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Depicting latent variables considering different pig genetics and nutritional plans in crossbred pigs

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ABSTRACT - We aimed to reduce the dimensionality of quantitative traits in pigs applying factor analysis. Quantitative variables were collected, and the factor analysis extracted five factors with biological meaning related to performance, carcass quality, carcass yield, meat quality, and initial pH. These factors were posteriorly used as dependent variable to evaluate the effects of genetic groups (Piau, Duroc, and Pietrain crossbreds), nutritional plans (low, medium and high lysine levels) and sex. An interaction effect between genetic group and sex was observed in performance, in which Duroc crossbred showed the greatest scores. The Pietrain genetic group showed greater values of carcass quality compared with Duroc and Piau, while Piau crossbred pigs had greater values for meat quality compared with Pietrain and Duroc. A greater carcass yield was observed in Pietrain crossbred compared with Duroc pigs. Pigs fed under low lysine level had the lowest performance values. Carcass yield was affected by nutritional plans, in which the medium lysine level showed the greatest values. Meat quality was improved by the nutritional plan with high lysine level compared with the low lysine level. Initial pH showed increased means when using nutritional plans with low and medium lysine levels in diet composition. With regard to sex effects, a greater carcass quality was found for gilts compared with barrows. The reduction of the data dimensionality allowed the joint evaluation of genetic group, nutritional plan, and sex based on new latent variables that represented the original dataset under easier framework based on factors' biological interpretation.

Keywords: carcass, factor analysis, meat quality, multivariate, performance

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1. Introduction

Selection efforts in pig production were primarily focused on performance traits to the detriment of carcass and meat quality (Balatsky et al., 2016). Even though differences in carcass and meat quality traits across genetic groups have been observed, pigs usually show similar performance traits (Ventura et al., 2012; Veloso et al., 2019; Nakev and Popova, 2020). Differences in performance are more evident when comparing animals with outstanding genetics to not selected animals (Zhang et al., 2015, 2016).

In animal production systems, profitability is directly linked to animal performance traits. However, carcass and meat quality traits contribute to the production system success and consumer satisfaction as well (Marzoque et al., 2020). Therefore, evaluating performance, carcass, and meat quality together is crucial to improve pig production and pork market by sharing and providing better information for breeding and genetic improvements.

The simultaneous evaluation of local and commercial pig breeds allows visualizing different variation patterns and the selection effects on carcass and meat quality traits. Knowledge regarding the distinct genetic groups and the environmental factors affecting these traits makes it possible to designate which would be the best genotypes and also which environment would favor a target group of traits. Genetically improved animals have higher lysine requirements than not selected genetic groups. Therefore, different nutritional plans and nutrient levels should be evaluated according to animal genetic group (Argemí-Armengol et al., 2019; Veloso et al., 2019).

Most of the studies regarding quantitative traits in pigs have numerous variables (Argemí-Armengol et al., 2019; Formenton et al., 2019; Veloso et al., 2019) that commonly are highly correlated, and the use of those variables for univariate analysis may have outcomes that are difficult to interpret. Thus, multivariate methods enable an easier understanding of their results. The identification of latent unobserved variables may allow consistent biological explanations of the analysis outcomes. Factor analysis can provide latent variables that will reduce the original data dimension (Ferreira, 2011).

In the current study, we aimed to reduce the dimensionality of quantitative traits in pigs applying factor analysis. Thus, the resulted latent variables were used to evaluate the effects of three different genetic groups subjected to three nutritional plans.

2. Material and Methods

2.1. Experimental data

Data used on this study were collected from an experiment carried out in 2014 in Viçosa, MG, Brazil (20°46'35.9" S, 42°51'32.6" W, altitude of 648.74 m), and research on animals was conducted according to the institutional committee on animal use (No. 20/2014-CEUAP).

The genetic groups were derived from the mattings of different sires with F1 sows (Pietrain × Large White). Two commercial sire lines were used, a Pietrain and a Duroc-based line (Duroc). In addition, sires from the local Piau pig breed was also used to provide a contrast with the selected commercial lines.

A total of 102 progenies of the mattings were used in the experiment (52 barrows and 50 gilts), which were individually housed in pens (3 m^2) with concrete floor, semi-automatic feeders, and nipple drinkers. The animals were assigned to the treatments according to a completely randomized design in factorial scheme 3×3×2 (three genetic groups, three nutritional plans, and two sexes).

The nutritional plans were based on different digestible lysine (DL) levels: Low (7 g DL fed from 70 to 98 days of age; 6 g DL fed from 99 to 134 days of age; and 5 g DL fed from 135 to 156 days of age), Medium (9 g DL fed from 70 to 98 days of age; 8 g DL fed from 99 to 134 days of age; 7 g DL fed from 135 to 156 days of age), and High (11 g DL fed from 70 to 98 days of age; 10 g DL fed from 99 to 134 days of age; and 9 g DL fed from 135 to 156 days of age).

