

Genetic divergence between genotypes for male and female broilers

Divergência genética entre genótipos de frangos de corte machos e fêmeas

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ABSTRACT

The aim of this study was to verify the genetic divergence amongst three broiler genotype, from both sexes, by means of a multivariate performance analysis and carcass traits. Nine hundred and ninety sexed, one-day chicks were utilized; belonged to the following genetic groups: Cobb 500, Hubbard Flex, and Ross 308. The study evaluated the daily average weight gain, the daily average ration consumption, feed conversion, body weight, weight and performance for breast, and carcass over the period from 1 to 35, and from 1 to 42 days of age. Performance of the genetic groups was evaluated by means of multivariate analysis of variance and by Fisher's linear discriminant function, using Roy's largest eigenvalue and Roy's union-intersection test for multiple comparisons. The genetic divergence study was carried out through the analysis of canonical variables and through Tocher method. Female animals from Cobb 500, Hubbard Flex, and Ross 308 genetic groups presented different canonical averages from males of the same groups. First two canonical variables explained 88.10% of variation between genetic groups. Genetic divergence between the evaluated groups allowed formation of two clusters with the following genotypes: Cluster 1 - Cobb 500, Hubbard Flex and Ross 308 females; Cluster 2 - Cobb 500, Hubbard Flex and Ross 308 males.

Key words: grouping, discriminating analysis, genetic group.

RESUMO

Objetivou-se com este estudo verificar a divergência genética entre três genótipos de frangos de corte, de ambos os sexos, utilizando o desempenho e as características de carcaça por meio da análise multivariada. Utilizaram-se 990 pintos de um dia, sexados, dos seguintes grupos genéticos: Cobb 500, Hubbard Flex, e Ross 308. Avaliaram-se as seguintes variáveis: ganho em peso médio diário, consumo de ração médio diário, conversão

alimentar, peso corporal, peso e rendimento do peito e da carcaça, nos períodos: 1 a 35 dias e 1 a 42 dias de idade. O desempenho dos grupos genéticos foi avaliado por meio da Análise de Variância Multivariada e da função discriminante linear de Fisher, usando os testes do maior autovalor de Roy e da união-interseção de Roy para as comparações múltiplas. O estudo da divergência genética foi feito por meio da análise por variáveis canônicas e pelo método de otimização de Tocher. As fêmeas dos grupos genéticos Cobb 500, Hubbard Flex e Ross 308 apresentaram médias canônicas diferentes dos machos desses mesmos genótipos. As duas primeiras variáveis canônicas explicaram 88,10% da variação entre os grupos genéticos. A divergência genética entre os grupos genéticos avaliados permitiu a formação de dois grupos com os seguintes genótipos: grupo 1 - Fêmeas Cobb 500, Hubbard Flex e Ross 308; e grupo 2 - Machos Cobb 500, Hubbard Flex e Ross 308.

Palavras-chave: agrupamento, análise discriminante, grupo genético.

INTRODUCTION

The economically relevant characteristics, such as performance and carcass, used to evaluate broilers or genetic groups, are of quantitative nature and; therefore, are subjected to different genetic bases and different degrees of environmental influence, making difficult to understand the set of characteristics from univariate analyses (SAKAGUTI et al., 1996). A way to address this matter is the utilization of multivariate analysis techniques (FRANCI et al., 2001); since, differently from the univariate analysis, they

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simultaneously match multiple pieces of information from an experimental unit (VIANA et al., 2000).

There are several approaches in the field of multivariate analyses that allow the joint analysis of these characteristics. Amongst them, canonical variables technique represents an important tool in discriminating genetic groups, allowing the verification of the degree of similarity through uni- or multi-dimensional dispersion diagrams involving canonical averages. Cluster analysis is used by several authors (PIRES et al., 2002; YAMAKI et al., 2008; VENTURA et al., 2012) as another type of multivariate technique which allowing sampling units to be synthesized in a number of groups. So, homogeneity in cluster and heterogeneity between the clusters are maintained (CRUZ et al., 2004). Therefore, this study aimed to verify the genetic divergence amongst three broiler genotypes, from both sexes, by using performance and carcass traits with the multivariate analysis technique.

