# COMPARATIVE ANALYSIS OF PROCEDURES FOR PREDICTING BREEDING VALUE FOR TRAITS OF ECONOMIC IMPORTANCE IN A SHEEP POPULATION

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*Abstract*

*The objective of the paper is the comparative analysis of three selection methods, from the point of view of breeding values, for production traits (the amount of milk, milk fat and protein) and reproduction traits (prolificacy) in the Palas Milk Line sheep population. Totally, 486 sheep were analyzed. The heritabilities for breeding values were estimated by the REML method, using an animal model for the four traits analyzed, and were: 0.197, 0.209, 0.263 and 0.235. The comparison of the three methods was carried out by means of the Spearman rank correlation, which allows the comparison of the ranking of the same observation units (individuals), on different criteria (different selection methods): The Spearman rank correlation was applied for the following couples of methods: BLUP and BLP; BLUP and own performances and BLP and own performances. The results for each couple were: 0.998, 0.89 and 0.899, for the amount of milk; 0.996, 0.907 and 0.919, for the amount of fat in milk and 0.998, 0.89 and 0.897, for the amount of protein in milk. For prolificacy, the rank correlation values were 0.953, 0.837 and 0.912. These results show that the highest agreement was achieved between the BLUP and BLP methods.*

*Key words: BLP method, BLUP methodology, breeding values, prediction, selection.*

## INTRODUCTION

By 2050, global demand for animal-based food products is expected to increase by 70%. Meeting this demand while minimizing environmental impact would necessitate the use of innovative technologies and strategies for improving animal genetic quality (Georges et al., 2019). The selection index is a mechanism for determining an animal's breeding value by collecting all relevant information on the animal and its relatives. It provides the most accurate linear estimate of an individual breeding value. When records are available from various sources, such as records on the animal, its dam, half sibs, progeny, and so on, it is obviously preferable to use all records to estimate the breeding value (Endris, 2020). Knowing the genetic correlations (rg) and heritability ($h^2$) of the variables included in the breeding aim and selection index is necessary for breeding value estimation (Scholtens, 2016). Selection is an important aspect of animal breeding and is usually done on the basis of a collection of qualities, each of which is distinguished by its breeding value and economic value. As a result, a recalculation of the economic importance of profit-related traits in sheep is required for the adaptation of the enterprises' breeding objectives based on their economic importance (Slavova, 2022). Genetic improvement is a fundamental means of boosting livestock productivity, and to attain genetic benefits, well-designed animal genetic improvement schemes are required (Haileselassie et al., 2022). The accepted method for genetic evaluation is best linear unbiased prediction (BLUP) applied to an animal model. It has the advantage that all available information is optimally considered, and selection or special mating has little to no impact on the judgement. Due to the relatively low number of offspring produced by natural mating in dairy sheep, information from other relatives is even more crucial in this operation

(Grosu & Rotar, 2015). Best Linear Prediction (BLP) is a technique for calculating breeding values based on linear models, it is a fundamental strategy that takes into account individual relationships (descent) and phenotypic information (Mueller et al., 2021). Animals with higher estimated breeding value are expected to produce offspring with more desirable traits because their breeding values indicate their genetic potential to transmit those traits, by selecting animals with higher estimated breeding value as parents, breeders aim to increase the frequency of desired genes in the population, leading to improvements in overall trait expression (Khatib, 2015). The breeding value as a ratio to the population mean provides an assessment of the animal's performance position in relation to the population mean from which it is drawn; the breeding value given in relation to the population mean provides a measure of the animal's genetic potential (Liu et al., 2023). The selection index is a technique for calculating the breeding value of an animal that incorporates all data about the animal and its relatives. It is the most accurate linear prediction for a single improvement value. Using all available records - i.e. information about the animal, mother, half-siblings, offspring, etc. will undoubtedly be the most advantageous approach for estimating the breeding value of the specimen (Endris, 2020). Estimates of heritability can be used to create selection indices, predict genetic response to selection, and assess how much an individual's own phenotype can be depended on for selection. Heritability estimations for multiple economic features are required for effective cattle operations (Lalit et al., 2016). Estimates of a trait's heritability vary between breeds of sheep and alter gradually over time; animal performance data and pedigree data used to detect genetic linkages between those animals are used to evaluate heredity. Heritability is used to calculate genetic evaluations, anticipate response to selection, and assist producers in determining whether it is more effective to increase qualities through management or selection. Heritability also helps explain how genes influence trait expression (Sutera, 2018). The objective of the paper is the comparative analysis of three selection methods, from the point of view of breeding value, for production and reproduction characters in the Palas Milk Line sheep population. The three selection methods are represented by: selection based on own performance, selection based on the BLP method (Selection Indices) and selection based on the BLUP - Individual Animal Model methodology. The study focuses on the evaluation of two groups of characters in the analyzed herd Milk production, expressed by the amount of milk, milk fat and protein, and reproductive characteristics, especially prolificacy.

