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Genetic parameters for performance and carcass traits in a paternal 1 lineage of broiler

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Abstract: The objective of this study was to estimate variance components for performance and carcass traits in a paternal broiler line. The (co)variance components were estimated by the restricted maximum likelihood method applied to the animal model, including the fixed effect of group (sex and hatch) and additive genetic and residual as random effects. Estimated heritability for performance traits ranged from 0.09 to 0.42. The genetic correlations between traits ranged from -0.50 to 0.97. The heritability estimates of feed intake, weight gain, and feed conversion from 35 to 41 days of age were of low magnitude. The genetic correlations among them were favorable to genetic selection. These results suggest that moderate genetic gain can be obtained to the feed intake and weight gain when the selection criterion is the body weight and prime cuts traits. The feed conversion that had low heritability estimation and low genetic correlation with the body weight and prime cut traits needs to pay greater attention due to the economic importance in the high-meat production lineage breeding programs.

Key words: Carcass, feed conversion, genetic correlation, heritability, weight gain.

INTRODUCTION

The increased demand for high-quality protein to human consumption pushed the animal production industry to a higher level in livestock. The animal production was accelerated by biological, environmental and economic factors (Webb & Casey 2010). Also, the developing countries have increased their contribution to the world's livestock, which are characterized by the growing productivity compared to the number of animals increasing (Steinfeld 2004). The global changes in eating habits during the last decades with a strong preference for chicken cuts and processed meat have encouraged the industry to adapt to the poultry industry level, providing specific lineages of meat production. Consequently, it is possible to obtain genotypes with higher performance for local environmental conditions (Vayego et al. 2008).

The selection of broiler chickens during the last 40 years has brought bigger changes in their growth curves. It not only maximized the birds' production performance but also, allowed the reduction of the market age and minimized the production cost in the hybrid system (Schmidt 2008). Besides, broilers production has adopted important criteria for the selection while aiming to reduce the slaughter age by the performance evaluation, focusing on a carcass, breast, and leg meat yield, but also their quality.

According to Moreira et al. (2003), up to 35 days of age, broiler chickens that consume a higher amount of feed present higher weight gain. However, selected birds after weight at 42 or 49 days have presented higher fat deposition in the carcass (Zerehdaran et al. 2004), affecting the carcass yield. The body weight at 42 days of age as selection criteria has been shown great results, due to at this period the broiler presents an equilibrium point between body weight, the yield of traits at slaughter and feed conversion than older ages.

The feed efficiency traits have been studied in several domestic species, focusing on improving feed utilization. Inefficient animals cause economic and biological losses in the production system. The feed intake that was not deposited as protein can be redirected to produce fat, which is undesirable in excess in the carcass. On the other hand, the food excess that crossed the gastro-intestinal tract is eliminated, causing environmental impacts. The feed conversion ratio is measured as the ratio of feed consumption and weight gain, and consequently, it is difficult to forecast the effect of selection for traits from its components, without the knowledge of their respective genetic and phenotypic parameters (Gunsett 1984). For past time, the feed efficiency breeding in commercial line was obtained as the correlated response to the selection to the higher growth (Crawford 1990). Mignon-Grasteau et al. (2004) showed that the animal ability to digest the feed can be included as selection criteria. Although weight gains have been evaluated in different periods of growth across the species to get the appropriate period to apply the selection. The weight gain depends on the nutrients harnessing, however, the genetic potential is a strong determinant of how much food is ingested and converted into muscle tissue. This factor reflects directly in feed costs, which represent a higher cost of the total production chain (Havenstein et al. 2003).

Besides the feed efficiency, the gain in prime cut traits has become one of the main lineage breeding, once the chicken cuts suppressed the market of a whole chicken (Schmidt 2008). Le Bihan-Duval et al. (2008) observed that the higher breast muscle weight was registered in the broilers selected to fast growth, correlating positively with the muscle fiber size, which would cause higher protein deposition and meat yield. The maximum growth and protein deposition are different among lineages; besides the body weight and maturity traits (Goliomytis et al. 2003, Eyng et al. 2013) and it can be explored by genetic selection.

