The Estimation of Genetic Parameters for Body Weight, Body Dimension, and Carcass Traits in Four Egyptian Chickens Strains

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ABSTRACT

Body weight and carcass traits are important traits in the poultry industry. Breeding programs are powerful strategies to improve these economic traits. The challenge, however, is to choose an appropriate strategy to increase production. The estimation of genetic parameters in target strains could provide valuable information to determine the potent breeding strategy. Therefore, the aim of the current study was to assess the heritability and the genetic correlations of the Body Weight (BW), Body Dimensions (BD), and Carcass Traits (CT) in four Egyptian strains (Matrouh, Mandarah, Inshas, and Silver Montazah) of dual-purpose chickens. The BW was measured at hatching (BW0), 8 weeks (BW8), and 16 weeks (BW16) of age, and weight gain was calculated from 8 to 16 weeks of age. The BD traits included shank length (SL), keel length (KL), and Body Circumference (BC). Carcass, liver, gizzard, heart, head, and leg percentages were also determined. Data were collected on 2800 dual-purpose chickens with pedigree information. A Multitrait animal model with a restricted maximum likelihood procedure was applied to estimate heritability, genetic and phenotypic correlations for BW, BD, and CT using Wombat software. Heritability estimates for BW traits were between 0.24 and 0.41 for BW0 and BW8, respectively. Heritability estimates of SL, KL, and BC were 0.49, 0.41, and 0.52, respectively. The heritability estimates for CT were low to moderate, ranging from 0.15 to 0.37 for head and gizzard percentage, respectively. The least-square means for BW, BD, and CT varied significantly between strains. The genetic correlation estimates among BW and BD traits indicated a close genetic relationship between these traits. Positive genetic correlations were found between BW and BD with CT (from 0.12 to 0.78). Based on the present results, there were strong positive genetic correlations between all traits, including BW and BD as the most important ones. Therefore, the selection for these traits would improve the carcass traits in the four strains of chickens. Hence, the inclusion of BW and BD as selection criteria in breeding programs would potently affect the improvement in carcass performance, which might positively increase the production profit of such strains.

Keywords: Body dimensions, Carcass, Egyptian strains, Genetic parameters, Heritability

INTRODUCTION

Poultry has been considered as one of the main sources of high-quality animal protein (FAO, 2005; Hosny, 2006; Randazzo et al., 2021). Egypt possesses a wide variety of chickens, including indigenous ones, which are characterized by high resistance to various diseases and performing well in harsh environments and nutritional conditions (Hosny, 2006). Despite the fact that Egyptian chickens are valuable native breeds, the information about their genetic variability and relationships is limited (Eltanany et al., 2011; Ramadan et al., 2012; El-Attrouny et al., 2020). Parameters of growth traits had a genetic basis and vary between chicken breeds (Kosba and Abd El-Halim, 2008; Hermiz et al., 2020). The growth rate is a critical trait and could be considered as a direct fitness trait. Evaluating the differences between chicken breeds on growth traits is essential to increase the production efficiency and consequently decreased production costs (Iraqi et al., 2002; El-Attrouny et al., 2017; Chu et al., 2020).

The genetic response of breeding programs depended on estimates of genetic parameters, such as heredity, phenotypic, and genetic correlations between the traits in the breeding goal and the corresponding selection index. To support genetic improvement, it is important to define the breeding objective, production, and breeding systems. Knowledge of the genetic parameters is crucial to accurately estimate the breeding values, optimize the combination of traits in a selection program as well as breeding schemes, and improve the prediction of the

response to the selection (Prado-Gonzalez et al., 2003; Adeogun and Adeoye, 2004; Norris et al., 2004; Gaya et al., 2011). Accordingly, the lack of information on genetic components of variance and genetic parameters limited genetic improvement. In this context, heritability estimated for Body Dimensions (BD) and Carcass Traits (CT) in chickens varied from medium to high (Chabault et al., 2012; Abou El-Ghar and El-Karim, 2016; Bungsrisawat et al., 2018; Ullengala et al., 2020).

