OPTIMIZATION OF THE SELECTION PLAN, FOR PRODUCTION AND REPRODUCTION TRAITS, IN THE MILK-PALAS SHEEP POPULATION

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Abstract

The purpose of this study is to optimize the selection plan for production and reproduction traits in the milk-Palas sheep population totally 486 sheep. The selection criterion is represented by an estimate of the global breeding value, calculated based on the BLP method. Among the four traits considered in terms of economic weights, the most important in the selection turned out to be prolificacy (55%), followed by the amount of milk (24%), the amount of fat (12%) and the amount of protein (9%). The greatest genetic progress per generation was obtained in the case of variant 5 (Milk + Fat + Protein + Prolificacy), the genetic gain being 7.6623 kg milk and of 0.0407 lambs/calving. Compared to the control variant (1), the total genetic gain increased by 102.8%. The next variant is variant 2 (Milk + Fat + Prolificacy), which practically ensures a genetic gain similar to variant 5, namely 102.7%. This result is explained by a higher genetic correlation between the amount of milk and the amount of fat (0.836) compared to the value of the correlation between the amount of milk and the amount of protein (0.441).

Key words: correlation, fat, milk, production and reproduction traits, prolificacy, protein, selection indices.

INTRODUCTION

Sheep are among the most economically significant animals since they provide human society with necessities including meat, milk, wool, and fur (Gebreselassie et al., 2019). One of the main ways to increase livestock output is through genetic improvement, and in order to reap the genetic benefits, carefully thought out animal genetic improvement programmes are required (Villalba et al., 2019). Livestock genetic improvement is a particularly effective way to increase output, it entails determining the breeding objectives, calculating the traits' economic values, creating suitable schemes that define the population structure, gene flow, and selection tactics, as well as creating and carrying out the breeding plan (Gizaw et al., 2014). The effectiveness of a breeding programme in terms of realised genetic advancement and inbreeding rate is dictated by flock size, which is likely to vary across the breeding tract of a breed that is being improved, to increase the overall productivity of sheep, it is crucial to investigate alternative breeding techniques. Both the short-term (high rate of genetic gain) and long-term (preservation of genetic variety and avoidance of inbreeding depression) effects of selection

decisions must be considered in order to optimise breeding strategies (Fimland, 2007). With the correct index trait weights, indexes can be simply generated as measurements become available on site, and selection can be performed promptly. The application of selection indexes would be a simple expeditious approach for efficient selection that would not delay farmer's animal sale chances, requiring only a little amount of support from extension officers or regional personnel (Mueller et al., 2021). Genetic parameter estimation is used to determine the selection criterion and future breeding strategies, as well as to enable the efficient prediction of breeding value and selection procedures, it can serve as the foundation for any sound livestock improvement programme (Alemayehu, 2022). Both genetic and economic factors must be considered when evaluating the effectiveness of the selection strategy. These factors must be optimally integrated to guarantee that the chosen variant maximises genetic gain while requiring the least amount of time, money, or effort (Popa et al., 2011). A method for determining an animal's breeding value that takes into account all of the information about the animal and its ancestors is called the selection index. It is the

linear forecast with the highest accuracy for a single improvement value, employing all accessible records - that is, details about the animal, mother, half-siblings, progeny, etc. - will surely be the most beneficial method for determining the specimen's breeding value (Endris, 2020). Heritability estimates are useful in predicting genetic responses to selection, generating selection indices, and determining the degree to which an individual's phenotype may be relied upon for selection. Effective cattle operations require heritability estimates for several economic characteristic

cs (Lalit et al., 2016).

The purpose of the research is to optimize the selection plan for production and reproduction traits in the milk-Palas sheep population.

In the first phase, being partial results, the selection criterion was optimized by considering several selection indices, based on 2, 3 and 4 traits. The optimal variant of the selection criterion is represented by the index that maximizes genetic progress per generation.

MATERIALS AND METHODS

The study was carried out on the basis of the production and reproduction performances of a number of 486 sheep from the Palas milk Line.The three production traits (amount of milk, amount of milk fat and amount of milk protein) and the one reproduction trait (prolificacy) were analysed.

