

PHENOTYPIC VARIATION, BODY CONFORMATION, AND RELATIONSHIPS BETWEEN BIOMETRIC TRAITS AND LIVE WEIGHT IN YOUNG SHEEP FROM THREE GENETIC COMBINATIONS

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Abstract

The study evaluated phenotypic variation and body conformation in young sheep obtained by crossing Tigaie ewes with rams of French meat breeds, namely Berrichon du Cher (BC×TI), Blanche du Massif Central (BMC×TI), and Vandein (V×TI). To characterize body development, trunk length, withers height, rump height, chest circumference, cannon circumference, trunk depth, and live weight were measured. Descriptive statistics, factorial ANOVA with the effects of genetic group, sex, and genetic group × sex interaction, Pearson correlations, conformation indices, principal component analysis, and multiple regression were used. Differences among genetic combinations were detected for withers height, cannon circumference, trunk depth, and live weight. Live weight showed the strongest correlations with trunk length ($r=0.826$; $p<0.001$) and trunk depth ($r=0.763$; $p<0.001$). The multiple regression model based on trunk length, chest circumference, and trunk depth explained 75.65% of the variation in live weight ($R^2=0.7565$). The results describe phenotypic differentiation at the age of evaluation and were not used to estimate heterosis because the available values for the parental breeds were obtained from adult animals.

Key words: sheep; young stock; body conformation; biometry; live weight; PCA; regression

INTRODUCTION

Research in the field of animal science is significant and essential, as it aims to develop new animal populations with traits, properties, and characteristics that render them more productive, more resilient, and more cost-effective to maintain [1].

Crossbreeding is a method used to combine traits from different populations; however, interpreting differences among the resulting offspring requires consideration of age, sex, rearing conditions, and group structure [2,3,4].

Under these conditions, the differences between the offspring resulting from

crosses must be evaluated objectively, taking into account age group, sex, rearing conditions, and flock structure [5,6,7].

For new animal populations, characterization of body dimensions provides useful information on skeletal development, trunk conformation, and body mass. Body measurements are used for morphometric description of sheep populations and for estimating live weight when direct weighing is not available. Studies conducted in different sheep populations have demonstrated relationships between weight and body length, chest circumference, trunk depth,

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The manuscript was received: 20.04.2026

Accepted for publication: 31.05.2026



and other body dimensions. Multivariate analysis can complement univariate comparisons, given that biometric traits are intercorrelated and can collectively describe body size and shape [8].

The objective of the present study was to characterize the phenotype and body conformation of young sheep from three genetic combinations and to evaluate relationships between body measurements and live weight. The available values for the adult parental breeds were not used to calculate heterosis because the parental animals and the young stock were not at the same physiological age.

MATERIAL AND METHOD

Biological material and measurements. A total of 24 young animals were analyzed and assigned to three genetic combinations: BC×TI (7 animals; 3 females and 4 males), BMC×TI (11 animals; 7 females and 4 males), and V×TI (6 animals; 4 females and 2 males).

Seven variables were recorded for each animal: trunk length, withers height, rump height, chest circumference, cannon circumference, trunk depth, and live weight.

Statistical analysis. Mean and standard deviation were calculated for each genetic combination. The effects of genetic group, sex, and genetic group × sex interaction were evaluated using a factorial model of the form $Y = \mu + G + S + G \times S + e$. Statistical significance was set at $p < 0.05$. Partial eta-squared (η^2_p) was used to quantify effect size.

Relationships between biometric traits and live weight were evaluated using the Pearson correlation coefficient.

The following conformation indices were calculated: form = trunk length/withers height × 100; massiveness = chest circumference/withers height × 100; bone = cannon circumference/withers height × 100; depth = trunk depth/withers height × 100.

For multivariate analysis, principal component analysis (PCA) was performed on the seven standardized variables, namely six biometric traits and live weight. A reduced multiple linear regression model was constructed to estimate live weight using trunk length, chest circumference, and trunk depth as predictors.

RESULTS and DISCUSSION

Evaluation of morphological traits and body development.

Descriptive statistical analysis revealed differences among the three genetic combinations for several of the morphometric traits evaluated, although their magnitude varied by trait. Mean values and standard deviations for trunk length, withers height, rump height, chest circumference, cannon circumference, trunk depth, and live weight are presented in Table 1.

