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Genetic parameter estimation and genetic evaluation of important economic traits in white and yellow broilers

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ABSTRACT

1. This study calculated descriptive statistics for the production traits of two broiler populations: 1) the Northeast Agricultural University broiler lines divergently selected for abdominal fat content (NEAUHLF white broilers), including fat and lean lines; and 2) the Guangxi yellow broilers. Their genetic parameters were estimated, including (co)variance components, heritability (h^2) and genetic correlations (r_g), using the REML method.

2. Heritability estimates (h^2) for NEAUHLF white broilers ranged from 0.07 to 0.61. Traits with high heritability $(h^2 > 0.3)$ included body weight at 3, 5 and 7 weeks of age (BW3, BW5, BW7), carcass weight (CW), metatarsal circumference (MeC), liver weight (LW), gizzard weight (GW), spleen weight (SW) and testis weight (TeW), while in Guangxi yellow broilers, heritability estimates ranged from 0.18 to 0.76, with every trait exhibiting high heritability, except for SW (0.18).

3. Positive genetic correlations for NEAUHLF were found ($r_g > 0.3$, ranging from 0.31 to 0.84) between BW7 and metatarsal length (MeL), MeC, body oblique length (BoL), chest angle (ChA), LW, GW, heart weight (HW) and SW. Genetic correlations between abdominal fat weight (AFW) and BW1, BW3, BW5, CW, MeL, keel length (KeL), BoL and LW were positive ($r_g > 0.3$, ranging from 0.31 to 0.58).

4. Among the Guangxi population, BW (125 d of age) showed strong positive genetic correlations with all other traits (r_g >0.3, ranging from 0.30 to 0.99), while AFW displayed strong positive genetic correlations with leg muscle weight (LeW), CW, BW and thigh diameter (TD) (r_g >0.3, ranging from 0.44 to 0.51).

5. It was concluded that the characteristics of the two populations were different, which means there is a need to use different strategies when performing the breeding work to improve productivity and efficiency in both broiler populations.

Introduction

Chicken (*Gallus gallus*) has become one of the main meat sources in China, comprising 30% of the entire domestic meat market as of 2022 (Jin 2023). Chinese broilers can be divided into two major categories – white or yellow. White broilers have a higher growth rate and account for the majority of commercial production, while yellow broilers grow slower but have better meat quality (Leng et al. 2016). Selective breeding for superior broiler lines is crucial for further development of the poultry industry in China. In poultry breeding, there is an aim to select and cultivate certain economic traits as a means to improve productivity to meet human needs (Aslam et al. 2011). However, complex correlations exist among various economic traits, posing difficulties in achieving balanced improvement if solely relying on single-trait selection.

Modern broiler chickens have been intensely selected for rapid growth and increased muscle mass. However, this has led to issues such as increased fat deposition, metabolic disorders and impaired reproductive performance (Closter et al. 2012; C. Wu et al. 2021; Zuidhof et al. 2014). Striking a balance between growth, health and reproduction is an important breeding goal. Genetic parameter estimates have been extensively utilised in poultry breeding (Aggrey 2002; Grossman and Bohren 1985; Grosso et al. 2010; Koots et al. 1994; Laird 1966; Ricklefs 1985). Therefore, it is important to analyse genetic parameters, including heritability and genetic correlations, which can help with optimal design of breeding schemes targeting multiple traits simultaneously (Aggrey 2002; Koots et al. 1994).

Genetic parameter estimates for growth, body composition and abdominal fat deposition traits can provide insights into the genetic architecture underlying these differences and are used for improving the accuracy of breeding strategies. Moderate heritability has been reported for body weight and abdominal fat in broilers, indicating a degree of genetic control (Gaya et al. 2006; Zerehdaran et al. 2004). However, estimates vary widely between populations and analytical methods (Mignon-Grasteau, et al. 2001). Few studies have compared genetic parameters between white and yellow broiler lines.

The following research aimed to estimate heritability and determine genetic and phenotypic correlations for growth and body composition traits in both white and yellow broilers.

*These authors contributed equally to this work and should be considered co-first authors.

