



# Multivariate modelling to estimate carcass characteristics and commercial cuts of Boer goats

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## Abstract

The objective was to establish a multivariate model using two complementary multivariate statistical techniques, factor analysis and multiple stepwise regression to predict carcass characteristics, carcass cuts, internal fat, viscera and loin eye area from body measurements of goats Boer mestizos. Thirty-two goats were used, with initial average weights of  $3.3 \pm 0.61$  kg and final average weights of  $16 \pm 2.5$  kg. Before slaughter and after 16 h of fasting, body weight was measured along with the biometric measurements (BMs) of each animal: body length, withers height, croup height, chest width, croup width, croup perimeter, thoracic perimeter, leg length and thigh circumference. The half carcasses were sectioned in six anatomical regions that made up the commercial cuts: neck, palette, rib, handsaw, loin and ham. BMs showed a high correlation with a few exceptions; most of the correlations are above 50%. What also happens with the Carcass weight and cuts were also correlated above 50% with BMs. The data presented an index for the Kaiser–Meyer–Olkin test of 0.80, demonstrating the adequacy of the factor analysis. Through factor analysis, it was possible to observe that the first two factors extracted accumulated 75.47% of the total variance of the studied characteristics. Moderate to high and positive correlations of morphological characteristics with body weight, carcass characteristics and primary carcass cuts suggested the adequacy of morphological characteristics as criteria for early selection of crossbred Boer goats for their body weight and carcass characteristics without slaughter.

## Introduction

The prediction of the carcass characteristics, including the own weight of the cuts, can provide a viable alternative to estimate their value and assist in marketing for some niches (Bonny *et al.*, 2018). The ultimate goal of the meat industry is to have an accurate and objective measurement method to assess the economically important characteristics of the animals and to determine the value and merit of the carcass while the animal is still alive (Younas *et al.*, 2013). A quick and easy-to-use tool is needed to predict the live weight and carcass characteristics of the animals by the breeders, as they depend on visual assessment to estimate the live weight of the goats under field conditions (Tesema *et al.*, 2019).

Biometric measurements (BM) are essential to predict the quantitative characteristics of the meat and are also useful in the development of suitable selection criteria (Tesema *et al.*, 2019). BMs can also be used as an indirect way of estimating live weight and carcass characteristics due to the relative ease of measuring linear dimensions (Bingol *et al.*, 2011; Assan, 2013; Ricardo *et al.*, 2016; Bautista Diaz *et al.*, 2017). The BM correlation matrix can be used to predict live weight and carcass averages in goats (Abdel-Mageed and Ghanem, 2013; Tesema *et al.*, 2019) and sheep (Bautista-Diaz *et al.*, 2017; Costa *et al.*, 2020).

Multivariate models allow the analysis of the relationship between multiple explanatory variables. Part of the research aimed at examining the effect of two or more independent variables on a dependent variable uses multiple regression analysis (Ellies-Oury *et al.*, 2019).

Multiple regression analysis has been used to interpret the complex relationships between live weight and some BM. However, the interpretation of these multiple regressions can be misleading when there is multicollinearity between the predictor variables (Ogah *et al.*, 2011; Yakubu and Mohammed, 2012; Tesema *et al.*, 2019). To address this problem, multivariate factor analysis is best suited as a statistical method to reduce a complex system of correlations to one of the smaller dimensions by extracting some unobservable latent variables called

factors (Woods and Edwards, 2011). Factor scores can be derived from this multivariate analysis, which can be almost uncorrelated or orthogonal. Factor scores could, therefore, be used for prediction, thus solving the problem of multicollinearity, which can occur when data are collected on a small basis because, for ethical and economic reasons, a good experimental design requires the use of the minimum number of animals needed to achieve the desired goal given the required accuracy (Festing and Altman, 2002).

The work hypothesizes that BMs are capable of estimating carcass, cuts, viscera and internal fat characteristics. As the information used to estimate the carcass composition of goats through physiological characteristics is weak the objective was to establish a multivariate model using two complementary multivariate statistical techniques, factor analysis and multiple stepwise regression to predict carcass characteristics, carcass cuts, internal fat, viscera and loin eye area (LEA) from body measurements of goats Boer mestizos.

## Materials and methods

### Place of experiment

The experiment was carried out at the Pendência Experimental Station, belonging to the Paraíba State Agricultural Research Corporation (EMEPA-PB), located in the municipality of Soledade, micro-region of Cariri Paraibano, located between the geographical coordinates of 7°8'18" south and 36°27'2" latitude west of Greenwich, with an altitude of 534 m, the average temperature of 30°C and average relative humidity of 70%.

### Ethical aspects and animals

The Animal Ethics Committee approved the study of the Federal University of Paraíba-UFPA, Brazil approved the study (Protocol number 2305/14).