The BMC×TI group had the highest mean live weight (33.14 ± 2.39 kg) and one of the highest mean values for trunk depth (17.09 ± 0.83 cm), whereas BC×TI had the highest mean values for withers height (59.71 ± 1.25 cm), chest circumference (85.86 ± 3.02 cm), and cannon circumference (8.71 ± 0.49 cm). The V×TI group had the highest mean trunk depth (17.17 ± 1.17 cm), whereas mean trunk length and rump height were relatively similar among the three groups.

For live weight, the mean values were 30.36 ± 1.89 kg in BC×TI, 33.14 ± 2.39 kg in BMC×TI, and 29.87 ± 2.59 kg in V×TI. The difference between the maximum and minimum mean values was 3.27 kg, indicating descriptive variation among the genetic combinations analyzed. The statistical significance of these differences and the contribution of genetic group, sex, and their interaction are examined using the factorial model presented in Table 2.

Table 1 Means $\pm$ standard deviations of body measurements and live weight by genetic combination

Trait	BC $\times$ TI (n=7)	BMC $\times$ TI (n=11)	V $\times$ TI (n=6)
Trunk length (cm)	65.14 $\pm$ 1.57	65.64 $\pm$ 2.01	64.50 $\pm$ 3.78
Withers height (cm)	59.71 $\pm$ 1.25	57.18 $\pm$ 1.40	59.33 $\pm$ 3.08
Rump height (cm)	63.43 $\pm$ 1.51	62.09 $\pm$ 1.51	61.83 $\pm$ 2.32
Chest circumference (cm)	85.86 $\pm$ 3.02	82.64 $\pm$ 2.46	82.33 $\pm$ 4.18
Cannon circumference (cm)	8.71 $\pm$ 0.49	7.55 $\pm$ 0.52	7.83 $\pm$ 0.41
Trunk depth (cm)	16.00 $\pm$ 0.82	17.09 $\pm$ 0.83	17.17 $\pm$ 1.17
Live weight (kg)	30.36 $\pm$ 1.89	33.14 $\pm$ 2.39	29.87 $\pm$ 2.59

Note: p = statistical significance level; η^2p = partial eta-squared, used as a measure of effect size.

Effects of genetic group, sex, and genetic group $\times$ sex interaction. Factorial analysis (Table 2) revealed significant effects of genetic group on withers height ($p < 0.001$; $\eta^2p = 0.564$), cannon circumference ($p = 0.001$; $\eta^2p = 0.532$), trunk depth ($p = 0.004$; $\eta^2p = 0.464$), and live weight ($p < 0.001$; $\eta^2p = 0.590$). For trunk length, rump height, and chest circumference, the effect of genetic group did not reach statistical significance ($p > 0.05$).

Sex had a significant effect on trunk length, withers height, rump height, chest circumference, trunk depth, and live weight ($p \leq 0.011$), whereas the effect of sex was not significant for cannon circumference ($p = 0.295$). The largest effect sizes associated with sex were observed for trunk length ($\eta^2p = 0.714$), rump height ($\eta^2p = 0.625$), and withers height ($\eta^2p = 0.621$).

The genetic group $\times$ sex interaction was significant for trunk length ($p = 0.017$; $\eta^2p = 0.362$) and withers height ($p = 0.001$; $\eta^2p = 0.517$). For rump height, chest circumference, cannon circumference,

trunk depth, and live weight, the interaction was not statistically significant ($p > 0.05$). These results indicate that the effect of sex on trunk length and withers height varied according to genetic combination.

Figure 1 shows descriptive differences among the three genetic combinations in withers height. BC $\times$ TI had a higher median, whereas BMC $\times$ TI had the lowest median. The V $\times$ TI group had an intermediate position and greater variability in individual values. These observations are consistent with the significant effect of genetic group identified by the factorial model ($p < 0.001$; $\eta^2p = 0.564$).