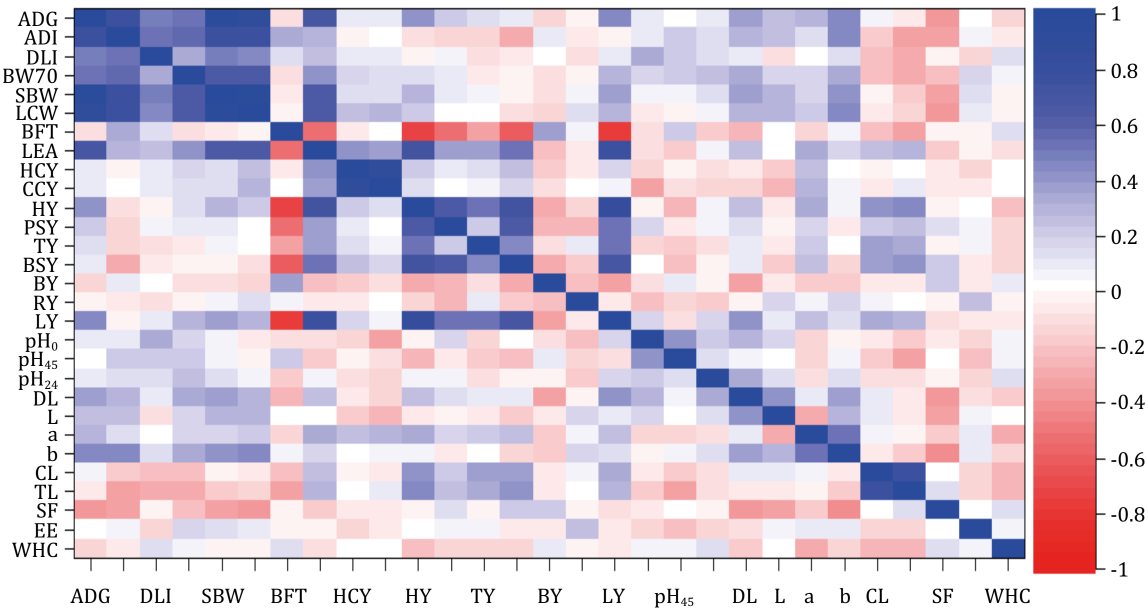
The experimental diets were formulated based on corn and soybean meal, supplemented with minerals, vitamins, and aminoacids to attend the nutritional requirements of the animals with except of digestible lysine, according to Rostagno et al. (2011). The proportions of essential aminoacids and digestible lysine were met according to the ideal protein concept (Rostagno et al., 2011). Feed and water were provided *ad libitum*.

The following quantitative variables were recorded: average daily weight gain (ADG), average daily intake (ADI), digestible lysine intake (DLI), body weight at 70 days (BW70), slaughter body weight

(SBW), left carcass weight (LCW), backfat thickness (BFT), loin eye area (LEA), belly yield (BY), Boston shoulder yield (BSY), ribs yield (RY), tenderloin yield (TY), loin yield (LY), picnic shoulder yield (PSY), ham yield (HY), hot carcass yield (HCY), cold carcass yield (CCY), water-holding capacity (WHC), cooking loss (CL), drip loss (DL), total loss (TL), redness (a*), yellowness (b*), lightness (L*), shear-force (SF), pH at slaughter (pH_0), pH at 45 min postmortem (pH_{45}), pH at 24 h postmortem (pH_{24}), and ether extract (EE). More details about this experiment can be found in Veloso et al. (2019).

2.2. Statistical analyses

The suitability of the original quantitative variables for factor analysis was evaluated by Pearson correlation values (Figure 1).



ADG - average daily weight gain; ADI - average daily intake; DLI - digestible lysine intake; BW70 - body weight at 70 days; SBW - slaughter body weight; LCW - left carcass weight; BFT - backfat thickness; LEA - loin eye area; HCY - hot carcass yield; CCY - cold carcass yield; HY - ham yield; PSY - picnic shoulder yield; TY - tenderloin yield; BSY - Boston shoulder yield; BY - belly yield; RY - ribs yield; LY - loin yield; pH_0 - pH at slaughter; pH_{45} - pH at 45 min postmortem; DL - drip loss; L* - lightness; a* - redness; b* - yellowness; CL - cooking loss; TL - total loss; SF - shear force; EE - ether extract; WHC - water-holding capacity.

Figure 1 - Correlogram between the quantitative pig traits.

The factorial model adopted for an observable variable X_i with mean μ_i can be represented as follows (Johnson and Wichern, 2007):

$$X_i - \mu_i = l_{i1}F_1 + l_{i2}F_2 + \cdots + l_{ij}F_m + e_i,$$

in which $i = 1,2,...,p$ and $m \leq p$, p is the number of observable variables; m is the number of commons factors; the coefficient l_{ij} is the factor loading of the i-th phenotypic variable on the j-th factor, in which $j = 1,2,..,m$; $F_1, F_2, ..., F_m$ are named common factors (unobservable random variable); and e_i is the random error vector that is only associated with the i-th phenotypic variable X_i.