However, knowing genetic variability in the development and maturity body, and cuts traits along the growth period that is sold as separated traits may increase the production economic efficiency. Also, according to Verdal et al. (2011), changes in the broiler digestive capacity have been observed, due to the gastrointestinal tract being extensively modified by the selection process. Increases in carcass quality traits may favor protein deposition and reduce fat accumulation.

The knowledge regardless of the genetic parameters across the generations in breeding programs is essential to detect possible differences in genetic selection response of the traits, allowing evaluation of the selection efficiency. Thus, the aim of the present study was to estimate the genetic parameters for performance and prime cut traits in a paternal lineage in broiler chicken.

MATERIALS AND METHODS

Ethics statement

This study was performed with the approval of the Embrapa Swine and Poultry Ethical Committee for Animal Use (CEUA) under protocol number 011/2011, following international guidelines for animal welfare.

Population and the collection of data

Phenotypic records were obtained from 1,454 animals from a paternal lineage of broilers. This line has been developed and is owned by the Poultry Genetic Improvement Program from EMBRAPA Swine and Poultry (Brazilian Agricultural Research Corporation, https://www.embrapa.br/en/home). The experimental research center is located in the city of Concórdia (27º 14’ 03” S - 52º 01’ 40” W), Santa Catarina state, Brazil. This line of broilers has been under development since 1992 and aims to: increase body weight and carcass yield, improve viability, fertility, hatchability, and feed conversion, and reduce abdominal fat and metabolic problems (Vayego et al. 2008). The original population was randomly sampled and then 20 males and 100 females were mated to produce an initial population of approximately 1,500 animals. A pedigree of two generations from 2007 to 2008 containing a total of 1570 individuals was used.

The birds were housed collectively until 35 days of age and to evaluate feed conversion, were moved to individual cages from 35 to 41 days. The birds were banded for identification and fed a three-phase diet, starter from the 1st to 21st day (21% crude protein and 3,150 kcal metabolizable energy), grower from the 22nd to 35th day (20% protein gross and 3,200 kcal metabolizable energy) and finisher from the 31st to 41st day (18.5% crude protein and 3,200 kcal metabolizable energy). The birds were housed collectively until 35 days of age and then to evaluate feed conversion, were moved to individual cages for days 35 to 41.

The birds were slaughtered at 42 days following a 6 hour fast. Eighty-five characteristics relating to performance, carcass composition, organ and bone integrity in broilers were collected from this population as described by Cruz et al. (2015). For this study, the weight at 35 (W35), 41 (W41), 42 (W42) days of age, feed intake (FI35_41), weight gain (WG35_41) and feed conversion (FC35_41) at 35 to 41 days of age, weights of drumstick (WDS), thigh (WTH), and breast (WBT) were evaluated. The feed conversion ratio was calculated by dividing feed intake and weight gain in the period 35-41 days of age.

The phenotypic data used in this study are available upon request to Dr. Mônica Côrreia Ledur (Embrapa Swine and Poultry. Address: Rodovia BR-153, Km 110, Distrito de Tamanduá Caixa Postal: 21 CEP: 89700-899, Concórdia, Santa Catarina, Brazil).

Statistical analysis

Preliminary analyses, including descriptive statistics, normality test and testing of fixed effects to be included in the model, were done using the *UNIVARIATE* and *GLM* procedures in the Statistical Analysis System (SAS 2001). Outliers were identified using *Box-plot* and were removed from the data set, resulting in 1,343 animals in the final data file to posterior genetic analysis.

Phenotypic and genetic (co)variance components used to obtain the heritability estimates and genetic correlations were estimated in a multi-trait analysis by the Restricted Maximum Likelihood Method via WOMBAT (Meyer 2007).