In order to optimize the selection criteria, as work steps, the following activities were carried out:

1. Estimation of genetic parameters (heritability, genetic and phenotypic correlations between traits).
2. Estimation of the economic weights of the traits.
3. Estimation of genetic progress per generation. The genetic parameters were obtained by the REML method, for several traits.

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:

$$\begin{bmatrix} X_1' \cdot r^{11} \cdot X_1 & X_1' \cdot r^{12} \cdot X_2 & X_1' \cdot r^{11} \cdot Z_1 & X_1' \cdot r^{12} \cdot Z_2 \\ X_2' \cdot r^{21} \cdot X_1 & X_2' \cdot r^{22} \cdot X_2 & X_2' \cdot r^{21} \cdot Z_1 & X_2' \cdot r^{22} \cdot Z_2 \\ Z_1' \cdot r^{11} \cdot X_1 & Z_1' \cdot r^{12} \cdot X_2 & Z_1' \cdot r^{11} \cdot Z_1 + A^{-1} \cdot g^{11} & Z_1' \cdot r^{12} \cdot Z_2 + A^{-1} \cdot g^{12} \\ Z_2' \cdot r^{11} \cdot X_1 & Z_2' \cdot r^{21} \cdot X_2 & Z_2' \cdot r^{21} \cdot Z_1 + A^{-1} \cdot g^{21} & Z_2' \cdot r^{22} \cdot Z_2 + A^{-1} \cdot g^{22} \end{bmatrix} \cdot \begin{bmatrix} \hat{b}_1 \\ \hat{b}_2 \\ \hat{a}_1 \\ \hat{a}_2 \end{bmatrix}$$

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

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"

$$W = \begin{bmatrix} X_1 \oplus X_2 & Z_1 \oplus Z_2 \end{bmatrix};$$

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

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

$$e_i = P_i - W \cdot \begin{bmatrix} \tilde{b}_1 & \tilde{b}_2 & \hat{a}_1 & \hat{a}_2 \end{bmatrix}$$

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

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

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).

For estimation of the weight of the characters in the selection objective according to the formula:

$$\begin{bmatrix} h_1 & h_2 \cdot r_{G12} & h_3 \cdot r_{G13} & h_4 \cdot r_{G14} \\ h_2 \cdot r_{G12} & h_2 & h_3 \cdot r_{G23} & h_4 \cdot r_{G24} \\ h_3 \cdot r_{G13} & h_3 \cdot r_{G23} & h_3 & h_4 \cdot r_{G34} \\ h_4 \cdot r_{G14} & h_4 \cdot r_{G24} & h_4 \cdot r_{G34} & h_4 \end{bmatrix} \cdot \begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_4 \end{bmatrix} = \begin{bmatrix} d_1 \\ d_2 \\ d_3 \\ d_4 \end{bmatrix}$$

$h_i = \sqrt{h_i^2}$ = heritability of trait i,

r_{Gij} = genetic correlation between traits i and j,

d_i = standardized genetic distance for trait i,

$d_i = (\overline{P}_P - \mu_{Act})/\sigma_{Ai}$,

$\overline{P}_P$ = average trait performance, in perspective, μ_{Act} = current population mean,

σ_{Ai} = genetic standard deviation of trait i.

The technical coefficients are obtained by standardizing the partial regression coefficients, to bring all traits to the same denominator, according to the formula:

$$v_i = \frac{\beta}{K \cdot \sigma_{Aij}}$$

$K = \sqrt{\beta^T \cdot r_P \cdot \beta}$ = variance of the regression coefficients; = matrix of phenotypic correlation coefficients between traits.

By relating the value of each technical coefficient to their sum, the relative weight of the four traits is obtained.

The significance of the values of the relative coefficients shows us the importance that must be assigned to each trait in the selection process.