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Materials and methods

Ethical statement

All animal work was conducted according to the guidelines for the Care and Use of Experimental Animals established by the Ministry of Science and Technology of the People's Republic of China (approval number 2006–398) and was approved by the Lab-oratory Animal Management Committee of Northeast Agricultural University (Harbin, P.R.China) (NEAUEC20170201). Reporting results complied with the Animal Research: Reporting In Vivo Experiments (ARRIVE) guidelines.

Experimental birds and management

A total of 1087 birds were used in this study, including 556 male birds from the 23rd generation of Northeast Agricultural University (NEAU) broiler lines divergently selected for abdominal fat content in 2019, named as the Northeast Agricultural University High and Low Fat (NEAUHLF) white broilers. Among them, birds from the NEAUHLF population could be classified into two lines, which had significantly different abdominal fat weight but no significant difference in other growth and composition traits. The other 531 male birds were Guangxi yellow broilers obtained from Guangdong Wens Nanfang Poultry Breeding Co., Ltd in the year 2018. The population of Guangxi yellow broilers is a characteristic yellow broiler line which has advantages such as good feed conversion ratio (FCR), good meat quality and strong disease resistance, but relatively low reproductive performance and a longer growth cycle. In the trial period, every bird was placed into an individual cage, kept in similar environmental condition and had free access to feed and water.

Trait measurements

For the NEAUHLF white broilers, during rearing their body weight was recorded after fasting for 12 h at 1 (BW1), 3 (BW3), 5 (BW5) and 7 weeks of age (BW7). At week 7, white broilers were slaughtered and growth traits measured, including carcass weight (CW), keel length (KeL), body oblique length (BoL), chest angle (ChA), metatarsal length (MeL), metatarsal circumference (MeC), keel length (KeL), body oblique length (BoL), AFW, liver weight (LW), gizzard weight (GW), proventriculus weight (PW), heart weight (HW), spleen weight (SW) and testicle weight (TeW).

For the Guangxi yellow broilers, their BW, CW, AFW, HW, LW, SW, PW, GW and TeW were recorded at 125 d of age. In addition, the head and neck weight (HNW), leg muscle weight (LeW), feet weight (FeW) and thigh diameter (TD) of Guangxi yellow broilers were measured. Slaughtering was conducted according to standard procedures and carcass traits were measured.

The BW1, BW3, BW5, BW7 and BW125d were measured using a digital electronic scale (TCS-60 model, Kaifeng Electronics Co., Ltd., Zhejiang, China) with 0.01 kg (10 g) precision and a range of 0 ~ 60 kg. The CW, LeW and HNW were measured using the same digital electronic scale as body weights due to their larger mass. The AFW, LW, GW, PW, HW, SW, TeW and FeW were recorded after slaughter using a precision electronic balance (JA5003B model, Shanghai Precision Scientific Instrument Co., Ltd., Shanghai, China) with 0.001 g precision and a range of $0 \sim 500$ g. MeL, MeC, KeL, BoL and TD were measured using both a digital caliper ($0 \sim 300$ mm model, Guanglu Measuring Instrument Co., Ltd., Guilin, China) with 0.01 mm precision and a flexible tape measure (3 m model, Deli Group Co., Ltd., Zhejiang, China) with 1 mm precision. The ChA was measured using a poultry chest angle metre (ZUI-1 model, Wuxi Livestock and Veterinary Instrument Factory, Jiangsu, China) with 1° precision and a range of $0 \sim 180^\circ$. All measurements were performed by trained technicians following standardised protocols to ensure consistency and accuracy.

