



## Genetic and phenotypic parameters of carcass and organ traits of broiler chickens

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**ABSTRACT.** The objective of this study was to estimate the genetic and environmental parameters for carcass, carcass part, and organ weights in a paternal strain of broiler chickens that was selected mainly for body weight at 42 days of age (BW42) to provide support for poultry genetic improvement programs. A total of 1448 chickens were used that resulted from the expansion of a pure paternal strain named TT, which was developed by Embrapa Suínos e Aves. The following weights were evaluated: BW42, chilled carcass, wing, drumstick meat, thigh meat, breast meat, breast fillet, back, liver, heart (HRT), and gizzard (GIZ). The variance component was estimated by the restricted maximum likelihood method using a multi-trait animal model. The general model included the additive genetic and residual random effects and the fixed effect of the sex-hatch group (10 levels). The heritability estimates ranged from  $0.27 \pm 0.06$  for HRT to  $0.44 \pm 0.08$  for GIZ. These results indicated that all the traits have enough additive genetic variability to respond to selection. The genetic correlation estimates between BW42 and the carcass and carcass part weights were high and positive. However, the genetic correlation estimates between BW42 and organ weights were

low. In this population, the carcass traits might respond indirectly to selection applied to BW42. It can be concluded that selection to increase BW42 is not effective in improving broiler organ weight. Therefore, to obtain suitable genetic improvement for these traits, the selection indexes for broilers should include organ weight-based criteria.

**Key words:** Breast fillet; Breast weight; Heritability; Body weight; Wing weight

## INTRODUCTION

The constantly growing worldwide demand for low-cost protein of animal origin has led to major investments in genetics by the poultry industry. Prior knowledge of heritability estimates and genetic correlations is fundamental because this makes it possible to have information about the nature of the action of genes that are involved in the inheritance of traits and to monitor the genetic variability of traits that are to be selected in the strains.

Because traits that are related to body performance and carcass parts have economic importance, they have been evaluated in genetic improvement programs for broiler chickens (Le Bihan-Duval et al., 1998; Rance et al., 2002; Zerehdaran et al., 2004). There is a constant search for birds with greater body weight and part weights. The hoped-for genetic gains can be achieved through selection applied to body weight at 42 days of age (BW42) because this trait presents high positive genetic correlations with most carcass parts (Singh and Trehan, 1994; Le Bihan-Duval et al., 1998, Xu et al., 2011).

The weights of organs also require considerable attention because they are linked to the birds physiology. Gaya et al. (2006) observed that there was a moderate genetic correlation between BW42 and the weight of the liver (LIV) (0.43) and low correlations between BW42 and the weights of the gizzard (GIZ) (0.21) and heart (HRT) (0.28). Verdal et al. (2011) also found a low-magnitude genetic correlation between carcass weight and organs weights. According to Aliabad et al. (2011), the great selection pressure applied to achieve weight increases has caused physiological problems in poultry. For this reason, the introduction of these traits into studies on genetic parameters becomes a matter of interest with the aim of seeking alternatives in genetic improvement programs that would diminish the physiological disorders that might result from selection for body weight.

Drumstick, thigh, and wing weights are also traits that should be evaluated in genetic improvement programs to ascertain how they would respond to the process of selection for BW42. Studies conducted by Vali et al. (2005), Gaya et al. (2006), and Xu et al. (2011) indicated that drumstick and thigh weights present heritability estimates ranging from  $0.28 \pm 0.14$  to 0.38. Gaya et al. (2006) observed that there was a high positive genetic correlation (0.84) between BW42 and leg weight. Therefore, the objective of this study was to estimate the genetic and environmental parameters for carcass, carcass part, and organ weights in a paternal strain of broiler chickens that was selected mainly for BW42 with the aim of providing support for poultry genetic improvement programs.