MATERIAL AND METHODS

The experiment was conducted in the poultry sector of the Animal Sciences Department at the “Universidade Federal dos Vales do Jequitinhonha e Mucuri” (UFVJM), located at the JK *campus*, in Diamantina/MG, Brazil, from October 31 to December 12, 2011.

Nine hundred and ninety one-day chicks, male and female, were utilized; the chicks derived from three broiler genotypes: Cobb 500, Hubbard Flex, and Ross 308, and were distributed in an entirely randomized design, with five repetitions. Sexed chicks were kept in an experimental wooden shed, measuring 40 meters in length and 8 meters wide, with a ceiling height of 3 meters, allocated into thirty sections of 1.65x1.55m, with thirty-three animals in each section. Experimental ration was maize and soy-meal based, according to HUBBARD (2011).

Genetic groups (treatments) consisted of combination between genotypes and sex, for a total of six treatments. Performance and carcass traits were the following: daily average gain weight (DAGW), daily average ration consumption (DARC), feed conversion (FC), body weight (BW), breast weight (BSW), breast performance (BP), carcass weight (CW), and carcass performance (CP), over the following periods: 1 to 35 days (DAGW35, DARC35, FC35, BW35, BSW35, BP35, CW35, and CP35, respectively) and 1 to 42 days (DAGW42, DARC42, FC42 e BW42, BSW42, BP42, CW42, and CP42, respectively). For the carcass traits, two broilers were slaughtered for each

repetition, one of each sex, after eight hours of solid food fasting; carcass was composed of head and feet.

Statistical analyses were conducted with the “proc candisc” procedure of SAS software (2002), preceded by the multivariate analysis of variance (MANOVA) according to the model: $Y_{ijk} = u_k + G_{ik} + e_{ijk}$; Y_{ijk} = value observed for the k characteristic, for the j repetition, of the i genetic group (i = 1, 2, ..., 6; j = 1, 2, 3, 4, 5; k=1, 2, ..., 18); u_k = average of the k characteristic; G_{ik} = effect of the i genetic group over the k characteristic; e_{ijk} = random error associated with the Y_{ijk} observation.

The discard criteria for the variables was adopted after evaluating the importance of characteristics from weighting coefficient of every characteristic in the final canonical variables, which, by estimation, withhold the minimal proportion of total variation (CRUZ et al., 2004). After discarding variables, researchers carried out average tests for comparison of variables amongst genetic groups with characteristics that were maintained.

In contrast to the univariate analysis, MANOVA generates A, H, and E matrices for sum of squares and products. The hypothesis tested by MANOVA is the equality of average vectors between the groups, *i.e.*: $H_0 : G_1 = G_2 = G_3 = G_4 = G_5 = G_6$

In order to test this hypothesis Roy’s largest eigenvalue test was conducted; it consisted of the determination of characteristic roots (eigenvalues) of the characteristic equation: $|E^{-1}\lambda I| = 0$ or $|H - \lambda E| = 0$

I = identity matrix; λ = eigenvalues; E^{-1} = residual sum-of-squares-and-products matrix inverse; and H = sum-of-squares-and-treatment-products matrix.

Considering that l_{max} is the largest eigenvalue of E-1 H, the following statistic is as

$$\theta = \frac{l_{max}}{1_{max}}$$

established: The obtained value (θ) is compared to the significance limit given in tables (MORRISON, 1967; HARRIS, 1975).

Afterwards, contrast comparison test amongst averages was carried out amongst the averages through Roy’s union-intersection test. For cluster analysis, it was used Tocher method, adopting Mahalanobis distance as the dispersion measure, as mentioned by RAO (1952). Several authors have used these tests to study genetic divergence (VIANA et al., 2000; CARNEIRO et al., 2002; PIRES et al., 2002; VENTURA et al., 2012).

The discriminating function was estimated based on the canonical variable with the largest correlation with the data, the first canonical variable, which obtained a score for each genetic group.

Unidimensionally representing genetic groups, an analysis of variance (ANOVA), from these scores, was conducted to test the hypothesis of genotypic equality: $H_0 : g_1 = g_2 = g_3 = g_4 = g_5 = g_6$.

