



Use of multivariate analysis to evaluate genetic groups of pigs for dry-cured ham production

Henrique T. Ventura^a, Paulo S. Lopes^{a,*}, José V. Peloso^a, Simone E.F. Guimarães^a, Antonio P.S. Carneiro^b, Paulo L.S. Carneiro^c

^a Departamento de Zootecnia, Universidade Federal de Viçosa, 36570-000 Viçosa, MG, Brazil

^b Departamento de Estatística, Universidade Federal de Viçosa, 36570-000 Viçosa, MG, Brazil

^c Departamento de Ciências Biológicas, Universidade Estadual do Sudoeste da Bahia, 45200-000 Jequié, BA, Brazil

ARTICLE INFO

Article history:

Received 27 April 2011

Received in revised form

5 June 2012

Accepted 6 June 2012

Keywords:

Canonical variable

Cluster analysis

Single linkage method

Tocher optimization method

ABSTRACT

Records of a pig population used for dry-cured ham production were used to evaluate genetic groups by multivariate analysis. The investigated genetic groups were as follows: DULL=Duroc × (Landrace × Large White), DULA=Duroc × Landrace, DUWI=Duroc × Large White, WIWI=Large White and DUDU=Duroc. Two groups were obtained for the carcass traits hot carcass weight (HCW), backfat thickness (BT) and loin depth (LD), with the groups including 597 and 341 animals harvested at 130 kg and at 160 kg weights, respectively. Two groups were also found for ham traits gross ham weight (GHW), trimmed ham weight (THW), ham inner layer fat thickness (HIFT), ham outer layer fat thickness (HOFT), pH (PH), and Göfo value, with 393 and 91 animals harvested at 130 kg and 160 kg weights, respectively. The analysis was performed within each group of traits and harvest weights, and the animals without records were excluded. The first and the second canonical variables explained 97.5% and 93.6% of the total variation for the carcass traits at 130 kg and 160 kg, respectively, and 88.8% of ham traits at 130 kg. In the dispersion graph concerning the canonical means, a significant distance was observed between the genetic groups DUDU and WIWI for the carcass traits at 130 kg and 160 kg and the ham traits at 130 kg. The 50% Duroc animals exhibited little dispersion regarding the carcass traits at 130 kg and 160 kg and were not divergent from the DUDU genetic group for the ham traits at 130 kg. In a cluster analysis using the single linkage method, DULL, DULA and DUWI were grouped with a high similarity level for the carcass traits at 130 kg and 160 kg and ham traits at 130 kg. Using the Tocher optimization method, 50% Duroc crossbred and 100% Duroc purebred animals were grouped for the ham traits at 130 kg, suggesting that for ham traits, 50% Duroc animals were similar to 100% Duroc purebred animals. In this context, the genetic groups Duroc × Large White, Duroc × Landrace and Duroc × (Landrace × Large White) are recommended for use in producing dry-cured ham.

© 2012 Elsevier B.V. Open access under the [Elsevier OA license](http://creativecommons.org/licenses/by/3.0/).

1. Introduction

The pork meat industry has considerably increased the production of items with high aggregated value to meet the demand in a market niche that consumes products of

superior quality, and dry-cured ham is significant within this segment. In the production of dry-cured ham, such as Parma and San Daniele, the quality of the raw material in its unprocessed state is considered to be of fundamental importance because original defects in the meat cannot be corrected due to the fact that the curing process consists basically of adding salt and controlling the environment. Thus, ham is sought that can reach the end of curing with the desired sensorial traits and minimum loss during the

* Corresponding author. Tel.: +55 31 3899 3319; fax: +55 31 3899 2275.
E-mail address: plopes@ufv.br (P.S. Lopes).

process (Bosi and Russo, 2004). Traits related to product acceptance include fat cover thickness, intramuscular fat quantity and muscle and fat coloring (Candek-Potokar et al., 2002). Sabbioni et al. (2004) recommended that ham for dry-cured ham production should have a high percentage of intramuscular fat and a fat thickness greater than 8 mm.

Weight at harvest is a factor to be considered because it is also linked to the ham weight and fat cover that are correlated negatively with losses during the curing process. Harvesting is recommended at approximately 160 kg live weight (Bosi and Russo, 2004).

According to Bosi and Russo (2004), the genotype of the animals used has a direct effect on ham traits. Pure Duroc breed animals and crossbreeds of Durocs with Landrace and Large White animals have been used in high-quality dry-cured ham production (Garcia-Rey et al., 2004). However Duroc animals are inappropriate for industrial use at 160 kg live weight due to their low feed efficiency on the farm, excess fat on the carcass, as well as occurrence of deep seated hair on the hams (Peloso et al., 2010). Generating crosses with the Duroc breed has resulted in meat with desirable traits for obtaining greater intramuscular fat deposition and small losses during the dry-cured ham production process (Candek-Potokar et al., 2002).