## MATERIALS AND METHODS

The study focuses on the evaluation of two groups of traits in the analyzed herd Milk production, expressed by the amount of milk, milk fat and protein, and reproductive traits, especially prolificacy. In the study carried out, 486 sheep from the Palas Milk Line were analyzed. The heritabilities used in calculating the breeding values were estimated by the REML method, using an animal model for the four traits analyzed. The three selection methods are represented by: selection based on own performance, selection based on the BLP method (Selection Indices) and selection based on the BLUP - Individual Animal Model methodology. The comparison of the three listed methods was carried out by means of the Spearman rank correlation, which allows the comparison of the ranking of the same observation units (individuals), on different criteria (different selection methods). This correlation study was conducted between the following pairs of methods: (BLUP and BLP), (BLUP and own performances) (BLP and own performances).

**Statistical analysis:** The data were analyzed with animal model with R software [1, 2]. The model for trait "i" is as follows:

$$P_i = X_i b_i + Z_1 a_i + e_i$$

For two traits, Mixed Model Equations of BLUP can be written as follows:

$$= \begin{bmatrix} X_1' \cdot r^{11} \cdot P_1 + X_1' \cdot r^{12} \cdot P_2 \\ X_2' \cdot r^{21} \cdot P_1 + X_2' \cdot r^{22} \cdot P_2 \\ Z_1' \cdot r^{11} \cdot P_1 + Z_1' \cdot r^{12} \cdot P_2 \\ Z_2' \cdot r^{21} \cdot P_1 + Z_2' \cdot r^{22} \cdot P_2 \end{bmatrix}$$

G and R are variances and covariances matrices for genotypic and environmental effects:

$$G^{-1} = \begin{bmatrix} \sigma_{a1}^2 & \sigma_{a12} \\ \sigma_{a21} & \sigma_{a2}^2 \end{bmatrix}^{-1} = \begin{bmatrix} g^{11} & g^{12} \\ g^{21} & g^{22} \end{bmatrix};$$

$$R^{-1} = \begin{bmatrix} \sigma_{e1}^2 & \sigma_{e12} \\ \sigma_{e21} & \sigma_{e2}^2 \end{bmatrix}^{-1} = \begin{bmatrix} r^{11} & r^{12} \\ r^{21} & r^{22} \end{bmatrix}$$

The elements of G and R were estimated using the formulas:

$$\sigma_{a\,ii}^2 = \frac{\hat{a}_i' \cdot A^{-1} \cdot \hat{a}_i + tr(A^{-1} \cdot C_{ii})}{q}$$

$$\sigma_{a\,jj}^2 = \frac{\hat{a}_j' \cdot A^{-1} \cdot \hat{a}_j + tr(A^{-1} \cdot C_{jj})}{q}$$

$$\sigma_{a\,ij} = \frac{\hat{a}_i' \cdot A^{-1} \cdot \hat{a}_j + tr(A^{-1} \cdot C_{ij})}{q}$$

$$\sigma_{e\,ii}^2 = \frac{\hat{e}_i' \cdot \hat{e}_i + tr(B_{ii})}{n}$$

$$\sigma_{e\,ij} = \frac{\hat{e}_i' \cdot \hat{e}_j + tr(B_{ij})}{n}$$

$$\sigma_{e\,jj}^2 = \frac{\hat{e}_j' \cdot \hat{e}_j + tr(B_{jj})}{n}$$

$\sigma_{a\,ij}$ = additive covariance between trait "i" and "j"

$\sigma_{e\,ii}^2$ = environmental variance for trait "i",

$\sigma_{e\,ij}$ = environmental covariance between trait "i" and "j"

$$W = [X_1 \oplus X_2 \quad Z_1 \oplus Z_2];$$

$$B = W \cdot C \cdot W' = \begin{bmatrix} B_{ii} & B_{ij} \\ B_{ji} & B_{jj} \end{bmatrix};$$