For estimation of genetic progress per generation according to the equations:

$$H = v_1 \cdot A_1 + v_2 \cdot A_2 + ,..., + v_m \cdot A_m$$

$$I = b_1 \cdot P_1 + b_2 \cdot P_2 + ,..., + b_n \cdot P_n$$

$$\begin{bmatrix} V_{P_1} & Cov(P_1,P_2) & ... & Cov(P_1,P_n) \\ Cov(P_2,P_1) & V_{P_2} & ... & Cov(P_2,P_n) \\ ... & ... & ... & ... \\ Cov(P_n,P_1) & Cov(P_n,P_2) & ... & V_{P_n} \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \end{bmatrix} = \begin{bmatrix} V_{A1} & Cov(A_1,A_2) & ... & Cov(A_1,A_n) \\ Cov(A_2,A_1) & V_{A2} & ... & Cov(A_2,A_n) \\ ... & ... & ... & ... \\ Cov(A_n,A_1) & Cov(A_n,A_2) & ... & V_{An} \end{bmatrix} \begin{bmatrix} v_1 \\ v_2 \\ v_3 \\ v_4 \end{bmatrix}$$

$$b = v' \cdot C' \cdot V^{-1}$$

$$r_{HI} = \sqrt{\frac{S_I^2}{S_H^2}} = \sqrt{\frac{b' \cdot C \cdot b}{v' \cdot G \cdot v}}$$

$$\Delta H = r_{IH} \cdot i \cdot \sigma_H$$

$$\Delta G_i = \frac{b_i \cdot C}{\sigma_I}$$

RESULTS AND DISCUSSIONS

Table 1 shows the population's mean amount of milk produced is 104.22 kg, with a relatively small standard deviation of 1.87 kg, indicating that the values are closely clustered around the mean.

The coefficient of variation (CV) is 41.15%, suggesting moderate variability in milk production across individuals. The observed range spans from 16 kg to 261 kg, showcasing significant variability in milk production among the population. And the population's mean amount of fat produced is 7.22 kg, with a low standard deviation of 0.14 kg, indicating a relatively tight distribution around the mean value. The coefficient of variation (CV) is quite low at 3.03%, suggesting low variability in fat production across individuals. The observed fat production ranges from 1 kg to 19 kg, showcasing some variability but not as wide-ranging as the amount of milk. The population's mean amount of protein produced is 5.54 kg, with a standard deviation of 0.15 kg, indicating

a relatively tight distribution around the mean value. The coefficient of variation (CV) is 3.21%, similar to fat production, suggesting low variability in protein production across individuals. The observed protein production ranges from 0.4 kg to 19 kg, showcasing variability but with a more extended range than fat production. Finally the population's mean prolificacy is 1.3, with a small standard deviation of 0.02, indicating a narrow distribution around the mean value.The coefficient of variation (CV) is 0.46, suggesting low variability in prolificacy across individuals. The observed prolificacy ranges from 1 to 2, indicating limited variation within the population for this trait.

These results are similar to what Dhaoui et al. (2019) found that the average production in D'man sheep Over the course of 78.60 ± 0.24 days of lactation, the D'man ewe produced an average of 128.91 ± 3.14 l of milk, 9.23 ± 0.26 kg of fat, and 5.26 ± 0.12 kg of total protein.

Table 1. Statistical indicators of the analyzed population

No. trait	traits	unit	n	$\overline{X} \pm s_{\overline{X}}$	S	CV %	Limit Min-Max
1	amount of milk	kg	486	104.22 ±1.87	41.15	39.48	16-261
2	amount of fat	kg	486	7.22 ± 0.14	3.03	42	1-19
3	amount of protein	kg	486	5.54 ± 0.15	3.21	58	0.4-19
4	prolificacy	nr	486	1.3 ± 0.02	0.46	35	1-2

Table 2 observed genotypic variances and covariances between traits (amount of milk amount of fat, amount of protein and prolificacy) in the sheep. These values offer insights into the genetic relationships and variability among these traits.

There's significant genotypic variance in the amount of milk compared to the other traits. The covariances between amount of milk and the other traits (amount of fat, amount of protein, and prolificacy) are relatively higher, indicating a stronger relationship between milk production and these traits.

Prolificacy shows the least genotypic variance and has relatively lower covariances with the other traits, indicating less shared genetic variability compared to the other traits.

Strong Genetic Influence on Milk Production: The high genotypic variance and substantial covariances suggest that milk production has a strong genetic basis within this population. Traits like fat production, protein production, and to a lesser extent, prolificacy, seem to share genetic influences with milk production, indicating potential interconnectedness or co-inheritance.