In matrix notation, the same model can be written as follows (Ferreira, 2011):

$$y - \mu = \Gamma F + \epsilon,$$

in which y is the vector of observations; μ is the vector of means for all observations; Γ is a matrix ($p \times m$) of coefficients known as factor loadings, which measure the association between each observable variable and the factors; F is a vector ($m \times 1$) of latent common factors; and ϵ is a vector ($p \times 1$) of random errors.

In the context of factor analyses, the following assumptions were established: $E(y) = \mu$; $E(c) = 0$; $E(s) = 0$; $Cov(c) = I_m$; $Cov(y) = \Sigma$; $Cov(s) = \psi$; $Cov(c, s) = 0$, in which ψ is $\text{diag}(\psi_i)$, s is the specific factor, and c are the common factors.

The suitability of a dataset for factor analysis was evaluated based on the Kaiser-Meyer-Olkin criterion (KMO) and Bartlett's test. The KMO measures the difference between the Pearson and partial correlations, which is calculated as follows:

$$KMO = \frac{\sum_{i \neq j} R_{ij}^2}{\sum_{i \neq j} R_{ij}^2 + \sum_{i \neq j} Q_{ij}^2},$$

in which R_{ij} and Q_{ij} are, respectively, Pearson and partial correlation between the variables i and j.

The higher value of the KMO, the better the suitability of the dataset for factor analysis. In this study, the threshold was used according to Sarstedt and Mooi (2019), which suggests a value above 0.6.

The Bartlett's test (T) was calculated according to Bartlett (1950), as follows:

$$T = -[n - (1/6)(2p + 11)] \left[\sum_{j=1}^{p} \ln \hat{\lambda}_i \right],$$

in which $\ln \hat{\lambda}_i$ is the Napierian logarithm of the i-th eigenvalue of the sample correlation matrix R_{pxp}, n is the sample size, and p is the number of variables.

The number of factors was determined based on the amount of variance explained by the extracted factors. According to Ferreira (2011), the factors should explain a minimum of 70% of the total variability. The Kaiser criterion was also evaluated to determine the number of factors, in which the factors with eigenvalues higher than one should be used. The factors readability in terms of biologically interpretable meanings was also considered.

The principal components method (Bartlett, 1950) was applied based on spectral decomposition of correlation matrix. The individual factor scores were calculated by regression method for each pig (Ferreira, 2011) and used as a new variable after the VARIMAX rotation procedure. The *psych* and *GPArotation* packages of the R software (R Core Team, 2021) were used to obtain the factor scores.

To evaluate the effects of the treatments and their interaction on individual factors scores, an Analysis of Variance (ANOVA) and Tukey tests were performed using the *ExpDes* package of the R software (R Core Team, 2021). The ANOVA assumption of residuals normality was verified using the Shapiro-Wilk test by *ExpDes* package, and the residual homoscedasticity was checked using Levene test by *Car* package, both packages used were from R software (R Core Team, 2021). The ANOVA was based on the following linear model:

$$y = \mu + g + d + s + g \times d + g \times s + d \times s + g \times d \times s + e,$$

in which y is the vector of observations; μ is the vector of means for all observations; g is the vector of genetic group effects; d is the vector of nutritional plan effects; s is the vector of sex effects; $g \times d$ is the vector of interaction between genetic group and nutritional plan effects; $g \times s$ is the interaction between genetic group and sex effects; $d \times s$ is the interaction between nutritional plan and sex effects; $g \times d \times s$ is the interaction between genetic group, nutritional plan, and sex effects; and e is the vector of random errors associated to observations, $e \sim N(0,\sigma^2)$.

3. Results

The number of observations, mean, standard deviation, and respective coefficient of variation, along with the minimum and maximum values observed for each quantitative variable, are presented in Table 1.

Table 1 - Number of observations (N), mean values (M), standard deviation (SD), coefficient of variation (CV%), minimum (Min), and maximum (Max) values for quantitative traits in pigs

Trait	Unit	N	M	SD	CV%	Min	Max
ADG	g/d	102	858.64	142.07	16.55	443.00	1,136.00
ADI	g/d	102	2,403.34	303.69	12.64	1,516.00	3,084.00
DLI	g/d	102	20.32	5.29	26.02	10.06	32.14
BW70	kg	102	24.87	3.55	14.28	16.95	33.05
SBW	kg	102	97.59	14.01	14.35	66.00	126.30
LCW	kg	102	38.96	5.87	15.06	26.55	51.50
BFT	Mm	102	16.85	6.40	38.01	6.75	37.89
LEA	cm^2	102	37.99	9.93	26.13	15.89	55.41
HY	%	102	25.54	2.02	7.92	20.86	29.75
BSY	%	102	15.24	0.99	6.49	13.25	17.23
TY	%	102	1.00	0.14	14.47	0.67	1.37
PSY	%	102	1.34	0.19	14.44	0.97	1.79
LY	%	102	5.06	0.95	18.72	3.20	7.42
HCY	%	102	79.60	1.79	2.25	75.13	82.97
CCY	%	102	77.46	1.91	2.46	72.44	81.25
DL	%	102	8.94	2.70	30.21	1.77	14.70
L*	Absorbance	102	60.09	2.70	4.50	54.25	67.23
SF	kg/cm^2	102	3.04	0.58	18.90	1.80	4.78
pH_0	pH	102	6.38	0.29	4.61	5.68	7.02
pH_{45}	pH	102	6.22	0.32	5.18	5.64	6.96
CL	%	102	20.94	2.63	12.55	15.65	25.99
TL	%	102	28.63	3.30	11.54	22.28	36.29
EE	%	102	2.34	0.46	19.74	1.10	3.00
a*	Absorbance	102	6.59	1.10	16.67	3.88	8.94
b*	Absorbance	102	15.24	1.11	7.26	13.02	18.16
WHC	%	102	77.72	3.44	4.42	69.54	86.21
BY	%	102	7.89	0.54	6.81	6.52	9.38
RY	%	102	11.72	1.13	9.67	8.74	14.59
pH_{24}	pH	102	6.10	0.33	5.42	5.61	6.93