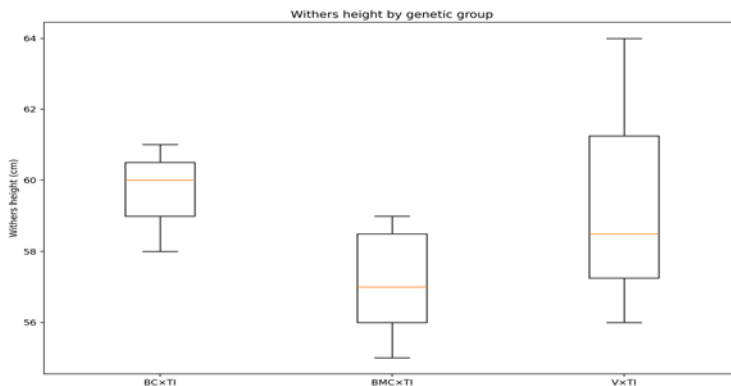
Figure 2 shows a higher median live weight in the BMC $\times$ TI group compared with BC $\times$ TI and V $\times$ TI. The distribution of individual values also indicates greater dispersion in the BMC $\times$ TI group.

These descriptive observations are consistent with the significant effect of genetic group on live weight ($p < 0.001$; $\eta^2p = 0.590$).

Table 2. Effects of genetic group, sex, and genetic group $\times$ sex interaction on body measurements and live weight.

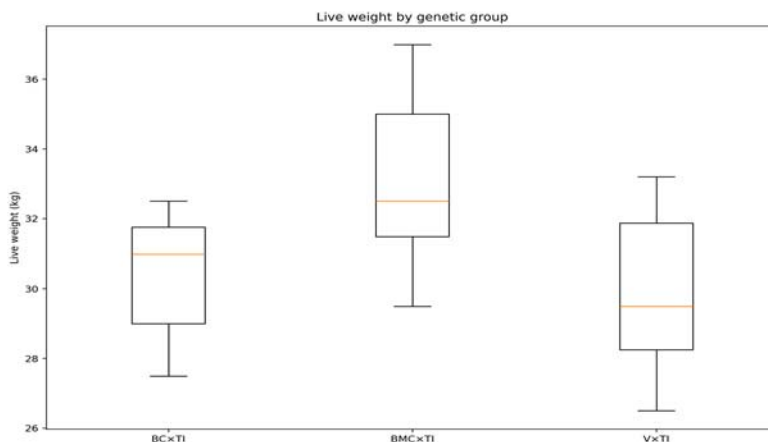
Trait	Genetic group, p	η^2p	Sex, p	η^2p	Genetic group $\times$ sex, p	η^2p
Trunk length	0.128	0.205	<0.001	0.714	0.017	0.362
Withers height	<0.001	0.564	<0.001	0.621	0.001	0.517
Rump height	0.241	0.146	<0.001	0.625	0.138	0.197
Chest circumference	0.108	0.219	0.011	0.311	0.139	0.197
Cannon circumference	0.001	0.532	0.295	0.061	0.893	0.013
Trunk depth	0.004	0.464	0.007	0.342	0.086	0.239
Live weight	<0.001	0.590	<0.001	0.549	0.112	0.216

Note: η^2p = partial eta-squared.



Note: Boxplots show the median, interquartile range, and extreme observed values

Figure 1. Distribution of withers height in young sheep from the three genetic combinations (BC×TI, BMC×TI, and V×TI).



Note: Boxplots show the median, interquartile range, and extreme observed values.

Figure 2. Distribution of live weight according to genetic combination.

Relationships between biometric traits and live weight. Pearson correlation analysis revealed positive associations between live weight and several of the biometric traits analyzed (Table 3). The strongest association was observed for trunk length ($r=0.826$; $p<0.001$), followed by trunk depth ($r=0.763$; $p<0.001$). These results show that, in the analyzed flock, greater trunk length and depth were associated with higher live weight.

Rump height showed a positive, moderate-strength correlation with live weight ($r=0.649$; $p<0.001$). Chest

circumference was also positively and significantly correlated with weight ($r=0.542$; $p=0.006$). These results indicate that longitudinal and thoracic body development is associated with variation in live weight in the studied flock, although the strength of these relationships differs among traits.

Withers height showed a weak, non-significant positive correlation with live weight ($r=0.315$; $p=0.134$), whereas the association for cannon circumference was very small and non-significant ($r=0.059$; $p=0.785$). Therefore, biometric traits did not

show the same strength of association with live weight. Trunk length and trunk depth had the strongest correlations, whereas withers height and cannon circumference did not show significant linear relationships. These results represent phenotypic associations in the studied flock and should not be interpreted as genetic relationships between traits.

The graphical representation of the relationship between trunk length and live weight (Figure 3) shows the positive trend identified by the correlation analysis. Greater trunk length was generally associated with higher live weight, as supported by the high Pearson coefficient ($r=0.826$; $p<0.001$). Observations from the three genetic combinations partially overlapped, indicating that this association was present across the entire flock.

