Genetic Correlation For Real-Time Ultrasound And Fleshing Of Breast Muscle With Carcass Traits In Broilers

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Introduction

The success of poultry meat production has been strongly related to the intense selection process carried out and the use of crossbreeding among breeds, producing specific lines with particular characteristics. The focus for the selection of commercial broiler lines, considering mainly the male lines (Lesson and Summers 2000), has been much more intense for the carcass traits, as a consequence of a world trend of the largest consumption of chicken meat being in parts, mainly breast meat (Pollock 1997). The establishment of appropriate and efficient selection criteria becomes extremely necessary to the development of poultry breeding programs (Lopes and Quaas 1997). Traditionally, body weight is the most important trait in broiler breeding programs; however, many other traits are being incorporated into the selection process. Indirect carcass measurements provide the opportunity to collect information from live birds and as a result the own performance information for carcass traits would be available on selection candidates (Zerehdaran *et al.* 2005). Body conformation traits are good indicators for predicting breast meat weight. Recently, the thickness of breast muscle has been measured by ultrasonic apparatus. Therefore, the estimates of genetic parameters of traits used as selection criteria are required to remain updated, as quantifying the genetic variation of traits, by heritability, and the genetic association between different traits, by genetic correlation (Campos and Pereira 2004). Thus, the objective of current study was to estimate heritabilities and genetic and phenotypic correlations for real-time ultrasound and fleshing of breast muscle with carcass traits in a commercial broiler line.

Material and methods

Data. Data of 69,577 broilers from an elite population of a commercial breeding program were used. Information from full-sib testing was also used to evaluate carcass traits, whose purpose is helping to choose the best animals during the selection program of the elite population. The information collected from the individuals included: fleshing of breast muscle at 35 days (FL), corresponding to notes of breast conformation from one to five, one being the worst conformation and five the best conformation; ultrasound measure of beast muscle thickness at 35 days (RTU), recorded *in vivo* by real-time ultrasound; carcass weight (CW), corresponding to the warm carcass weight, eviscerated, without neck, feet, abdominal fat, and internal organs; breast meat weight (BRW), the breast was boneless and skinless,

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recorded after the carcass was refrigerated; and leg weight (LW), corresponding to the thigh plus drumstick weight with skin and bones. The yield of carcass (CY), breast meat (BRY) and leg (LY) were calculated as the ratio between the absolute weight of each trait and the body weight (BW) at 6 week recorded after 10 h of feed and water withdrawal. Carcass data of 24,001 broilers were collected at the Experimental Processing Plant of the University of São Paulo, Pirassununga, SP, Brazil, from November 2002 to December 2006.

Statistical analyses. The pedigree contained 132,442 animals. Components of (co)variance and genetic parameters were estimated by the restricted maximum likelihood method using the software MTDFREML (Boldman *et al*. 1995). The animal models used in the univariate analyses to estimate heritabilities included as random effects, maternal genetic and permanent environmental for FL, RTU, CY, and BRY, and maternal permanent environmental for LY, besides the direct genetic and residual effects. Such model is in accordance with the preliminary analysis that shows significant reduction on the estimate of -2 log L, according to the likelihood ratio test (Dobson 2002). Bivariate analyses were used to estimate genetic and phenotypic correlations between all combinations of traits. In matrix notation, the most complete model of analysis was set up as follows:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} W_1 & 0 \\ 0 & W_2 \end{bmatrix} \begin{bmatrix} m_1 \\ m_2 \end{bmatrix} + \begin{bmatrix} S_1 & 0 \\ 0 & S_2 \end{bmatrix} \begin{bmatrix} c_1 \\ c_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix},$$

where y_1 and y_2 are the vectors of records; b_1 and b_2 are vectors of fixed effects; a_1 and a_2 are vectors of random direct genetic effects; m_1 and m_2 are vectors of random maternal genetic effects; c_1 and c_2 are vectors of random maternal permanent environmental effects as there were five recorded offspring per dam; and e_1 and e_2 are vectors of random residual effects. Hatch week, mating group, and sex of the animals were included as fixed effects for RTU, CY, BRY, and LY, and only mating group for FL. The mating groups are the flocks from which the parents of each individual originated, representing the total environmental condition in which these flocks were submitted and that influenced the progeny performance. The age of the animal at measurement was considered as covariate for FL. The importance of these effects was determined by the GLM procedure of SAS software (SAS Institute 2004), which was significant ($P<0.0001$) for the traits under study.

Results and discussion

The statistical description of the data is summarized in Table 1. Estimated (co)variance components and heritabilities for the traits analyzed are presented in Table 2. The direct heritability estimates were moderate for FL, RTU, CY, and LY, and high for BRY, suggesting that the traits analyzed can be selected and significant results to the selection can be obtained. These estimates were lower than those obtained by Argentão *et al*. (2002) for RTU (0.46) and Zerehdaran *et al*. (2004) for CY (0.41) and BRY (0.73), all working with an animal model including as random effects, direct genetic and residual. Le Bihan-Duval *et al*. (1998) found higher direct heritability for BRY in males (0.64) and females (0.66), using an animal model including direct genetic and common environmental effects. Heritability estimates for CY and BRY were in agreement with estimates obtained by Gaya *et al*. (2005) who reported values of 0.30 and 0.51, respectively. However, these authors, using an animal model including as random effects, direct genetic and residual, reported lower estimates of the heritability for RTU and LY (0.29 and 0.35, respectively).