## MATERIAL AND METHODS

### Population used

The chickens used in this study resulted from the expansion of a pure paternal line

named “TT”, which was developed through a poultry genetic improvement program by Embrapa Suínos e Aves in the municipality of Concordia, SC, Brazil. This strain has been undergoing selection since 1992 with the aim of improving the traits of body weight, feed conversion, carcass yield, carcass part yield, viability, fertility, and hatchability.

The study population was created to be a reference population for validating genomic results. It was formed by mating 20 males with 92 females in a hierarchical scheme (proportions of 1:5). The broiler chickens were reared using vaccination and nutritional management programs recommended by Embrapa Suínos e Aves.

The chickens were kept in collective boxes until the age of 35 days; from 35 to 41 days of age they were housed in individual cages in order to evaluate their feed conversion. At the age of 42 days, 1465 of the 1600 chickens were slaughtered, and the performance records of 1448 of them (696 females and 752 males) were used to estimate genetic parameters.

### Traits analyzed

The traits analyzed were as follows:

- Slaughter weight and carcass weight expressed in grams: BW42 and chilled carcass weight (CCW)
- Weights of the carcass parts in grams: wing (WNG), drumstick meat (DRM), thigh meat (THM), breast meat (BRM), breast fillet (BRF), and back (BCK)
- Weights of the organs in grams: LIV, HRT, and GIZ

### Statistical analysis

Analyses using the least-squares method were performed before hand using the GLM procedure of SAS (SAS 9.1, SAS Institute, Cary, NC, USA) to ascertain the influence of the fixed effects of hatch (5 levels) and sex (2 levels), totaling 10 sex-hatch groups. These fixed effects were significant ( $P < 0.05$ ) for the 11 traits studied. The descriptive statistics on the traits of slaughter weight, carcass weight, carcass part weight, and weights of the organs involved in the study (Table 1) were obtained through the PROC MEANS procedure of SAS (SAS 9.1, SAS Institute).

**Table 1.** Number of animals (N), mean (M), standard deviation (SD), minimum (MIN), maximum (MAX), and coefficient of variation (CV) of the weights (in grams) of the carcass, carcass parts, and organs of broiler chickens.

Trait	N	M	SD	MIN	MAX	CV (%)
Slaughter and carcass weights						
BW42	1393	2224.39	253.55	1276.00	2971.00	11.40
CCW	1380	1639.11	196.48	850.00	2185.00	11.98
Carcass part weights						
WNG	1389	83.76	9.84	48.30	121.50	11.74
DRM	1392	66.63	10.48	22.20	112.20	15.73
THM	1391	115.93	18.65	46.30	175.60	16.09
BRM	1393	293.96	42.58	106.50	419.50	14.48
BCK	1390	264.60	36.42	124.10	390.60	13.76
BRF	1393	77.47	11.76	37.80	119.10	15.18
Organ weights						
LIV	1393	52.53	9.03	25.40	98.25	17.19
HRT	1387	12.39	2.14	7.40	19.70	17.27
GIZ	1390	32.08	6.08	17.80	58.90	18.95

BW42 = body weight at 42 days of age; CCW = chilled carcass weight; WNG = wing weight; DRM = drumstick meat weight; THM = thigh meat weight; BRM = breast meat weight; BRF = breast fillet weight; BCK = back weight; LIV = liver weight; HRT = heart weight; GIZ = gizzard weight.

The variance components were estimated using the restricted maximum likelihood method on a multi-trait animal model involving all 11 traits, using the WOMBAT computer software (Meyer, 2007). The general model included the direct additive genetic and residual random effects and the fixed effect from the sex-hatch group (10 levels). The mixed model for all traits was as follows:

$$y = Xb + Za + e$$

Where  $y$  is the vector of the dependent variable,  $X$  is the incidence matrix for fixed effects associated elements  $b$  and  $y$ ,  $b$  is the vector of fixed effects (sex-hatch group),  $Z$  is the incidence matrix of random additive effects associating the elements  $a$  and  $y$ ,  $a$  is the vector of random effects for the additive direct genetic effect, and  $e$  is the vector of residual effects.

