Henderson, 1963).

Thus, we used two methods to estimate heritability:

a) ANOVA (Analysis of Variance) method in order to obtain start heritability and b) Individual Animal Model, based on start heritability was estimated the final heritability. For ANOVA was used a two-way model, nested model.

$$P_{ijk} = \mu + A_i + B_{j(i)} + e_{ijk}$$

where:

P_{ij} = the trait „j” of a daughter belonging to sire „i” in year „k”; μ = overall mean of population; A_i = the fixed effect of the year ($i=1\dots 12$); $B_{j(i)}$ - the genetic effect of sire j ($j=1\dots 97$), nested within year; e_{ij} = the residual effect.

For Animal Model we used the following equation:

$$y = Xb + Za + e$$

with the Mixt model equation:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1} \cdot k \end{bmatrix} \cdot \begin{bmatrix} \tilde{b} \\ \hat{a} \end{bmatrix} = \begin{bmatrix} X'P \\ Z'P \end{bmatrix}$$

$$\text{where: } k = \frac{1 - h_0^2}{h_0^2}$$

The variance components were estimated as follows:

$$\sigma_e^2 = \frac{P'P - \tilde{b}' \cdot X'P - \hat{a}' \cdot Z'P}{n - r(X)}$$

(residual variance)

$$\sigma_A^2 = \frac{\hat{a}' \cdot A^{-1} \cdot \hat{a} + \sigma_e^2 \cdot \text{tr}(A^{-1} \cdot C_{22})}{q}$$

(additive genetic variance)

where: C_{22} is the sub-matrix corresponding to random effects in the system of equations obtained after reversed throughout the system of equations (including equation fixed effects):

$$C = \begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1} \cdot k \end{bmatrix}^{-1} = \begin{bmatrix} C_{11} & C_{12} \\ C_{21} & C_{22} \end{bmatrix}$$

Spearman Rank Correlation:

$$\frac{6 \cdot \sum d^2}{n \cdot (n^2 - 1)}$$

Prediction of the breeding value. It was done in several versions, then compared with each other in order to identify the best of them. In this context, the breeding value was estimated in next variants:

- Own Performance;
- Average performance of paternal half-sister;
- Performance + Average performance of paternal half-sister(LUSH index);
- Individual Animal Model.

RESULTS AND DISCUSSIONS

Estimation of genetic parameters and breeding value prediction of candidate farm animals are essential links of any breeding program, aiming to improve the livestock genetics. Knowing the animal performance allows us to characterize phenotypically the considered population.

Phenotypic Characterization

Table 1 shows several parameters characterizing the milk production. The yield ranges between 42 and 141.7 kg with an average of 104 kg.

Table 1. Average performance of analyzed sample

No.	Specification	Unit of measurement	Value
1	Number of animals with performance	number	455
2	$\bar{X} \pm s_{\bar{X}}$	kg.	104.09 ± 0.98
3	Lower limit	kg.	42.005
4	Maximum Limit	kg.	141.70
5	S (Standard deviation)	kg^2	20.87
6	CV (Coefficient of variation)	%	20.05

The coefficient of variation (20.05%) shows a good homogeneity of milk yield which is better

than that measured by Creanga et al. (2004), 33.1%.

Since for data processing we used an iterative procedure, a starting value was necessary as input, the so-called start heritability (h_0^2). In our study start heritability was obtained by classical two-way analysis of variance.

Genetic Parameters

Table 2 shows the analysis of variance (ANOVA nested) estimating the necessary

variance to obtain the heritability values for milk yield; we can observe that the variance value had the correct distribution and the heritability obtained (0.276) is normal for milk yield. Puledda et al. (2016) reported a heritability of 0.23 for milk yield in a population of Sarda sheep, while Bittante et al., (2017) reported a lower heritability of 0.16 for Sarda dairy sheep, but all of these values are representative for milk yield.

Table 2. Heritability of milk in the population under study (ANOVA Nested)

Sources	Degrees of freedom(DF)	Sum of squares(SS)	Average of squares(AS)	Variance
Between years (A)	DF _A = 11	SS _A =3379.60	AS _A =5761.78	V _A =91.02
Between rams in the years (B:A)	DF _{B:A} =85	SS _{B:A} =177115.77	AS _{B:A} =2083.71	V _{B:A} =117.62
Error (E)	DF _E =388	SS _E =580289.80	AS _E =1495.59	V _E =1495.59
Total (T)	DF _T =484	SS _T =820785.17	AS _T =1695.83	V _T =1704.23

$$h^2 = \frac{4 * V_{B:A}}{V_T} = \frac{4 * 117.62}{1704.23} = 0.276$$

Spearman rank correlation

The comparison of the methods of selection was done by Spearman rank correlation value (Table 3)

Table 3. Spearman rank correlation case the ordering different criteria

Number	The combination of selection methods	$\sum d^2$	$6 \cdot \sum d^2$	$n \cdot (n^2 - 1)$	r_s
1	Animal Model- Performance	62367	374202	1685040	0.78
2	Animal Model- Average performance of paternal half sister	282826	1696956	1685040	-0.0071
3	Animal Model- Lush index	50324	301944	1685040	0.82
4	Lush index-Performance	58449	350694	1685040	0.79
5	Lush index- Average performance of paternal half sister	191072	1146432	1685040	0.32
6	Performance - Average performance of paternal half sister	243803	1462818	1685040	0.13

The highest rank correlation was obtained using the combination between *Animal model* and *LUS Hindex*, 0.82 respectively, also due to the multitude of information sources (Performance + Average performance of paternal half-sister) as already mentioned as already mentioned in material and methods.

The opposite is the combination of *Animal model* and *Average performance* of paternal half-sister, whose rank correlation value indicates no correspondence between the two criteria (-0.0071).

The combinations in which Performance is present (ex. Animal model and Performance or LUSH index and Performance) led to higher

rank of correlation, which shows that this source of information is the basic piece in relation to information provided by the average performance of paternal half-sister. All the combinations of Average performance of paternal half-sister led to low values of rank correlation.

The second criterion for comparison of the combination considered was the accuracy of selection, which can be analyzed on the basis of the parameters presented in Table 4. It can be observed that the highest accuracy was obtained by using BLUP-Animal Model and on the opposite was by using Average performance of paternal half-sister.

Table 4. Selection accuracy

No.	Selection Method	Accuracy selection	Relative efficiency of selection methods (%)
1	Animal model – BLUP	0.52	-
2	Lush Index	0.50	-
3	Performance	0.48	-
4	Average performance of paternal half sister	0.19	-
The combination of selection methods			
5	Animal Model-Lush index	-	4 %
6	Animal Model – Performance	-	8.33 %
7	Lush index-Performance	-	4.17 %

CONCLUSIONS

The main conclusion of this study is that the best results were obtained with the combination: the *Individual Animal Model* and *LUSH index*, resulting in a 0.82 rank correlation. Oppositely was the combination *Animal Model* and *Average Performance of paternal half-sister* which result in a negative rank correlation -0.0071.

To achieve a more accurate evaluation of animal breeding, all available sources of information should be use in calculations. Also, the combination of these sources is recommended to be performed by using BLUP methodology, applied to an animal model.

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