Table 1: Means, standard deviations, coefficients of variation, and minimum and maximum values of the traits analyzed

Trait[1]	N	Mean	SD	CV (%)	Minimum	Maximum
FL	69,577	3.03	0.97	31.96	1.00	5.00
RTU	35,669	26.17	3.54	13.53	14.00	43.50
CY	24,001	70.56	1.85	2.62	62.23	78.62
BRY	23,529	19.52	1.87	9.58	12.49	27.51
LY	23,515	24.47	1.44	5.87	17.47	31.80

[1] FL = fleshing of breast muscle at 35 days; RTU = real-time ultrasound measure of breast muscle thickness at 35 days (mm); CY = carcass yield (%); BRY = breast meat yield (%); LY = leg yield (%).

Table 2: Estimates of (co)variance components and heritabilities with their approximate standard errors (in parenthesis) for fleshing of breast muscle (FL), real-time ultrasound measure of breast muscle thickness (RTU), yield of carcass (CY), breast meat (BRY) and leg (LY), from univariate analyses

	Variance components[1]					Genetic parameters[2]	
Trait	$\hat{\sigma}^2_a$	$\hat{\sigma}^2_m$	$\hat{\sigma}_{a,m}$	$\hat{\sigma}^2_c$	$\hat{\sigma}^2_e$	$\hat{h}^2_a$	$\hat{h}^2_m$
FL	0.3082	0.0345	-0.5779	0.0427	0.6461	0.32 (0.03)	0.04 (0.01)
RTU	1.2066	0.1109	-0.2031	0.1260	2.1926	0.35 (0.03)	0.03 (0.01)
CY	0.6116	0.0354	-0.0639	0.0524	1.2714	0.32 (0.03)	0.02 (0.01)
BRY	0.8341	0.0573	-0.1207	0.1075	0.7163	0.52 (0.04)	0.04 (0.01)
LY	0.4237	-	-	0.0161	0.5510	0.43 (0.03)	-

[1] $\hat{\sigma}^2_a$ = direct genetic variance; $\hat{\sigma}^2_m$ = maternal genetic variance; $\hat{\sigma}_{a,m}$ = covariance between direct and maternal genetic effects; $\hat{\sigma}^2_c$ = maternal permanent environmental variance; $\hat{\sigma}^2_e$ = residual variance.

[2] $\hat{h}^2_a$ = direct heritability; $\hat{h}^2_m$ = maternal heritability.

The genetic and phenotypic correlation estimates for real-time ultrasound and fleshing of breast muscle with carcass traits are presented in Table 3. Positive genetic correlations were observed between indirect carcass measurements (FL and RTU) and carcass traits (CY and BRY); in other words, the direct selection for FL or RTU will result in increased CY and BRY. Therefore, including FL or RTU in the selection index could be justified, especially for lines that are used for further processing. However, selection for FL or RTU decreases LY, because there is a negative genetic correlation between these traits. These finding ware in agreement with Gaya et al. (2005), who reported positive genetic correlations between RTU and CY (0.40) and RTU and BRY (0.51), and negative genetic correlation between RTU and LY (-0.29). The genetic association between CY and BRY and CY and LY seemed to exist based on the genetic correlation estimates between these traits (0.63 and 0.33, respectively). Therefore, direct selection for total carcass yield would increase its parts. However, a selection for BRY decreases LY and vice-versa, because there is a negative genetic correlation between these traits. The small differences between genetic and phenotypic correlations for traits analyzed may imply a relatively small influence of environmental conditions for these traits.

Table 3: Estimates of genetic (above the diagonal) and phenotypic (below the diagonal) correlations of the traits analyzed, from bivariate analyses

Trait[1]	FL	RTU	CY	BRY	LY
FL		0.77	0.43	0.62	-0.20
RTU	0.57		0.49	0.58	-0.13
CY	0.29	0.36		0.63	0.33
BRY	0.42	0.48	0.53		-0.50
LY	-0.11	0.08	0.30	-0.21	

[1] FL = fleshing of breast muscle at 35 days; RTU = real-time ultrasound measure of breast muscle thickness at 35 days (mm); CY = carcass yield (%); BRY = breast meat yield (%); LY = leg yield (%).

Conclusion

The current study suggests that the traits analyzed can be selected and significant response to selection can be obtained. The results also indicate that it is possible to increase CY and BRY from indirect carcass measurements on selection candidates.

Acknowledgments

Research supported by FAPESP (Fundação de Amparo à Pesquisa do Estado de São Paulo) .

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