The following multivariate animal model, given matrix notation, was used to estimate the genetic parameters:

$$\begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 & 0 \\ 0 & X_2 & 0 & 0 \\ 0 & 0 & \ddots & \vdots \\ 0 & 0 & \cdots & X_n \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ \vdots \\ b_n \end{bmatrix} + \begin{bmatrix} Z_1 & 0 & 0 & 0 \\ 0 & Z_2 & 0 & 0 \\ 0 & 0 & \ddots & \vdots \\ 0 & 0 & \cdots & Z_n \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ \vdots \\ a_n \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ \vdots \\ e_n \end{bmatrix}$$

In which:

$y_1, y_2, ..., y_n$ = vector of phenotypic observations for the n^{th} trait (n=1, 2, ..., 9), $X_1, X_2, ..., X_n$ = incidence matrices for fixed effects, elements associated from b_1 to y_1, b_2 to y_2,..., b_n to y_n, $b_1, b_2, ..., b_n$ = vector of the fixed effect group (sex and hatch) for the n^{th} trait, $Z_1, Z_2, ..., Z_n$ = incidence matrix of additive genetic direct effects elements associating elements g_1

to y_1, g_2 to y_2,...,g_n to y_n, $a_1, a_2, ..., a_n$ = vector of additive genetic effects for the n^{th} trait for traits, $e_1, e_2, ..., e_n$ = vector of random residual effects, with random standard error supposed normal and independently distributed (e_1~NID(0, σ^2) for each dependent variable.

We assume that $Var(y) = ZGZ' + R$, $G = A\sigma_a^2$, being A the parental matrix and σ_a^2 and σ_e^2 the additive and environmental genetic variances, respectively, $R = I\sigma_e^2$, being I the identity matrix with order similar to the number of observations.

RESULTS

Descriptive statistics showed higher phenotypic variations to WG35_41 (22%) and FC35_41 (21%) traits. The feed conversion observed variation may have followed weight gain variation, which is used to calculate the feed conversion (Table I). In this context, the breast weight phenotypic variation was the closest to the body weight at 42 days, with a higher proportion when compared to the other traits.

The heritability estimates in a multi-trait analysis for the traits are presented in Table II. The estimative for the evaluated traits in this study ranged from lower (0.09±0.04 to FI35_41) to high (0.42±0.07 to W35). Estimates of heritability for the body weight (W35, W41, and W42) were 0.42±0.07, 0.40± 0.07, and 0.38± 0.06, respectively, and the values decreased as the age increased. Among the prime cut traits, the heritability estimates for WBT (0.38±0.03) was closer to W42 when compared to the WDS (0.35±0.06) and WTH (0.31±0.06). This result may be explained due to the WBT represents the higher weight corporal proportion at this age (22.6%, according to Table I) than the others. The heritability estimate for FC35_41 (0.09±0.04) was limited by the FI35_41 (0.18±0.05) and WG35_41 (0.10±0.04) that showed the low magnitude of heritability (Table II).

Genetic and residual correlations for all traits are shown in Table III. The estimated genetic correlations between W35 and W41 and between W35 and W42 were respectively 0.97±0.01 and 0.98±0.01 (Table III), indicating a strong genetic association between the traits. To the corporal weight and the other performance traits, the genetic correlations were positive, although the magnitude was from low to moderate, varying from 0.03±0.21 to 0.66±0.10. The smaller genetic correlation obtained between W42 and FC35_41 (0.03±0.21), indicating a lower genetic linear association between them and the higher was between W41 and FI35_41 (0.66±0.10).

The W35 was correlated with FC35_41, WG35_41, and FI35_41, with a magnitude of 0.20±0.19, 0.30±0.19, and 0.59±0.12, respectively. Also, higher and favorable genetic correlations were found among the body weights and the prime cuts traits, varying from 0.76±0.07 to 0.87±0.04. Among these traits, WDS was presenting the lowest association with all body weights. The genetic correlation estimates between the performance traits were negative for WG35_41 and FC35_41 (-0.50±0.21) and positive between FI35_41 and WG35_41 (0.59±0.15), and FC35_41 (0.39±0.23).