Multiple regression model for estimating live weight. To simultaneously evaluate the contribution of selected morphometric traits to variation in live weight, a multiple linear regression model was constructed using trunk length, chest circumference, and trunk depth as predictive variables (Table 4). The resulting model was: $\text{Live weight} = -25.333 + 0.737 \times \text{trunk length} - 0.083 \times \text{chest circumference} + 0.935 \times \text{trunk depth}$.

The model had a coefficient of determination of $R^2=0.7565$ and an adjusted $R^2=0.7200$, indicating that the predictors included in the model explained approximately 75.7% of the variation in live weight observed in the analyzed flock. The root mean square error (RMSE) was 1.300 kg.

The negative coefficient associated with chest circumference should not be interpreted as a biological negative relationship between chest circumference and live weight. It represents the partial effect of chest circumference in the presence of the other two predictors and may reflect overlapping information among body traits.

Therefore, the main interpretation of the model is based on its overall ability to explain variation in live weight, rather than on the isolated sign of an individual coefficient.

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Therefore, the main interpretation of the model is based on its overall ability to explain variation in live weight, rather than on the isolated sign of an individual coefficient.

This result is consistent with the correlation analysis, in which trunk length and trunk depth showed the strongest simple associations with live weight. Multiple regression extends this analysis by evaluating several predictors simultaneously and indicates that this combination of traits can explain an important proportion of the variation in live weight in the studied flock.

Table 3. Pearson correlations between biometric traits and live weight.

Trait	r Pearson	p
Trunk length	0.826	<0.001
Withers height	0.315	0.134
Rump height	0.649	<0.001
Chest circumference	0.542	0.006
Cannon circumference	0.059	0.785
Trunk depth	0.763	<0.001

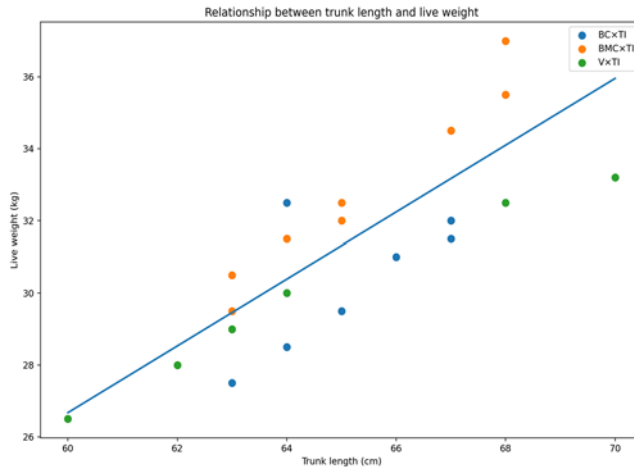
Figure 3. Relationship between trunk length and live weight in young sheep ($r=0.826$; $p<0.001$).

Table 4. Multiple linear regression model for estimating live weight

Predictor	Coefficient
Constant (intercept)	-25.333
Trunk length	0.737
Chest circumference	-0.083
Trunk depth	0.935
R^2	0.7565
Adjusted R^2	0.7200
RMSE (kg)	1.300

Body conformation indices. Four morphometric indices were calculated to characterize body conformation: form index, massiveness index, bone index, and depth index. These were determined by relating the main body dimensions to withers height (Table 5; Figure 4).

The form index, calculated as trunk length/withers height $\times 100$, had mean values of $109.10 \pm 2.15\%$ in BC×TI, $114.77 \pm 1.25\%$ in BMC×TI, and $108.68 \pm 0.88\%$ in V×TI. These values indicate descriptive differences in the ratio between trunk length

and withers height, with the highest mean value observed in BMC×TI.

The massiveness index, calculated as chest circumference/withers height $\times 100$, had similar values in BC×TI ($143.75 \pm 2.36\%$) and BMC×TI ($144.52 \pm 2.54\%$), whereas the mean value in V×TI was $138.77 \pm 1.24\%$. These results indicate similar descriptive values for the ratio between chest circumference and withers height in BC×TI and BMC×TI.

The bone index, calculated from cannon circumference/withers height $\times 100$, had

values of $14.59 \pm 0.55\%$ in BC×TI, $13.19 \pm 0.74\%$ in BMC×TI, and $13.22 \pm 0.78\%$ in V×TI. The highest mean value was observed in BC×TI, whereas the BMC×TI and V×TI values were very similar.