The breeding strategies to improve meat production concentrate on rapid growth and CT. Choosing the specific body weight that corresponds to the market weight is the most common practice among breeders. As a result, the age of selection became progressively earlier as the potential for growth increased (Aslam et al., 2011; Saxena and Kolluri, 2018).

There are two more selection strategies, which are chosen in the commercial age or in a multi-stage selection. Various breeding and selection strategies at different time intervals have been used to improve the genetic components of poultry (Johansson et al., 2010; Ahsan et al., 2013; Jambui et al., 2017). Feed Conversion Ratio (FCR), BD, Carcass Percentage (CP), and meat quality are the major traits in broilers. Moreover, carcass traits are important in determining income from meat production, meaning that the profitability of any enterprise largely depends on the weight and quality of the carcass. Body dimensions have usually been used as an indicator of skeletal development in poultry and could be used to predict carcass yield percentage (Das et al., 2015). Previous studies have shown that selection based on measurement of breast area across the length and width of the breast along with BW resulted in a genetic gain of 277% per generation (Thiruvenkadan et al., 2011; Saxena and Kolluri, 2018). High and positive correlations between BW and BD were reported in recent studies of Das et al. (2015) and Ullengala et al. (2020). Despite the great importance of such correlations in constructing proper selection indices and consequently performing selection at young ages of chickens, to our knowledge, a few limited studies discussed the genetic and phenotypic correlation among Egyptian strains.

The authors hypothesized that the strain genotype could affect the genetic and phenotypic correlation among economic traits. Therefore, the objective of the present study was to estimate the heritability and the genetic correlation coefficients for BW, BD, and CT in four different Egyptian chicken strains. The association between these economic traits in Egyptian chickens could provide useful information in determining a successful breeding strategy.

MATERIALS AND METHODS

The study was conducted on the Poultry Research Farm, Faculty of Agriculture, Benha University, Egypt. All experimental procedures were approved by the Institutional Animal Care and Use Committee (IACUC) at Benha University.

Ethics approval
The protocol for the conducted animal experiments was approved by the institutional animal care and use committee (IACUC) of Benha University.

Population structure
The experiment started in November 2019 and lasted 12 months. Four pedigreed indigenous Egyptian dual-purpose strains of chickens were used in the current study, including Matrouh strain (MT), Mandarah strain (MN), Inshas strain (IN), and Silver Montazah strain (SM).

A total of 2800 chickens were used in this experiment (n = 700 chickens per strain). The chickens were produced from four strains in a pedigree that mated to 120 sires and 600 dams (30 sires and 150 dams for each strain), with each sire was mated to five dams. The eggs were collected daily and labeled according to dam number to identify pedigree information. Before the incubation, the collected eggs were disinfected with formaldehyde and then placed in the incubator for 21 days (18 days in the setter and 3 days in the hatchery). After hatching, chickens were weighed individually and the wings were banded.

Feeding management and diet
All chickens were from the same hatching batch and subjected to the same feeding management and diet. At one to four weeks of age, chickens were raised with brooders on a litter floor using incandescent lamps, 24-hour lights, and no darkness. After four weeks of age, all chickens were placed in a slatted floor barn and fluorescent lighting (20 hours of light and 4 hours of darkness) was arranged up to the 16 weeks of age. Feed and fresh water were provided *ad libitum*. The diets were formulated to meet the nutritional recommendations for broilers (NRC, 1994). From one day to four weeks of age, all chickens received a starter diet containing 21% crude protein and 3050 kcal/kg metabolizable energy. After four weeks up to 16 weeks of age, the chickens were provided

with grower feed containing 18% crude protein and 3000 kcal/kg metabolizable energy.

Traits

All chickens were weighed at hatching (BW 0), 8 weeks (BW 8), 16 weeks (BW 16) of age, and the Weight Gain (WG) was calculated at the age of 8 to 16 weeks (WG 8-16). The BW was measured using a digital balance to an accuracy of 0.1-gram.

Body dimensions were measured, including Shank Length, distance from the hock to the extremity of the digitus pedis, keel length, distance from the anterior to the posterior end of the keel; and Breast Circumference (BC: the circumference of the breast around the deepest region of the breast behind the wings through the anterior edge of the keel and middle thoracic vertebra). Measurements were done according to FAO (2012).