Several studies have been carried out to investigate the influence of genotype on ham traits (Candek-Potokar et al., 2002; Carrapiso and García, 2008; Cilla et al., 2005; Garcia-Rey et al., 2004; Guerrero et al., 1996; Peloso et al., 2010). However, all of these studies used univariate analysis techniques, which are limited because they do not take into consideration possible correlations among the investigated traits.

There are several approaches in the area of multivariate analysis that allow joint analysis of such traits. The canonical variables technique represents an important tool in discriminating genotype groups because it allows verification of the degree of similarity by uni- or two-dimensional dispersion diagrams involving canonical means. Cluster analysis is another type of multivariate technique that is often used with the objective of obtaining a scheme that enables the sample units to be summarized in a number of groups so that there is homogeneity within and heterogeneity between groups.

Most such cluster techniques begin with the calculation of a similarity or dissimilarity matrix among the sample units. A recommended dissimilarity measurement is the Mahalanobis distance (D^2) when there are repetitions within the sample units and when the traits are correlated (Cruz et al., 2004).

Once the Mahalanobis distance (D^2) has been determined, the Tocher optimization method (Rao, 1952) is a viable alternative for grouping the sample units. This methodology always maintains an intergroup distance greater than the mean intragroup distance (Cruz et al., 2004).

Therefore, the objective of the present study was to assess pig genetic groups for dry-cured ham production and also to determine whether crossbred Duroc fit a high-quality ham production as purebred Duroc using multivariate analysis techniques.

2. Materials and methods

The data used in the present study were derived from five pig genetic groups produced in a multiplier farm in the state of Santa Catarina in the south of Brazil. The following genetic groups were included in our analyses: DULL=Duroc × (Landrace × Large White), DULA=Duroc × Landrace, DUWI=Duroc × Large White, WIWI=Large White and DUDU=Duroc.

After weaning at 28 days of age, the piglets were transferred weekly in batches of 20 to a nursery and growing barns and separated based on their genetic group into pens of mixed gender. The animals remained inside these facilities until they reached 83 days of age and a mean weight of 48.3 kg. They were then transferred to finishing barns and kept in groups of 5–8 animals per stall, separated by genetic group and gender. Throughout the experimental phase, the animals received a corn and soybean meal-based diet ad libitum (Peloso et al., 2010). The animals were harvested in two periods (130 and 160 kg live weights). In the first period animals reached on average 135.3 kg ($SD=5.9$ kg) at 163 days after birth, whereas in the second period animals reached on average 163.8 kg ($SD=8.8$ kg) at 202 days. The animals in the Duroc (DUDU) genetic group with 160 kg harvest weights were not tested because animals in this class are inappropriate for industrial use due to their low feed efficiency on the farm, excess fat on their carcasses and the occurrence of deep seated hair on their hams. Twenty-five consecutive harvest were performed (two harvest per week), with the number of pigs per harvest ranging from 13 to 60. Animals were harvested following the routine standard operational procedures of the plant according to the technical standards of the Federal Inspection Service (SIF) of the Ministry of Agriculture, Livestock and Food Supply. The following carcass traits were obtained: hot carcass weight (HCW), backfat thickness (BT) and loin depth (LD). Additionally, we determined the following ham traits: gross ham weight (GHW), trimmed ham weight (THW), ham inner layer fat thickness (HIFT), ham outer layer fat thickness (HOFT), pH at 24 h post-mortem (pH) and the ham color based on objective surface light reflectance of semimembranous muscle at 24 h after harvest (Göfo value, ranging from 0=pale to 100=dark). Details of the measurements of the traits are described by Peloso et al. (2010).

The number of individuals in each genetic group and the mean and coefficient of variation are shown in Tables 1 (harvest at 130 kg) and 2 (harvest at 160 kg).

The condition number test was used according to the description of Montgomery and Peck (1992) to detect the effect of multicollinearity or linear correlation among the variables that could lead to the formation of singular or ill-conditioned matrices. No variables were discarded because the condition number for all of the data groups was less than 100. The data were previously adjusted for the fixed effect of gender by the least squares method. The variables were then standardized according to the method of Cruz et al. (2004).

The statistical analyses were carried out using SAS for Windows version 9.1 (SAS[®] Institute, 2002–2003) with

Table 1

Number of individuals in each genetic group, mean and coefficient of variation (CV, %) for animals harvested at 130 kg.