Thirty-two goats were used (16 males: 8 slaughtered at 70 days and 8 slaughtered at 100 days + 16 females: 8 slaughtered at 70 days and 8 at 100 days), crossbred Boer breed with native goats. The animals had average weights at birth of 3.3 ± 0.62 kg (males) and 3.1 ± 0.76 kg (females) for those slaughtered at 70 days and weights of 4.1 kg ± 0.71 (males) and 3.2 kg ± 0.38 (females), for those slaughtered at 100 days of age.

### Diet

The diet was formulated according to the NRC (2007), aiming at a weight gain of 200 g/day, with forage: concentrate ratio of 12 : 84, composed of Tifton grass hay (*Cynodon dactylon*), and the concentrates were composed of ground corn, soybean meal, finely ground, mineral supplement and calcitic limestone. The adaptation of the animals was made for 14 days, and the weight gain was carried out weekly. All experimental animals were selected 1 week before the first weaning (70 days). From 10 days of age, the pups received a complete diet *ad libitum* in their own troughs.

### Slaughter, BMs and carcass components

Before slaughter and after 16 h of fasting, body weight was measured along with the BMs of each animal: body length (BL), withers height (WH), croup height (CH), chest width (CW), croup width (CRW), croup perimeter (CRP), thoracic perimeter (TP), leg length (LL) and thigh circumference (TC). For all measurements, flexible tape fiberglass (Truper®) and a large caliper of

**Table 1.** Descriptive analyses of the data measured on the live animal

Variables	$\mu \pm$ s.d.	CV (%)	Maximum	Minimum
<i>BMs (cm)</i>				
Body length	50 ± 3.8	7.37	60	43
Leg length	48 ± 5.2	10.65	57	38
Withers height	48 ± 4.5	9.27	58	40
Croup height	47 ± 3.9	8.29	55	40
Thoracic perimeter	48 ± 9.2	18.91	62	37
Croup perimeter	39 ± 3.8	9.51	45	32
Thigh circumference	29 ± 2.2	7.51	37	26
Chest width	10.8 ± 0.64	5.96	12	10
Croup width	12 ± 1.0	8.18	14	11
<i>Carcass measurement (kg)</i>				
SBW	16 ± 2.5	15.57	21	11
EBW	13 ± 2.0	14.97	18	10
HCW	8 ± 1.4	16.39	19	10
CCW	8 ± 1.3	16.99	10	5
Internal fat	2.6 ± 0.77	29.97	4	1
LEA	6 ± 1.1	19.97	8	4
Viscera	3.2 ± 0.70	22.20	4	2
Waste parts of the carcass	5.6 ± 0.93	16.82	7	4
<i>Cuts</i>				
Neck	0.4 ± 0.09	19.04	0.65	0.29
Pallette	0.7 ± 0.11	14.92	1.02	0.57
Rib	0.9 ± 0.18	19.11	1.40	0.58
Loin	0.4 ± 0.08	19.76	0.60	0.28
Ham	1.2 ± 0.20	16.07	1.70	0.85

$\mu \pm$  s.d., mean ± standard deviation; CV, coefficient of variation.

65 cm (Haglof®) were used. The BM was expressed in centimetres so that it could be related to the composition of the carcass (Fernandes *et al.*, 2010).

All goats were slaughtered the same day using standard commercial procedures following Brazilian welfare codes of practice (Brasil, 2000). Goats were fasted at the farm for 8 h and transported to an accredited slaughterhouse and were then weighed to obtain the slaughter body weight (SBW). At the slaughterhouse, goats had an 8 h rest period with full access to water but not to feed. Experimental animals were left unconscious by electrical stunning and slaughtered by bleeding. After slaughter, the carcasses were chilled at 4°C in a refrigerated chamber, where they remained for 24 h hanging from hooks by the Achilles tendon with the metatarsal joints spaced 17 cm apart. The animals were subsequently skinned and eviscerated.

The hot carcass weight (HCW) was calculated following slaughter, with the carcass divided by the dorsal median line into two halves and refrigerated for a period of 24 h at 1°C.

**Table 2.** Pearson's correlation of BMs of crossbred Boer goats

Variable	CRW	CRP	WH	CH	BL	LL	TP	TC
Chest width – CW	0.43*	0.39*	0.19	0.24	0.33	–0.16	0.28	0.18
Croup width – CRW	1.00	0.85*	0.67*	0.70*	0.69*	–0.60*	0.71*	0.24
Croup perimeter – CRP		1.00	0.67*	0.72*	0.76*	–0.60*	0.77*	0.39*
Withers height – WH			1.00	0.90*	0.88*	–0.46*	0.83*	0.37*
Croup height – CH				1.00	0.91*	–0.49*	0.81*	0.44*
Body length – BL					1.00	–0.44*	0.83*	0.53*
Leg length – LL						1.00	–0.70*	–0.20
Thoracic perimeter – TP							1.00	0.34
Thigh circumference – TC								1.00

\*Significant at 5%.