The relationship among the prime cuts and the other performance traits, the genetic correlation between FC35_41 and WTH was close to zero (0.02±0.21), and between FI35_41 and WBT (0.48±0.15) was the highest genetic correlation observed. However, FC35_41 presented a low and negative genetic correlation to WDS (-0.17±0.20). The genetic correlations were favorable between the prime cut traits, varying from 0.58±0.10 to 0.78±0.07. In general, the traits studied in this study were correlated among them, except the FC35_41 with body weights and prime cuts traits.

Table I. Average (in grams) ± standard deviations (SD) and coefficient of variations (CV%) for performance and carcass traits measured in a paternal broiler line.

Trait	Average	CV(%)	Min	Max	Male		Female	
					Average±SD	CV(%)	Average±SD	CV(%)
W35	1,737.37±192.80	11.00	1,156.00	2,444.00	1864.22^{a} ±162.22	8.70	1622.88^{b} ±139.06	8.57
W41	2,226.52±240.00	10.80	1,542.00	2,908.00	2399.30^{a} ±191.64	7.99	2070.58^{b} ±158.78	7.67
W42	2,231.51±247.20	11.00	1,510.00	2,919.00	2410.65^{a} ±199.30	8.27	2069.82^{b} ±159.07	7.69
FI35_41	1,093.56±149.10	13.60	508.00	1,590.00	1155.75^{a} ±139.57	12.08	1037.42^{b} ±134.56	12.97
WG35_41	488.00±108.25	22.00	128.00	802.00	532.67^{a} ±111.76	20.98	447.69^{b} ±86.98	19.43
FC35_41	2.31±0.50	21.00	1.40	5.20	2.22^{b} ±0.49	22.07	2.39^{a} ±0.45	18.83
WDS	206.84±30.30	14.60	138.00	306.60	230.54^{a} ±22.72	9.86	185.46^{b} ±17.80	9.60
WTH	311.92±44.30	14.00	199.20	462.80	340.69^{a} ±39.48	11.59	285.96^{b} ±30.21	10.56
WBT	503.25±60.17	11.90	334.10	710.80	532.53^{a} ±57.45	10.79	476.83^{b} ±49.16	10.31

Body weight at 35 (W35), 41 (W41), and 42 (W42) days of age, feed intake (FI35_41), weight gain (WG35_41) and feed conversion (FC35_41) from 35 to 41 days of age, weight of drumstick (WDS), thigh (WTH) and breast (WBT), number of animals (1,347), number of females (708) and males (639).

$^{a\text{-}b}$ **Average in same row with different superscripts significantly different ($P \leq 0.05$).**

Table II. Estimates of heritability and genetic and environment variance and respective standard error for performance and carcass traits.

Traits	σ_a^2	σ_e^2	σ_p^2	h^2
W35	9184.94	12658.50	21843.50	0.42±0.07
W41	11632.10	17259.00	28891.10	0.40±0.07
W42	11196.90	18449.10	29646.10	0.38±0.06
FI35_41	3091.54	13778.70	16870.30	0.18±0.05
WG35_41	736.40	6397.60	7134.00	0.10±0.04
FC35_41	0.015	0.143	0.157	0.09±0.04
WDS	128.34	236.67	365.01	0.35±0.06
WTH	326.76	724.35	1051.11	0.31±0.06
WBT	949.30	1576.94	2526.24	0.38±0.03

Weight at 35 (W35), 41 (W41), and 42 (W42) days of age, feed intake (FI35_41), weight gain (WG35_41) and feed conversion (FC35_41) from 35 to 41 days of age, weight of drumstick (WDS), thigh (WTH) and breast (WBT), number of animals per trait = 1,347.

Table III. Genetic (above diagonal) and phenotypic (below diagonal) correlations and respective standard errors among performance and carcass traits.