Statistical analysis

Based on the measurements, the descriptive statistics for the investigated traits of two populations were calculated by the JMP 7.0 program (SAS Inc., Cary, NC, U.S.A.). A mixed model (Model 1) was used to estimate the Least Squares Means (LSM) of each trait separately for the fat line and lean line of NEAUHLF population and their significant differences were defined as p < 0.05. Model 1 was used to calculate the LSM for the entire NEAUHLF population, including both the fat and lean lines. For Guangxi yellow broilers, the analysis was performed using Model 2.

$$y_{ik} = \mu + L_i + BW + e_{ik}$$
 (Model 1)
 $y_k = \mu + BW + e_k$ (Model 2)

where y was the phenotypic value of each bird, μ was the value of the population mean, L was the fixed effect of fat and lean lines within the NEAUHLF white broilers, BW was a covariable in the analysis. For the NEAUHLF population, BW1 was the covariable for BW3, BW5, BW7, while BW7 was the covariable for the other body composition traits (CW, AFW, LW, GW, PW, HW, SW, TeW). For the Guangxi yellow broilers, BW (125 d of age) was the covariable in the analysis of all traits; and e was the random residual effect.

The genetic parameters for all traits were estimated by the restricted maximum likelihood (REML) method (McGilchrist and Yau 1995; Meyer and Hill 1997) using the WOMBAT 1.0 software (Meyer 2010). For the NEAUHLF white broilers the model employed was described as Model 3 and for Guangxi yellow broilers, the model used for estimating was Model 4:

$$y_{ik} = \mu + L_i + BW + ak + e_{ik} \pmod{3}$$
$$y_k = \mu + BW + ak + e_k \pmod{4}$$

where y_{ik} was the record of the kth broiler from the ith Line; μ was the population mean; L_i was the fixed effect of two lines within the NEAUHLF white broilers (i = 1,2-fat line/lean line); BW was taken as a covariate in the heritability estimation. For the NEAUHLF population, BW1 was the covariable for BW3, BW5, BW7, while BW7 was the covariable for the other body composition traits in Model 3 and BW (125 d of age) was used as a covariate in the heritability estimation of all traits for Guangxi yellow broilers in Model 4; a_k was the random direct addition genetic effect of individual k; e_{ik} was the random residual effect.

The heritability of traits was estimated using the univariate linear mixed-effects model and the genetic correlations between combinations of traits was computed by bivariate linear mixed-effects model. In this study, heritability estimates were interpreted as follows: values below 0.3 were considered low and those equal to or above 0.3 were considered moderate to high. This classification is based on common practice in poultry genetics research (*e.g.*, Alemu et al. 2021; Szwaczkowski et al. 2003). For genetic correlations, the widely used scale in quantitative genetics was adopted where correlations from 0.00 to 0.29 were interpreted as weak, 0.30 to 0.49 as moderate and 0.50 to 1.00 as strong (*e.g.*, Ghorbani et al. 2013; Niknafs et al. 2012).

Results

Descriptive statistics for the investigated traits

The descriptive statistics of the phenotypic traits are shown in Table 1 and Supplementary Tables S1 and S2.

For the results from NEAUHLF white broilers, the LSM of BW7 of fat line and lean line did not show significant difference between the two lines (1871.89 g and 1886.41 g, respectively). However, the AFW of fat line showed significant difference (p < 0.01) between two lines (107.51 g and 10.75 g, respectively). Besides, the BW1 and BW5 of fat line were similar with lean line, but the BW3 of fat line (479.65 g) was significantly lower than the lean line (567.71 g; p < 0.01). In addition to this, for body composition traits, no significant differences were found for MeL, MeC, BoL or ChA. The only significant difference was observed in KeL (0.01) between the fat (9.76 g) and lean (13.81 g) lines of the NEAUHLF white broilers.

For the Guangxi yellow broilers, the LSM of BW (125 d of age) was 1819.03 g, which was close to BW7 in NEAUHLF white broilers (1884.04 g). For body composition in Guangxi yellow broilers, AFW was 35.75 g,

which fell between the AFW of the fat line (107.51 g) and lean line (10.75 g) in the NEAUHLF population and was significantly different from the overall AFW of the NEAUHLF population (59.20 g; p < 0.01). The LW, HW and TeW showed significant differences between the white (43.73 g, 7.13 g, 0.73 g, respectively) and yellow (27.17 g, 10.11 g, 29.39 g, respectively) broiler populations (p < 0.01). Besides, the GW (28.08 g), PW (4.69 g) and SW (2.72 g) of Guangxi yellow broilers showed differences with the NEAUHLF white broilers (20.93 g, 7.68 g, 4.39 g, respectively) (0.01).