The depth index, calculated as trunk depth/withers height ×100, was $26.78 \pm$

0.83% in BC×TI, $29.88 \pm 0.93\%$ in BMC×TI, and $28.92 \pm 0.96\%$ in V×TI. These values indicate descriptive differences among genetic combinations in the ratio between trunk depth and withers height.

Table 5. Body conformation indices by genetic combination.

Index	BC×TI	BMC×TI	V×TI
Form (%)	109.10 ± 2.15	114.77 ± 1.25	108.68 ± 0.88
Massiveness (%)	143.75 ± 2.36	144.52 ± 2.54	138.77 ± 1.24
Bone (%)	14.59 ± 0.55	13.19 ± 0.74	13.22 ± 0.78
Depth (%)	26.78 ± 0.83	29.88 ± 0.93	28.92 ± 0.96

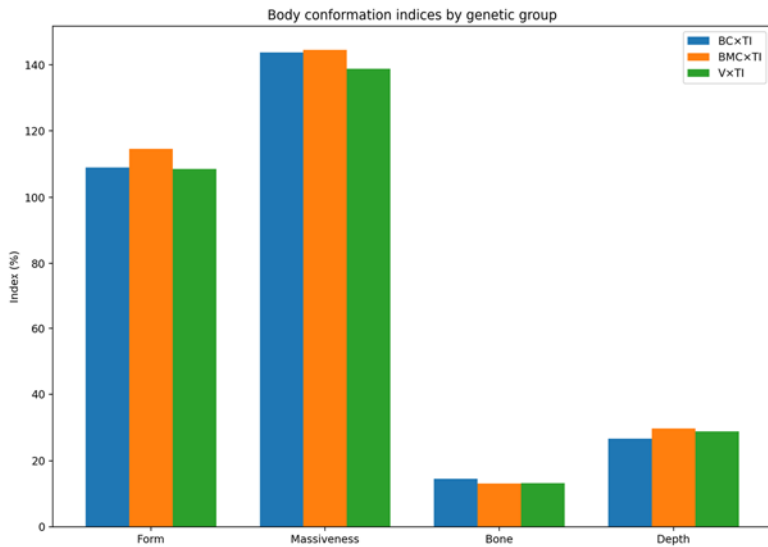


Figure 4. Body conformation indices for the three genetic combinations.

Overall, the body indices reveal descriptive differences in conformation among the three genetic combinations, with the most evident differences observed for the form and depth indices.

The massiveness index showed similar values in BC×TI and BMC×TI, whereas the bone index had similar values in BMC×TI and V×TI. These indices complement the information provided by absolute body measurements by expressing body dimensions relative to withers height.

Principal component analysis (PCA) was used to synthesize the multivariate

information from the seven variables analyzed, namely six biometric traits and live weight (Table 6). The variables were standardized before analysis, and the principal components were obtained as linear combinations of the original variables.

The first two principal components jointly explained 88.34% of the total variation, whereas the first three accounted for 93.47%. PC1 had an eigenvalue of 4.890 and explained 66.95% of the variation, while PC2 had an eigenvalue of 1.562 and explained 21.39%. PC3 had an eigenvalue

of 0.375 and contributed 5.13% of the total variation.

PC1 can be interpreted as a general body-size dimension because all variables had positive loadings, with the largest loadings associated with rump height, chest circumference, and trunk length.

PC2 highlights a contrast between cannon circumference and, to a lesser extent, withers height and chest circumference, on the one hand, and live weight, trunk depth, and trunk length, on the other hand, according to the sign and magnitude of the factor loadings.

The first two components explained 88.34% of the total variation, while the first

three explained 93.47%. The representation in the space of the first two principal components (Figure 5) shows differentiated distribution of observations from the three genetic combinations. PC1 explains 66.95% of the total variation and PC2 21.39%, so the first two components jointly summarize 88.34% of the initial variation. The distribution of observations suggests more evident descriptive differentiation along PC2, with BMC×TI values predominantly negative, BC×TI values predominantly positive, and V×TI showing a more intermediate distribution and greater variability.

Table 6. Eigenvalues and explained variance of the principal components.