To determine carcass characteristics, 600 chickens (n = 150 per strain) were randomly selected and weighed prior to slaughter based on the average group weight of each strain at 16 weeks of age. Chickens were fasted for a period of 10-hours before slaughter, however, they had unlimited access to water. After slaughter and bleeding, the carcasses were de-feathered and eviscerated (Adeyemi, 2021). The weight of hot carcass, eviscerated, without neck and feet, the edible inner organs (Liver, Gizzard, and Heart), head, and leg were measured after slaughter and as a percentage of live BW expressed.

Statistical analysis

Descriptive statistics of the performance traits (body weight, body dimension, and carcass traits) were calculated using the UNIVARIATE procedure in the SAS software (SAS, 2004). Differences were considered significant at p < 0.05 and significant differences between means were tested by Duncan's multiple range test (Duncan, 1955).

The statistical model was $Y_{ij} = \mu + S_i + e_{ij}$

Where, y_{ij} is the individual observation for each trait, µ refers to the overall mean, Si denotes the fixed effect of hatching batch with strain (i =1….4), and e_{ij} signifies the random residual effect ~ NID (0, s^2e).

The information from the pedigree and performance data was used to estimate the genetic (co) variance components. The fixed effect was genotype and the random effects were additive genetic and residual effects. Variance and covariance components were obtained using the Average Information Restricted Maximum Likelihood method (AI-REML; Johnson and Thompson, 1995) with the WOMBAT software (Meyer, 2012). The mixed linear animal model for multiple traits is shown in the following equation.

$$y = Xb + Zu + e \qquad \text{Equation 1}$$

Where, y is a vector of observing all traits, b is a vector of the fixed effects made up of strains (4 levels), X represents a design matrix relating the appropriate fixed effects to each trait, u is a vector of the direct genetic effect of trait, Z is a design matrix relating the appropriate random effect to each individual and e is a vector of random residual effects.

The mathematical model used in the two-trait analysis is presented in Equation 2.

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix} + \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix} + \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix},$$
Equation 2

Where, y_1 and y_2 represent different traits. The vectors of fixed effects for trait 1 (b_1) and trait 2 (b_2) are the same as described in the univariate model. The vectors a_1 and a_2 are random additive genetic effects, and e_1 and e_2 are residual effects for trait1 and trait2, respectively. The incidence matrices X_1 and X_2 associated elements of b_1 and b_2 with the records in y_1 and y_2. The incidence matrices Z_1 and Z2 associate elements of a_1 and a_2 with the records in y1 and y2.

Estimates of heritability were computed from the variance components and (co)variance components were used to calculate genetic correlation and phenotypic correlation using the equation of Falconer and Mackay (1996).

RESULTS AND DISCUSSION

The descriptive statistics for the studied traits including mean, standard deviation, coefficient of variation, minimum and maximum values, and heritability are presented in Table 1.

Heritability estimates

The heritability estimates for the traits studied are shown in Table 1. The heritability estimate for BW8 was greater than the heritability estimates for BW16 (0.41 and 0.30), meaning that detecting that genetic variability for BW appeared to be more difficult after 16 weeks of age, compared to 8 weeks of age. Thus, using BW8 as a selection criterion appeared to be more efficient than the use of BW16. The heritability estimates for BW8 and BW16 were similar to those found by Le Bihan-Duval et al. (2001), Iraqi et al. (2002), Resende et al. (2005), and El-Attrouny et al. (2017) and different from those found by Das et al. (2015), and Bungsrisawat et al. (2018).

Table 1. Descriptive statistics and heritability estimates for body weight (0-16 weeks), and body dimensions, and carcass traits at 16 weeks of age, of four Egyptian dual-purpose chickens (Matrouh, Mandarah, Inshas, and Silver Montazah).