	Genetic groups ^a									
	DULL		DULA		DUWI		WIWI		DUDU	
	Mean	(CV, %)	Mean	(CV, %)	Mean	(CV, %)	Mean	(CV, %)	Mean	(CV, %)
Number of pigs	133		158		116		64		126	
Carcass traits ^b										
HCW (kg)	95.2	5.9	94.8	5.4	95.6	5.2	96.2	5.6	93.5	5.1
BT (mm)	18.3	24.4	18.7	21.6	18.9	24.5	16.4	23.6	20.7	23.9
LD (mm)	56.7	9.9	55.6	10.5	56.1	10.8	58.7	9.2	55.3	11.3
Number of pigs	102		116		59		32		84	
Ham traits ^c										
GHW (kg)	15.2	5.8	15.1	5.3	15.4	5.4	16.0	4.9	14.9	5.0
THW (kg)	10.8	6.0	10.8	4.6	11.0	5.6	11.3	4.7	10.7	5.4
pH	5.58	3.22	5.56	2.33	5.96	3.04	5.57	2.51	5.59	2.50
Göfo value	55.7	8.6	54.2	7.4	57.0	8.8	58.0	10.4	54.6	9.5
HIFT (mm)	4.1	58.5	4.6	61.9	4.1	54.8	4.1	56.8	4.7	68.2
HOFT (mm)	25.7	33.2	26.7	34.0	23.3	37.2	25.1	36.7	30.2	29.2

^a DULL=Duroc × (Landrace × Large White), DULA=Duroc × Landrace, DUWI=Duroc × Large White, WIWI=Large White, DUDU=Duroc.^b HCW=hot carcass weight, BT=backfat thickness, LD=loin depth.^c GHW=gross ham weight, THW=trimmed ham weight, pH=pH 24 h post-mortem, Göfo value ranging from 0=pale to 100=dark, HIFT=ham inner layer fat thickness, HOFT=ham outer layer fat thickness.**Table 2**

Number of individuals in each genetic group, mean and coefficient of variation (CV, %) for animals harvested at 160 kg.

	Genetic groups ^a							
	DULL		DULA		DUWI		WIWI	
	Mean	(CV, %)	Mean	(CV, %)	Mean	(CV, %)	Mean	(CV, %)
Number of pigs	111		114		85		31	
Carcass traits ^b								
HCW (kg)	116.4	5.9	116.7	6.2	115.4	6.3	114.9	7.8
BT (mm)	22.8	25.3	23.9	24.1	24.6	27.8	20.0	25.0
LD (mm)	54.8	11.6	53.3	10.7	52.7	12.1	56.5	9.8
Number of pigs	32		34		18		7	
Ham traits ^c								
GHW (kg)	18.5	6.4	18.6	6.6	19.1	8.5	19.6	5.4
THW (kg)	12.8	6.1	12.9	6.9	13.1	9.0	13.8	8.0
pH	5.65	2.83	5.67	1.94	5.65	1.94	5.66	1.94
Göfo value	56.1	5.9	57.2	6.5	55.7	6.7	56.5	5.3
HIFT (mm)	6.4	77.3	6.8	57.9	5.9	57.3	5.5	29.5
HOFT (mm)	22.5	27.1	24.3	23.9	22.3	22.8	20.1	31.5

^a DULL=Duroc × (Landrace × Large White), DULA=Duroc × Landrace, DUWI=Duroc × Large White, WIWI=Large White.^b HCW=hot carcass weight, BT=backfat thickness, LD=loin depth.^c GHW=gross ham weight, THW=trimmed ham weight, pH=pH 24 h post-mortem, Göfo value ranging from 0=pale to 100=dark, HIFT=ham inner layer fat thickness, HOFT=ham outer layer fat thickness.

the following model:

$$Y_{ijk} = \mu_k + GG_{ik} + e_{ijk}$$

where μ_k is the mean of variable k , GG_{ik} is the effect of genetic group i on variable k , and e_{ijk} is the random error associated to each observation.

To test the hypothesis of equality among the vectors of the means of the genetic groups, multivariate analysis of variance (MANOVA) was used. The matrices of the residual (E) and genetic groups (H) sums of squares and products were estimated, and the Wilks test was performed. Multiple comparisons among the vectors of the means were performed using the T^2 Hotelling statistic (Hotelling, 1931).

The canonical means were estimated to construct two-dimensional dispersion diagrams from the two first canonical variables. The normalized eigenvectors associated with the non-nil eigenvectors of the $E^{-1}H$ matrix constituted the canonic vectors containing the weighted coefficients for the respective canonical variables (Cruz et al., 2004).

For the cluster analysis, the Mahalanobis distances were first estimated among the genetic groups (Cruz et al., 2004; Mahalanobis, 1936). Considering possible divergences in the results, two clustering methods were used to obtain high levels of certainty: the single linkage method, as described by Sokal and Sneath (1963), and the

Tocher optimization method, as reported by Rao (1952). The cophenetic correlation coefficient (CPCC) proposed by Sokal and Rohlf (1962), which measures the fit between the dissimilarity matrices and the matrices resulting from the simplification provided by the cluster method, was obtained for the single linkage method.

3. Results

The hypothesis of equality among the vectors of the means of the genetic groups for the carcass traits in animals harvested at 130 kg and 160 kg and ham traits harvested at 130 kg was rejected ($p < 0.01$) by the Wilks significance test. No significant differences were observed among the mean vectors of the genetic groups for the ham traits in the animals harvested at 160 kg by the same significance test ($p > 0.05$).