Component	Eigenvalue	Explained variance (%)	Cumulative (%)
PC1	4.890	66.95	66.95
PC2	1.562	21.39	88.34
PC3	0.375	5.13	93.47
PC4	0.314	4.29	97.76
PC5	0.094	1.28	99.04
PC6	0.049	0.67	99.71
PC7	0.021	0.28	100.00

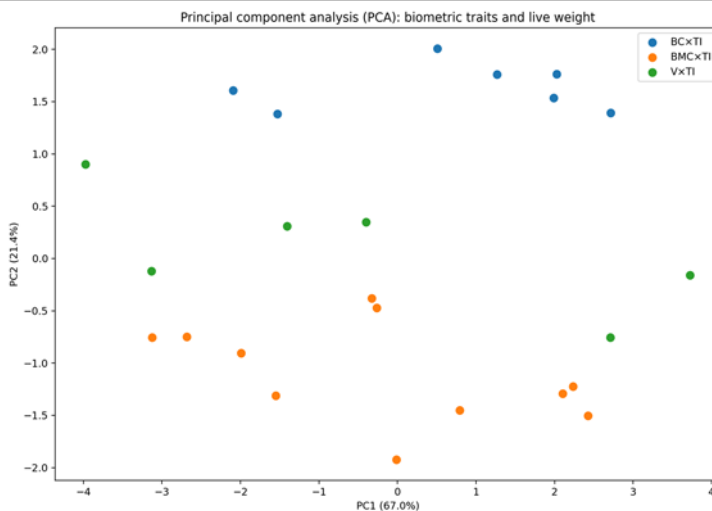


Figure 5. Principal component analysis (PCA) based on biometric traits and live weight.

This representation shows that an important proportion of the observed morphometric variation can be summarized

by the first two principal components. The results should be interpreted as a statistical reduction of phenotypic and morphometric

variation, without assigning direct genetic meaning to the components. Differences among genetic combinations observed in principal-component space should likewise be considered descriptive and do not

represent direct estimates of heterosis or other genetic parameters.

Loadings for the first three principal components are presented in Table 7 to facilitate interpretation of the multivariate structure.

Table 7. Loadings of the first three principal components

Variable	PC1	PC2	PC3
Trunk length	0.420	-0.235	-0.149
Withers height	0.390	0.273	0.562
Rump height	0.447	0.111	-0.202
Chest circumference	0.428	0.221	-0.147
Cannon circumference	0.276	0.586	-0.129
Trunk depth	0.312	-0.474	0.605
Live weight	0.338	-0.491	-0.465

The PCA analysis highlights three principal components that summarize the morphometric structure of the sample. PC1 shows positive loadings for all variables with the highest values observed for height at the croup (0.447), chest circumference (0.428), and body length (0.420)-suggesting a general dimension associated with body development. PC2 highlights a contrast between cannon bone circumference (0.586) and height at the withers (0.273) on the one hand, and live weight (-0.491), body depth (-0.474), and body length (-0.235) on the other. PC3 is characterized primarily by positive loadings for body depth (0.605) and height at the withers (0.562), in opposition to live weight (-0.465), indicating a distinct third morphometric dimension.

CONCLUSIONS

- Phenotypic differences were identified among the three genetic combinations, with a significant effect of genetic group on withers height, cannon circumference, trunk depth, and live weight.

- Sex significantly influenced several morphometric traits, and the genetic group $\times$ sex interaction was significant for trunk length and withers height.

- Trunk length and trunk depth showed the strongest phenotypic associations with

live weight, with correlation coefficients of 0.826 and 0.763, respectively.

- The multiple regression model based on trunk length, chest circumference, and trunk depth explained 75.65% of the variation in live weight ($R^2=0.7565$); however, its predictive applicability requires validation on independent flocks.

- The first two principal components explained 88.34% of the total variation, highlighting the usefulness of PCA for synthesizing morphometric information and describing the multivariate structure of the analyzed flock.

- The results do not allow heterosis to be estimated by comparison with the available parental values because those values were obtained from adult animals, whereas the young-stock data were obtained at a different physiological stage. The results should also be interpreted in the context of the small sample size and the juvenile status of the animals.

In issuing them, it is not recommended to repeat the data from the text, tables, figures or schemes, but it must highlight the practical and scientific value and importance of the study.

ACKNOWLEDGMENTS

Sincere thanks to the Romanian Minister of Agriculture and Rural Development for

funding the research, provided through the ADER 716 Sectoral Plan.

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