The gastrointestinal tract was weighed both full and empty to determine the empty body weight (EBW). The kidneys and perirenal fat were removed and were subtracted from the HCW and cold carcass weight (CCW) (Cézar and Sousa, 2007). In the left half carcass, a cross section between the 12th and 13th ribs was performed, exposing the cross section of the *longissimus dorsi* muscle, whose area was dashed using a permanent marker with a 2.0 mm mean tip on a transparent plastic film to determine the LEA.

Subsequently, the carcasses were sectioned at the ischio-pubic symphysis, following the body and spinous apophysis of the sacrum, lumbar and dorsal vertebrae. Then, the carcass was subjected to a longitudinal cut. The left half carcass was weighed. The half carcasses were sectioned in six anatomical regions that made up the commercial cuts: neck, palette, rib, loin and ham, according to the methodology of Cézar and Sousa (2007). Then the individual weight of each cut was recorded to calculate its proportion concerning the sum of the reconstituted half carcass, thus obtaining the yield of the carcass cuts.

### Statistical analysis

Mean, range and variance (s.d.) and Pearson correlations were determined for all measurements as well as regression analyses. Regressions were developed with PROC REG of SAS (SAS Ver. 9.3, 2010). The biometric variables used in the development of the prediction equation. The equations were selected taking into account the model determination coefficient ( $R^2$ ), the root means square error (RMSE) and the  $C_p$  statistic:

$$\frac{SQR}{\sigma^2} + 2p - n. \quad (1)$$

The  $SQR$  is the residual mean square,  $\sigma^2$  is the residual variance,  $p$  is the number of parameters in the model (including the intercept) and  $n$  is the number of records. According to MacNeil (1983),  $C_p$  relates  $R^2$  and residual variance, and it is a more appropriate equation selection criterion than  $R^2$  alone, allowing the identification of optimal subsets. The goal is to find the best model involving a subset of predictors. Hence, in general, a small value of  $C_p$  means that the model is relatively precise (Mallows, 1973). For regression analysis, the stepwise procedure was adopted, which aims to assess the statistical significance of

the parameters of certain explanatory variables and includes only those that are relevant to a certain level of confidence.

The multiple regression analysis using the stepwise method was performed using the model:

$$Y = \alpha + \beta_1 X_1 + \beta_2 X_2 + \dots + \beta_n X_n + e \quad (2)$$

where  $Y$  is the dependent variable or response; carcass characteristics and carcass cuts;  $\alpha$  is the intercept of the regression equation;  $\beta_1$ ,  $\beta_2$  and  $\beta_n$  are regression coefficients of the variables  $X_1$ ,  $X_2$  and  $X_n$  are the explanatory variables or morphological characteristics and  $e$  is the residual random error.

Factor analysis based on principal components was used to summarize the set of original variables in latent independent variables (factors). The Kaiser–Meyer–Olkin test (KMO) test was used to assess the adequacy of factor analysis to the data set (Kaiser, 1974), and the most critical factors were extracted based on the method of Kaiser (1974), which considers for selection the eigenvalues higher than 1. The varimax orthogonal rotation was adopted, which seeks to improve the interpretability of the extracted factors.

The model used in the analysis was:

$$X_1 = a_{11}F_1 + a_{12}F_2 + \dots + a_{1m}F_m + \varepsilon_1$$

$$X_2 = a_{21}F_1 + a_{22}F_2 + \dots + a_{2m}F_m + \varepsilon_2$$

$$X_p = a_{p1}F_1 + a_{p2}F_2 + \dots + a_{pm}F_m + \varepsilon_p$$

The factorial model constituted by the factors  $F_1, \dots, F_m$ ,  $m \leq p$ . Here,  $X_1$ ,  $X_2$  and  $X_p$  are the variables under study;  $a$  is the factor load;  $F = F_1, F_2, \dots, F_m$  are the  $m$  uncorrelated factors and  $\varepsilon = \varepsilon_1, \varepsilon_2, \dots, \varepsilon_p$  are variables with means 0 and variance 1. Factorial analysis has been used in the morphological evaluation of goats, and mainly as a tool in the evaluation of the size and shape of the animals' bodies (Yakubu *et al.*, 2011; Arandas *et al.*, 2016).