Items	Mean	SD	CV (%)	Min	Max	$h^2 \pm SE$
Body weight						
BW0 (g)	33	3.5	10.6	25	41	0.24 ± 0.02
BW8 (g)	560	104	19	402	753	0.41 ± 0.02
BW 16 (g)	1351	334	25	842	1820	0.30 ± 0.02
WG8-16 (g)	782	115	15.0	511	1012	0.26 ± 0.02
Body dimension						
SL (cm)	7.97	1.02	12.79	7	9	0.49 ± 0.03
KL (cm)	14.75	1.49	10.10	13	16	0.41 ± 0.03
BC (cm)	26.7	2.04	7.64	25	29	0.52 ± 0.03
Carcass traits						
CP (%)	63.42	4.20	7.0	58.12	70.28	0.36 ± 0.03
LIV (%)	2.17	0.15	6.9	1.40	2.65	0.27 ± 0.02
GIZ (%)	2.42	0.13	5.3	1.92	3.59	0.37 ± 0.03
HRT (%)	0.59	0.08	13.5	0.43	0.84	0.39 ± 0.03
HD (%)	3.06	0.41	13.3	3.12	4.48	0.15 ± 0.03
Leg (%)	3.10	0.25	8.06	2.73	3.53	0.33 ± 0.03

BW 0, 8, and 16: Body weight at day old, week 8 and week 16, repectively; WG8-16: Weight gain from 8 to 16 weeks; SL: Shank length; KL: Keel length; BC: Breast circumference; CP: Carcass percentage; LIV: liver percentage; GIZ: Gizzard percentage; HRT: Heart percentage; HD: Head percentage; h^2: Heritability; BD: Body dimensions; CT: Carcass traits; SD: Standard deviation; Min: Minimum; Max: Maximum; SE: Standard error.

The heritability estimates for BD in the current study ranged from moderate to high. The heritability estimates of the shank length and keel length values were 0.49 and 0.41, respectively. The current heritability estimates of shank length and keel length values were lower than those reported by Adebambo et al. (2006), Das et al. (2015). However, Singh and Jilani (2005) reported a lower heritability of keel length (0.15) than the current study (0.36). These variations in the results could be related to the statistical model, genetic groups, and the number of chickens used in the study (El-Attrouny et al., 2020).

The heritability estimate for body circumference (0.52) was similar to that reported by Abd El-Karim and Ashour (2014), and higher than that described by Padhi et al. (2015). The moderate heritability estimate for carcass percentage in the present study was 0.36, which is similar to that reported by Zerehdaran et al. (2004); Grosso et al. (2010), and as an intermediary to that reported by Gaya et al. (2006) and Felício et al. (2013). This indicated that selection based on carcass percentage will result in a high genetic gain for CT.

Considerable direct additive genetic effects seem to exist in the expression of CT based on their heritability estimates. The heritability estimate for the liver was 0.27, which was similar to the value reported by Gaya et al.

(2006) and Venturini et al. (2014). In contrast, Cahaner and Nitsan (1985) observed higher heritability estimates for the liver (0.50). This suggests that the liver trait would be responsive to the selection. Nevertheless, the heritability estimates for gizzard in the present study (0.37) differed from those reported by Cahaner and Nitsan (1985) and Rance et al. (2002), who observed higher heritability estimates for gizzard of 0.57 and 0.52, respectively.

The heritability estimate for the heart was 0.39, suggesting that this trait could respond to selection. This estimate was similar to those described by Gaya et al. (2006) and Salvian et al. (2020) and was within the range of values observed in the literature for this trait from 0.27 (Venturini et al., 2014) to 0.30 (Rance et al., 2002). In the current study, liver, gizzard, and heart traits were not used as a selection criterion. Although, they may be potentially useful if these traits become limiting factors in the physiological integrity of chickens. Thus, the direct selection to modify organ (liver, gizzard, and heart) traits could be efficient if necessary (Venturini et al., 2014).

The heritability estimate obtained for the leg (0.33), was similar to that presented by Le Bihan-Duval et al. (1998); Gaya et al. (2006); Grosso et al. (2010), but lower than those found by Cahaner and Nitsan (1985); Rance et

al. (2002); Khalid et al. (2012). The heritability estimate for the head was low (0.15). Khalid et al. (2012) estimated the heritability estimate for head to be 0.20, suggesting that selection, by itself, might not improve this trait.

