Estimation of Heritability and Genetic Correlation of Quantitative Traits as a Basis for Selection Program of Indonesian Native Chickens

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Abstract. Native chicken is a potential genetic source to produce new superior and productive strains. The genetic parameter information is needed as basis data for the selection program to improve the genetic quality of native chickens. This study aimed to estimate the heritability and genetic correlation of quantitative traits in local Indonesian chickens. The material used is the offspring from outbreeding, crossbreeding, and reciprocal crosses of four native chicken lines: White, Lurik, Wareng, and Ranupane. The traits observed were Body Weight (BW), Body Height (BH), Body Length (BL), Body Circumference (BC), Wing Length (WL), Beak Length (BeL), Head Circumference (HC), Thigh-Shank Length (TSL), and Thigh Circumference (TC). The ANOVA and ANCOVA were used to estimate heritability and genetic correlation based on the mating lines of each cage/pen. The mating line significantly affected all the measured traits ($P < 0.05$). The highest heritability was obtained for BW ($h^2 = 0.25$, moderate category). A positive genetic correlation was found between BW and all other traits except for BeL and HC. In conclusion, body weight can be considered for early selection because it has the highest heritability and positive genetic correlation with other traits related to body size.

Keywords: Body measurement, *Gallus domesticus* (Linnaeus, 1758), genetic parameter, mating lines.

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1 Introduction

Indonesia is rich in native chicken germplasm with very different characteristics between regions [1]. Native chickens have advantages in aspects of good meat and egg quality [2], disease resistance [3], high adaptability to traditional rearing systems and the local environment [4, 2], and have great potential as a source of family income [5, 6]. Native chicken products are a source of healthy food [7] and become national food security [8]. The genetic advantages of native chickens have not been fully exploited optimally [5] through a serious, targeted, and sustainable breeding program. New strains of native chicken's superior in egg and meat products have not been produced. In Indonesia, the crossbreeding between commercial and native chickens is carried out instantaneously, and the first offspring (filial-1/F1) is directly sold in the market. The performance of the crossbred chicken was not pure like the native chicken but a mixture of the performance.

Based on this reality, it is necessary to carry out a breeding program to increase the productivity of native chickens. Native chickens are a genetic source to produce new strains for laying and broiler types [9]. The diversity of characteristics in native chickens reflects the high genetic variation, so it has potential and opportunity for genetic improvement [10, 11]. Improving the genetic quality of native chickens can be done through a strict selection program and by controlling the mating system. The wide range of diversity provides materials for selection programs to produce new strains of superior native chicken.

The selection process should be started with a recording program. Recording of production in chickens needs to be done to increase selection efficiency [12, 13] which can predict genetic parameters. Information on genetic parameters is essential in quantitative genetics [14, 15] and genetic improvement programs [16]. The genetic parameters consist of heritability, repeatability, and genetic correlation; hereafter, they can be used to estimate the Estimated Breeding Value (EBV) as a reflection of genetic quality.

John-Jaja *et al.* [17] stated that heritability is a coefficient of inheritance whose values range from 0 to 1, with categories: low (0.00 to 0.19), moderate (0.20 to 0.39), and high (above 0.4). Understanding heritability as the basis for initial consideration of whether a trait needs to be selected is essential. The higher the heritability value, the better the selection will be because the selection is faster. Hill [18] stated that heritability can also estimate the collateral relatives and selection responses. Genetic correlation is a coefficient that shows the degree of closeness of the relationship between several genetically evaluated traits. Genetic correlation values range from -1 to +1 [19]. Previous studies have examined genetic parameters, especially heritability and genetic correlation of several quantitative features of local chickens [20–22, 12, 13, 16, 17]. Genetic parameters that are widely measured include characteristics related to body weight and growth [23, 24, 16], egg production [25–28, 10, 13], reproduction [29–31], perch habit-related traits [32], and feather-related traits [33, 34].

Methods for estimating the heritability and genetic correlation of several traits in livestock have long been formulated and developed. The difference in this estimation method depends on the condition of the offspring data from different mating systems, resulting in offspring with varying collateral relatives. The methods that are often used include parent-offspring regression analysis [31], fullsib analysis, half-sib correlation, pedigree relationship [35, 36], and animal model [37]. Because the mating system applied to chickens is a colony system that makes it challenging to record individual production systems, estimating genetic parameters in chickens is based on the cage/batch/flock as a database as applied by Biscarini *et al.* [38], Grams *et al.* [33] and Rajkumar *et al.* [39].