Traits	W35	W41	W42	FI35_41	WG35_41	FC35_41	WDS	WTH	WBT
W35		0.98±0.01	0.97±0.01	0.59±0.12	0.30±0.19	0.20±0.19	0.76±0.07	0.85±0.05	0.87±0.04
W41	0.87±0.01		0.99±0.00	0.66±0.10	0.49±0.15	0.08±0.20	0.77±0.06	0.84±0.05	0.85±0.04
W42	0.86±0.01	0.95±0.01		0.62±0.11	0.49±0.16	0.03±0.21	0.78±0.06	0.86±0.04	0.85±0.04
FI35_41	0.30±0.03	0.56±0.02	0.55±0.02		0.59±0.15	0.39±0.23	0.28±0.16	0.40±0.15	0.48±0.15
WG35_41	0.01±0.03	0.46±0.02	0.44±0.02	0.64±0.02		–0.50±0.21	0.37±0.18	0.26±0.19	0.29±0.18
FC35_41	0.19±0.03	-0.15±0.03	-0.09±0.03	0.03±0.03	–0.55±0.02		-0.17±0.20	0.02±0.21	0.14±0.21
WDS	0.67±0.02	0.75±0.02	0.79±0.01	0.42±0.03	0.36±0.03	-0.09±0.03		0.78±0.07	0.58±0.10
WTH	0.70±0.02	0.78±0.01	0.81±0.01	0.45±0.03	0.37±0.03	-0.09±0.03	0.66±0.02		0.72±0.08
WBT	0.76±0.02	0.82±0.01	0.84±0.01	0.43±0.03	0.33±0.03	-0.06±0.03	0.66±0.02	0.66±0.02	

Body weight at 35 (W35), 41 (W41), and 42 (W42) days of age, feed intake (FI35_41), weight gain (WG35_41) and feed conversion (FC35_41) from 35 to 41 days of age, weight of drumstick (WDS), thigh (WTH) and breast (WBT), number of animals per trait = 1,347.

DISCUSSION

The fixed effect that included sex and hatching was significant for all traits. According to Zuidhof et al. (2014), the sexual dimorphism in several traits has become more pronounced in modern strains due to the divergent responses of females versus males to commercial selection pressures. Also, the average of the evaluated traits can be higher in broilers from younger than ones from older mothers. Peebles et al. (1999) reported that broiler offspring from hens at 35 and 51 weeks old performed best at different periods during grow-out then broiler from 63 weeks old. The significant effect of hatching in our research study providing pieces of evidence that the age of the mother may affect the performance of the broiler progeny.

Heritability

The W42 heritability estimate in this study is similar to the observed (0.37) by Le Bihan-Duval et al. (2008). However, the results of heritability estimates for W42 and W35 disagree with those reported in the literature (Gaya et al. 2006, Vayego et al. 2008, Aggrey et al. 2010, Zerehdaran et al. 2004). Although the body weight heritability estimates can vary between different broiler populations. The selection for these traits has modified the growth curve, reducing the age of broiler at slaughter over the generations (Neme et al. 2006).

Similarly, to this study, other authors also reported higher heritability when the body weight was measured at a younger age. A high estimate for body weight at 28 days (0.59) was found by Beaumont et al. (1998). Pakdel et al. (2005) evaluated body weight at 23 and 48 days and observed heritability estimates of 0.52 and 0.27, respectively. Also, Gaya et al. (2006) found different heritability estimates for W38 and W42. It implies that to detect genetic variability for body weight sounds to be hard at 42 days broilers when compared to younger broilers. Thus, our find suggests that the W35 could be used as selection criteria instead of W42 to select animals for early age at slaughter. However, decision regardless of the selection criteria must be taken carefully, due to the genetic progress evaluation across the generations must be done based on the same selection criteria.