To test the contrast amongst the group averages (treatments), the minimum significant difference (DMS), at the probability of 1%, was calculated through Roy's test (MORRISON, 1967; HARRIS, 1975).

RESULTS AND DISCUSSION

The CW35, BSW35, and CW42 variables are disposable (Table 1), because they retain a minimum proportion of the total variation; they present large absolute values for the last canonical variables (Can5, Can4, and Can2, respectively) and; thus, account for a practically insignificant variation (CRUZ et al., 2004).

From the analyses, regarding only the non-discarded characteristics, no significant difference was observed ($P \leq 0.01$) between the genetic groups by Roy's test, considering every characteristic (Table 2). It is evident that, overall, male broilers, independently of their genetic group, had greater tendency for performance. Similarly MORO et al. (2005) and LIMA et al. (2008) research achieved similar results. Male Cobb 500 group

presented a greater tendency for performance at 35 days of age and greater breast weight and performance at 42 days. Ross, the best performance for 308 male Ross broilers had been seen at the final breeding stage, *i.e.*, at 42 days of age, aside from having a better carcass performance at the same age.

These results demonstrated that the Cobb 500 male group was the most precocious, because it presented a largest growth rate when compared to the male Ross 308 group; however, at 42 days of age, the male Ross 308 broilers were superior to the other groups, which may had occurred due to the fact that they s had a better compensatory gain because they were more efficient in converting ration into muscle within the same period, most notably by their greater body weight at 42 days of age. Female Cobb 500 group presented greater breast and carcass efficiency at 35 days of age, and the male Cobb 500 group displayed greater weight and higher breast efficiency at 42 days of age, which evinces that broilers from the Cobb 500 genotype, regardless sex, presented higher efficiency in muscle deposition for carcass and breast. Similar results were found by FERNANDES et al. (2013).

There is a difference ($P \leq 0.01$) in the performance between sexes in the genetic groups evaluated by Roy's test, applied to the discriminating function on the basis of the canonical variable of greater

Table 1 - Standardized canonical coefficients for the performance characteristics in broilers.

Characteristic	Can1	Can2	Can3	Can4	Can5
CW35	-2.15	34.56	-153.80	-12.47	-90.18
CP35	-1.22	-4.36	34.75	10.27	19.18
BSW35	8.47	-18.06	32.64	-28.07	17.71
BP35	-6.01	9.92	-12.65	12.88	-7.45
DARC35	3.53	-0.44	6.98	1.66	-0.40
DAGW35	-2.20	-4.14	-7.71	-3.04	-0.87
FC35	-2.71	2.40	-7.29	-1.46	-0.11
BW35	0.62	4.51	4.39	1.46	2.33
CW42	27.17	-56.96	4.18	4.79	11.70
CP42	-12.49	12.15	-2.69	-1.20	-1.59
BSW42	7.38	36.06	2.54	-0.44	-8.79
BP42	-2.20	-20.90	-1.72	-0.27	3.17
DARC42	-4.62	-0.34	-3.84	-4.09	2.19
DAGW42	5.27	2.93	3.54	3.31	-1.67
FC42	2.94	0.42	5.74	4.56	-0.92
BW42	-2.93	-2.35	-1.48	-0.19	0.61

CW35 = carcass weight at 35 days of age; CP35 = carcass efficiency at 35 days of age; BSW35 = breast weight at 35 days of age; BP35 = breast efficiency at 35 days of age; DARC35 = daily average ration consumption from 1 to 35 days of age; DAGW35 = daily weight gain from 1 to 35 days of age; FC35 = feed conversion from 1 to 28 days of age; BW35 = body weight at 35 days of age; CW42 = carcass weight at 42 days of age; CP42 = carcass efficiency at 42 days of age; BSW42 = breast weight at 42 days of age; BP42 = breast efficiency at 42 days of age; DARC42 = daily average ration consumption from 1 to 42 days of age; DAGW42 = daily weight gain from 1 to 42 days of age; FC42 = feed conversion from 1 to 42 days of age; BW42 = body weight at 42 days of age.