Many studies have been conducted to estimate the heritability and genetic correlation of several traits in chickens. Still, the results cannot be directly applied to the Estimation of Breeding Values (EBV) in different chicken lines. The heritability and genetic correlation values for the same trait did not always have similar results due to differences in methods, chicken strains, age, and measurement time. Heritability only applies to a specific population in the same environment and cannot be used to estimate the genetic quality of individuals [18]. Therefore, it is crucial to conduct this research to assess the genetic parameters (heritability and genetic correlation) of several traits in native chickens as a basis for selection in producing new superior native laying hens. Furthermore, these genetic parameters will be used to estimate the breeding value of several traits, which are then used as the basis for early selection (end of the starter period) in offspring from crossbreeding and reciprocal crosses of native chickens.

2 Materials and methods

2.1 Genetic source and mating line

This study was conducted at the Poultry Breeding House, Experimental Farm of Animal Science Department, the University of Muhammadiyah Malang, starting in July 2020. The coordinate point of the research site is at the 7°55'16.659827296257"S, and 112°35'50.738020678142"E. The ethical approval was issued with the number of E.5.a/048.a/KEPK-UMM/III/2022 under ethic of commission for medical reseach in University of Muhammadiyah Malang. Furthermore, the genetic sources used were four strains of native chicken's endemic to East Java: White, Lurik, Wareng, and Ranupane. The mating system used was outbreeding (within strain) and crossbreeding and reciprocal crossing (between strain) with a male: female ratio = 1: 4 to 6. There were sixteen mating lines from the three mating systems. A total of 436 offspring were observed on quantitative traits at 12 wk of age (end of the starter period) without separating males and females (unsexed).

Fig. 1. Four native chicken lines as genetic sources: White, Lurik, Wareng, and Ranupane.

2.2 Quantitative traits

Quantitative traits measured were Body Weight (BW), Body Height (BH), Body Length (BL), Body Circumference (BC), Wing Length (WL), Thigh-Shank Length (TSL), Beak Length (BeL), Head Circumference (HC), and Thigh Circumference (TC). The measurement of traits follows the previous researchers [40, 41] with some modifications developed ourselves (Figure 2). The outputs of measurement were then used to estimate heritability and genetic correlation. Quantitative traits data were analyzed by ANOVA of two-levels unequally nested classification followed by unequally-LSD test.

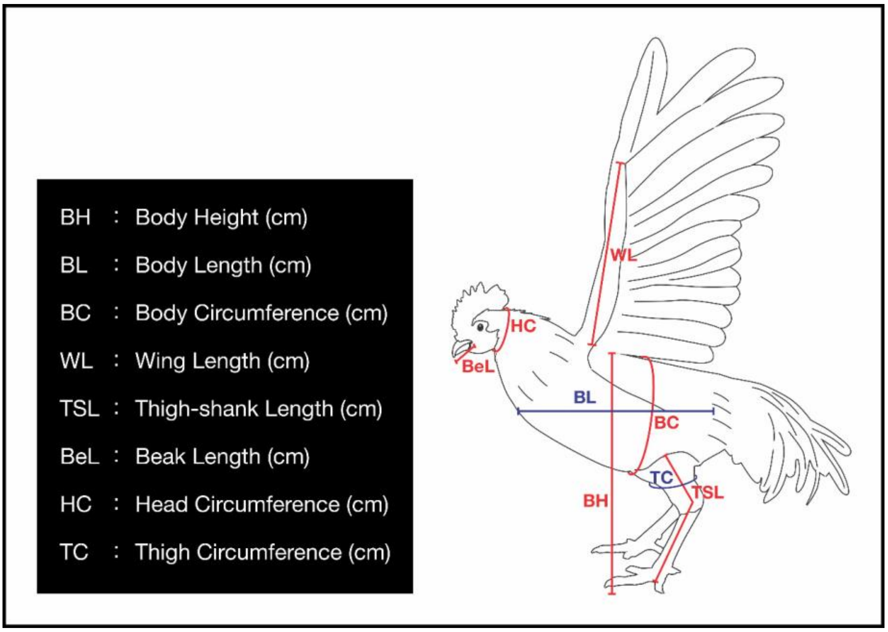

Fig. 2. Measurement of quantitative traits in chickens.