The heritability estimates for WTH, WDS, and WBT in our study were in agreement with different reports in the literature. Gaya et al. (2006) observed heritability for WBT of 0.33, similar to our study. Grosso et al. (2009) and Gaya et al. (2006) studied WDS and WTH as a single trait (LEG) and observed heritability estimates of 0.31 and 0.33, respectively. However, the LEG trait when splitting into WDS and WTH traits allows visualizing differences of the genetic variance estimates to them, and it may indicate that these traits could have different selection responses.

The heritability estimates for FI35_42, WG35_42, and FC35_42 in this study were in agreement with the ones found by Gaya et al. (2006), who evaluated FI35_42 and FC35_42 and observed low heritability (0.20 and 0.16, respectively) for these traits. Pakdel et al. (2005) evaluated the chicken performance from 23 to 48 days, obtaining heritability of 0.35 (FI23_48) and 0.16 (WG23_48), superior to the ones found in this study. Beaumont et al. (1998) evaluated the genotype-environment interaction considering two temperatures and observed differences in the heritability estimates for WG28_42 (0.24 at 22°C and 0.13 at 32°C) though to FC28_42 the estimates did not differ between temperatures (0.28 at 22°C and 0.27 at 32°C). According to the authors, the environmental differences were while weight gain was evaluated and it shows evidence of the interaction genotype-environment. Besides, to differences between the populations studied in the researchers of Pakdel et al. (2005) and Beaumont et al. (1998), the heritability estimates for feed intake, weight gain and feed conversion in this study, may be explained by the fact that the authors evaluated periods covering younger ages and these may show higher estimative, as observed for body weight. Despite the low magnitudes of heritability estimates for FI35_41, WG35_41, and FC35_41 in this study, we must be considered in the genetic evaluation in breeding programs to improve these traits in broilers chicken, even the genetic variability in these phenotypes are small.

Heritability estimates for the evaluated traits (Table II) indicate that the body weight, drumstick, thigh, and breast have enough additive genetic variability to response selection. The variation among the heritability estimated reported in the literature can be affected by different factors, such as methodologies and by the fixed and random effects considered in the analysis models, sample sizes, besides the population and selection criteria differences used in the breeding programs.

Genetic correlations

Body weight and prime cuts

High genetic correlation estimates between the body weights at 35 and 42 days (Table II) showed that the body weight selection in any age could lead to changes in the body weight in other ages. This result also suggests that they are influenced by the same genes, determining the high genetic correlations. Genetic correlation estimates for weight of different ages were described in the literature by Zerehdaran et al. (2004) of 0.94 between body weight at 35 and 42 days of age. Pakdel et al. (2005) found a genetic correlation of 0.70 between W23 and W48 days, i.e., heavier birds at W23 can be also heavier at W48. However, when increases the interval between ages the genetic correlation decreases.

There was a high genetic association between body weight and prime cuts, indicating that these traits expressed by a set of common genes. In this way, the selection process of weight at 35 and 42 days increases the weight of cuts traits. Gaya et al. (2006) found genetic correlations between W38 and W42 with WBT of 0.75 and 0.43, and LEG (WDS+WTH) of 0.93 and

0.84, respectively. In our study, WDS had an inferior genetic correlation with body weights comparing to WTH. We can emphasize that this difference could be taken into account when LEG weight is evaluated, i.e., WDS and WTH, because these traits would not respond to selection indirectly with the same intensity if the selection is done based on the body weights.

Body weights, FI35_41, WG35_41, and FC35_41

The body weights did not have a genetic association to FC35_41, the genetic correlations estimated were low, also since had standard errors close or higher to the estimates themselves. Genetic correlations between W35 and FI35_41, WG35_41, and FC35_41 are scarce in the literature. Gaya et al. (2006) evaluated the performance of the period from 38 to 42 days. They observed moderate to higher genetic correlations of W38 (0.61) and W42 (0.91) with FI. For FC the genetic correlation was close to zero with W38 (0.07) but increase with the W42 (0.35). Performance traits from 23 to 48 days of age were evaluated by Pakdel et al. (2005), these authors reported a positive genetic correlation of W23 and W48 with FI (0.73 and 0.78) and WG (0.64 and 0.98), respectively. Also, they suggested that broilers with higher gains from 23 to 48 days had a higher feed intake, reflecting in the genetic correlation between weight gain and feed intake.