Genetic parameter analysis

The results of estimating genetic parameters of traits are shown in Figures 1 and 2 and Supplementary Tables S3–S6

For the NEAUHLF white broilers, heritability estimates ranged from 0.07 to 0.61, while for the Guangxi yellow broilers, this ranged from 0.18 to 0.76. In the results from NEAUHLF white broilers, BW3, BW5, BW7, CW, MeC, LW, GW, PW, SW and TeW had high heritability ($h^2 > 0.3$), MeL, BoL, ChA, AFW, HW had medium heritability ($0.2 < h^2 < 0.3$), BW1 and KeL had low heritability ($h^2 < 0.2$). For the Guangxi yellow broilers, most traits of yellow broilers had high heritability (ranging from 0.36 to 0.76) except SW (0.18), the heritability of BW, CW and AFW were 0.67, 0.63 and 0.41, respectively. The highest heritability was observed in LeW (0.76).

For body weight traits (BW), in the results of NEAUHLF, BW1, BW3, BW5, BW7 and CW all showed strong positive genetic correlations with each other ($r_g > 0.3$) and similar results could be found in their phenotypic correlation results ($r_p > 0.3$). In addition, eight body composition traits had strong positive genetic correlations with BW7: MeL, MeC, BoL, ChA, LW, GW, HW and SW (0.75, 0.84, 0.60, 0.77, 0.84, 0.31, 0.53 and 0.58, respectively). Among above traits, MeL,

Table 1. Descriptive statistics of phenotypic traits and differences between the fat and lean lines of NEAUHLF white broilers, as well as between NEAUHLF white broilers and Guangxi yellow broilers.

Traits	NEAUHLF white broilers Fat line/Lean line		NEAUHLF white broilers/Guangxi yellow broilers	
	LSM(SE)	LSM(SE)	LSM(SE)	LSM(SE)
BW1 (g)	94.14 (1.89) ^a	106.89 (1.90) ^a	109.37 (0.55)	_
BW3 (g)	479.65 (5.78) ^A	567.71 (5.39) ^B	533.45 (3.37)	
BW5 (g)	1083.16 (8.42) ^a	1105.36 (8.49) ^a	1094.42 (6.00)	_
BW7/BW125d (q)	1871.89 (12.93) ^a	1886.41 (12.96) ^a	1884.04 (8.39) ^a	1819.03 (13.08) ^a
CW (g)	1673.40 (11.29) ^a	1682.23 (11.24) ^a	1677.83 (7.96) ^a	1665.47 (8.24) ^a
AFW (g)	107.51 (0.89) ^A	10.75 (0.89) ^B	59.20 (2.18) ^A	35.75 (1.26) ^B
LW (g)	45.31 (0.38) ^a	42.66 (0.37) ^a	43.73 (0.24) ^A	27.17 (0.19) ^B
MSW (g)	20.46 (0.18) ^a	21.39 (0.18) ^a	20.93 (0.13) ^a	28.08 (0.21) ^b
GSW (g)	7.15 (0.13) ^a	8.19 (0.13) ^a	7.68 (0.09) ^a	4.69 (0.05) ^b
HW (g)	6.89 (0.06) ^a	7.37 (0.06) ^a	7.13 (0.05) ^A	10.11 (0.08) ^B
SW (g)	4.57 (0.08) ^a	4.22 (0.08) ^a	4.39 (0.05) ^a	2.72 (0.05) ^b
TeW (g)	0.55 (0.03) ^a	0.87 (0.03) ^b	0.73 (0.03) ^A	29.39 (0.44) ^B
MeL (mm)	91.04 (0.25) ^a	90.39 (0.25) ^a	90.72 (0.18)	
MeC (cm)	4.62 (0.01) ^a	4.81 (0.01) ^a	4.69 (0.03)	_
KeL (cm)	9.76 (0.06) ^a	13.81 (0.06) ^b	11.78 (0.10)	
BoL (cm)	17.08 (0.06) ^a	17.98 (0.06) ^a	17.54 (0.04)	_
ChA (°)	54.59 (0.34) ^a	55.25 (0.34) ^a	54.68 (0.23)	_
LeW (q)				470.09 (2.35)
HNW (g)		_	_	224.96 (1.24)
FeW (g)	_	_	_	57.27 (0.28)
LCD (mm)	_	_	_	37.80 (0.23)

