Genetic Evaluation Of Body Weight, Skin Weight And Carcass Yield Of Broilers.

G.C. Venturini[1,2], D.A. Grossi[1,3], M.E. Buzanskas[1], L.E. Faro[4], M.C. Ledur[5], J.O. Peixoto[5], G.S. Schmidt[5] and D.P. Munari[6‡]

Introduction

Genetic evaluation of body weight and carcass yield, are of fundamental importance for the broiler breeding. The productive performance of the broiler strains needs to be evaluated according to traits connected with the quantity and quality of the meat produced. For meat quality, few studies on genetic parameters for skin weight were found in literature.

Heritability estimates for broiler body weight range from moderate value to high value (Le Bihan-Duval et al. (2001), Zerehdaran et al. (2004) Adeyinka et al. (2006) and Vayego et al. (2008)) and for carcass component yields, from 0.62 ± 0.03 (Le Bihan-Duval et al. (2001)) to 0.82 ± 0.28 (Cahaner and Nitsan (1985)). Heritability estimate for skin weight (0.28 ± 0.06) was reported by Zerehdaran et al. (2004).

The present investigation aims to estimate heritabilities and genetic correlations for body weight, skin weights and carcass cuts yields, providing tools for selection of a male broiler line.

Material and methods

Animals and data file. Data of 1,462 animals were used for evaluation of body weight at 42 days of age (BW42), feed conversion ratio from 35 to 41 days (FCR), skin thigh weight (SThigh), skin breast weight (SBreast) and skin drumstick weight (SDrum) and abdominal fat percentage (AFP), thigh yield (THY), drumstick yield (DRY) and breast yield (BRY) at 42 days of age of a male broiler line developed at the National Research Center for Swine and Poultry - EMBRAPA, Brazil.

Data editing. The present study was limited to offspring whose parents were known. Preliminary analyses of all traits were performed to eliminate inconsistent data. Least square

---

1 Programa de Pós-Graduação em Genética e Melhoramento Animal, FCAV/UNESP, Jaboticabal, SP, Brazil
2 CAPES Grantee
3 FAPESP Grantee
4 Agência Paulista de Tecnologia dos Agronegócios – APTA/SAA, Brazil
5 Embrapa Suínos e Aves, Concórdia, SC, Brazil
6 Departamento de Ciências Exatas FCAV/UNESP Via de Acesso Prof. Paulo D. Castellane, 14884-900, Jaboticabal, SP, Brazil.
‡ E-mail address: danisio@fcav.unesp.br

analysis, using the GLM procedure of SAS (SAS 9.1, SAS Institute, Cary, NC, USA), aided in defining the fixed effect (ten groups of animals of same sex and incubation) considered in the model (sex-incubation group) which affected significantly ($P < 0.05$) all traits. A total of 700 sires and 762 dams were used in the analysis.

Assumptions for the fixed-effects model. Residual normality was verified for each trait using Guided Data Analysis - SAS (SAS 9.1, SAS Institute, Cary, NC, USA). Observations exhibiting a standardized residual 3.5-fold above or below the standard deviation were excluded.

Statistical analysis. Estimation of genetic parameters was performed using the Restricted Maximum Likelihood Method (REML) for multi-trait animal model, using the WOMBAT software (Meyer, 2007). The relationship matrix included 2212 animals. The mixed model used for all traits was $y=Xb + Za + e$, in which: y is the vector of the dependent variable; X is the incidence matrix for the fixed effect, thereby associating the elements of b and y; b is the fixed-effects vector (sex-incubation group); Z is the incidence matrix for additive random effects, thereby associating the elements of a and y; a is the random-effects vector for direct additive genetic effects and e is the residual-effects vector.

Results and discussion

Descriptive statistics and heritability estimates for all studied traits are in Table 1. Similar means for BW42 were found by Gaya et al., (2006) and Vayego et al. (2008). For carcass component yield (AFP; THY; DRY and BRY), the presented means were close to that verified by Le Bihan-Duval et al. (2001). However, Zerehdaran et al. (2004) found means slightly higher for AFP at 7 weeks of age (3.38 ± 0.89%).

The highest heritability estimate was found for AFP (0.40 ± 0.07) and the lowest for FCR (0.04 ± 0.02). Beaumont et al. (1998) verified higher estimates for food conversion ratio between 4 and 6 weeks, working with the effect of two temperature in body weight (0.28 ± 0·04 and 0.27 ± 0.04) and Gaya et al (2006) reported heritability estimate of 0.16 ± 0.03 for FCR in a male broiler line. The result found in this study shows that the FCR is strongly influenced by environmental effects. The heritability estimates of BW42, SDrum, AFP, THY, DRY and BRY indicated that direct selection for any of these traits could result in genetic progress.