ADG - average daily weight gain; ADI - average daily intake; DLI - digestible lysine intake; BW70 - body weight at 70 days; SBW - slaughter body weight; LCW - left carcass weight; BFT - backfat thickness; LEA - loin eye area; HY - ham yield; BSY - Boston shoulder yield; TY - tenderloin yield; PSY - picnic shoulder yield; LY - loin yield; HCY - hot carcass yield; CCY - cold carcass yield; DL - drip loss; L* - lightness; SF - shear force; pH_0 - pH at slaughter; pH_{45} - pH at 45 min postmortem; CL - cooking loss; TL - total loss; EE - ether extract; a* - redness; b* - yellowness; WHC - water-holding capacity; BY - belly yield; RY - ribs yield; pH_{24} - pH at 24 h postmortem.

3.1. Multivariate factor analysis

The KMO index (0.69) indicated that the correlation matrix is suitable to explain most of the variance (74%) (Pallant, 2007; Hair et al., 2009; Sarstedt and Mooi, 2019). Bartlett's sphericity test shows that the present database fits a multivariate factor analysis.

Eight latent common factors were extracted from the 29 initial variables (Table 2). The proportion of the explained variance (74%) was maximized with these eight factors (Table 2) in accordance with the Kaiser parameter of sampling adequacy (Figure 2).

Coefficients obtained as factor loadings were used to assign variables to the eight factors because they express the relationship of each variable, in which variables with highest factor loading was represented by the respective factor. Factor analysis indicated five common factors with biologically

Table 2 - Factor loadings for each trait in relation to the eight factors extracted, communalities (h^2), unicities (u^2), and the accumulated variance explained by each factor

Trait	F1	F2	F3	F4	F5	F6	F7	F8	h^2	u^2
ADG	0.91	0.21	−0.01	0.15	0.03	0.09	0.14	0.00	0.93	0.07
ADI	0.85	−0.27	−0.08	0.10	0.13	−0.08	0.17	0.09	0.87	0.13
DLI	0.60	−0.02	0.07	−0.21	0.46	−0.16	−0.07	0.08	0.65	0.35
BW70	0.62	0.14	0.05	0.19	0.07	−0.40	0.01	0.07	0.61	0.39
SBW	0.94	0.13	0.05	0.21	−0.03	−0.05	0.04	−0.01	0.96	0.05
LCW	0.92	0.04	0.19	0.21	−0.09	−0.04	0.02	−0.11	0.95	0.05
BFT	0.05	−0.88	0.01	−0.18	0.07	0.01	0.05	−0.03	0.81	0.19
LEA	0.58	0.67	0.28	0.07	−0.14	0.14	0.03	−0.01	0.90	0.1
HY	0.18	0.87	0.07	0.02	−0.13	0.21	0.13	0.06	0.88	0.12
BSY	0.02	0.74	−0.07	−0.12	0.13	0.01	0.07	0.08	0.60	0.4
TY	0.03	0.48	0.00	−0.06	−0.18	0.30	0.13	−0.18	0.41	0.59
PSY	−0.12	0.82	0.14	−0.16	−0.01	0.17	0.07	0.07	0.78	0.22
LY	0.25	0.86	0.05	0.20	0.01	0.10	0.01	0.05	0.86	0.14
HCY	0.10	0.14	0.92	−0.04	0.00	−0.03	0.02	0.00	0.88	0.12
CCY	0.11	0.03	0.93	−0.09	−0.16	−0.02	0.08	−0.04	0.91	0.09
DL	0.22	0.26	−0.12	0.70	0.21	−0.01	0.14	0.10	0.69	0.31
L*	0.24	−0.10	−0.26	0.68	−0.05	0.12	−0.29	−0.09	0.70	0.3
SF	−0.32	0.12	−0.13	−0.62	−0.01	−0.07	−0.25	0.07	0.59	0.41
pH_0	0.01	0.14	−0.25	0.17	0.74	−0.13	−0.11	0.09	0.71	0.3
pH_{45}	0.05	−0.20	−0.01	−0.01	0.71	−0.12	0.02	0.08	0.58	0.42
CL	−0.07	0.29	−0.08	0.09	−0.13	0.80	0.02	−0.05	0.75	0.25
TL	−0.19	0.36	0.02	−0.04	−0.27	0.73	−0.06	0.00	0.77	0.23
EE	0.09	0.07	−0.29	−0.12	−0.44	−0.45	0.08	−0.43	0.70	0.3
a*	0.12	0.23	0.20	−0.04	−0.13	−0.12	0.85	−0.03	0.86	0.14
b*	0.34	−0.09	−0.02	0.48	−0.10	−0.16	0.58	−0.01	0.72	0.28
WHC	−0.03	−0.10	0.10	−0.08	−0.08	−0.42	−0.59	0.08	0.57	0.43
BY	0.04	−0.44	−0.21	−0.43	−0.18	0.13	−0.10	0.44	0.68	0.32
RY	−0.01	−0.13	−0.03	0.21	−0.22	−0.03	−0.03	−0.75	0.67	0.33
pH_{24}	0.04	0.13	−0.12	0.38	0.01	−0.29	−0.14	0.64	0.69	0.31
Variance	0.22	0.39	0.48	0.56	0.61	0.66	0.71	0.74	-	-