Abbreviations: BW1 = body weight at week 1; BW3 = body weight at week 3; BW5 = body weight at week 5; BW7 = body weight at week 7; BW125d = body weight at 125 days of age in Guangxi yellow broilers; CW = carcass weight; AFW = abdominal fat weight at slaughtering age; LW = liver weight; MSW = muscle stomach weight; GSW = glandular stomach weight; HW = heart weight; SW = spleen weight; TeW = testicle weight; MeL = metatarsal length; MeC = metatarsal circumference; KeL = keel length; BoL = body oblique length; ChA = chest angle; LeW = leg muscle weight; HNW = head and neck weight; FeW = feet weight; LCD = Leg circumference; LSM(SE) = Least Square Means (Standard Error). The different lowercase letters annotation in data in same row means there were difference between the data (p < 0.05), and the different capital letters annotation in data in same row means there were significant difference between the data (p < 0.01).



Figure 1. Heritability (on diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations for phenotypic traits of NEAUHLF white broilers. Abbreviations: BW1 = body weight at week 1; BW3 = body weight at week 3; BW5 = body weight at week 5; BW7 = body weight at week 7; CW = carcass weight; MeL = metatarsal length; MeC = metatarsal circumference; KeL = keel length; BOL = body oblique length; CA = chest angle; AFW = abdominal fat weight; LW =liver weight; MSW = muscle stomach weight; GSW = glandular stomach weight; HW = heart weight; SW = spleen weight; TeW = testicle weight.



Figure 2. Heritability (on diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations for phenotypic traits of Guangxi yellow broilers. Abbreviations: AFW = abdominal fat weight; LW = liver weight; HNW = head and neck weight; FeW = feet weight; LeW = leg muscle weight; HW = heart weight; SW = spleen weight; GSW = glandular stomach weight; MSW = muscle stomach weight; TeW = testicle weight; CW = carcass weight; BW = body weight at 125 days of age; LCD = leg circumference.

MeC, BoL, LW and HW showed strong positive phenotypic correlations with BW7 ($r_p > 0.3$). As for Guangxi yellow broilers, all traits showed strong positive genetic correlations with BW at (125 d of age; ranging from 0.30 to 0.99) and AFW, LW, HNW, FeW, LeW, HW, PW, TeW, CW and TD showed strong positive phenotypic correlations with BW at

125 d of age (0.60, 0.34, 0.72, 0.62, 0.92, 0.52, 0.38, 0.40, 0.98 and 0.57, respectively).

Moreover, to investigate the factors influencing abdominal fat weight (AFW), in the results of NEAUHLF white broilers, BW1, BW3, BW5, CW, MeL, KeL, BoL and LW showed strong positive genetic correlations with AFW (0.58, 0.33, 0.45, 0.31, 0.36, 0.35, 0.37 and 0.54, respectively). The BW7 only had strong positive phenotypic correlations with AFW (0.53) and BW3, BW5, CW had strong positive phenotypic correlations with AFW (0.33, 0.49 and 0.55, respectively). For Guangxi yellow broilers, only LeW, CW, BW and TD showed strong positive genetic correlations with AFW (0.44, 0.50, 0.51 and 0.44, respectively) and the phenotype correlation results were consistent with this (0.46, 0.60, 0.60 and 0.36, respectively).

Discussion

Genetic estimation plays an important role in livestock breeding and production and can elucidate the direct and indirect effects on offspring outcomes from parental inheritance and even individual factors (Baylan 2017; Romé et al. 2021). The current study estimated the genetic parameters for growth and body composition traits in two broiler populations to summarise the factors that influenced broiler production.