Least square means

As shown in Table 2, there was a significant influence of the genotype on BW and WG traits of chickens. The SM strain exhibited the highest BW and WG compared to MN, MT, and IN strains through the entire experimental period (p ≤ 0.05). The SM strain had the greatest value of WG8-16 (830 g), followed by MN (782 g) and IN (774 g), while MT had the lowest value of WG8-16 (755 g). This could be due to the differences in the genetic make-up of the four strains. Similar results were reported by Kosba and Abd El-Halim (2008) and Debes (2017).

The SM strain revealed the highest significant value of BD followed by MN, MT, and IN strain (Table 2). Comparing the four strains, the SM strain surpassed shank length, keel length, and body circumference by 8.5, 15.8, and 28.2cm, respectively. Identifying relationships between studied traits was very useful in selecting fast-growing chickens. The least-square means of BD in the present study were similar to those reported by Abd El-Karim and Ashour (2014), and El-Attrouny et al. (2020).

The MT strain revealed the highest (p ≤ 0.05) value of carcass percentage (68.36 %) compared to the other three strains (61.78 % for MN, 61.98% for IN, and 61.57% for SM strain) as shown in Table 2. A significant difference was recorded between all strains for liver percentage; however, a non-significant difference was recorded for head percentage. The IN and MT strains had a significantly higher percentage (p ≤ 0.05) of the gizzard and heart than MN and SM strains. The MT chickens had a significantly higher percentage (p ≤ 0.05) of leg compared to MN, IN, and SM chickens. Rayan et al. (2017) reported that MT strain had a significantly higher carcass percentage (60.85%) compared to the SM strain (57.97%).

Table 2. Least square means and standard errors for body weight, body dimension, and carcass traits in different strains.

Items	Mandarah	Matrouh	Inshas	Silver Montazah	p value
Body weight					
BW0 (g)	33 ± 0.13^b	32 ± 0.13^c	33 ± 0.13^b	34 ± 0.13^a	<0.001***
BW8 (g)	548 ± 9.6^b	486 ± 8.7^c	575 ± 9.1^b	630 ± 8.4^a	<0.001***
BW 16 (g)	1340 ± 15.8^c	1260 ± 1.2^d	1380 ± 12.9^b	1460 ± 12.9^a	<0.001***
WG8-16 (g)	782 ± 12.3^b	755 ± 14.2^c	774 ± 11.2^b	830 ± 13.5^a	<0.001***
Body dimension					
SL (cm)	7.8 ± 0.05^{bc}	8.0 ± 0.05^b	7.6 ± 0.05^c	8.5 ± 0.05^a	<0.001***
KL (cm)	13.8 ± 1.10^b	15.2 ± 1.10^a	14.2 ± 1.10^b	15.8 ± 1.10^a	<0.001***
BC (cm)	26.4 ± 2.21^b	26.4 ± 2.21^b	26.8 ± 2.21^b	28.2 ± 2.21^a	<0.017**
Carcass traits					
CP (%)	61.78 ± 3.21^b	68.36 ± 3.21^a	61.98 ± 3.21^b	61.57 ± 3.21^b	<0.003***
LIV (%)	2.08 ± 0.05^b	2.01 ± 0.05^b	2.39 ± 0.05^a	1.69 ± 0.05^c	<0.004***
GIZ (%)	2.69 ± 0.08^b	2.97 ± 0.08^a	2.98 ± 0.08^a	2.31 ± 0.08^{bc}	<0.012**
HRT (%)	0.55 ± 0.02^b	0.68 ± 0.02^a	0.62 ± 0.02^a	0.49 ± 0.02^b	<0.018**
HD (%)	3.63 ± 0.09	3.55 ± 0.09	3.71 ± 0.09	3.52 ± 0.09	0.5764^{ns}
Leg (%)	3.05 ± 0.07^b	3.36 ± 0.07^a	3.07 ± 0.07^b	2.94 ± 0.07^b	0.030***

[a-d] Means followed by different superscripts within a row differ significantly (p ≤ 0.05). BW 0, 8, and 16: Body weight at day old, week 8 and week 16, repetively; WG8-16: Weight gain from 8 to 16 weeks; SL: Shank length; KL: Keel length; BC: Breast circumference; CP: Carcass percentage; LIV: liver percentage; GIZ: Gizzard percentage; HRT: Heart percentage; HD: Head percentage; h2: Heritability; BD: Body dimensions; CT: Carcass traits.