ADG - average daily weight gain; ADI - average daily intake; DLI - digestible lysine intake; BW70 - body weight at 70 days; SBW - slaughter body weight; LCW - left carcass weight; BFT - backfat thickness; LEA - loin eye area; HY - ham yield; BSY - Boston shoulder yield; TY - tenderloin yield; PSY - picnic shoulder yield; LY - loin yield; HCY - hot carcass yield; CCY - cold carcass yield; DL - drip loss; L* - lightness; SF - shear force; pH_0 - pH at slaughter; pH_{45} - pH at 45 min postmortem; CL - cooking loss; TL - total loss; EE - ether extract; a* - redness; b* - yellowness; WHC - water-holding capacity; BY - belly yield; RY - ribs yield; pH_{24} - pH at 24 h postmortem.

interpretable meanings, grouping 20 variables. Thus, only these five factors were used in ANOVA. The first latent factor (F1) included ADG, ADI, DLI, BW70, SBW, and LCW, and explained about 22% of the total variance. All these variables came from measures taken during the growth of the animal and at slaughter. Therefore, this factor was labeled as performance. It was observed that the factor loadings of F1 were positive like the correlation among these variables. The second latent factor (F2) was associated with carcass measurements (BFT, LEA, HY, BSY, TY, PSY, and LY), and was labeled as carcass quality. Loading factors were positive in all variables of F2, except for BFT. Negative loading in BFT means opposite increment in relation to the other variables.

Variables HCY e CCY were grouped in third latent factor (F3) and labeled as carcass yield. Factor loadings indicated positive relationship between the two referred variables. The fourth latent factor

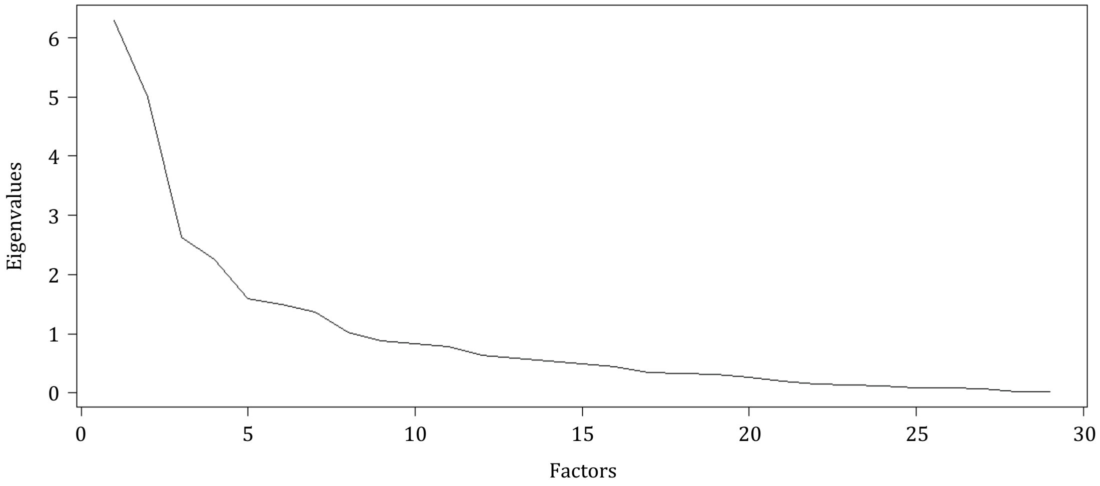


Figure 2 - Scree plot from factor analysis for pig quantitative traits, with eigenvalues against their factor numbers before rotation.

(F4) was associated with meat quality. It was labeled as meat quality because of the biological relationship between the variables, i.e., DL, L*, and SF, which is associated to better or worse meat quality, according to their magnitude. Factor loadings were positive in DL and L* and negative in SF.