The carcass traits harvested at 130 kg indicated a significant difference ($p < 0.01$) between DUDU and the other genetic groups as well as between WIWI and DULA and between WIWI and DUWI by the T^2 Hotelling test. For the animals harvested at 160 kg, the means vectors of the WIWI group differed from those of DULA and DUWI ($p < 0.05$). Differences were not observed among the means for DULL, DULA and DUWI ($p > 0.05$), for harvest at either 130 kg or 160 kg.

There was a significant difference ($p < 0.01$) found for the ham traits harvested at 130 kg between WIWI and the other genetic groups; between DUDU compared to DULL and DUWI; and between DULA and DUWI. No significant difference was observed between DUDU and DULA; DULL and DULA; and between DULL and DUWI ($p > 0.05$).

The $E^{-1}H$ eigenvalues, proportion of variance and weighted coefficients of the canonical variables are shown in Tables 3, 4 and 5 for the carcass traits harvested at 130 kg and 160 kg and ham traits harvested at 130 kg, respectively.

The first two canonical variables were sufficient to explain 97.5%, 93.6% and 88.8% of the total variation in the data for the carcass traits harvested at 130 kg and 160 kg and the ham traits harvested at 130 kg, respectively. It was observed in the dispersion diagram for the canonical means obtained from the first two canonical pairs for the carcass traits harvested at 130 kg that there was divergence between DUDU and the other genetic groups, and the greatest distance observed was between WIWI and DUDU. Little distance was observed between DULL, DULA and DUWI. In the diagram for the carcass traits for animals harvested at 160 kg, divergence was observed between

Table 3

$E^{-1}H$ eigenvalues, proportion of variance and canonical coefficients of the canonical variables (Can) for carcass traits harvested at 130 kg.

Trait	Can 1	Can 2	Can 3
Hot carcass weight	−0.63	−0.11	−0.82
Backfat thickness	1.02	0.60	0.52
Loin depth	0.18	1.24	0.07
Eigenvalues of $E^{-1}H$	0.116	0.011	0.003
Variation (%)	89.1	8.4	2.5
Accumulated variation (%)	89.1	97.5	100

Table 4

$E^{-1}H$ eigenvalues, proportion of variance and canonical coefficients of the canonical variables (Can) for carcass traits harvested at 160 kg.

Trait	Can 1	Can 2	Can 3
Hot carcass weight	−0.13	0.90	−0.48
Backfat thickness	0.80	0.45	1.42
Loin depth	−0.29	0.57	1.52
Eigenvalues of $E^{-1}H$	0.046	0.008	0.004
Variation (%)	79.4	14.2	6.4
Accumulated variation (%)	79.4	93.6	100

WIWI and the other genetic groups, but little distance was seen between DULL, DULA and DUWI.

The dispersion of the genetic groups in relation to the canonical means for the ham traits harvested at 130 kg showed a large distance between WIWI and DUDU, whereas there was little distance between DULL and DULA and little difference between DUDU and the groups formed by crosses with the Duroc breed.

The Mahalanobis (D^2) distances for the data for the carcass and ham traits in animals harvested at 130 kg and the carcass traits harvested at 160 kg are shown in Tables 6 and 7, respectively.

For the carcass traits harvested at 130 kg (Table 6), the greatest distance was observed between WIWI and DUDU, whereas the smallest distances were found for DULL vs. DULA, DULL vs. DUWI and DULA vs. DUWI. In the data for the carcass traits harvested at 160 kg (Table 7), the smallest distances were seen among the 50% Duroc crossbred animals.

The results obtained from the ham traits harvested at 130 kg (Table 6) showed that WIWI and DUDU were at the greatest Mahalanobis distance (D^2) from each other and that the smallest differences were between DULL and DULA and between DULL and DUWI.

Figs. 1, 2 and 3 show the dendrograms for the carcass traits harvested at 130 kg and 160 kg and ham traits harvested at 130 kg, respectively, obtained by the single linkage method based on the Mahalanobis distance (D^2). Even without fixing a number of groups, it was possible to observe in the dendrograms for the data on carcass traits harvested at 130 kg (Fig. 1) and ham traits harvested at 130 kg (Fig. 3) that jointly group WIWI and DUDU, it would be necessary to significantly relax the minimum level of similarity required to consider these genotype as close. However, it was observed that DULL, DULA and DUWI would be grouped with a relatively low minimum distance among them. The cophenetic correlation coefficient (CPCC) was over 0.7 for the three datasets, which indicated that the method used was adequate for the cluster analysis (Rohlf, 1970).