Table 2 - Average of the considered characteristics for broilers of both sexes.

Characteristics	Genetic group					
	Cobb_F	Cobb_M	Hubbard_F	Hubbard_M	Ross_F	Ross_M
CP42	81.41	83.30	82.97	83.39	83.48	83.71
BSW42	692.00	881.00	732.60	829.60	679.20	839.80
BP42	37.45	37.68	34.44	34.20	34.34	35.44
CP35	83.81	83.53	81.78	82.58	81.77	82.08
BSW35	509.00	594.00	488.40	524.40	511.20	582.40
BP35	35.57	34.87	32.83	30.96	34.19	33.68
DARC35	87.88	94.38	86.95	89.67	89.04	91.46
DAGW35	47.66	58.01	49.41	53.61	49.15	55.83
FC35	1.76	1.55	1.61	1.56	1.75	1.57
BW35	1710.00	2068.00	1771.00	1909.00	1802.00	1997.00
DARC42	104.72	109.54	102.25	105.95	107.80	107.64
DAGW42	52.34	62.77	54.78	61.97	57.43	62.86
FC42	1.88	1.71	1.71	1.61	1.80	1.65
BW42	2364.00	2631.00	2386.00	2615.00	2543.00	2679.00

CP35 = carcass performance at 35 days of age; BSW35 = breast weight at 35 days of age; BP35 = breast efficiency at 35 days of age; DARC35 = daily average ration consumption from 1 to 35 days of age; DAGW35 = daily weight gain from 1 to 35 days of age; FC35 = feed conversion from 1 to 28 days of age; BW35 = body weight at 35 days of age; CP42 = carcass efficiency at 42 days of age; BSW42 = breast weight at 42 days of age; BP42 = breast efficiency at 42 days of age; DARC42 = daily average ration consumption from 1 to 42 days of age; DAGW42 = daily weight gain from 1 to 42 days of age; FC42 = feed conversion from 1 to 42 days of age; BW42 = body weight at 42 days of age.

Averages not followed by a different letter in the same line are equal according to Roy's test at 1% probability.

correlation with the data (Table 3). Female Cobb 500 group presented a greater average; excepting of Cobb 500 male group, which did not differ statistically when compared to others. Performance of every genetic group, for each studied characteristic, is explained by Roy's largest eigenvalue test.

In this study, obtained information were employed for comparison amongst groups, as well as in evaluation amongst lineages of a same breed of core livestock, such as in studies of VIANA et

al. (2000) and CARNEIRO et al. (2002), when the gathered data were used along with other information for the disposal or selection of lineages.

Canonical variables technique is normally considered efficient when the most part of the variation among characteristics may be explained in the first three main components, since transformation in new scale stores all the variability explained by variables in original scale, which results in non-correlated variables. In the present study, the first two canonical variables explained 88.10% of the observed variation (Table 4) and; therefore, were utilized to generate two canonical averages (MC1 and MC2) used in the bidimensional representation. From figure 1, it is possible to visualise the graphical distances that