Genetic and phenotypic correlation estimates

Genetic parameters including genetic and phenotypic correlations for BW and BD are presented in Table 3. The genetic and phenotypic correlations between all BW measures (BW0, BW8, and BW16) were strong and positive, ranging from rg = 0.35 to 0.50 and rp = 0.27 to 0.38. These current results are in agreement with the corresponding correlation reported by Niknafs et al. (2012), El-Attrouny et al. (2017), and Tongsiri et al. (2019). Selection for rapid early growth in market age (35-45 days) has been the most common approach in broiler chickens breeding programs (Emmerson, 2003). The current results showed that BW at 16 weeks of age was positively correlated to BW traits from 0 to 8 weeks of age. The genetic correlations were particularly strong (0.50) with certain BW traits with BW8. Since chickens were raised in Egypt for both meat and egg production, 8

weeks selection could be the most suitable approach to improving growth. The genetic correlations for BD (shank length, keel length, and body circumference) were positive and ranged from 0.47 between keel length and body circumference to 0.62 between shank length and keel length (Table 3). Phenotypic correlations between BD were positive and ranged between 0.25 and 0.31. This was in agreement with the findings of Abd El-Karim and Ashour (2014), who reported a positive and high genetic correlation between BD (shank length, keel length, and body circumference). The estimate of genetic correlation of BD in the current study was lower than that reported by Ige (2013), who indicated that genetic correlation between shank length and keel length was high (0.97), between shank length and body circumference was 0.99, and between keel length and body circumference was 0.85 in crossbred Fulani Ecotype chickens.

Table 3. Estimates of genetic correlations (above the diagonal) and phenotypic correlations (below the diagonal), with their standard errors (between parentheses), between body weight, weight gain, and body dimension traits

Items	BW0	BW8	BW16	WG8-16	SL	KL	BC
BW0	-	0.41(0.02)	0.35(0.02)	0.25(0.03)	0.31(0.03)	0.32(0.01)	0.30(0.01)
BW8	0.27(0.02)	-	0.50(0.03)	0.31(0.01)	0.36(0.01)	0.37(0.02)	0.40(0.02)
BW16	0.28(0.02)	0.38(0.02)	-	0.38(0.03)	0.64(0.02)	0.56(0.03)	0.62(0.03)
WG8-16	0.21(0.01)	0.15(0.01)	0.22(0.01)	-	0.32(0.01)	0.39(0.03)	0.43(0.03)
SL	0.24(0.02)	0.22(0.01)	0.41(0.02)	0.22(0.02)	-	0.62(0.03)	0.51(0.03)
KL	0.11(0.01)	0.19(0.01)	0.29(0.03)	0.19(0.01)	0.31(0.01)	-	0.47(0.02)
BC	0.19(0.01)	0.31(0.02)	0.33(0.03)	0.24(0.02)	0.28(0.02)	0.25(0.02)	-

BW 0, 8, and 16: Body weight at day old, week 8 and week 16, repectively; WG8-16: Weight gain from 8 to 16 weeks; SL: Shank length; KL: Keel length; BC: Breast circumference.

It is very important to consider the relationship between BD and BW traits as this could be useful as a selection criterion to improve the BW. Traits representing BD (shank length, keel length, and body circumference) appeared to be highly genetically associated with BW (BW0, BW8, and BW16) because the genetic correlation estimates between these traits ranged from 0.30 between BW0 and body circumference to 0.64 between BW16 and shank length as presented in Table 3. The strong genetic correlation suggested that the direct selection for BD at different ages could bring indirect genetic gains for BW. Similar genetic correlation estimates between these traits were obtained by Haunshi et al. (2012), Rajkumar et al. (2012), and Ullengala et al. (2020).