The fifth latent factor (F5) was labeled initial pH, because it included the variables pH_0 and pH_{45}, which were both measured in early moments after slaughter.

All the communalities observed for the five factors with biologically interpretable meanings were considered satisfactory (h^2>0.5) (Sarstedt and Mooi, 2019), except for TY (h^2 = 0.41).

3.2. Effects of genetic group, nutritional plan, and sex on latent factors

To analyze the effects of the genetic group, nutritional plan, and sex, and their interactions, analyses of variance were conducted using the scores generated by the five factors with biological interpretation. Interaction (P<0.05) between genetic group and sex was found for the non-observable performance latent variable (Figure 3). No interaction between the effects was observed for the other factors. For barrows, better performance was observed for Duroc compared with Piau, and it did not differ between Duroc and Pietrain. For gilts, a better performance was observed for Duroc when compared with Piau and Pietrain.

Means followed by the same letter are not significantly different by Tukey's test (P>0.05).

Figure 3 - Comparison between genetic group and sex for performance factor.

The latent variables carcass quality, carcass yield, and meat quality were affected by different genetic groups ($P<0.05$) (Table 3). Pietrain crossbred animals had the greatest average of carcass quality. Pietrain and Piau showed the highest means, whereas the Duroc crossbred exhibited the lowest mean in carcass yield. Meat quality showed greater averages in Piau when compared with Pietrain. That is, higher average of the factor meat quality means a meat with lower SF and higher DL and L*.

The latent variables performance, carcass yield, meat quality, and initial pH were affected by the nutricional plans ($P<0.05$), but no difference was observed for carcass quality ($P>0.05$) (Table 3). High and medium lysine levels in nutritional plans showed higher means for performance and carcass yield compared to low lysine level ($P<0.05$). The nutritional plan with high lysine level resulted in lower meat quality compared with the nutritional plan with low lysine level ($P<0.05$); however, it did not differ from the medium level ($P>0.05$). For initial pH, the nutritional plan with high lysine level showed the highest mean when compared with the other nutritional plans assessed ($P<0.05$). Effect of sex was observed only for carcass quality, in which gilts showed higher means than barrows ($P<0.05$).

4. Discussion

4.1. Multivariate factor analysis

Databases with high number of variables are frequently observed in animal production studies. Multivariate techniques proved to be adequate for the evaluation of high dimensional data analyses because it decreases the complexity involved in the univariate analyses of multiple variables, being a useful tool to investigate variable relationship (Macciotta et al., 2012; Teixeira et al., 2015; Conte et al., 2016; Paiva et al., 2020). Among other multivariate techniques, factor analysis can reduce the dimensionality, while capturing a certain amount of the overall variance in the observed variables and generating satisfactory results in pig research (Silva et al., 2011; Teixeira et al., 2015, 2016). Factor analysis can represent a large number of correlated variables extracting maximum common variance from all variables. Correlated variables usually show correlation even in sample error, therefore making it difficult to understand the results when tested one by one (Bolormaa et al., 2010). In this study, the correlation matrix observed among the original quantitative variables was used for factor analysis. The database dimensionality was reduced from 29 variables to five factors or latent variables, which presented biological interpretation and captured a considerable amount of the variance (61%).

The new latent variables were labeled according to the variable importance inside each factor in performance, carcass quality, carcass yield, meat quality, and initial pH. Six original variables (ADG, ADI, DLI, BW70, SBW, and LCW) had high and positive loadings in the first factor, providing the creation of the performance factor. Positive loadings observed among the variables in this factor indicates that the higher the values of the variables, the higher the score observed for the latent variable performance. Thus, the scores observed for performance may be understood as the inference for the set of variables that compose it (Teixeira et al., 2015).

Using pig carcass quality variables recorded by using Brazilian and American carcass grade methods, Silva et al. (2011) also reported a latent variable (factor) related to carcass quality besides a correlation structure between variables. When using univariate analysis, variables BFT and LEA are the most common variables for carcass quality evaluation. This is because of the high and negative correlation between BFT and LEA and the high correlation between these two variables with most carcass variables (Nakano et al., 2015). The negative factor loading for BFT and positive for the other original variables (LEA, HY, BSY, TY, PSY, LY) observed in the factor carcass quality are in line with the correlations observed for these variables when considered in univariate analyses (Figure 1). Nakano et al. (2015) observed a correlation of −0.43 between BFT and LEA in a study evaluating carcass variables in Duroc pigs. Thus, according to the correlation observed between variables, lower factor loadings for BFT result in better scores for this factor.