The white broilers used in this study were 23rd generation of Northeast Agricultural University High and Low abdominal Fat (NEAUHLF) broiler population. These had been divergently selected into fat and lean lines for abdominal fat weight over twenty generations while maintaining similar body weight, which provided an ideal experimental model for investigating the growth and fatness of broilers (Guo et al. 2011). The AFW showed a significant difference (p < 0.01) between the fat and lean lines, confirming the long-term divergent selection has successfully generated two lines with markedly different fatness. Comparing the two lines of NEAUHLF white broilers allows elucidation of genetic factors controlling fat deposition and growth traits in broilers. Moreover, the BW3 of fat line was significantly lower than lean line (p < 0.01). This might be because the growth rate at the early stage of the lean line is higher than in the fat line, and then, with advancing age, will be increased and the body weight of fat line catches up with the lean line.

As a Chinese native breed, the genetic selection of Guangxi yellow broilers likely focused more on preserving meat quality and unique flavour profiles before largescale commercialisation, rather than selecting for fast growth or high muscle yield. Now emerging in the market as a speciality breed, less intensive past selection of Guangxi yellow broilers may have contributed to its distinct characteristics, such as slower growth rate and differences in body conformation compared to modern broilers. The heritability patterns observed in Guangxi yellow broilers could be linked to more stabilised trait expression during longer growth periods. As the results showed, distinct differences were found in growth performance and genetic parameters between NEAUHLF white broilers and Guangxi yellow broilers. For the Guangxi yellow broilers, BW (125 d of age) was close to BW7 of NEAUHLF white broilers, but the time to slaughter for Guangxi yellow broilers was much longer. Therefore, it can be seen that the growth rate of Guangxi yellow broilers was lower. Similarly, LSM for most other traits differed between these two breeds. The heritability of BW, AFW, HW, GW and TeW (0.67, 0.42, 0.53, 0.74 and 0.74, respectively) were much higher in Guangxi yellow broilers than

NEAUHLF (0.38,0.24, 0.25, 0.52 and 0.41, respectively). This result may be related to the longer time it took for Guangxi yellow broilers to market, which enabled more mature phenotypic expression of these traits, leading to higher stability of phenotypic expression, which contributed to increased heritability estimates (Huang et al. 2016; C. Wu 2001; G. X. Zhang et al. 2015).

For body weight, there were moderate heritability estimates for NEAUHLF white broilers, including 0.45 for BW3, 0.40 for BW5 and 0.38 for BW7. These aligned well with the estimates of 0.42 and 0.35 for BW4 and BW7 reported by Chen et al. (2021). The heritability of 0.38 for BW7 and 0.37 for CW in NEAUHLF population was comparable to estimates of 0.33 for both traits in white Plymouth Rock broilers (Zerehdaran et al. 2004). In a study on TT broilers (developed by Embrapa Suínos e Aves), the heritability values of BW and CW at 42 d of age were 0.41 and 0.39, respectively (Venturini et al. 2014), similar to the current study (0.38 and 0.37). For Guangxi yellow broilers, a higher heritability of 0.67 was estimated for 125d BW compared to white broilers, likely due to its distinct genetic background and more stabilised growth after a longer period.

There are not many studies on the research results of yellow broilers. In the research reported by Liu et al. (2014), the heritability values of BW of Chinese triplevellow chicken at 6 and 12 weeks of age were 0.26 and 0.13, respectively, which were much lower than the heritability of 125d BW of Guangxi yellow broilers in the current study. While the current BW heritability estimates for the NEAUHLF white broilers aligned well with values reported in other broiler lines, the higher estimate of 0.67 in Guangxi yellow broilers needed more interpretation. As a Chinese native breed, Guangxi yellow broilers have likely undergone less intense selection for rapid growth initially. This could contribute to more genetic variation for body weight versus highly selected modern broilers. The 125 d BW was measured at a much later age compared to white broilers, which enabled full expression of genetic potential for body weight. Heritabilities above 0.5 are generally considered relatively high, though estimates exceeding 0.7 are less common. The high 125 d BW heritability suggested that genetics plays a major role in determining this trait's variation in Guangxi yellow broilers, with less influence from environmental or non-additive genetic factors. The heritability of the estimated BW was not higher than 0.7 in both white and yellow broiler populations.