2.3 Heritability and genetic correlation estimation

The heritability and genetic correlation were estimated based on the offspring data of each cage/group, not by blood-relationship (fullsib, half-sib, pedigree) according to the method developed by previous researchers [33, 38]. Due to cage/pen/group mating systems, recording individual offspring data from each parent/lineage is complicated.

Heritability (h^2). The heritability value of a trait was estimated based on the component values of the cage variance ($\sigma^2 a$) and the error variance ($\sigma^2 e$) by taking into account the number of parents in each cage (d). The $\sigma^2 a$ and $\sigma^2 e$ were obtained through ANOVA of the unequal two-level nested classification. The modified formula for heritability from Biscarini *et al.* [38] is in Equation (1) and Equation (2):

$$h^2 = \frac{\sigma^2 a}{\sigma^2 a + \left(\frac{\sigma^2 e}{d}\right)} \quad (1)$$

$$d = \frac{1}{c-1}\left[\sum n - \frac{\sum n^2}{\sum n}\right] \quad (2)$$

Where d is the coefficient of the number of hens per cage, calculated by the formula: c is the number of pens, and n is the total number of offspring per cage.

2.4 Genetic correlation (r_G)

The estimated genetic correlation is between Body Weight (BW) as variable Y and other quantitative traits as variable X. Calculations include cage variance ($\sigma^2 a$) and covariance (cova) obtained through ANOVA and ANCOVA of two-level unequally nested classification, respectively. The basic formula for genetic correlation used is in Equation (3) [38]:

$$r_{g12} = \frac{4\,cov_a}{\sqrt{4\sigma^2_{a1} + 4\sigma^2_{a2}}} \qquad (3)$$

Where a1 is for trait-1 and a2 is for trait-2, which is correlated.

3 Result and discussions

3.1 Result

The identification of several quantitative traits of 12 wk offspring from sixteen mating lines (outbreeding, crossbreeding, and reciprocity) between strains is presented in Table 1. Chicken lines showed a significant effect ($P < 0.05$) on all quantitative characteristics: Body Weight (BW), Body Height (BH), Body Length (BL), Body Circumference (BC), Wing Length (WL), Thigh-Shank Length (TSL), Beak Length (BeL), Head Circumference (HC), and Thigh Circumference (TC).

Table 1. Quantitative traits of 12 wk offspring form different mating lines in native chickens.