Table 2. Genotypic variances and covariances between traits

No. trait	traits	amount of milk	amount of fat	amount of protein	prolificacy
1	amount of milk	280.553	18.153	11.733	1.737
2	amount of fat	18.153	1.68	0.67	0.128
3	amount of protein	11.733	0.67	2.527	0.052
4	prolificacy	1.737	0.128	0.052	0.048

Table 3 provides information on phenotypic variances and covariances between different traits within a population. Phenotypic variances encompass both genetic and environmental influences on traits, so they offer a broader perspective compared to genotypic variances, which focus solely on genetic influences.

The phenotypic variance for milk production is high (1424.953), indicating substantial overall variability in milk production within the population, considering both genetic and environmental factors.

The phenotypic variance for fat production is relatively lower (8.052) compared to milk production, signifying less overall variability in fat production considering both genetic and environmental factors. This trait displays a moderate phenotypic variance (9.608), suggesting a moderate level of overall variability in protein production considering

both genetic and environmental influences. Prolificacy shows the lowest phenotypic variance (0.204) among all the traits, indicating the least overall variability within the population for this trait considering both genetic and environmental factors.

Table 3. Phenotypic variances and covariances between traits

Nr. trait	traits	amount of milk	amount of fat	amount of protein	prolificacy
1	amount of milk	1424.953	100.967	59.614	9.896
2	amount of fat	100.967	8.052	4.129	0.724
3	amount of protein	59.614	4.129	9.608	0.631
4	prolificacy	9.896	0.724	0.631	0.204

Heritabilities
The heritabilities and errors ($h2\pm$ s.e.) for the traits (amount of milk, milk fat, milk protein, and prolificacy) that were analysed and used to determine breeding values are shown on table 1's diagonal. These values are 0.197 ± 0.263, 0.209 ± 0.278, 0.263 ± 0.347, and 0.235 ± 0.311, indicating that these traits have an intermediate genetic determinism.

Heritability is one of the four variables for which genetic parameters have been calculated in a great deal of research. Shihab et al. (2022) reported that Awassi sheep had a heritability rate of 0.19, which is comparable to the percentage we found in Palas sheep. Heritability estimations for milk production in Italian dairy sheep from Valle del Belice were a low 0.15 (Sutera et al., 2021). For milk production traits in dairy sheep, the heritability estimates were 0.24, 0.21, and 0.22 for milk yield, fat yield, and protein yield, respectively (Mucha et al., 2022). According to Raoof and Khidhir's (2023) study, there was a high 0.22 heritability for daily milk output in local sheep in Iraq. In Istrian sheep, the daily milk yield (kg), fat content (kg), and protein content (kg) had low heritabilities of 0.09, 0.03, and 0.06 on dairy characteristics, respectively (Špehar et al., 2022). In dairy herds in southern Chile, genetic parameter estimation was used to estimate milk yield, fat and protein yield, and estimated heritability for milk yield, fat, and protein was 0.16 ± 0.004, 0.44 ± 0.007, and 0.42 ± 0.006, respectively (Muñoz et al., 2017). The heritability values for milk yield, fat yield, protein yield, and prolificacy that Scholtens (2016) determined were 0.25, 0.21, 0.20, and 0.13 for dairy sheep in New Zealand, respectively, and were taken into consideration in a breeding aim. According to Murphy and Thomas (2016), the number of lambs born per ewe lambing had a low heredity estimate of 0.07, whereas the milk output, fat yield, and protein yield had intermediate heritability estimates of 0.32, 0.26, and 0.30. Baluchi sheep reproductive characteristic estimations based on genetic parameters. According to Esmaeili-Fard et al. (2021) the heritability for prolificacy was 0.22. When Xinggao sheep's genetic parameters were evaluated, the heritability for prolificacy was 0.12 (Liu et al., 2023). The proportion was 0.23 in another study that estimated sheep heritability for prolificacy, which was considered moderate (Pascal et al., 2019).

Genetic correlations
The genetic correlations between each pair of the four qualities studied are shown on the off diagonal of table 1, along with their errors (rg s.e):
The degree to which genetic variables influencing one trait also influence another trait is measured by genetic correlation. For example, there is a substantial positive genetic connection between the amount of milk and milk fat qualities. This suggests that the genetic variables driving increased milk production are also connected with increased milk fat content. The genetic link between the amount of milk and the amount of milk protein is positive, but it is weaker than the genetic correlation between the amount of milk and the amount of milk fat.