Thus, the multiple regression analysis was also used to predict the carcass characteristics and cuts from the extracted factors,

**Table 3.** Pearson's correlation of BMs, carcass characteristics and cuts of crossbred Boer goats

Variables	EBW	SBW	HCW	CCW	Neck	Pallete	Rib	Loin	Ham	IF	LEA	VISC	OFF
Chest width	0.46*	0.50*	0.49*	0.51*	0.46*	0.47*	0.43*	0.42*	0.51*	0.15	0.44*	0.35*	0.29
Croup width	0.77*	0.76*	0.43*	0.77*	0.63*	0.70*	0.65*	0.72*	0.76*	0.18	0.58*	0.72*	0.46*
Croup perimeter	0.84*	0.86*	0.51*	0.83*	0.69*	0.77*	0.62*	0.83*	0.82*	0.27	0.66*	0.76*	0.55*
Withers height	0.85*	0.81*	0.61*	0.81*	0.71*	0.82*	0.59*	0.74*	0.78*	-0.05	0.56*	0.70*	0.35*
Croup height	0.87*	0.82*	0.67*	0.82*	0.64*	0.80*	0.73*	0.76*	0.77*	0.06	0.51*	0.76*	0.43*
Body length	0.92*	0.90*	0.77*	0.91*	0.73*	0.88*	0.76*	0.84*	0.90*	0.11	0.63*	0.73*	0.51*
Leg length	-0.55*	-0.57*	-0.32	-0.55*	-0.53*	-0.38*	-0.49*	-0.63*	-0.51*	-0.54*	-0.54*	-0.68*	-0.66*
Thoracic perimeter	0.89*	0.90*	0.63*	0.88*	0.64*	0.84*	0.64*	0.85*	0.84*	0.35*	0.72*	0.86*	0.69*
Thigh circumference	0.47*	0.50*	0.56*	0.50*	0.39*	0.51*	0.35	0.48*	0.51*	0.14	0.35	0.33	0.32

EBW, empty body weight; SBW, slaughter body weight; HCW, hot carcass weight; CCW, cold carcass weight; IF, internal fat; LEA, loin eye area; VISC, viscera; OFF, waste parts of the carcass.  
\*Significant at 5%.

according to the model:

$$Y = \alpha + \beta_1 F_1 + \beta_2 F_2 + \dots + \beta_n F_n + e, \tag{3}$$

where  $Y$  is the dependent/response variable; carcass characteristics and carcass cuts;  $\alpha$  is the interception of the regression equation;  $\beta_1, \beta_2$  and  $\beta_n$  are the regression coefficients of scores  $F_1, F_2$  and  $F_n$  are the explanatory variables or factors and  $e$  is the residual random error.

**Results**

The internal fat presented the highest coefficient of variation (30%), followed by the viscera (22%) among the biometric, carcass and weight measurements (Table 1). The variables LEA, neck, rib and loin varied around 19%. Body length, leg length, withers height, rump height, rump circumference, thigh circumference, chest width and rump width varied below 11% (Table 1).

BMs showed a high correlation with each other (Table 2) with a few exceptions; most of the correlations are above 50%. This also occurs with the weight of the carcass and cuts that showed a high correlation with BMs (Table 3). The croup width showed a correlation of 43% with HCW. However, with other weight, croup width showed a correlation that varied from 63 to 77%. The croup perimeter, withers height, croup height, body length and thoracic perimeter showed the highest correlations, with emphasis on BL with correlation ranging from 77 to 92% and thoracic perimeter ranging from 63 to 90%.

The chest width showed a correlation ranging from 46 to 51% with the carcass weights at slaughter, the empty glass, hot carcass and cold carcass and from 42 to 51% with the weight of the cuts. The thigh circumference showed a correlation ranging from 47 to 56% with the carcass weights and from 35 to 51% with the weight of the cuts. Leg length, on the other hand, showed an inverse correlation (-32 to -63%) with carcass and cut weights. Consider other carcass measures such as the weight of internal fat, which only correlated with leg length (-54%) and thoracic perimeter (35%). The LEA and viscera weight correlated with all BMs, except for the thigh circumference, and being inverse with the leg length. The weight of waste parts of the carcass (OFF) did not show any correlation with chest width and thigh circumference (Table 3).

It was observed that in the prediction equations as the number of variables increases, the  $R^2$  value increases, and the  $C_p$  decreases as well as the RMSE decreases (Tables 4 and 5). Although there are divergences in the literature in deciding which individual variable is the most suitable to be used in the prediction of animal carcasses, the accuracy of the prediction has been improved especially when more than one variable is considered in the model, that is, the inclusion of several variables produce an increase in the precision of the estimates obtained.

The chest width, body length, thoracic perimeter, croup perimeter and croup width are the biometric measures that best fit the prediction equations of the SBW, EBW, HCW and CCW where the  $R^2$  value was 92, 94, 70 and 94% and the  $C_p$  value was 4.05; 3.54; 1.26 and 2.34, respectively (Table 4). The LEA and the viscera had in their prediction equations only the thoracic perimeter with  $R^2 = 51$  and 73% and  $C_p = 1.85$  and 1.31, respectively. The equations for predicting the weight of the rib, loin, shoulder and ham were better adjusted, as they presented high  $R^2$  and the  $C_p$  remained close to the number of variables included

**Table 4.** Prediction equations for carcass characteristics based on original morphological characteristics of crossbred Boer × Savanna goats