Two groups were formed using the Tocher optimization method for the data for the carcass traits harvested at 130 kg. The first consisted of DULL, DULA, DUWI and WIWI, and the second contained only Duroc (DUDU). Two groups were formed in the data regarding the carcass traits harvested at 160 kg, one containing DULL, DULA and DUWI and the other including only WIWI. Additionally, two groups were formed using the Tocher optimization

Table 5

$E^{-1}H$ eigenvalues, proportion of variance and canonical coefficients of the canonical variables (Can) for ham traits harvested at 130 kg.

Trait	Can 1	Can 2	Can 3	Can 4
Gross ham weight	0.76	0.79	-1.00	-0.99
Trimmed ham weight	-0.02	-0.33	0.77	1.42
pH	-0.17	-0.15	0.30	0.07
Göfo value ^a	0.58	0.21	0.74	-0.15
Ham inner layer fat thickness	-0.30	0.29	-0.19	0.75
Ham outer layer fat thickness	-0.30	0.93	0.37	-0.13
Eigenvalues of $E^{-1}H$	0.195	0.033	0.025	0.004
Variation (%)	76.0	12.8	9.6	1.6
Accumulated variation (%)	76.0	88.8	98.4	100

^a Göfo value ranging from 0=pale to 100=dark.

Table 6

Generalized Mahalanobis distance (D^2) among the genetic groups (GG) for carcass traits (above diagonal) and ham traits (below diagonal) harvested at 130 kg.

GG ^a	DULL	DULA	DUWI	WIWI	DUDU
DULL	0	0.04	0.02	0.26	0.49
DULA	0.16	0	0.04	0.44	0.42
DUWI	0.20	0.59	0	0.36	0.45
WIWI	1.27	1.79	0.86	0	1.42
DUDU	0.48	0.30	1.11	2.63	0

^a DULL=Duroc × (Landrace × Large White); DULA=Duroc × Landrace; DUWI=Duroc × Large White; WIWI=Large White; DUDU=Duroc.

Table 7

Generalized Mahalanobis distance (D^2) among the genetic groups (GG) for carcass traits harvested at 160 kg.

GG ^a	DULL	DULA	DUWI	WIWI
DULL	0	0.06	0.16	0.24
DULA	-	0	0.06	0.42
DUWI	-	-	0	0.59
WIWI	-	-	-	0

^a DULL=Duroc × (Landrace × Large White); DULA=Duroc × Landrace; DUWI=Duroc × Large White; WIWI=Large White.

method for the dataset regarding the ham traits harvested at as 130 kg, one containing DULL, DULA, DUWI and DUDU and another including only WIWI.

4. Discussion

The absence of significant differences among the mean vectors of the genetic groups for the ham traits in the animals harvested at 160 kg obtained in the present study differs from the findings of all previous studies on this topic we found reported in the literature. Sabbioni et al. (2004) observed differences in ham weight between 50% Duroc and Large White × Landrace animals in the 160–170 kg harvest weight range. Thus, the hypothesis may be considered that the data structure, specifically in the set of ham measurements harvested at 160 kg (limited number of WIWI and no DUDU genetic group), influenced the results obtained.

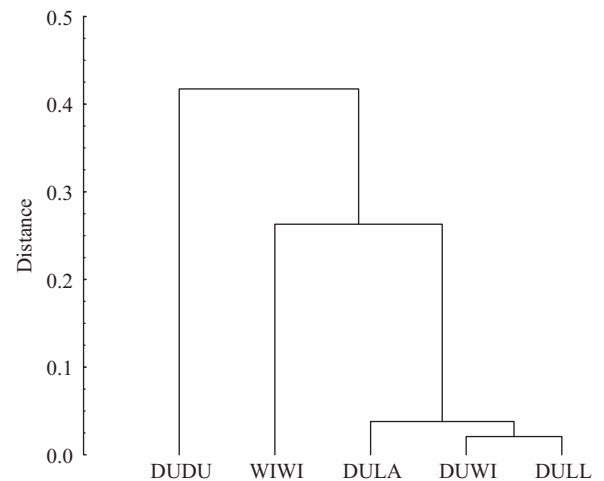


Fig. 1. Similarity dendrogram among the genetic groups obtained by the single linkage method based on the Mahalanobis distance (D^2) for carcass traits harvested at 130 kg. DULL=Duroc × (Landrace × Large White); DULA=Duroc × Landrace; DUWI=Duroc × Large White; WIWI=Large White, DUDU=Duroc.