$\oplus$ = Direct sum (S.R. Searle, 1982)

$$e_i = P_i - W \cdot [\tilde{b}_1 \quad \tilde{b}_2 \quad \hat{a}_1 \quad \hat{a}_2]$$

For the trait "i", the heritability was obtained as the ratio between the additive genetic variance and the total phenotypic variance ($\sigma_f^2$), according to the formula:

$$h_{ii}^2 = \frac{\sigma_{\hat{a}\,ii}^2}{(\sigma_{\hat{a}\,ii}^2 + \sigma_{e\,ii}^2)}$$

Genetic correlation according to the formula:

$$rg_{ij} = \frac{\sigma_{aij}}{\sqrt{\sigma_{ii}^2 * \sigma_{jj}^2}}$$

Spearman's rank correlation coefficient according to the formula:

$$rs = 1 - \frac{6\Sigma d_i^2}{n(n^2 - 1)}$$

Where: n - rank number; d - the difference between the rank occupied by the same animal (candidate to selection), in two rankings based on different criteria (different biometric models).

## RESULTS AND DISCUSSIONS

Taking into account the all information disponible, the heritabilities and genetic correlations between each pair of traits, have obtained (Table 1):

Table 1. The heritability (on diagonal) and genetic correlations (above the diagonal) between the four traits analized

| Traits | Amount of Milk | Milk Fat | Milk Protein | Prolificacy |
|---|---|---|---|---|
| Amount of Milk | **0.197** ± 0.263 | 0.836 ± 0.284 | 0.441 ± 0.757 | 0.473 ± 0.731 |
| Milk Fat | | **0.209** ± 0.278 | 0.325 ± 0.839 | 0.451 ± 0.749 |
| Milk Protein | | | **0.263** ± 0.347 | 0.149 ± 0.915 |
| Prolificacy | | | | **0.235** ± 0.311 |

## Heritabilities

On the diagonal of Table 1, we can find the heritabilities and their errors ($h^2 \pm$ s.e) for each trait analized (amount of milk, milk fat, milk protein, and prolificacy), used in calculating the breeding values and were the following: 0.197 ± 0.263, 0.209 ± 0.278, 0.263 ± 0.347 and 0.235 ± 0.311, highlighting the fact that these traits have an intermediate genetic determinism. Many studies have been conducted on calculating genetic parameters for four traits, especially heritability. Shihab et al. (2022) found that the heritability rate in Awassi sheep was 0.19, which is a percentage near to what we

found in Palas sheep. Another study on local sheep in Iraq estimated heritability for daily milk production was high 0.22 (Raoof & Khidhir, 2023). In Valle del Belice dairy sheep from Italy, heritability estimates for milk production was low 0.15 (Sutera et al., 2021). Genetic-parameter estimation of milk yield in White Maritza sheep, heritability estimates was between 0.35-0.34 (Zhelyazkova et al., 2023). The heritability estimates for milk production traits (milk yield, - fat yield and protein yield) were 0.24, 0.21 and 0.22 respective in dairy sheep (Mucha et al., 2022). The heritabilities of daily milk yield (kg), fat content (%), and protein content (%) were low 0.09, 0.03, and 0.06, respectively, on dairy traits in Istrian sheep (Špehar et al., 2022). In a previous study heritability estimates for milk yield, fat yield and protein yield were low and ranged between 0.060, 0.065 and 0.067 with standard error ranging from 0.037, 0.039 and 0.037 respectively, in Valle del Belice dairy sheep (Sutera, 2018). Genetic parameter estimation to milk yield and fat and protein yield in dairy herds of southern Chile, estimated heritability for milk yield, and fat and protein were 0.16±0.004, 0.44±0.007 and 0.42±0.006, respectively (Uribe Muñoz et al., 2017). Genetic parameter estimates for composite reproductive traits in Baluchi sheep. the heritability for prolificacy was 0.22 (Esmaeili-Fard et al., 2021). The heritability for prolificacy was 0.12 when evaluating genetic parameters in Xinggao sheep (Liu et al., 2023). In another study to estimate heritability in sheep, the percentage was moderate and amounted to 0.23 (Pascal et al., 2019). Estimates of heritability for number of lambs born per ewe lambing was lowly heritable (0.07), and for milk yield, fat yield and protein yield were all moderately heritable (0.32, 0.26 and 0.30) (Murphy, & Thomas, 2016). In another study the heritability for the number of born lambs was low (0.01) (Pelmuş et al., 2019). The heritability estimates for prolificacy traits was low 0.08 traits in Afshari sheep breed (Pourtahmasebian Ahrabi et al., 2021). Scholtens (2016) estimated of heritability values for milk yield, fat yield, protein yield and prolificacy considered in a breeding objective for dairy sheep in New Zealand were 0.25, 0.21, 0.20 and 0.13 respectively. In another study, the estimated heritabilities for milk, fat, protein