## RESULTS AND DISCUSSION

The additive, phenotypic, and environmental variances and heritability estimates with respective standard errors for the traits studied can be seen in Table 2. The heritability estimates ranged from  $0.27 \pm 0.06$  (HRT) to  $0.44 \pm 0.08$  (GIZ).

**Table 2.** Additive genetic variance ( $\sigma_a^2$ ), phenotypic variance ( $\sigma_p^2$ ), environmental variance ( $\sigma_e^2$ ), and heritability estimates ( $h^2$ ), with their respective standard errors (between parentheses), for the weights (in grams) of the carcass, carcass parts, and organs of broiler chickens.

Trait	$\sigma_a^2$	$\sigma_p^2$	$\sigma_e^2$	$h^2$
Slaughter and carcass weights				
BW42	15157.8 (3414.77)	36194.9 (1963.8)	21037.1 (2121.61)	0.41 (0.08)
CCW	9541.68 (2185.3)	23643.7 (1266.1)	14102.0 (1372.9)	0.39 (0.08)
Carcass part weights				
WNG	18.91 (4.42)	52.82 (2.67)	33.92 (2.90)	0.35 (0.07)
DRM	21.42 (5.01)	61.44 (3.07)	40.01 (3.33)	0.35 (0.07)
THM	60.31 (14.87)	203.44 (9.64)	143.13 (10.48)	0.29 (0.06)
BRM	531.71 (124.48)	1436.79 (73.94)	905.08 (80.68)	0.37 (0.07)
BRF	49.20 (11.01)	122.04 (6.46)	72.84 (6.94)	0.40 (0.07)
BCK	321.34 (78.09)	959.57 (47.80)	638.23 (52.29)	0.33 (0.07)
Organ weights				
LIV	25.80 (6.12)	75.04 (3.75)	49.24 (4.07)	0.33 (0.07)
HRT	0.73 (0.18)	2.68 (0.12)	1.95 (0.13)	0.27 (0.06)
GIZ	14.43 (3.09)	33.19 (1.79)	18.76 (1.91)	0.44 (0.08)

BW42 = body weight at 42 days of age; CCW = chilled carcass weight; WNG = wing weight; DRM = drumstick meat weight; THM = thigh meat weight; BRM = breast meat weight; BRF = breast fillet weight; BCK = back weight; LIV = liver weight; HRT = heart weight; GIZ = gizzard weight.

The heritability estimates varied from moderate (HRT, THM, BCK, and LIV) to high magnitude (DRM, WNG, BRM, CCW, BRF, BW42, and GIZ), and the standard errors associated with these estimates were low (less than 0.08). This was possible because the structure and size of the population presented a hierarchical mating scheme, because the numbers of progeny per male and female reproducers were sufficient to make estimates of genetic parameters, and because ancestral records were available in the relationship matrix for all of the birds.

Both BW42 and CCW showed enough genetic variability to respond for selection. Heritability estimates for CCW showed a wide range of magnitudes in the literature. For live weight at slaughter, Nunes et al. (2011) and Xu et al. (2011) observed heritability estimates of  $0.31 \pm 0.07$  and  $0.53$ , respectively. Grosso et al. (2009), Narinc et al. (2010), and Xu et al. (2011) observed heritability estimates for CCW of  $0.17 \pm 0.02$ ,  $0.42$ , and  $0.52$ , respectively. The genetic correlation (Table 3) estimated between BW42 and CCW was  $0.98 \pm 0.01$ . This estimate was greater than that obtained in the study by Xu et al. (2011), who obtained a genetic correlation of  $0.85$  between live weight at 49 days of age and carcass weight. The CCW trait may respond positively, in terms of genetic gains, through indirect selection for BW42 because of its high positive genetic correlation with BW42.

**Table 3.** Estimates of genetic correlations (above the diagonal) and environmental correlations (below the diagonal), with their respective standard errors (between parentheses), between slaughter, carcass, carcass part, and organs weights (in grams) of broiler chickens.