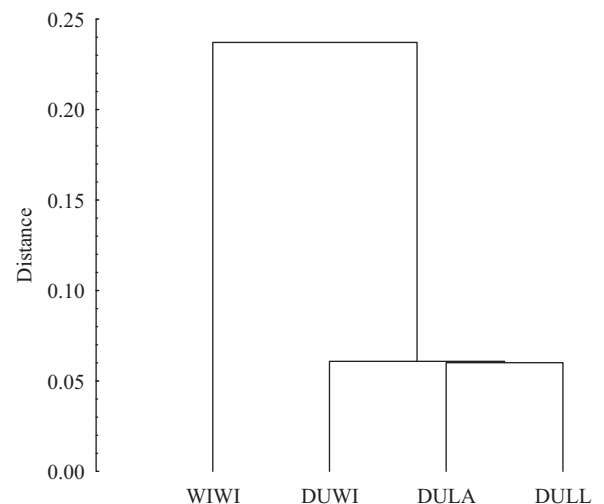


Fig. 2. Similarity dendrogram among the genetic groups obtained by the single linkage method based on the Mahalanobis distance (D^2) for carcass traits harvested at 160 kg. DULL=Duroc × (Landrace × Large White); DULA=Duroc × Landrace; DUWI=Duroc × Large White; WIWI=Large White.

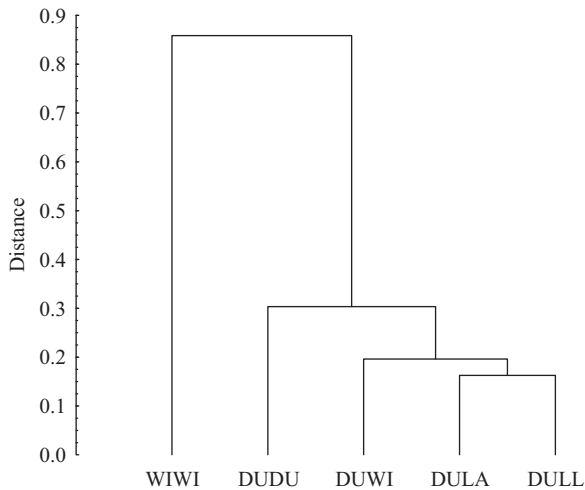


Fig. 3. Similarity dendrogram among the genetic groups obtained by the single linkage method based on the Mahalanobis distance (D_2) for ham traits harvested at 130 kg. DULL=Duroc \times (Landrace \times Large White); DULA=Duroc \times Landrace; DUWI=Duroc \times Large White; WIWI=Large White, DUDU=Duroc.

Our results showed that the use of Landrace, Large White or Landrace \times Large White sows mated with Duroc breed boars did not result in differences in the carcass traits of the progenies produced from these crosses. These results were somewhat expected because the Landrace and Large White breeds are considerably similar with respect to carcass traits, such that high lean meat yield has been observed in these breeds (Briggs, 1983). The results in agreement with those of the present study were reported by Gispert et al. (2007), who did not find any significant differences among animals of the Landrace and Large White breeds in the carcass measurements of HCW, BT, and LD, and by Peloso et al. (2010), who examined carcass traits through univariate analysis and did not observe significant differences among crossbred Duroc \times Large White, Duroc \times Landrace or Duroc \times (Landrace \times Large White) animals. Nevertheless, Bunter et al. (2008) observed differences in some carcass traits in animals of the Landrace and Large White breeds, but the authors attributed these differences to the occurrence of variation within each genetic group.

The differences in the ham traits of the Duroc and Large White breeds observed in this study are in agreement with the results obtained by Schivazappa et al. (2002), Bosi and Russo (2004) and Sabbioni et al. (2004). Furthermore, some studies have reported significant differences among the ham of animals of the Duroc and Large White breeds in the quantity of ham after deboning, such that Duroc breed animals gave the highest yields (Franci et al., 1997; Sabbioni et al., 2004).

The differences observed between DULA and DUWI by the T^2 Hotelling test regarding the ham traits were not expected because according to Briggs (1983), the Landrace and Large White breeds are fairly similar with respect to meat traits. No distinction has been made between the Landrace and Large White breeds in the production of dry-cured ham, such as Parma and San Daniele because both are used as pure breeds or in

crossings with the Duroc breed (Beek, 2009; Bosi and Russo, 2004).

Examination of the divergence among genetic groups in dispersion diagrams is possible when canonical variables explain a sufficient proportion of total variance. According to Cruz et al. (2004), at least 80% of total variance should be explained by the first and second canonical variables. The results similar to those of the present study, in which the first two canonical variables explained more than 80% of the total variance, were obtained by Sakaguti et al. (1996) with data from diallelic crossings in rabbits, Fonseca et al. (2000) regarding litter traits of pure pig breeds, and Viana et al. (2000) in broiler lines.

The results observed in the dispersion diagrams from the two first canonical variables for the carcass traits harvested at 130 kg and 160 kg supported the idea that using Landrace, Large White and Landrace \times Large White sows in crosses with Duroc boars probably results in little difference among the animals produced for the traits hot carcass weight (HCW), backfat thickness (BT) and loin depth (LD). Gispert et al. (2007) subjected carcass measurements to a principal components analysis technique and observed proximity of the Landrace and Large White breeds in the resulting dispersion graph but a large distance between these breeds and the Duroc breed, and these results were in line with the proximity between DULL, DULA and DUWI and the divergence between WIWI and DUDU observed in the present study.