Ige (2013) reported that the highest values of the genetic correlation between BW8 and keel length (0.98), shank length (0.90), and body circumference (0.85) were obtained in crossbred Fulani Ecotype chickens. Egena et

al.(2014) indicated that BW was positively correlated with body length and body girth traits. This suggested that including BD in the breeding scheme would have a significant effect on improving growth characteristics through favorable genetic correlations (Rajkumar et al., 2012; Padhi et al., 2015). The phenotypic correlations between the BW and BD traits were positive and ranged from 0.11 between BW0 and keel length to 0.41 between BW16 and shank length (Table 3).

The genetic and phenotypic correlation estimates among BW, BD, and CT are presented in Tables 4 and 5. The genetic correlation estimates between carcass percentage and BW traits indicated an important genetic association between these traits. It was recorded that the increase in the carcass percentage was associated with higher BW, and the higher the BW, the higher the carcass percentage (Venturini et al., 2014).

Table 4. Estimates of genetic correlations of body weight, weight gain, shank length, keel length, body circumference with carcass traits. All genetic correlation estimates are shown with corresponding standard errors in parenthesis.

Traits	CP	LIV	GIZ	HRT	HD	Leg
BW0	0.30(0.02)	0.12(0.02)	0.14(0.03)	0.18(0.02)	0.21(0.03)	0.23(0.03)
BW8	0.45(0.06)	0.29(0.03)	0.26(0.02)	0.24(0.01)	0.38(0.04)	0.44(0.04)
BW16	0.78(0.06)	0.51(0.06)	0.35(0.03)	0.60(0.05)	0.32(0.02)	0.68(0.04)
WG8-16	0.24 (0.03)	0.32(0.03)	0.22(0.02)	0.19(0.02)	0.22(0.01)	0.28(0.03)
SL	0.46(0.04)	0.29(0.02)	0.30(0.03)	0.32(0.03)	0.27(0.03)	0.47(0.04)
KL	0.62(0.06)	0.27(0.02)	0.19(0.02)	0.25(0.02)	0.16(0.02)	0.39(0.03)
BC	0.71(0.04)	0.19(0.02)	0.27(0.02)	0.17(0.02)	0.27(0.02)	0.53(0.04)

BW 0, 8, and 16: Body weight at day old, week 8 and week 16, repectively; WG8-16: Weight gain from 8 to 16 weeks; SL: Shank length; KL: Keel length; BC: Breast circumference; CP: Carcass percentage; LIV: Liver percentage; GIZ: Gizzard percentage; HRT: Heart percentage; HD: Head percentage.

Table 5. Estimates of phenotypic correlations of body weight, weight gain, Shank length, keel length, breast circumference with carcass traits. All genetic correlation estimates are shown with corresponding standard errors in parenthesis

Traits	CP	LIV	GIZ	HRT	HD	Leg
BW0	0.11(0.01)	0.08(0.02)	0.07(0.01)	0.11(0.01)	0.07(0.01)	0.16(0.01)
BW8	0.26(0.02)	0.19(0.06)	0.18(0.01)	0.19(0.02)	0.10(0.01)	0.20(0.02)
BW16	0.42(0.03)	0.23(0.02)	0.24(0.02)	0.23(0.01)	0.11(0.01)	0.17(0.01)
WG8-16	0.19(0.01)	0.22(0.03)	0.16(0.01)	0.12(0.02)	0.13(0.01)	0.15(0.02)
SL	0.23(0.02)	0.16(0.01)	0.18(0.01)	0.18(0.01)	0.21(0.02)	0.24(0.02)
KL	0.26(0.02)	0.18(0.02)	0.07(0.01)	0.17(0.02)	0.17(0.01)	0.24(0.01)
BC	0.30(0.02)	0.09(0.02)	0.19(0.02)	0.09(0.02)	0.16(0.01)	0.31(0.02)

BW 0, 8, and 16: Body weight at day old, week 8 and week 16, repectively; WG8-16: Weight gain from 8 to 16 weeks; SL: Shank length; KL: Keel length; BC: Breast circumference; CP: Carcass percentage; LIV: Liver percentage; GIZ: Gizzard percentage; HRT: Heart percentage; HD: Head percentage.