	BW42	CCW	WNG	DRM	THM	BRM	BRF	BCK	LIV	HRT	GIZ
BW42		0.98 (0.01)	0.86 (0.04)	0.83 (0.05)	0.86 (0.05)	0.82 (0.06)	0.76 (0.07)	0.93 (0.03)	0.64 (0.10)	0.48 (0.13)	0.38 (0.14)
CCW	0.97 (0.00)		0.86 (0.05)	0.80 (0.06)	0.91 (0.03)	0.89 (0.04)	0.78 (0.06)	0.93 (0.03)	0.56 (0.12)	0.44 (0.14)	0.32 (0.14)
WNG	0.76 (0.02)	0.77 (0.02)		0.83 (0.06)	0.79 (0.07)	0.72 (0.08)	0.70 (0.08)	0.82 (0.06)	0.41 (0.14)	0.47 (0.14)	0.30 (0.15)
DRM	0.65 (0.03)	0.68 (0.03)	0.51 (0.04)		0.92 (0.04)	0.57 (0.11)	0.63 (0.10)	0.78 (0.07)	0.44 (0.14)	0.43 (0.14)	0.28 (0.15)
THM	0.74 (0.02)	0.75 (0.02)	0.57 (0.04)	0.46 (0.04)		0.75 (0.08)	0.70 (0.09)	0.84 (0.06)	0.41 (0.15)	0.24 (0.17)	0.28 (0.15)
BRM	0.72 (0.03)	0.72 (0.03)	0.54 (0.04)	0.53 (0.04)	0.54 (0.06)		0.85 (0.06)	0.78 (0.08)	0.47 (0.14)	0.16 (0.17)	0.29 (0.15)
BRF	0.61 (0.04)	0.62 (0.04)	0.48 (0.05)	0.44 (0.05)	0.48 (0.04)	0.52 (0.04)		0.71 (0.09)	0.36 (0.14)	0.36 (0.15)	0.22 (0.15)
BCK	0.66 (0.03)	0.68 (0.03)	0.49 (0.04)	0.42 (0.04)	0.42 (0.04)	0.50 (0.04)	0.42 (0.05)		0.55 (0.12)	0.51 (0.13)	0.27 (0.15)
LIV	0.43 (0.05)	0.39 (0.05)	0.34 (0.05)	0.22 (0.05)	0.25 (0.05)	0.23 (0.05)	0.19 (0.06)	0.29 (0.05)		0.56 (0.13)	0.44 (0.14)
HRT	0.47 (0.05)	0.44 (0.05)	0.38 (0.04)	0.27 (0.05)	0.36 (0.04)	0.38 (0.05)	0.28 (0.05)	0.30 (0.05)	0.22 (0.05)		0.38 (0.15)
GIZ	0.29 (0.06)	0.25 (0.06)	0.22 (0.06)	0.11 (0.06)	0.20 (0.06)	0.12 (0.06)	0.11 (0.07)	0.20 (0.06)	0.05 (0.07)	0.16 (0.06)	

BW42 = body weight at 42 days of age; CCW = chilled carcass weight; WNG = wing weight; DRM = drumstick meat weight; THM = thigh meat weight; BRM = breast meat weight; BRF = breast fillet weight; BCK = back weight; LIV = liver weight; HRT = heart weight; GIZ = gizzard weight.

The traits of carcass part weights also presented heritability estimates that implied that considerable gains would be obtained through direct selection for each of them. Among these, THM presented the lowest heritability estimate ( $0.29 \pm 0.06$ ), while BRF presented the highest ( $0.40 \pm 0.07$ ). This class of traits (carcass part weights) showed genetic correlation estimates with BW42 and CCW that were greater than  $0.76$  (Table 3). This result indicated that these traits would be capable of responding positively to selection for BW42 or CCW.