Mating lines	Quantitative traits								
	Body weight (g)	Body height (cm)	Body length (cm)	Body circ. (cm)	Wing length (cm)	TSL (cm)	Beak length (cm)	Head circ. (cm)	Thigh circ. (cm)
White × white	689.80 ± 119.57[bc]	20.2 ± 1.76[bc]	14.86 ± 2.48[ab]	19.88 ± 2.58[abc]	13.30 ± 1.40[b]	18.04 ± 2.08[a]	2.92 ± 0.19[a]	9.70 ± 0.19[a]	6.50 ± 1.66[bc]
Lurik × lurik	810.54 ± 228.13[a]	22.1 ± 2.54[ab]	16.23 ± 1.88[a]	21.05 ± 2.75[a]	15.88 ± 1.51[a]	18.13 ± 1.63[a]	2.89 ± 0.35[a]	9.05 ± 0.35[ab]	7.73 ± 1.54[ab]
Wareng × wareng	628.00 ± 115.14[c]	18.74 ± 2.45[c]	13.54 ± 3.70[ab]	18.98 ± 3.06[bc]	14.90 ± 2.41[ab]	16.10 ± 2.38[b]	2.82 ± 0.22[ab]	8.72 ± 0.22[ab]	5.98 ± 1.28[c]
Ranupane × ranupane	708.82 ± 127.13[c]	20.62 ± 2.21[bc]	13.54 ± 2.06[ab]	19.58 ± 2.80[abc]	14.79 ± 1.29[ab]	16.42 ± 1.62[b]	2.87 ± 0.37[ab]	8.60 ± 0.37[ab]	8.75 ± 4.67[a]
White × lurik	688.57 ± 173.32[bc]	20.95 ± 1.96[bc]	15.48 ± 2.14[ab]	19.40 ± 2.51[bc]	14.82 ± 1.52[ab]	16.63 ± 1.78[ab]	2.85 ± 0.29[ab]	9.16 ± 0.29[ab]	7.11 ± 1.16[bc]
Lurik × white	736.43 ± 123.81[abc]	20.07 ± 2.82[bc]	15.79 ± 2.00[ab]	20.36 ± 1.94[abc]	15.86 ± 1.38[a]	17.74 ± 1.50[a]	3.03 ± 0.08[a]	9.29 ± 0.08[ab]	7.11 ± 1.84[bc]
White × wareng	768.00 ± 150.81[abc]	21.36 ± 2.61[ab]	16.06 ± 2.61[ab]	20.28 ± 3.08[abc]	15.94 ± 1.92[a]	18.49 ± 2.12[a]	2.94 ± 0.25[a]	8.93 ± 0.25[ab]	7.58 ± 1.89[ab]
Wareng × white	708.33 ± 223.02[bc]	22.17 ± 1.72[ab]	16.50 ± 1.38[a]	19.82 ± 1.17[abc]	15.83 ± 1.47[a]	16.83 ± 2.32[ab]	2.57 ± 0.46[ab]	9.42 ± 0.46[a]	7.58 ± 0.58[ab]
White × ranupane	684.67 ± 207.29[bc]	20.89 ± 2.31[bc]	14.69 ± 2.53[ab]	17.91 ± 2.41[c]	14.82 ± 1.60[ab]	16.76 ± 2.05[ab]	2.75 ± 0.33[ab]	8.35 ± 0.33[b]	6.30 ± 1.42[bc]
Ranupane × white	794.33 ± 133.88[ab]	20.58 ± 1.13[bc]	15.42 ± 2.42[ab]	20.62 ± 2.14[ab]	15.58 ± 1.86[ab]	17.51 ± 1.98[a]	2.50 ± 0.41[b]	8.58 ± 0.41[ab]	7.55 ± 2.43[ab]
Lurik × wareng	767.78 ± 127.04[abc]	23.01 ± 2.53[a]	15.85 ± 1.77[ab]	20.37 ± 2.19[ab]	15.82 ± 1.18[a]	16.52 ± 3.73[ab]	2.78 ± 0.49[ab]	8.87 ± 0.49[ab]	7.17 ± 1.51[bc]
Wareng × lurik	840.94 ± 150.69[a]	21.90 ± 2.51[b]	16.22 ± 1.83[a]	20.86 ± 2.77[a]	15.82 ± 1.73[a]	17.43 ± 2.83[ab]	2.83 ± 0.44[ab]	8.88 ± 0.44[ab]	7.95 ± 1.40[ab]
Lurik × ranupane	805.04 ± 174.87[ab]	21.13 ± 1.81[abc]	16.33 ± 2.51[a]	20.86 ± 2.12[a]	15.83 ± 1.64[a]	18.39 ± 1.79[a]	2.95 ± 0.35[a]	9.39 ± 0.35[a]	7.46 ± 1.01[abc]
Ranupane × lurik	772.63 ± 172.66[abc]	21.37 ± 2.01[ab]	15.61 ± 2.18[ab]	19.76 ± 2.47[abc]	15.01 ± 1.91[ab]	17.79 ± 1.85[a]	2.79 ± 0.29[ab]	9.43 ± 0.29[a]	7.55 ± 1.34[ab]
Wareng × ranupane	786.94 ± 129.83[ab]	20.98 ± 1.23[bc]	14.42 ± 2.96[ab]	17.91 ± 2.41[c]	14.64 ± 1.79[ab]	16.76 ± 2.05[ab]	2.88 ± 0.24[ab]	8.99 ± 0.24[ab]	6.78 ± 1.47[bc]

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Table 1. Continue.