For abdominal fat, both of the heritability of AFW in white and yellow broilers in this research (0.24 and 0.42, respectively) were lower than 0.62 reported for Rock broilers (Zerehdaran et al. 2004). In both two populations, most body composition traits showed high genetic and phenotypic correlations with body weight, which was expected as body weight is influenced by tissue components. For organ composition traits, BW of two populations in this study both showed strong genetic correlations with GW, HW, LW and SW. This indicated significant interactions between growth rate and development of these vital organs. In research by Venturini et al. (2014), genetic correlations between 42 d BW with LW and HW were 0.64 and 0.48, respectively, which were lower than the current results, but were still high. The liver was involved in the regulation of carbohydrate and other energy metabolism and is the main site of fat synthesis in poultry (Na et al. 2018). Both the liver and heart are intricately related to body development and metabolism and research has shown that excessively pursuit for high growth rate in broilers will lead to the imbalance between the development of heart and the rapid growth and metabolic syndrome. This may manifest as cardiac hypertrophy, ascites, obesity, wooden breast and even mortality (Julian 1993; Pakdel et al. 2005; Scheele 1997; Shen et al. 2022; M. Zhang et al. 2020; Y. Zhang et al. 2020).

To investigate the effect of fat deposition, the current analysis revealed that in NEAUHLF white broilers, AFW showed a strong positive genetic correlation with MeL, KeL, BoL and LW (0.36, 0.35, 0.37 and 0.54, respectively) and had medium correlations with BW7 (0.25). While in Guangxi yellow broilers, AFW was strongly correlated with BW, CW, LeW and TD (0.51, 0.50, 0.44 and 0.44, respectively). The differing correlation patterns may reflect distinct fat deposition distributions between the two populations. Further quantitative studies comparing fat patterning are needed to determine whether white and vellow broilers exhibit different storage across body regions. According to research, fatness is one of the factors that significant impact on poultry meat quality, as it can influence the taste of chicken through flavour, juiciness and nutrient content. However, excessive fat laydown will cause obesity and ascites (Mir et al. 2017; C. Y. Wu et al. 2016; M. Zhang et al. 2020; Y. Zhang et al. 2020). In research on 22nd and 23rd HEAUHLF populations, correlations between the combine of AFW-BW4 and AFW-BW7 were 0.34 and 0.14, respectively (Chen et al. 2021), which was close to the current estimate of 0.31 in NEAUHLF white broilers. In the other research, the genetic correlation between AFW and BW in sevenweek-old Plymouth white broilers was 0.38 (Zerehdaran et al. 2004), which was between the current results for white and yellow broilers. The lower correlation for NEAUHLF white broilers might have resulted from more efficient metabolism and lipolysis rates supporting lean growth after generations of selection. In contrast, a higher positive correlation was observed (0.51) between AFW and BW in the Guangxi yellow broilers, compared to the value of 0.31 in the NEAUHLF population. Increased association in Guangxi yellow broilers could arise from relatively less selection pressure for efficient nutrient partitioning, allowing greater fat deposition during growth. Additionally, some strong negative genetic correlations were found between MeC-KeL (-0.67) and MeL-KeL (-0.42), which suggested possible trade-offs to optimise both traits.

Conclusions

This study revealed moderate-high heritability of body weight, body composition and fatness in white and yellow broilers. Body weight and abdominal fat weight showed positive genetic correlations with other economic traits in both populations, but followed different patterns. Based on the results, rapid growth may lead to negative consequences and excessive obesity, which can reduce economic efficiency. In practical breeding programs, reasonable multi-trait selection strategies should be formulated according to the genetic background and specific breeding objectives for each population and there may be indirect impacts on physiology and metabolism to achieve optimal breeding efficiency.

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Disclosure statement

No potential conflict of interest was reported by the author(s).

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Data availability statement

The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

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