production, and prolificacy for East Friesian milk sheep were 0.15, 0.09, 0.20, and 0.04 (Hamann et al., 2004).

## Genetic correlations

On the off diagonal of table 1, there are the genetic correlations between each pair of the four analized traits, together with their errors (rg ± s.e):

Genetic correlation measures the degree to which the genetic factors influencing one trait also influence another trait, there is a strong positive genetic correlation between the amount of milk and milk fat traits. This means that the genetic factors influencing higher milk production tend to also be associated with higher milk fat content. The genetic correlation between amount of milk and milk protein is positive but weaker compared to amount of milk and milk fat. There is a positive genetic correlation between amount of milk and prolicacy, indicating that some genetic factors associated with higher milk production may also be associated with higher prolicacy (the ability to give birth to multiple offspring at once). The genetic correlation between milk fat and milk protein is positive but relatively weak. There is a positive genetic correlation between milk fat and prolicacy. The genetic correlation between milk protein and prolicacy is positive but quite weak. Genetic correlations between daily milk yield and fat content, daily milk yield and protein content were negative, and fat content and protein content were positive (-0.22, -0.27, and 0.70), respectively on dairy traits in Istrian sheep (Špehar et al., 2022). The genetic association between the amount of milk yield, fat yield, and protein yield was shown to be substantially genetically associated (0.91 to 0.96). Milk fat percentage and protein production were moderately genetically linked (0.61). Milk yield was negatively associated to fat yield and protein yield (-0.31 and -0.34, respectively). Ewe prolicacy was not significantly (> 0.67) genetically linked with milk yield or protein yield, but was slightly negatively (-0.26) correlated with milk fat (Murphy et al., 2017). According to a Eurosheep study, the genetic correlations between milk and fat and protein yields are favorable and relatively strong (between 0.77 and 0.93). Estimates of genetic correlations between milk

output and content are negative and highly variable. Correlations between fat and protein yields and their correlations contents vary according on the breed (Eurosheep, 2022). In dairy herds of southern Chile, estimated genetic correlations were -0.285 and -0.331 between milk yield and fat and protein respectively (Uribe Muñoz et al., 2017). Prolificacy was estimated to have low genetic correlations with yield traits (-0.06 to 0.05). Genetic correlation for Milk, fat, and protein yields were all moderately positively (0.91 to 0.96) in dairy sheep (Murphy & Thomas, 2016). Another study significantly positive genetic association between total prolificacy and milk production (0.16) in prolific Chios dairy sheep (Tsartsianidou et al., 2023). For New Zealand dairy sheep, estimated genetic correlations between milk yield, fat yield, protein yield, and prolificacy were taken into account in the breeding objective. Milk yield correlations with fat yield, protein yield, and prolificacy were 0.85, 0.96, and 0.06, respectively; fat yield correlations with prolificacy were 0.76 and -0.03, and protein yield correlations with prolificacy were 0.02 (Scholtens, 2016).

**Breeding values**

In the Tables 2, 3, 4 and 5 were shown the breeding values for the best 20 animals from sheep population for amount of milk, milk fat, milk protein, and prolificacy, for three selection methods.

Breeding values for amount of fat is presented in Table 3.

Breeding values for amount of protein is evaluated in Table 4.

Breeding values for prolificacy in presented in Table 5.