Among the carcass part weights, the lowest genetic correlation observed was between DRM and BRM ( $0.57 \pm 0.11$ ), and the highest was between DRM and THM ( $0.92 \pm 0.04$ ). Among this set of traits, indirect genetic gains could also occur positively between the carcass parts if selection was implemented for one of them (Table 3). Between the carcass part weights and the organ weights, the genetic correlation estimates ranged from low ( $0.16 \pm 0.17$  between BRM and HRT) to medium magnitude ( $0.55 \pm 0.12$  between BCK and LIV). Therefore, if selection was undertaken for the carcass part traits, the organs would have a correlated response that was low or close to zero (BRM and HRT).

The heritability estimates for organ weights were  $0.27 \pm 0.06$ ,  $0.33 \pm 0.07$ , and  $0.44 \pm 0.08$  for HRT, LIV, and GIZ, respectively. Cahaner and Nitsan (1985) observed higher heritability estimates for LIV ( $0.50 \pm 0.21$ ) and GIZ ( $0.57 \pm 0.24$ ). However, Gaya et al. (2006)

found heritability estimates that were similar to those obtained in this study for LIV and GIZ ( $0.25 \pm 0.03$  and  $0.39 \pm 0.04$ , respectively). Rance et al. (2002) obtained similar heritability estimates for HRT ( $0.30 \pm 0.08$ ). These estimates indicate that selection for organ weights, like HRT, LIV, and GIZ, is promising.

The genetic correlation estimates (Table 3) between BW42 and LIV, HRT, and GIZ were higher than those found by Gaya et al. (2006), which were 0.28, 0.43, and 0.21 between BW42 and HRT, BW42 and LIV, and BW42 and GIZ, respectively. Closter et al. (2012) reported that the genetic correlations between body weight and the proportion of the heart decreased with a signal change as the age of the chickens increased ( $0.11 \pm 0.12$ ,  $-0.09 \pm 0.13$ , and  $-0.43 \pm 0.11$  for live weights at 14, 35, and 49 days of age relative to the proportion of the heart, respectively). A similar trend was observed by Kause et al. (2012), who found genetic correlation estimates of  $0.12 \pm 0.12$  between live weight at 14 days of age and the proportion of the heart, and  $-0.33 \pm 0.12$  between live weight at 49 days of age and the proportion of the heart.

With exception of the genetic correlation estimate between BW42 and LIV, the genetic correlation estimates between BW42 and organ weights were moderate, thus indicating that these traits will respond indirectly to selection when selection is applied directly to increase BW42. Havenstein et al. (1994) observed that the genetic relationship between weight gain and organ weight led to a relative decrease in the size of the heart. This can lead to a deficiency of this organ to serve adequately the demand for oxygen; consequently, the development of ascites and sudden death syndrome are possible. Julian (1998) also reported that these physiological problems were related to the effect of selection of chickens for higher body performance. Furthermore, in a study on genetic correlations between body weight and organ weights, Thiruvankadan et al. (2011) observed that the correlations were high between body weight and lung weight (0.49) and between body weight and heart weight (0.95). These authors emphasized that selection applied toward greater body weight might cause a disproportional increase in the organs.

The environmental correlation estimates (Table 3) ranged from  $0.05 \pm 0.07$  between LIV and GIZ to  $0.97 \pm 0.00$  between BW42 and CCW. The environmental correlation estimates between BW42 and CCW with carcass part weights were moderate to high (greater than 0.60), indicating that environmental factors and non-additive genetic effects affected this group of traits in the same direction.

The results obtained in this study demonstrate that selection for higher BW42 might cause favorable correlated genetic gains both for carcass weight and for carcass part weights. However, the correlated response in organ weights when selection for higher BW42 was applied would be low. This could contribute to increase the incidence of metabolic disorders (sudden death) and physiological problems (ascites), which are associated with alterations in organs due to rapid growth rates.

## CONCLUSION

In this population, the carcass traits might respond indirectly to selection applied to BW42. It can be concluded that the selection to increase BW42 is not effective for improving broiler organ weight. Therefore, to obtain suitable genetic improvement for these traits, the selection index for broilers should include organ weight-based criteria.

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