Mating lines	Quantitative traits								
	Body weight (g)	**Body height (cm)**	**Body length (cm)**	**Body circ. (cm)**	**Wing length (cm)**	**TSL (cm)**	**Beak length (cm)**	**Head circ. (cm)**	**Thigh circ. (cm)**
Ranupane × wareng	797.22 ± 200.11[ab]	20.98 ± 2.28[bc]	15.02 ± 1.64[ab]	20.62 ± 2.14[ab]	15.56 ± 1.82[ab]	17.51 ± 1.98[a]	2.73 ± 0.43[ab]	9.49 ± 0.43[a]	7.76 ± 1.94[ab]
Overall	772.08 ± 164.27	21.44 ± 2.81	15.83 ± 2.16	20.30 ± 2.57	15.54 ± 1.66	17.53 ± 2.25	2.86 ± 1.13	9.07 ± 1.13	20.30 ± 2.57

Note: Circ. = Circumference. TSL = Thigh-Shank Length. Columns with different superscripts differ significantly ($P < 0.05$).

Table 2 shows the heritability values (h^2) for all traits with an average of 0.10 + 0.07. Body weight has the highest heritability, which is 0.24, while the heritability of other traits ranges from 0.01 to 0.16. Table 3 shows the results of the estimated genetic correlation between body weight and other characteristics. The genetic correlation (rG) of BW-BH, BW-BL, BW-BC, and BW-WL were 0.75, 0.55, 0.89, and 0.54, respectively. At the same time, the BW-TSH and BW-TC were 0.43 and 0.36. However, the negative rG was found in BW-BeL (rG= -0.03) and BW-HC (rG= -0.16).

Table 2. Heritability of quantitative traits in 12 wk native chicken.

Quantitative traits	Heritability	
	h^2	**Category**
Body weight (g)	0.25	M
Body height (cm)	0.10	L
Body length (cm)	0.03	L
Body circumference (cm)	0.07	L
Wing length (cm)	0.16	L
Thigh length (cm)	0.13	L
Beak length (cm	0.09	L
Head circumference (cm)	0.01	L
Thigh circumference (cm)	0.10	L
Average	0.10 ± 0.07	L

Note: h^2 = Heritability. M = Moderate. L = Low.

Table 3. Genetic correlation (rG) between body weight with several quantitative traits of 12 wk native chicken.

Quantitative traits	Body weight (g)	
	r_G	**Category**
Body height (cm)	0.75	H+
Body length (cm)	0.55	H+
Body circumference (cm)	0.89	H+
Wing length (cm)	0.54	H+
Thigh-shank length (cm)	0.43	M+
Beak length (cm)	-0.03	L-
Head circumference (cm)	-0.16	L-
Thigh circumference (cm)	0.36	M+

Note: rG = Genetic correlation. H+ = High possitive; M+ = Moderate possitive; L+ = Low possitive; L- = Low negative.

3.2 Discussion

Table 2 shows the average body weight of 12 wk old crossbreds of 772.08 g ± 164.27 g (607.81 g to 936.36 g). Relatively similar results were reported by Singh *et al.* [42], who studied local chickens from Uttara, India, with an average weight of 12 wk old chickens of 837.00 g ± 24.23 g. Das *et al.* [23] also reported the same relative results for the body weight of 12 wk old chickens from Hilly × Fayoumi crosses, Bangladesh, of 710.7 g ± 5.6 g (female) and 1043 g ± 5.5 g (male). El-Tahawy and Habashy [28] studied local Egypt chickens (Lohman Brown/LB) aged 12 wk was relatively the same as this study, with an average of 757.5 g ± 7.7 g. In Sinai (SI) chickens and their crosses, the weight of 12 wk old chickens was higher: 925.6 g ± 9.8 g (Sinai), 983.8 g ± 13.9 g (LB-SI), and 989.7 g ± 15.9 g (SI-LB). Higher body weight results were also reported by Tongsiri *et al.* [43], who measured the local Thai chicken Lueng Hang Kao Kabinburi at 12 wk old with an average yield of 1 100 g ± 210 g.

Referring to the ANOVA and LSD test results, it can be further analyzed which crossbred chicken has the highest (superior) value for each trait, with a summary as presented in Figure 3. The mating between a male Lurik with Lurik and Wareng parent (yellow circle) produces offspring that are superior in primary traits related to body size (body circumference and body height). Likewise, the mating of Wareng males with White and Lurik parents (yellow circle) also tends to be superior in traits related to the size of the body (body length and body weight). White males with White and Wareng females and Lurik males with White females (green circle) tended to be superior in secondary traits (head circumference, wing length, thigh-shank length, and beak length). Likewise, male and female Ranupane (purple circle) mating results are also superior in the secondary traits of thigh circumference. Based on these results, it can be predicted that Lurik and Wareng chickens can be used as male lines to produce offspring superior in body size.