Table 2. Breeding values for the best 20 animals from sheep population for amount of milk

| Animal | BV-BLUP | Rank-BLUP | BV-BLP | Rank-BLP | BV-OP | Rank-OP |
|--------|---------|-----------|--------|----------|-------|---------|
| 453 | 26.09 | 1 | 25.91 | 1 | 27.60 | 1 |
| 29 | 20.75 | 2 | 20.66 | 2 | 20.66 | 3 |
| 481 | 19.59 | 3 | 19.47 | 3 | 19.47 | 5 |
| 253 | 18.01 | 4 | 18.07 | 4 | 16.08 | 8 |
| 370 | 16.66 | 5 | 16.38 | 5 | 15.78 | 9 |
| 139 | 16.40 | 6 | 16.09 | 6 | 15.39 | 11 |
| 335 | 16.26 | 7 | 15.81 | 7 | 13.37 | 21 |
| 340 | 15.30 | 8 | 15.09 | 8 | 15.57 | 10 |
| 221 | 15.20 | 9 | 15.01 | 9 | 11.95 | 31 |
| 452 | 14.73 | 10 | 14.41 | 11 | 21.96 | 2 |
| 31 | 14.50 | 11 | 14.27 | 12 | 9.64 | 53 |
| 258 | 14.38 | 12 | 14.46 | 10 | 13.61 | 16 |
| 99 | 14.00 | 13 | 13.70 | 14 | 12.19 | 30 |
| 350 | 13.89 | 14 | 13.78 | 13 | 13.58 | 18 |
| 25 | 13.83 | 15 | 13.65 | 15 | 20.07 | 4 |
| 445 | 13.70 | 16 | 13.45 | 16 | 9.07 | 57 |
| 23 | 13.46 | 17 | 13.20 | 17 | 11.53 | 32 |
| 32 | 13.30 | 18 | 13.11 | 18 | 7.32 | 77 |
| 321 | 13.14 | 19 | 12.72 | 20 | 10.61 | 43 |
| 298 | 12.90 | 20 | 12.45 | 21 | 10.78 | 38 |

Table 3. Breeding values for the best 20 animals from sheep population for amount of fat

| ANIMAL | BV-BLUP | Rank-BLUP | BV-BLP | Rank-BLP | BV-OP | Rank-OP |
|--------|---------|-----------|--------|----------|-------|---------|
| 453 | 5.07 | 1 | 5.00 | 1 | 5.80 | 1 |
| 481 | 4.78 | 2 | 4.72 | 2 | 4.72 | 2 |
| 29 | 3.86 | 3 | 3.84 | 3 | 3.84 | 4 |
| 221 | 3.62 | 4 | 3.51 | 4 | 2.95 | 20 |
| 335 | 3.46 | 5 | 3.33 | 5 | 3.39 | 14 |
| 340 | 3.31 | 6 | 3.23 | 7 | 3.48 | 8 |
| 350 | 3.29 | 7 | 3.30 | 6 | 3.08 | 18 |
| 25 | 3.14 | 8 | 3.10 | 8 | 4.28 | 3 |
| 211 | 3.10 | 9 | 3.07 | 9 | 2.36 | 36 |
| 370 | 3.07 | 10 | 2.86 | 13 | 2.86 | 21 |

| ANIMAL | BV-BLUP | Rank-BLUP | BV-BLP | Rank-BLP | BV-OP | Rank-OP |
|--------|---------|-----------|--------|----------|-------|---------|
| 357 | 3.05 | 11 | 2.96 | 11 | 2.56 | 27 |
| 362 | 2.99 | 12 | 3.06 | 10 | 3.26 | 16 |
| 446 | 2.91 | 13 | 2.83 | 14 | 3.07 | 19 |
| 132 | 2.80 | 14 | 2.90 | 12 | 3.40 | 11 |
| 32 | 2.71 | 15 | 2.67 | 15 | 2.08 | 46 |
| 81 | 2.62 | 16 | 2.56 | 18 | 3.67 | 6 |
| 253 | 2.53 | 17 | 2.56 | 19 | 2.47 | 29 |
| 127 | 2.49 | 18 | 2.41 | 21 | 3.37 | 15 |
| 369 | 2.43 | 19 | 2.60 | 16 | 3.47 | 9 |
| 139 | 2.36 | 20 | 2.28 | 26 | 2.37 | 34 |