Takahashi et al. (2006) observed an association in the feed conversion in chicken from low growth lineages at 64 days of age and they affirmed that the commercial lines are bred to reach maximum gain efficiency up to 42 or 49 days. The author comments that the FI and WG ratio observed in the first's experimental periods showed a better feed efficiency, however, the higher feed intake in the initial growth phase did not result in a higher weight gain for the total period. This may be worsening in the fast growth bird's feed efficiency. This probably occurs due to the big differences in the lineage digestive capacity, because the intestinal tract was extensively modified by the selection process (Verdal et al. 2011).

In this study we could verify that the final weights (W41 and W42) were the ones with has a higher correlation with FI35_41, although they presented smaller genetic correlations for feed conversion. We observed that, along the years, as the artificial selection made the individual body weight far from the natural body weight, it has changed the control mechanisms, either endocrine or neural, affecting the feed consumption in broiler chicken (Holanda et al. 2009).

Prime cuts, FI35_41, WG35_41, and FC35_41

Given our results, the genetic relationship between performance and prime cut traits presented a low magnitude of genetic correlations (Table II). Similar to the estimative found by Gaya et al. (2006), who estimated genetic correlations for FC and WBT of 0.10 and between FC and LEG of 0.10. Those authors observed a higher estimative for FI and WBT (0.86), which was superior to our study. The genetic association between FC and prime cut traits were low. Thus, the direct selection of carcass traits would have a small effect on FC. Although WDS, WTH, and WBT traits are the main products of the broiler industry. The lower estimative of genetic correlation between them and FC indicates how hard is to reduce the high costs with feeding in chicken production. It could be a real challenge in the production system.

Pakdel et al. (2005) found genetic correlations of 0.71 for FI23_48 with WG23_48. Aggrey et al. (2010) reported genetic correlation lower and negative between FC35_42 and WG35_42 (-0.14), and median for FC35_42 and FI35_42 (0.54). Also, Gaya et al. (2006) estimated a similar genetic correlation between FI and FC of 0.38. In addition, the way of the feed efficiency traits are measured and evaluated may influence the results (Aggrey et al. 2010). It can cause significant changes in the genetic parameter estimates (Campo & Rodriguez 1990).

The estimate heritabilities of the evaluated traits we may infer that birds with a higher body weight at 35 and 42 days tent to present higher WBT, WDS and WTH weight, interesting data to broiler lineages. However, the body weight selection does not favor relevantly the genetic gain of the feed conversion indirectly. Facing the results in our research together to the literature ones, the selection criteria and intensity used to obtain fast growth animals may have modified the broiler morpho-physiological aspects. The selected lineages improved the growth rate is associated mainly with appetite. It is characterized by the accelerated voluntary consumption rate, differently to the non-selected lineage feed, the selected ones use the digestive apparatus capacity in the maximum (Barbato et al. 1984). Barbato (1994) suggested that the fast growth selection in broiler lineage results is due to the hypothalamus failure in reducing the appetite control, leading to excessive consumption.

CONCLUSIONS

This study suggests that direct selection may be effective to obtain genotypes with higher body weights and prime cut traits according to the estimate heritability magnitudes. The genetic correlations between the traits may favor the correlated response to prime cut traits by body weight selection. We may obtain a correlated response to feed intake and weight gain with body weight and prime cut traits as selection criteria. However, the genetic gain would be moderate, because the FI35_41 and WG35_41 had low heritability estimates, facts that would lead to a slower genetic process. Our results showed that the FC did not contribute to the selection of high genetic gains in a pure lineage. Although, it deserves attention thanks to its economic importance in the breeding programs in high meat production lineages, focusing minimizes the high feed costs, a constant concern.

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