Table 3 - Effects of genetic group, nutritional plan, and sex on factors extracted by multivariate factor analysis for pig quantitative traits

Factor	Genetic group			P<F	Nutritional plan			P<F	Sex		P<F
	Piau N = 32	Duroc N = 36	Pietrain N = 34		Low	Medium	High		Barrows	Gilts	
Performance	−0.68±0.74	0.72±0.88	−0.13±0.79		−0.32±0.99b	0.12±0.99a	0.22±0.95a	0.020	0.31±0.85	−0.32±1.05	
Carcass quality	−1.11±0.69c	0.21±0.62b	0.81±0.54a	<.001	−0.12±1.01	0.01±1.06	0.12±0.94	0.354	−0.17±1.08b	0.18±0.88a	0.001
Carcass yield	−0.04±0.85ab	−0.38±1.06b	0.44±0.91a	0.001	−0.37±0.96b	0.30±0.90a	0.10±1.04ab	0.010	−0.07±1.12	0.07±0.87	0.380
Meat quality	−0.33±0.90b	−0.08±0.94ab	0.40±1.04a	0.005	0.41±0.97a	0.03±0.92ab	−0.48±0.92b	0.001	0.12±0.94	−0.13±1.05	0.186
Initial pH	0.19±1.02	−0.24±1.00	0.08±0.95	0.135	−0.33±0.80b	−0.11±0.96b	0.47±1.08a	0.002	0.18±0.93	−0.18±1.04	0.079

Means followed by the same letter in the row are not significantly different by Tukey’s test (P≥0.05).

Carcass yield involves not only the muscle quantity in carcass, as observed in most commercial cuts, but also fat, skin, and bones (Martins et al., 2015). Therefore, the factor carcass yield provides an evaluation of all these tissues simultaneously, and not only muscle tissue, although meat has the greatest market value.

In meat quality factor, a negative score for SF and positive for the other original variables were observed. This is in line with the biological interpretation. Lower scores for meat quality would imply better meat quality due to the direction of the variables, in which higher drip losses and brightness results in higher shear force (reduced tenderness). It is important to mention that meat quality variables have thresholds, in which exceeding these thresholds results in undesirable meat products such as PSE (pale, soft, exudative) and DFD (dark, firm, dry) meat (Marzoque et al., 2020).

The initial pH factor, including pH_0 and pH_{45} variables, allows inference on the pH measured in the first moments after slaughter by the use of a single latent variable. Meat quality is strongly associated to the pH decay in the first post-mortem hour. The initial pH can be used for detecting earlier undesirable effects on pig products, such as PSE meat, which can be generated mostly from carcasses with a pH_{45} lower than 5.8 (Cazedey et al., 2016), and DFD meat, resulting from a higher final pH (Marzoque et al., 2020).

Factorial scores allow subsequent analysis according to the correlation between the variables in each one of the factors, thus reducing the dimensionality of the data under study (Teixeira et al., 2016). Studies on animal genetics have been done using factors as new variables in univariate analyses with less complex interpretations than if taken using all original variables (Silva et al., 2011; Macciotta et al., 2012; Conte et al., 2016).

4.2. Effects of genetic group, nutritional plan, and sex on latent factors

Interaction between genetic group and sex was observed for the latent variable performance. Tukey test pointed that within gilts, the Duroc breed showed an improved performance compared with Piau and Pietrain crossbred. Among barrows, Duroc showed an improved performance compared with Piau crossbred, but did not differ from Pietrain crossbred pigs. When univariate studies approaching the original variables were employed, similar results were observed (Faria et al., 2009; Bertol et al., 2013). Pietrain pigs have lower growth rate and slaughter weight compared with Duroc pigs (Bertol et al., 2013). Unexpectedly, Pietrain crossbred barrows showed no difference in performance compared with Piau crossbred. Pigs of the naturalized Piau breed were not subjected to selection; however, in this study, F1 crosses of Piau with commercial dams were used. Thus, the results may be in part explained by heterosis, which is expected to be higher in the crosses with Piau than with Pietrain. Piau breed has lower scores for performance, similar to findings of Faria et al. (2009), who performed a univariate study that showed lower growth rates for Piau breed (Faria et al., 2009).

Nutritional plans with medium and high lysine levels provided higher performance in pigs in the present study, which is in agreement with other studies evaluating performance variables in univariate analysis (Lee et al., 2016; Coble et al., 2018; Totafurno et al., 2019). Trindade Neto et al. (2005) observed similar results to the ones found in the current study, wherein 1.03% supply of digestible lysine provided better trends in pig growth variables. Therefore, medium lysine level supply would be sufficient to provide higher performance of the pigs with lower costs. The performance factor contributed to the analysis of some variables together. The scores observed would allow the analysis of the effect on nutritional plans when considering correlations between the original variables.

The highest carcass quality was observed in Pietrain crossbred pigs, which shows the superiority of the animals of this genetic group. As expected, Piau crossbred pigs were the ones with the lower carcass quality. Faria et al. (2009) observed that Piau has higher fat content and lower lean meat deposition in the carcass, when working with F2 animals by univariate analyses. Piau is a genetic group known as having higher BFT and lower LEA when compared with commercial breeds because of the smaller genetic improvement efforts (Pinheiro et al., 2013).

Sex hormone action may promote the differences observed between sex effects for the variables in carcass quality factor (Pinheiro et al., 2013), in which gilts had better scores than barrows. The variables included in this factor were analyzed in a univariate way by Trindade Neto et al. (2005), who also reported superior gilts compared with barrows.