Eqn. no.	Equation	$C_p$	$R^2$	RMSE	$P$ -value
Slaughter body weight (SBW)					
1	$SBW = -15(\pm 2.5) + 0.6(\pm 0.05)BL$	25.7	0.83	1.03	<0.001
2	$SBW = -9(\pm 2.7) + 0.4(\pm 0.08)BL + 0.1(\pm 0.03)TP$	11.5	0.88	0.87	<0.001
3	$SBW = -15(\pm 3.0) + 0.7(\pm 0.23)CW + 0.4(\pm 0.07)BL + 0.1(\pm 0.03)TP$	4.1	0.92	0.77	<0.001
Empty body weight (EBW)					
1	$EBW = -11(\pm 2.1) + 0.5(\pm 0.04)BL$	54.3	0.82	0.88	<0.001
2	$EBW = -12(\pm 1.7) + 0.2(\pm 0.05)CRP + 0.3(\pm 0.05)BL$	25.0	0.89	0.70	<0.001
3	$EBW = -7(\pm 2.0) + 0.2(\pm 0.05)CRP + 0.2(\pm 0.06)BL + 0.1(\pm 0.02)TP$	14.0	0.92	0.62	<0.001
4	$EBW = -12(\pm 2.0) + 0.6(\pm 0.16)CW + 0.1(\pm 0.04)CRP + 0.2(\pm 0.05)BL + 0.1(\pm 0.02)TP$	3.5	0.94	0.52	<0.001
Hot carcass weight (HCW)					
1	$HCW = -17(\pm 3.8) + 0.5(\pm 0.07)BL$	6.4	0.59	1.56	<0.001
2	$HCW = -25(\pm 5.0) + 1.0(\pm 0.43)CW + 0.4(\pm 0.07)BL$	3.3	0.65	1.44	<0.001
3	$HCW = -25(\pm 4.7) + 1.3(\pm 0.43)CW - 0.7(\pm 0.35)CRW + 0.6(\pm 0.09)BL$	1.3	0.70	1.38	<0.001
Cold carcass weight (CCW)					
1	$CCW = -8(\pm 1.3) + 0.3(\pm 0.03)BL$	36.3	0.83	0.53	<0.001
2	$CCW = -5(\pm 1.4) + 0.2(\pm 0.03)BL + 0.1(\pm 0.02)TP$	19.6	0.88	0.45	<0.001
3	$CCW = -9(\pm 1.4) + 0.5(\pm 0.11)CW + 0.2(\pm 0.03)BL + 0.1(\pm 0.01)TP$	4.0	0.93	0.36	<0.001
4	$CCW = -9(\pm 1.3) + 0.4(\pm 0.10)CW + 0.1(\pm 0.03)CRP + 0.2(\pm 0.03)BL + 0.04(\pm 0.012)TP$	2.3	0.94	0.34	<0.001
Internal fat					
1	$IF = 7(\pm 1.1) - 0.1(\pm 0.02)LL$	8.7	0.29	0.66	0.001
2	$IF = 11(\pm 2.2) - 0.1(\pm 0.03)WH - 0.1(\pm 0.02)LL$	4.9	0.40	0.61	0.001
3	$IF = -10(\pm 2.0) - 0.2(\pm 0.04)WH - 0.1(\pm 0.03)LL + 0.1(\pm 0.02)TP$	-0.9	0.55	0.54	<0.001
Loin eye area (LEA)					
1	$LEA = 1.4(0.77) + 0.1(\pm 0.02)TP$	1.9	0.51	0.80	<0.001
Waste parts of the carcass (OFF)					
1	$OFF = 2.2(\pm 0.66) + 0.1(\pm 0.01)TP$	10.3	0.47	0.69	<0.001
2	$OFF = 6(\pm 1.3) - 0.2(\pm 0.04)WH + 0.1(\pm 0.02)TP$	0.8	0.63	0.59	<0.001
Viscera and organs (VISC)					
1	$VISC = -0.03(\pm 0.353) + 0.1(\pm 0.01)TP$	1.3	0.73	0.36	<0.001

<sup>a</sup>Regression coefficient RMSE,  $R^2$ ,  $C_p$  and  $P$ -value are updated with respect to a new independent variable to the prediction equation, the new independent variable is additionally with respect to the  $C_p \approx p$  independent variables, and root mean square error and cumulative  $R^2$ .  
BL, body length; TP, thoracic perimeter; CW, croup width; CRP, croup perimeter; CW, chest width; WH, withers height; LL, leg length.

in the model. The palette weight prediction equation presented  $R^2 = 90\%$ ,  $C_p = 6.22$ , and presented in its model 6 BMs a value similar to that of  $C_p$  (Table 5). The BMs that best fit the cut weight prediction equations were: chest width, withers height, body length, leg length, croup perimeter, thoracic perimeter, thigh circumference and croup height.