The estimates were positive and moderate to high, 0.30 between carcass percentage and BW0; 0.45 between carcass percentage and BW8; and 0.78 between carcass percentage and BW16 (Table 4). Similar genetic correlation estimates between these traits were obtained by Wang et al. (1991), Rance et al. (2002), and Gaya et al. (2006). Peertile et al. (2014) reported a positive and high (r = 0.95) genetic correlation between BW at the age of 38 days and carcass weight in broiler chickens. In contrast, Zerehdaran et al. (2004) reported that the genetic correlation value (0.22) between BW at 7 weeks and carcass percentage in broiler chickens was positive. As similar, Xu et al. (2011) confirmed the same results with a high value of genetic correlation (0.85). This suggested that using BW as a selection criterion could increase the carcass percentage, which might positively increase the production profit from these strains.

Body dimension traits played an important role in predicting the carcass weight of a chicken. In the current study, the genetic correlation estimates between carcass percentage with shank length, keel length, and body circumference were 0.46, 0.62, and 0.71, respectively (Table 4). These results were similar to those of Tyasi et al. (2018), who reported that the genetic correlations

between carcass percentage and body circumference, as well as carcass percentage and shank length, were 0.56 and 0.48, respectively. This revealed the importance of selection for higher body diameter and body length to increase the carcass percentage of chickens.

The phenotypic correlations of carcass percentage with BW and BD traits were positive and low or moderate (0.11-0.42; Table 5). A significant positive genetic correlation between these traits was desirable in a breeding program since the selection of one trait improves the performance of other traits as a correlated response (Ullengala et al., 2020).

The present study revealed that the genetic correlation estimates between BW and CT were low or moderate, except for the genetic correlation estimate of BW16 with liver, heart, and leg (Table 4). This indicated that these traits would react indirectly to the direct selection to increase BW. Similar genetic correlation estimates between these traits were obtained by Venturini et al. (2014). The genetic correlation estimates ranged from 0.12 between BW0 and liver to 0.68 between BW16 and leg (Table 4). Gaya et al. (2006) reported that the genetic correlation estimates were 0.28, 0.43, and 0.21 between BW and heart, BW and liver, and BW and

gizzard, respectively. Kause et al. (2012) found a genetic correlation estimate of 0.12 between BW at 14 days of age and the heart percentage. Ojedapo et al. (2008) reported that the correlation between live weight and leg weight was positive (0.93).

In the current study, the genetic correlation estimates between BD and CT were positive and low to moderate, ranged from 0.16 between keel length and head to 0.53 between body circumference and leg (Table 4). The current findings provided positive and moderate genetic correlation estimates (ranged 0.39-0.53) between leg and BD traits. Therefore, direct selection for BD would increase carcass traits. A small increase in gizzard, heart, and head by direct selection for shank length, keel length, and body circumference also appeared to be possible based on the genetic correlation estimate between these traits in the 0.16 to 0.32 range (Table 4). Phenotypically, in the current study, BW traits and BD correlated positively with the carcass traits in the range from low to moderate (0.07 - 0.31) as presented in Table 5.

CONCLUSION

In the present investigation, four Egyptian dual-purpose strains of chickens (Mandarah, Matrouh, Inshas and Silver Montazah) in terms of body weight, body dimensions, and carcass traits were characterized as essential economic traits in the poultry industry sector. The genetic estimations of these productive traits may provide useful information in determining a successful breeding strategy. Incorporating body dimension and weight as selection criteria in breeding programs will significantly increase the carcass percentage, and potentially improve the production benefit of the strains. Owing to positive genetic associations between body weight, body dimension, and carcass traits, assessing body weight and body dimension at a young age may be a fair and reliable predictor of carcass traits in future selection programs.

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Competing interests

The authors have declared that no competing interest exists.

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Ethical considerations

Ethical issues (Including plagiarism, consent to publish, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy) have been checked by the authors.

Author contributions

Mahmoud El-Attrouny and Mahmoud Iraqi designed the research project. Mahmoud El-Attrouny and Shereen Mohamed performed the experiment and collected data. Mahmoud El-Attrouny and Mahmoud Iraqi analyzed the data and interpreted the results. Mahmoud El-Attrouny and Shereen Mohamed wrote the initial manuscript. The authors revised the manuscript together and prepared it for publication.

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