Similar results regarding the distances between Duroc and Large White pure breed animals to those presented in this study were observed by Guerrero et al. (1996) working with ham traits of Duroc breed animals and progenies of crosses between Landrace and Large White breeds. The authors found a large distance between the Duroc and crossbred animals using a genetic group dispersion graph for canonical means.

The divergence observed among the purebred Duroc and Large White animals in the results of the present study can be explained by the set of traits associated with each breed. The Duroc breed presents a carcass with a high fat content and less lean meat yield and is used in finishing crossings to imprint desirable organoleptic traits on meat, while Large White breed pigs produce a carcass with a greater proportion of lean meat and are used largely to form maternal lines (Bosi and Russo, 2004; Guerrero et al., 1996; Taylor et al., 2005a, 2005c). Landrace and Large White breed maternal lines are selected for reproductive traits, unlike the Duroc breed, which is selected for use in terminal crossing (Taylor et al., 2005a, 2005b).

The Mahalanobis distances among the 50% Duroc crossbred animals indicate that DULL, DULA and DUWI were not divergent for carcass traits.

The distribution of purebred Duroc and Large White individuals in different groups observed in the present study can be attributed to the fact that these breeds present distinctly different carcass traits and meat quality traits, as has been reported in previous studies comparing the Duroc and Large White breeds (Bosi and Russo, 2004; Schivazappa et al., 2002).

The clustering of the 50% Duroc crossbred animals for carcass traits harvested at 130 kg and 160 kg indicated

that DULL, DULA and DUWI were not divergent. This clustering, together with the fact that these individuals did not differ significantly based on the Hotelling T^2 test, may indicate that there was no relevant influence of the Landrace and Large White maternal lines on the carcass traits, as was discussed previously.

For the ham traits harvested at 130 kg, the clustering of purebred Duroc animals with the DULL, DULA and DUWI genetic groups indicated that the crossbred individuals presented ham traits close to those of purebred Durocs. Peloso et al. (2010) working with the same data in a univariate analysis concluded that apart from the Durocs, a second option within the genetic groups studied is the DULA group. Thus, using multivariate analysis we could recommend 50% Duroc animals for dry-cured ham production because several studies have shown that the Duroc breed presents favorable traits in its raw ham that are important in the curing process, such as the ham's inner and outer layer fat thickness, pH and intramuscular fat (Bosi and Russo, 2004; Candek-Potokar et al., 2002; Sabbioni et al., 2004; Schivazappa et al., 2002).

5. Conclusion

The multivariate analysis showed to be an appropriate tool to confirm that crossbred Duroc animals fit a high-quality ham production as purebred Duroc. The Large White and Duroc genetic groups were found to diverge in their carcass and ham traits when harvested at 130 kg. The genetic groups Duroc × (Landrace × Large White), Duroc × Landrace and Duroc × Large White were similar with respect to the carcass traits harvested at 130 kg and 160 kg and ham traits at 130 kg. The genetic groups Duroc × Large White, Duroc × Landrace and Duroc × (Landrace × Large White) are recommended for use in producing dry-cured ham.

Conflict of interest statement

This paper does not cause any conflict of interest including financial, personal or other relationships with other people or organizations.

Acknowledgments

We thank the CNPq (National Council of Research and Development), FAPEMIG (Minas Gerais State Research Foundation) and INCT-CA (Brazilian Institute of Science and Technology—Animal Science) for financial support.

References

Beek, V., 2009. Producing for Parma ham. *Pig Prog.* 25, 6–8.
 Bosi, P., Russo, V., 2004. The production of the heavy pig for high quality processed products. *Ital. J. Anim. Sci.* 3, 309–321.
 Briggs, H.M., 1983. In: *Modern Breeds of Livestock* third ed. MacMillan Company, New York.