Independent factor scores were used to predict live weight, carcass characteristics and the weight of primary cuts of crossbred Boer goats (Table 6). This study demonstrated that the variation explained by the morphological variables (Tables 4 and 5) was smaller since the  $C_p$  was higher, already in the use of orthogonal variables (Table 6) to predict live weight, carcass characteristics and cut weight, the explained variation was more significant and  $C_p$  less. Evaluating the adjustment measures, it is observed that the values of the determination coefficient

( $R^2$ ) are high for some prediction equations, indicating a good correlation of the dependent variable with the independent ones. Thus, the model has a high explanation for the value variability of  $y$ .

## Discussion

These results suggest that producers who do not have a scale to weigh goats can estimate the live weight of their goats using biometric measures, that is, they can use a tape measure instead of a scale, a practice that is much easier to perform under field conditions and during the purchase and sale of the animals (Agamy *et al.*, 2015).

Live weight was not included in the models as an independent measure since it varies considerably between carcasses of domestic

**Table 5.** Prediction equations for carcass cuts based on original morphological characteristics of crossbred Boer × Savanna goats

Eqn. no.	Equation	$C_p$	$R^2$	RMSE	$P$ -value
1	Neck = $0.4(\pm 0.15) + 0.02(\pm 0.003)BL$	15.6	0.53	0.06	<0.001
2	Neck = $-0.7(\pm 0.20) + 0.03(\pm 0.017)CW + 0.02(\pm 0.003)BL$	12.4	0.59	0.06	<0.001
3	Neck = $-0.3(\pm 0.25) + 0.03(\pm 0.023)CW + 0.01(\pm 0.003)BL - 0.004(\pm 0.0021)LL$	9.5	0.64	0.05	<0.001
4	Neck = $-0.4(\pm 0.25) + 0.04(\pm 0.023)CW + 0.01(\pm 0.005)WH + 0.01(\pm 0.006)BL - 0.004(\pm 0.0021)LL$	8.8	0.67	0.05	<0.001
1	Rib = $-0.9(\pm 0.30) + 0.04(\pm 0.006)BL$	6.9	0.57	0.12	<0.001
2	Rib = $-1.4(\pm 0.40) + 0.06(\pm 0.004)CW + 0.003(\pm 0.0064)BL$	5.9	0.61	0.12	<0.001
3	Rib = $-0.8(\pm 0.53) + 0.1(\pm 0.03)CW + 0.03(\pm 0.006)BL - 0.01(\pm 0.004)LL$	4.5	0.64	0.11	<0.001
1	Loin = $0.05(\pm 0.044) + 0.01(\pm 0.001)TP$	12.8	0.72	0.04	<0.001
2	Loin = $-0.2(\pm 0.08) + 0.01(\pm 0.003)CRP + 0.01(\pm 0.001)TP$	3.6	0.80	0.04	<0.001
3	Loin = $-0.4(\pm 0.12) + 0.01(\pm 0.003)CRP + 0.01(\pm 0.003)BL + 0.003(\pm 0.0012)TP$	2.3	0.82	0.04	<0.001
1	Pallette = $-0.6(\pm 0.14) + 0.03(\pm 0.003)BL$	27.8	0.78	0.06	<0.001
2	Pallette = $-0.4(\pm 0.16) + 0.02(\pm 0.005)BL + 0.004(\pm 0.0021)TP$	20.9	0.81	0.05	<0.001
3	Pallette = $-0.7(\pm 0.19) + 0.03(\pm 0.012)CW + 0.02(\pm 0.004)BL + 0.004(\pm 0.0021)TP$	14.7	0.84	0.05	<0.001
4	Pallette = $-0.9(\pm 0.20) + 0.04(\pm 0.012)CW + 0.01(\pm 0.004)BL + 0.01(\pm 0.002)LL + 0.01(\pm 0.002)TP$	8.8	0.88	0.04	<0.001
5	Pallette = $-1.0(\pm 0.20) + 0.04(\pm 0.012)CW + 0.01(\pm 0.004)BL + 0.01(\pm 0.002)LL + 0.01(\pm 0.002)TP + 0.01(\pm 0.004)TC$	7.2	0.89	0.04	<0.001
6	Pallette = $1.1(\pm 0.20) + 0.03(\pm 0.012)CW + 0.01(\pm 0.003)CRP + 0.01(\pm 0.004)BL + 0.01(\pm 0.002)LL + 0.01(\pm 0.002)TP + 0.01(\pm 0.004)TC$	6.2	0.90	0.04	<0.001
1	Ham = $-1.2(\pm 0.21) + 0.05(\pm 0.004)BL$	24.6	0.81	0.09	<0.001
2	Ham = $-1.8(\pm 0.26) + 0.1(\pm 0.02)CW + 0.04(\pm 0.004)BL$	13.0	0.86	0.08	<0.001
3	Ham = $-1.7(\pm 0.24) + 0.1(\pm 0.02)CW + 0.01(\pm 0.005)CRP + 0.03(\pm 0.005)BL$	7.2	0.89	0.07	<0.001
4	Ham = $-1.6(\pm 0.23) + 0.1(\pm 0.02)CW + 0.02(\pm 0.001)CRP - 0.01(\pm 0.008)CH + 0.04(\pm 0.008)BL$	6.4	0.90	0.07	<0.001
5	Ham = $-1.3(\pm 0.26) + 0.1(\pm 0.02)CW + 0.01(\pm 0.005)CRP - 0.02(\pm 0.007)CH + 0.04(\pm 0.008)BL + 0.01(\pm 0.003)TP$	4.3	0.91	0.06	<0.001