There is a positive genetic association between milk production and prolificacy, indicating that some genetic variables associated with increased milk production may also be associated with higher prolificacy. The genetic relationship between milk fat and milk protein is positive but not strong. Milk fat and prolificacy have a positive genetic link. The genetic link between milk protein and procreation is positive but weak. For dairy qualities in Istrian sheep, there were genetic correlations that were negateve between daily milk yield and fat content, positive between daily milk yield and protein

content, and negative between daily milk yield and fat content (-0.22, -0.27, and 0.70), respectively (Špehar et al., 2022). It was demonstrated that there is a significant genetic correlation (0.91 to 0.96) between the yields of fat, protein, and milk. Protein synthesis and milk fat % showed a modest genetic correlation (0.61). Protein and fat yields had a negative correlation with milk yield (-0.31 and -0.34, respectively). Ewe prolificacy had a minor negative correlation (-0.26) with milk fat but no substantial genetic correlation (>0.67) with either milk yield or protein yield (Murphy et al., 2017). The genetic correlations between milk and fat and protein outputs are favourable and relatively substantial (between 0.77 and 0.93), according to a Eurosheep study. Genetic correlation estimates between milk output and content are negative and highly varied. Correlations between fat and protein yields, as well as their correlation contents, vary by breed (Eurosheep, 2022). According to Muñoz et al. (2017), the estimated genetic correlations between milk output and fat and protein in dairy herds in southern Chile were -0.285 and -0.331, respectively. Prolificacy was projected to have minimal genetic correlations with yield attributes (-0.06 to 0.05). Milk, fat, and protein yields were all somewhat positively correlated (0.91 to 0.96) in dairy sheep (Murphy & Thomas, 2016). In another study, total prolificacy and milk production (0.16) in prolific Chios dairy sheep showed a strong positive genetic connection (Tsartsianidou et al., 2023). The breeding objective for dairy sheep in New Zealand considered the estimated genetic correlations between milk yield, fat yield, protein yield, and prolificacy, the correlations between milk yield and fat yield, protein yield, and prolificacy were 0.85, 0.96, and 0.06, respectively; the correlations between fat yield and prolificacy were 0.76 and -0.03); and the correlation between protein yield and prolificacy was 0.02 (Scholtens, 2016).

Phenotypic correlations
Some phenotypic correlations have larger margins of error, indicating uncertainty in the estimation of overall relationships between certain traits. This might be due to environmental factors contributing more to these correlations or the variability within the population.

Table 4. Heritability (on the diagonal), genetic correlations (above the diagonal) and phenotypic correlations (below the diagonal) between the four analyzed traits

Nr.trait	traits	amount of milk	amount of fat	amount of protein	prolificacy
1	amount of milk	**0.197 ± 0.263**	0.836 ± 0.284	0.441 ± 0.757	0.473 ± 0.731
2	amount of fat	0.943 ± 0.015	**0.209 ± 0.278**	0.325 ± 0.839	0.451 ± 0.749
3	amount of protein	0.509 ± 0.039	0.469 ± 0.04	**0.263 ± 0.347**	0.149 ± 0.915
4	prolificacy	0.580 ± 0.037	0.565 ± 0.038	0.451 ± 0.041	**0.235 ± 0.311**

Table 5 to provide economic values associated with different traits related to milk production components and prolificacy. Among the four traits considered in terms of economic weights, the most important in the selection turned out to be prolificacy (55%), followed by the amount of milk (24%), the amount of fat (12%) and the amount of protein (9%). These values are used to quantify the economic impact or importance of each trait for estimation breeding value total and genetic progress, prolificacy could lead to higher economic gains compared to focusing solely on milk, fat, or protein production. These values are used in breeding programs, agricultural management, or decision-making processes to prioritize traits that yield higher economic returns or contribute significantly to the overall profitability.