The estimates of genetic correlation and respective standard errors between BW42 and SDrum, and SBreast and SThigh were 0.67 ± 0.09, 0.91 ± 0.06 and 0.48 ± 0.16, respectively. Selection for increased BW42 also increases the skin weight components. The estimates of genetic correlations between carcass components yields were -0.28 ± 0.17 (AFP x THY), -0.07 ± 0.18 (AFP x DRY), - 0.43 ± 0.14 (AFP x BRY), 0.43 ± 0.18 (THY x DRY), - 0.16 ± 0.18 (THY x BRY) and 0.23 ± 0.18 (DRY x BRY). The genetic correlation between AFP and BRY indicate that broilers with larger abdominal fat percentage at 42 days of age produce less percentage of breast yields. Genetic correlations between drumstick yield, and thigh yield and breast yield indicate positive genetic associations between these traits. Higher positive genetic associations were verified for skin traits. The estimates of genetic correlation were 0.79 ± 0.09 (SDrum x SBreast), 0.57 ± 0.16 (SDrum x SThigh) and 0.49 ± 0.19 (SBreast x SThigh).

Table 1. Number of animals (N), means, standard deviation (SD), coefficient of variation (CV), minimum (Min) and maximum (Max) values and heritability estimates (h^2) for body weight at 42 days of age (BW42), feed conversion ratio (FCR), skin drumstick weight (SDrum), abdominal fat percentage (AFP), thigh yield (THY), drumstick yield (DRY), breast yield (BRY), skin breast weight (SBreast) and skin thigh weight (SThigh).

Trait	N	Mean	SD	CV(%)	Min.	Max.	h^2
BW42 (kg)	1,462	2.22	0.26	11.69	0.99	2.97	0.37 (0.07)*
FCR	1,450	2.32	0.51	21.89	0.86	7.22	0.04 (0.02)
SDrum (g)	1,441	23.05	4.90	21.27	5.80	43.80	0.28 (0.06)
AFP (%)	1,444	2.14	0.62	29.17	0.25	4.67	0.40 (0.07)
THY (%)	1,445	4.62	0.37	8.10	1.79	7.88	0.21 (0.05)
DRY (%)	1,443	6.96	0.60	8.68	1.51	14.36	0.18 (0.05)
BRY (%)	1,444	22.54	1.53	6.78	14.38	34.58	0.36 (0.07)
SBreast (g)	1,443	31.47	6.99	22.23	8.40	80.50	0.15 (0.04)
SThigh (g)	1,442	8.72	2.42	27.68	2.70	28.60	0.13 (0.04)

*In parentheses are shown the standard errors for the heritability estimates

Conclusion

The positive and higher genetic correlations between BW42 and skin weights indicate that selection for increased BW42 can greatly affect SDrum, SBreast and SThigh. The lower magnitude of genetic correlations and its higher standard error between some carcass component yields (AFP x THY, AFP x DRY and THY x BRY) does not allow the establishment of reliable genetic associations between these traits.

Acknowledgements

Financial support for this project was provided by CNPq (National Council for Scientific and Technological Development), with grant number 481755/2007.

References

Adeyinka, I.A., Oni, O.O., Nwagu, B.I. *et al.* (2006). *Intern. J. Poul. Sci.,* 5(6):589-592.

Beaumont, C., Guillaumin, S., Geraert, P. A., *et al.* (1998) *Br. Poult. Sci.*, 39(4):488-491.

Cahaner, A.E and Nitsan, Z. (1985). *Poult. Sci.*, 64:1257-1263.

Gaya, L.G., Ferraz, J.B.S., Rezende, F.M., *et al.* (2006). *Poult. Sci.,* 85(5):837–843.

Le Bihan-Duval, E., Berri, C., Baeza, E., *et al.* (2001). *Poult. Sci.*, 80:839-843.

Meyer, K. (2007) *J. Zhejiang Uni. SCIENCE B,* 8:815–821.

Vali, N., Edriss, M.A. and Rahmani, H.R. (2005). *Intern. J. Poult. Sci.,* 4(5):296-300.

Vayego, S.A., Dionello, N.J.L. and Figueiredo, E.A.P. (2008) *R. Bras. Zootec.*, 37(7):1230-1235.

Zerehdaran, S., Vereijken, A.L.J., van Arendonk, J.A.M. *et al.* (2004) *Poult. Sci.*, 83(6):521–525.