<sup>a</sup>Regression coefficient RMSE,  $R^2$ ,  $C_p$  and  $P$ -value are updated with respect to a new independent variable to the prediction equation, the new independent variable is additionally with respect to the  $C_p \approx p$  independent variables, and root-mean-square error and cumulative  $R^2$ .

BL, body length; TP, thoracic perimeter; CW, croup width; CRP, croup perimeter; CW, chest width; WH, withers height; LL, leg length; TC, thigh circumference; CH, croup height.

**Table 6.** Prediction equations for carcass characteristics and cuts based on orthogonal characteristics of crossbred Boer × Savanna goats

Eqn. no.	Equation	$C_p$	$R^2$	RMSE	$P$ -value
<i>Slaughter body weight (SBW)</i>					
1	SBW = 16.3(±0.14) – 1.0(±0.06)PC	2.0	0.90	0.80	<0.001
<i>Empty body weight (EBW)</i>					
1	EBW = 13.5(±0.12) – 0.8(±0.05)PC	2.0	0.89	0.67	<0.001
<i>Hot carcass weight (HCW)</i>					
1	HCW = 7.9(±0.31) – 0.7(±0.13)PC	2.0	0.49	1.75	<0.001
<i>Cold carcass weight (CCW)</i>					
1	CCW = 7.5(±0.08) – 0.5(±0.03)PC	2.0	0.88	0.44	<0.001
<i>Neck</i>					
1	Neck = 0.5(±0.01) – 0.03(±0.004)PC	2.0	0.59	0.06	<0.001
<i>Pallete</i>					
1	Pallete = 0.8(±0.01) – 0.04(±0.004)PC	2.0	0.78	0.06	<0.001
<i>Loin</i>					
1	Loin = 0.4(±0.01) – 0.03(±0.009)PC	2.0	0.80	0.04	<0.001
<i>Ham</i>					
1	Ham = 1.2(±0.01) – 0.2(±0.01)PC	2.0	0.83	0.08	<0.001
<i>Rib</i>					
1	Rib = 1.0(±0.02) – 0.1(±0.01)PC	2.0	0.56	0.12	<0.001
<i>Waste parts of the carcass (OFF)</i>					
1	OFF = 5.6(±0.13) – 0.2(±0.06)PC	2.0	0.36	0.76	0.003
<i>Viscera and organs (VISC)</i>					
1	VISC = 3.2(±0.07) – 0.3(±0.03)PC	2.0	0.73	0.38	<0.001
<i>Loin eye area (LEA)</i>					
1	LEA = 5.6(±0.14) – 0.3(±0.06)PC	2.0	0.50	0.81	<0.001

<sup>a</sup>Regression coefficient RMSE,  $R^2$ ,  $C_p$ , and  $P$ -value are updated with respect to a new independent variable to the prediction equation, the new independent variable is additionally with respect to the  $C_p \approx p$  independent variables, and root-mean-square error and cumulative  $R^2$ . PC, principal component.

animals (Fernandes *et al.*, 2010; Hernandez-Espinoza *et al.*, 2012; De Paula *et al.*, 2013; Bautista-Diaz *et al.*, 2017; Costa *et al.*, 2020). There is a significant relationship between BMs and the live weight of animals (Assan, 2013), thus allowing breeders to make more informed selection decisions. This direct relationship between body weight and BMs in goats is reported by Mahieu *et al.* (2011), Souza *et al.* (2014) and Tesema *et al.* (2019). Therefore, the best results are obtained when other BMs are included in the predictive model. Tesema *et al.* (2019) observed that the bodyweight of crossbred Boer goats showed a high correlation with thoracic perimeter (0.94) and body length (0.91).

The moderate to high correlation value implies that BMs can be used as an indirect selection criterion to improve meat production (Agamy *et al.*, 2015; Tesema *et al.*, 2019). Therefore, the buyer of live goats can predict the weight of the characteristics and first cuts of the carcass from BMs.