Table 4. Breeding values for the best 20 animals from sheep population for amount of protein

| ANIMAL | BV-BLUP | Rank-BLUP | BV-BLP | Rank-BLP | BV-OP | Rank-OP |
|--------|---------|-----------|--------|----------|-------|---------|
| 139 | 3.05 | 1 | 3.03 | 1 | 3.19 | 1 |
| 298 | 3.02 | 2 | 2.93 | 2 | 3.14 | 2 |
| 321 | 2.95 | 3 | 2.87 | 3 | 2.56 | 6 |
| 394 | 2.62 | 4 | 2.68 | 4 | 2.58 | 5 |
| 168 | 2.55 | 5 | 2.56 | 5 | 2.31 | 9 |
| 482 | 2.20 | 6 | 2.22 | 6 | 2.52 | 7 |
| 388 | 1.98 | 7 | 2.05 | 7 | 1.73 | 15 |
| 370 | 1.93 | 8 | 1.95 | 8 | 2.13 | 11 |
| 25 | 1.91 | 9 | 1.90 | 9 | 2.71 | 4 |
| 312 | 1.87 | 10 | 1.79 | 12 | 1.12 | 47 |
| 212 | 1.86 | 11 | 1.87 | 10 | 1.87 | 14 |
| 423 | 1.77 | 12 | 1.85 | 11 | 2.75 | 3 |
| 178 | 1.72 | 13 | 1.74 | 13 | 1.72 | 16 |
| 284 | 1.69 | 14 | 1.70 | 15 | 1.70 | 18 |
| 481 | 1.68 | 15 | 1.70 | 16 | 1.70 | 19 |
| 395 | 1.67 | 16 | 1.73 | 14 | 2.19 | 10 |
| 241 | 1.63 | 17 | 1.63 | 18 | 1.63 | 23 |
| 69 | 1.60 | 18 | 1.59 | 19 | 1.37 | 31 |
| 393 | 1.58 | 19 | 1.66 | 17 | 2.49 | 8 |
| 51 | 1.53 | 20 | 1.52 | 21 | 1.29 | 34 |

Table 5. Breeding values for the best 20 animals from sheep population for prolificacy

| ANIMAL | BV-BLUP | Rank-BLUP | BV-BLP | Rank-BLP | BV-OP | Rank-OP |
|--------|---------|-----------|--------|----------|-------|---------|
| 221 | 0.2603 | 1 | 0.2615 | 1 | 0.2016 | 10 |
| 219 | 0.2533 | 2 | 0.2542 | 2 | 0.2038 | 7 |
| 253 | 0.2510 | 3 | 0.2524 | 3 | 0.2014 | 11 |
| 31 | 0.2352 | 4 | 0.2320 | 5 | 0.1923 | 14 |
| 211 | 0.2350 | 5 | 0.2363 | 4 | 0.1681 | 38 |
| 235 | 0.2350 | 6 | 0.2363 | 4 | 0.1681 | 38 |
| 362 | 0.2216 | 7 | 0.2179 | 6 | 0.1791 | 24 |
| 271 | 0.2122 | 8 | 0.2134 | 7 | 0.2134 | 5 |
| 284 | 0.2122 | 8 | 0.2134 | 7 | 0.2134 | 5 |
| 32 | 0.2107 | 9 | 0.2078 | 8 | 0.1440 | 65 |
| 81 | 0.2049 | 10 | 0.2004 | 10 | 0.2021 | 9 |
| 327 | 0.2032 | 11 | 0.1968 | 13 | 0.1856 | 17 |
| 168 | 0.1988 | 12 | 0.2019 | 9 | 0.1729 | 30 |
| 249 | 0.1972 | 13 | 0.1982 | 11 | 0.2211 | 1 |
| 140 | 0.1960 | 14 | 0.1957 | 14 | 0.1225 | 82 |
| 258 | 0.1955 | 15 | 0.1971 | 12 | 0.2184 | 3 |
| 53 | 0.1932 | 16 | 0.1893 | 16 | 0.1497 | 56 |
| 88 | 0.1932 | 16 | 0.1893 | 16 | 0.1497 | 56 |
| 199 | 0.1897 | 17 | 0.1909 | 15 | 0.1762 | 27 |
| 365 | 0.1851 | 18 | 0.1616 | 27 | 0.1041 | 87 |