Table 5. Economic values for milk production components and prolificacy

No. trait	traits	Economic values (%)
1	amount of milk	0.24
2	amount of fat	0.12
3	amount of protein	0.09
4	prolificacy	0.55

Table 6 shows optimization of the selection criteria in a sheep population and their impact on genetic progress, traits Considered: Milk (M), Fat (F), Protein (P), and Prolificacy (Pl).
Variant 1 (M+Pl): This is the control variant against which others are compared. It includes only milk and prolificacy traits.
Variants 2, 3, 5: These variants include milk, fat, protein, and prolificacy, resulting in similar aggregate genotype variance and accuracy index

compared to the control variant (Variant 1). They show slight improvements in total genetic progress and genetic progress for each trait.

Variant 4 (F+P+Pl): This variant excludes milk but includes fat, protein, and prolificacy. It demonstrates lower aggregate genotype variance and accuracy index compared to the control variant, leading to a decrease in total genetic progress and genetic progress for each trait.

Among the five variants of selection indices tested, the greatest genetic progress per generation was obtained in the case of variant 5 (M+F+P+Pl), with all four characters considered (the amount of milk, the amount of fat, the amount of protein and prolificacy), the genetic gain being 7.6623 kg. Milk and of 0.0407 lambs/calving. Compared to the control variant (1), the total genetic gain increased by 102.8%

Table 6. Optimization of the selection criteria in a sheep population

Nr. trait. (Var.)	Specification	Variance Index V_I	Aggregate genotype variance V_H	Accuracy Index r_{IH}	Total Genetic Progress ΔH	Genetic Progress each trait ΔG_i	Comparison (%). Variants 2,3,4,5, compared to variant 1.
1	M+Pl*	3.2780	16.6329	0.4440	1.8109·i	7.4508; 0.0414	100
2	M+F+Pl	3.4643	16.6329	0.4569	1.8612·i	7.6622; 0.0406	102,7**
3	M+P+Pl	3.2799	16.6329	0.4440	1.8110·i	7.4516; 0.0440	100
4	F+P+Pl	2.4831	16.6329	0.3863	1.5758·i	6.4544; 0.085	87
5	M+F+P+Pl	3.4644	16.6329	0.4570	1.8613·i	7.6623; 0.0407	102,8

M = milk = kg. F = fat = kg. P = protein = kg. Pl = prolificacy = the number of lambs at calving * Variant 1 = control variant
** = 102.8 = (1.8612/1.8109)*100.

The next variant in the ranking is variant 2 (M + F + Pl), which practically ensures a genetic gain similar to variant 5, namely 102.7%. This result is explained by a higher genetic correlation between the amount of milk and the amount of fat (0.836) compared to the value of the correlation between the amount of milk and the amount of protein (0.441). Correlating the economic values from Table 5 with the optimization results in Table 6 might shed light on aligning selection criteria with economic goals, maximizing profitability alongside genetic progress.

CONCLUSIONS

1. Heritability values in the investigated population were as follows: 0.197 ± 0.263, 0.209 ± 0.278, 0.263 ± 0.347 and 0.235 ± 0.311. The level of the respective values shows that these traits present an intermediate genetic determinism.

2. Of all traits pairs, milk quantity and fat quantity are the most highly correlated, both genetically (0.836) and phenotypically (0.943).

3. Among the four traits considered, the most important in the selection turned out to be prolificacy (55%), followed by the amount of milk (24%), the amount of fat (12%) and the amount of protein (9%).

4. Among the five variants of selection indices tested, the greatest genetic progress per generation was obtained in the case of variant 5 (M + F + P + Pl), with all four traits considered (the amount of milk, the amount of fat, the amount of protein and prolificacy), the genetic gain being 7.6623 kg. Milk and of 0.0407 lambs/calving. Compared to the control variant (1), the total genetic gain increased by 102.8%

5. The next variant in the ranking is variant 2 (M + F + Pl), which practically ensures a genetic gain similar to variant 5, namely 102.7%. This result is explained by a higher genetic correlation between the amount of milk and the amount of fat (0.836) compared to the value of the correlation between the amount of milk and the amount of protein (0.441).

As a general recommendation, it can be proposed for the practice of sheep selection, in the analyzed population, the selection based on a criterion that includes three characters: The amount of milk, the amount of fat and prolificacy. Future studies might benefit from more precise data collection, increased sample sizes, or alternative statistical methodologies to refine and validate the findings for robust decision-making.

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