Several studies have demonstrated a direct relationship between body weight and BMs in goats (Mahieu *et al.*, 2011; Souza *et al.*, 2014). There is a significant relationship between BMs, which can be used to estimate the live weight and carcass characteristics due to the practicality of the method, so the best results are obtained when other BMs are included in the

predictive model (Assan, 2013), thus allowing breeders to make selection decisions. These results suggest that breeders who do not have a scale to weigh goats can estimate live weight using morphometric measurements, that is, they can use a tape measure instead of a scale (Tesema *et al.*, 2019).

The selection of variables in the stepwise regression analysis was performed by calculating Mallows'  $C_p$ , which is a measure of the forecast equation (Mallows, 1973). This method provides a single combination of variables for each equation. The model size and the fit criteria ( $R^2$  and RMSE) are fixed, as the ideal  $C_p$  value must be close to the number of variables involved in the model (Laville *et al.*, 1996).

Multiple regression analysis has been used to interpret complex relationships between live weight and BMs. A fundamental step in the construction of a multiple regression model for predictive purposes is to determine the variables that best contribute to the response variable, with the elimination of non-significant variables ( $P > 0.05$ ) (Yakubu and Mohammed, 2012).

The data presented an index for the KMO test of 0.80, demonstrating the adequacy of the factor analysis. For Hair Júnior *et al.* (2014), the acceptable values of adequacy are between 0.5 and 1.0; therefore, below 0.5 indicates that the factor analysis is inadequate.

**Table 7.** Eigenvalue, total variance, commonality and loadings factor after varimax rotation with Kaiser normalization in crossbred Boer v. Savanna goats

Variable	Principal component	Commonality
Chest width	-0.40	0.16
Croup width	-0.85	0.72
Croup perimeter	-0.89	0.78
Withers height	-0.89	0.79
Croup height	-0.91	0.83
Body length	-0.92	0.85
Leg length	0.67	0.44
Thoracic perimeter	-0.92	0.84
Thigh circumference	-0.49	0.24
Eigenvalue	5.7	-
Total variance (%)	63	-

Kaiser (1974) indicates that, for the adequacy of fit of a factor analysis model, the KMO value must be greater than 0.8.

Through factor analysis, it was possible to observe that the first factor extracted by the method of Kaiser (1974), was responsible for accumulating 62% of the total variance of the studied characteristics (Table 7), that is, most of the variation was explained with the first factor, with reduced sample space. Gomes *et al.* (2013), when evaluating the carcass characteristics of five genetic groups of goats in Brazil, selected the first four factors that explained 77% of the total variance of the data.

Communalities ranged from 0.16 to 0.85, with chest width, thigh circumference and leg length being the variables with less commonality and the croup width, croup perimeter, withers height, croup height, length of body and thoracic perimeter of more significant commonality, to explain the total variability of the extracted factors (Table 7). Commonality is an index of total variability and indicates how much a given variable contributed to the total variation of the factors considered (Morrison, 1976), with 0.5 being the minimum acceptable value. Lower values of commonality are indicative of a low correlation between original variables evaluated and non-adequacy to the model. In our study, most variables showed high commonality; therefore, the characteristics used to evaluate the carcass characteristics and weight of the cuts demonstrate the adequacy in the analysis.

Factor loads or eigenvectors (weights) represent the correlation between the original variables and the factors. Thus the more significant, the higher the factor load of a variable, more significant the correlation with a given factor (Hair Júnior *et al.*, 2009). Croup width, croup perimeter, withers height, croup height, body length and chest circumference were the variables with the highest factor load and inversely related to factor 1 (Table 7). These variables showed correlations of moderate to high magnitude (Tables 2 and 3). The thoracic perimeter, body length, withers and croup height are the primary BMs that constitutes an essential database for the evaluation of animals (Souza *et al.*, 2014). Since these measures indicate the carcass yield and the digestive and respiratory capacity of the animals and in the genetic improvement can be used in indirect selection for body weight.

The use of morphological variables should be treated with caution since multicollinearity is associated with unstable estimates of

the regression coefficients (Ogah *et al.*, 2011). The use of orthogonal characteristics provides a better and reliable assessment of live weight and carcass characteristics, as it is capable of breaking multicollinearity; it is a problem associated with the use of biometric measures of the animals' bodies (Yakubu *et al.*, 2009; Ogah *et al.*, 2011; Yakubu and Mohammed, 2012), while Tesema *et al.* (2019) working with a prediction with original and orthogonal characteristics observed that the variation explained by the interdependent explanatory variables was superior to the use of orthogonal characteristics for live weight, carcass characteristics, and forecast of the primary cut weight of the Boer goat carcass.

Moderate to high and positive correlations of morphological characteristics with body weight, carcass characteristics and primary carcass cuts were obtained. They suggest the adequacy of morphological characteristics as criteria for early selection of crossbred Boer goats for their body weight and carcass characteristics without slaughter.

The use of factor scores in multiple regression models eliminates the problem of the interdependence of explanatory variables, thus improving the accuracy of the interpretation of the results. The information obtained in the present study may be useful to support the genetic improvement and commercialization of animals.

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