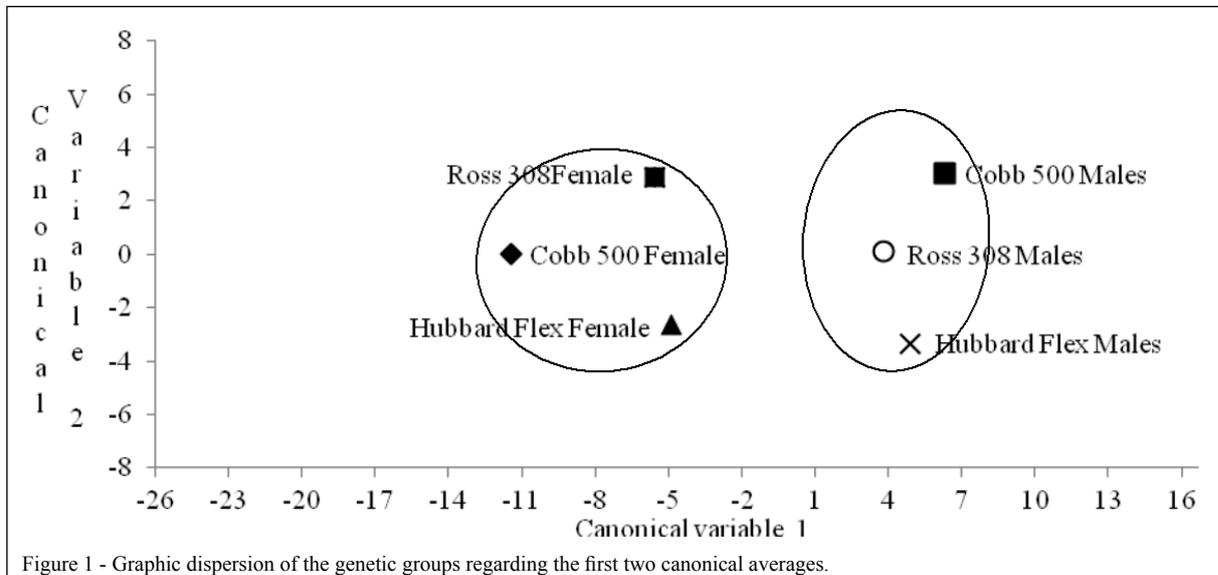
Table 3 - Scores and minimum significant difference (DMS) for the six groups, with basis on the discriminating function of the first canonical variable according to Roy's test.

Group	Scores of the discriminating function
Female Cobb 500	12.294 ^a
Male Cobb 500	11.800 ^b
Female Hubbard Flex	12.111 ^{ab}
Male Hubbard Flex	11.840 ^{ab}
Female Ross 308	12.130 ^{ab}
Male Ross 308	11.871 ^{ab}
DMS	0.460

Averages followed by different letters in their column are different according to Roy's test at 1% probability.

Table 4 - Canonical variables, eigenvalues, and variance percentages obtained with the analysis of the characteristics for the six broiler groups.

Canonical Variable (VCi)	Eigenvalue	Variance (%)	Accumulated Variance (%)
VC1	44.17	73.83	73.83
VC2	8.53	14.27	88.10
VC3	6.12	10.24	98.34
VC4	0.57	0.96	99.30
VC5	0.41	0.70	100.00



represent the similarities and dissimilarities between the genetic groups, where the greater differences were observed between the same variables; these variables are larger in MC1 and smaller in MC2, due to the fact that VC1, directly related to MC1, retains the greatest proportion of data variation: 73.83% (Table 4). Differences are big enough for female Cobb 500, Hubbard Flex, and Ross 308 groups to present MC1 with a negative value and; thus, an average in the opposite direction when compared to the other genetic groups, which evinces that these groups are different and that sex influences broilers performance. Regarding the second canonical average (MC2), results were less discrepant, which is justified by the percentage of total variance explained by VC2 (Table 4).

Six genetic groups were also gathered by Tocher method, resulting in two clusters, which are represented by the circles in figure 1; circles represent the genetic similarity in the cluster, and genetic divergence between clusters. Female Cobb 500, Hubbard Flex, and Ross 308 groups were gathered altogether, and male Cobb 500, Hubbard Flex, and Ross 308 groups were as well, supporting the hypothesis that, regardless of genotype, sex influences the performance and carcass of broilers. Other cluster analysis studies between genotypes were conducted by YAMAKI et al. (2008), with broiler matrices; PIRES et al. (2002), with leghorn poultry; and VENTURA et al. (2012) with a swine sample.

CONCLUSION

Multivariate analysis was an appropriate tool to indicate the traits that are amenable to disposal: carcass weight and breast at 35 days old and carcass weight at 42 days old. Males of Cobb and Ross genotypes were better and female Cobb group obtained higher carcass and breast yields. By cluster analysis it was possible to form two groups: 1 - Cobb female, Hubbard female and Ross female and group 2 - Male Cobb, Hubbard male and Ross male; thus, showing the influence of gender on performance and carcass of broilers.

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BIOETHICS AND BIOSSECURITY COMMITTEE APPROVAL

Protocolo CEUA-UFVJM nº 016/11.

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