Pietrain genetic group was outstanding compared with the Duroc crossbred based on the scores presented for the carcass yield factor, and this is because of the superiority of these animals for the variables represented by this factor. Unexpectedly, Piau breed did not differ from the other genetic groups evaluated and demonstrated a good carcass yield despite presenting lower carcass quality. It is noteworthy that the carcass yield is given in terms of the relationship between the hot and cold carcass weight and body weight (Martins et al., 2015). Contrasting this result, Bertol et al. (2013) reported higher hot carcass yields in Duroc pigs compared with a line composed mostly of Pietrain and naturalized Brazilian breeds being examined in a univariate way.

The medium lysine level nutritional plan improved the carcass yield compared with the low level of this aminoacid. Coble et al. (2018), when studying the variables as those that composed carcass yield, reported that lower lysine levels provide better results; however, the authors evaluated higher lysine levels (0.99, 1.07, and 1.14% of total lysine in the finishing phase) than those used in this study (0.5, 0.7, and 0.9% of total lysine in the finishing phase).

The Piau genetic group stood out in the meat quality factor when compared with the Pietrain genetic group, while Duroc genetic group did not differ from the other ones. Duroc pigs are often referred to as a breed of improved meat quality because they have tender meat and lower drip loss compared with other commercial genetic groups (Peloso et al., 2010; Zhang et al., 2016). Naturalized Brazilian pigs contribute positively for the meat quality (Silva et al., 2019), which may be justified by the higher fatness level in Piau pigs and for the fact that these animals are not under selection (Serão et al., 2011). It must be emphasized that the Pietrain genetic group also presented low scores for meat quality, as found by Kim et al. (2020) in a univariate approach, when evaluating Embrapa MS115 animals with mostly Pietrain genetic composition.

The different lysine levels also had an impact on meat quality. After carnitine synthesis, lysine is stored in muscle tissue, where it works in oxidation process of fatty acids (Lee et al., 2016). In this way, lower lysine levels have the potential to reduce the oxidation of fatty acids, resulting in higher intramuscular fat as a result of lower protein deposition and thus producing lighter meat (Lee et al., 2016) and also meat with higher tenderness.

Considering the initial pH factor, it can be noted that different lysine levels caused differences in pH reduction at early post-mortem period, even though the mean values for each treatment in each original variables were found to be within the normal ranges. The nutritional plans with lower lysine levels were related to lower initial pH values and higher lysine levels to higher initial pH. It should be noted that intensification of protein denaturation processes may result from severe reductions in the initial pH prior to carcass chilling (first 45 to 60 min after slaughter), which may increase the risk of PSE meat (Matarneh et al., 2017). However, it does not apply to the mean pH values observed in the variables that formed the initial pH factor. On the other hand, high initial pH values can result in deviations in postmortem glycolysis processes, which may intensify procedures that would cause meat with unwanted DFD-like aspects. Dark, firm, dry meat results in intensification of the coloring and reduction of the shelf life of the products (van der Wal et al., 1988).

5. Conclusions

Factor analysis allowed the reduction of data dimensionality, through the identification of the five orthogonal latent variables labelled as performance, carcass quality, carcass yield, meat quality, and initial pH, representing the original set of 29 variables. The use of these latent variables also allows a better understanding of the interrelations among the quantitative variables of pigs. By applying factor analysis, we found that Duroc crossbred shows the best performance among commercial breed assessed in the trial. However, Pietrain crossbred is the best genetic group regarding carcass quality, in which gilts have better results than barrows. Piau crossbred animals have better meat quality variables, followed by Duroc pigs. With regard to the nutritional plans evaluated, nutritional plan with low lysine level is related to the decrease of animal performance.

Conflict of Interest

The authors declare no conflict of interest.

Author Contributions

Conceptualization: R.F. Henriques, F.F. Silva, R. Veroneze and P.S. Lopes. Data curation: M.S. Duarte, R.C. Veloso and P.S. Lopes. Formal analysis: R.F. Henriques, F.F. Silva and R. Veroneze. Funding acquisition: F.F. Silva, R. Veroneze and P.S. Lopes. Investigation: R.F. Henriques, F.F. Silva, R. Veroneze, M.S. Duarte, J.T. Paiva and P.S. Lopes. Methodology: R.F. Henriques, F.F. Silva, R. Veroneze, J.T. Paiva and P.S. Lopes. Project administration: F.F. Silva, R. Veroneze and P.S. Lopes. Resources: F.F. Silva, R. Veroneze and P.S. Lopes. Software: R.F. Henriques, F.F. Silva and R. Veroneze. Supervision: F.F. Silva, R. Veroneze, M.S. Duarte and P.S. Lopes. Validation: R.F. Henriques, F.F. Silva, R. Veroneze, J.T. Paiva and P.S. Lopes. Visualization: F.F. Silva, R. Veroneze and P.S. Lopes. Writing – original draft: R.F. Henriques, F.F. Silva and P.S. Lopes. Writing – review & editing: R.F. Henriques, F.F. Silva, R. Veroneze, M.S. Duarte, J.T. Paiva and P.S. Lopes.

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