In the Tables 2, 3, 4 and 5 were shown the breeding values for the best 20 animals from sheep population for amount of milk, amount of fat, amount of protein, and prolificacy, for three selection methods, from the point of view of breeding value, selection based on the BLUP - Individual Animal Model methodology, selection based on the BLP method (Selection Indices) and selection based on own performance (OP). The breeding values of the best Palas sheep for amount of milk in our study the BLUP methodology and the BLP method and own performance, ranged from 12.90 to 26.09 , 12.45 to 25.91 and 10.78 to 27.60 kg, respectively for fat ranged from 2.36 to 5.07, 2.28 to 5.00 and 2.37 to 5.80 kg, for milk protein ranged from 1.53 to 3.05, 1.52 to 3.03 and 1.29 to 3.19 kg, and for prolificacy ranged from 0.1851 to 0.2603, 0.1616 to 0.2615 and 0.1041 to 0.2016 kg respectively. Popa et al. (2020) found that the average estimate breeding value for daily milk yield (kg) for the best 18 Teleorman Black Head Sheep were ranged between 14.57 and 28.48 kg. In another study the breeding value of the best 10 Teleorman Black sheep for the number of born lambs ranged from 0.013 to 0.022 (Pelmuş et al., 2019). Based on the Best Linear Unbiased Prediction value, breeding values for Karadi ewes for daily milk supply, protein, and fat percentages varied from -10.5293 to 10.7504, -2.0546 to 2.0097%, and -1.7033 to 1.4067%, respectively (Hama Khan et al., 2019). In another study estimated breeding values and selection index for milk yield, fat yield, protein yield and prolificacy of the top 20 dairy ewes of the Gunson's dairy sheep flock were (-10.78 to 16.4 kg, -0.35 to 0.82 kg, -0.24 to 0.74 and -0.15 and +0.30 lambs) respectively and significantly (P < 0.05) these values are lower than the values we found in our study (Sutera, 2018). Breeding values have been recorded, the breeding value of the first 19 ewes for milk production ranged from 70 to 86 kg (Buzu, 2016).

**Spearman Rank Correlation**
Spearman Rank Correlation between couples: (BLUP and BLP), (BLUP and own performances), (BLP and own performances) for the amount of milk, milk fat, protein, and prolificacy (Table 6).

Table 6. The Spearman Rank Correlation between the three methods

| Traits | BLUP and BLP | BLUP and Own Performances | BLP and Own Performances |
|---|---|---|---|
| Amount of Milk | 0.998 | 0.89 | 0.899 |
| Milk Fat | 0.996 | 0.907 | 0.919 |
| Milk Protein | 0.998 | 0.89 | 0.897 |
| Prolificacy | 0.953 | 0.837 | 0.912 |

Table 6 shows rank correlations (Spearman) between the following pairs of methods: (BLUP and BLP), (BLUP and own performances), (BLP and own performances). The results obtained, in the order of the method couples, were the following: 0.998, 0.89 and 0.899, for the amount of milk; 0.996, 0.907 and 0.919, for the amount of fat in milk and 0.998, 0.89 and 0.897, for the amount of protein in milk. For prolificacy, the rank correlation values were 0.953, 0.837 and 0.912. These results show that there is a high degree of concordance between the three selection methods, suggesting that any of the three methods can be used for selection candidates. Also, for each individual trait, the highest agreement was achieved between the BLUP and BLP methods (0.998, 0.996, 0.998 and 0.953), which can be explained by the proximity between the two calculation methods,
from the point of view of the calculation methodology.

**CONCLUSIONS**

Heritability plays a pivotal role in predicting breeding values and advancing genetic progress. Understanding the heritability and genetic correlations of the traits under consideration in the breeding objective and selection index is crucial for accurate breeding value estimation. Heritability estimates for the four examined traits were determined using the REML method within an animal model. These estimates were as follows: $0.197 \pm 0.263$, $0.209 \pm 0.278$, $0.263 \pm 0.347$ and $0.235 \pm 0.311$. These findings emphasize that these traits exhibit an intermediate level of genetic determinism. Genetic correlations between milk components

and prolificacy to be positive and significant, which may have important implications in the selection of animals for genetic improvement.

By conducting selection for sheep using three distinct approaches and subsequently comparing them-namely, selection based on individual performance, selection based on the Best Linear Unbiased Prediction (BLP) method (Selection Indices), and selection based on the BLUP - Individual Animal Model methodology-we observed a high degree of agreement among the three selection methods. This suggests that any of these three methods could be effectively employed for candidate selection, the breeding goal should be to improve milk performance, particularly milk quality, taking into account prolificacy.as indicated by the strong Spearman's rank correlation between the pairs identified in this study.

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