Bunter, K.L., Bennett, C., Luxford, B.G., Graser, H.U., 2008. Sire breed comparisons for meat and eating quality traits in Australian pig populations. *Animal* 2 (8), 1168–1177.
 Candek-Potokar, M., Monin, G., Žlender, B., 2002. Pork quality, processing, and sensory characteristics of dry-cured hams as influenced by Duroc crossing and sex. *J. Anim. Sci.* 80, 988–996.
 Carrapiso, A.I., García, C., 2008. Effect of the Iberian pig line on dry-cured ham characteristics. *Meat Sci.* 80, 529–534.
 Cilla, I., Altarriba, J., Guerrero, L., Gispert, M., Martínez, L., Moreno, C., Beltrán, J.A., Guàrdia, M.D., Diestre, A., Arnau, J., Roncalés, P., 2005. Effect of different Duroc line sires on carcass composition, meat quality and dry-cured ham acceptability. *Meat Sci.* 72, 252–260.
 Cruz, C.D., Regazzi, A.J., Carneiro, P.C.S., 2004. Modelos Biométricos Aplicados ao Melhoramento Genético, third ed. Universidade Federal de Viçosa, Viçosa.
 Fonseca, R., Pires, A.V., Lopes, P.S., Torres, R.A., Euclides, R.F., 2000. Estudo da divergência genética entre raças suínas utilizando técnicas de análise multivariada. *Arq. Bras. Med. Vet. Zootec.* 52, 403–409.
 Franci, O., Baldini, P., Bozzi, R., Bellatti, M., Pugliese, C., Acciaoli, A., Geri, G., 1997. Confronto fra progenie di verri Large White, Landrace Italiana, Landrace Belga, Duroc, Cinta Senese e scrofe Large White a 130e 160 kg di peso vivo, 5 Caratteristiche tecnologiche e sensoriali del prosciutto toscano. *Zootec. Nut. Anim.* 23, 67–79.
 García-Rey, R.M., Quiles-Zafra, R., Luque de Castro, M.D., 2004. Relationships of genotype and slaughter time with the appearance and texture of dry-cured hams. *Food Chem.* 94, 271–277.
 Guerrero, L., Gou, P., Alonso, P., Arnau, J., 1996. Study of the physico-chemical and sensorial characteristics of dry-cured hams in three pig genetic types. *J. Sci. Food Agric.* 70, 526–530.
 Gispert, M., Font i Furnols, M., Gil, M., Velarde, A., Diestre, A., Carrión, D., Sosnick, A.A., Plastow, G.S., 2007. Relationships between carcass quality parameters and genetic types. *Meat Sci.* 77, 397–404.
 Hotelling, H., 1931. The generalization of Student's ratio. *Ann. Math. Stat.* 2, 360–378.
 Mahalanobis, P.C., 1936. On the generalized distance in statistics. *Proc. Natl. Inst. Sci.* 2, 49–55.
 Montgomery, D.C., Peck, E.A., 1992. In: *Introduction to Linear Regression Analysis* second ed. John Wiley & Sons, New York.
 Peloso, J.V., Lopes, P.S., Gomide, L.A.M., Guimarães, S.E.F., Carneiro, P.L.S., 2010. Carcass and ham quality characteristics of heavy pigs from different genetic groups intended for the production of dry-cured hams. *Meat Sci.* 86, 371–376.
 Rao, C.R., 1952. In: *Advanced Statistical Methods in Biometric Research* first ed. John Wiley & Sons, New York.
 Rohlf, F.J., 1970. Adaptive hierarchical clustering schemes. *Syst. Zool.* 19, 58–82.
 Sabbioni, A., Beretti, V., Zanon, A., Superchi, P., Sussi, C., Bonomi, A., 2004. Effect of the proportion of Duroc genes in crosses with Large White and Landrace pigs on the characteristics of seasoned Parma ham. *Ital. J. Anim. Sci.* 3, 31–39.
 Sakaguti, E.S., Silva, M.A., Regazzi, A.J., Cruz, C.D., Sediya, C.S., 1996. Análise de divergência genética entre nove grupos de coelhos. *R. Bras. Zootec.* 25, 647–660.
 Schivazappa, C., Degni, M., Nanni Costa, L., Russo, V., Buttazzoni, L., Virgili, R., 2002. Analysis of raw meat to predict proteolysis in Parma ham. *Meat Sci.* 60, 77–83.
 Sokal, R.R., Rohlf, F.J., 1962. The comparison of dendrograms by objective methods. *Taxon* 11, 33–40.
 Sokal, R.R., Sneath, P.H.A., 1963. In: *Principles of Numerical Taxonomy* first ed. W.H. Freeman, San Francisco.
 Taylor, G., Roese, G., Hermes, S., 2005a. Breeds of pigs—Large White. Primefacts 62—NSW Farmers' Association. <http://www.dpi.nsw.gov.au/_data/assets/pdf_file/0008/45566/Breeds_of_pigs_-_Large_White_-_Primefact_62-final.pdf>.
 Taylor, G., Roese, G., Hermes, S., 2005b. Breeds of pigs—Landrace. Primefacts 63—NSW Farmers' Association. <http://www.dpi.nsw.gov.au/_data/assets/pdf_file/0008/45557/Breeds_of_pigs-Landrace_-_Primefact_63-final.pdf>.
 Taylor, G., Roese, G., Hermes, S., 2005c. Breeds of pigs—Duroc. Primefacts 64—NSW Farmers' Association. http://www.dpi.nsw.gov.au/_data/assets/pdf_file/0005/45545/Breed_of_pigs-Duroc_-_Primefact_64-final.pdf.
 Viana, C.F.A., Silva, M.A., Pires, A.V., Lopes, P.S., Piassi, M., 2000. Estudo da divergência genética entre quatro linhagens de matrizes de frango de corte utilizando técnicas de análise multivariada. *R. Bras. Zootec.* 29, 1074–1081.