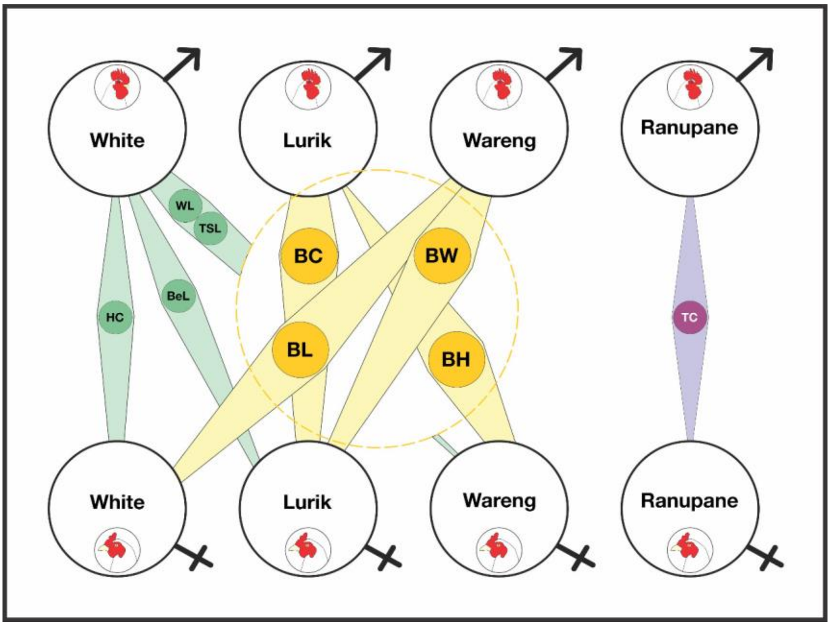

Fig. 3. Summary of the highest values of quantitative traits from crosses.

Note: BL = Body Length; BW = Body Weight; BC = Body Circumference; BH = Body Height; HC = Head Circumference; BeL = Beak Length; WL = Wing Length; TSL = Thigh-Shank Length; TC = Thigh Circumference.

Heritability for most estimated quantitative traits is low, except for body weight, which showed a moderate category (Table 2). That is under the statement of John-Jaja *et al.* [17] that heritability values range from 0 to 1 with details: 0 to 0.19 (low), 0.20 to 0.39 (moderate), and > 0.40 (high). The order of heritability value of all traits is body weight, wing length, thigh-shank length, body height, thigh circumference, beak length, body circumference, body length, and the end is the head circumference. Because the heritability of other traits is low, the discussion will focus on body weight, which has a heritability of 0.25 (moderate).

Research on local chickens in Mazandaran, Iran, obtained heritability of body weight relatively the same but with a more extensive range: 0.21 to 0.4 [22]. Das *et al.* [23] got lower results, which estimated heritability in crossbreds at the same age (12 wk) of 0.17. The results of the study by Ullengala *et al.* [37] that evaluated the heritability of local Indian Dahlem Red chickens were also lower: 0.16 (2 wk old), 0.16 (4 wk old), and 0.19 (6 wk old). Although both were in the moderate category, local Thai LHKK has higher yields: 0.37 [43]. Adeleke *et al.* [44] reported the heritability of several traits in local Nigerian chickens aged 12 wk with higher yields compared to this study: body weight (0.45), wing length (0.25), body length (0.41), shank length (0.52), and thigh length (0.37).

This study indicates that in local chickens, the level of inheritance of body weight traits is still relatively low compared to commercial broiler strains. Broilers, which are meat-producing strains, have been the result of rigorous selection over a long time so that their genetic quality is better than that of local chickens. As a result, broilers grow much faster than local chickens. This fact illustrates that the rate of inheritance of body weight traits in broilers is higher, as reported by Mebratie *et al.* [36] that the heritability of body weight of the broiler population aged 4 d is 0.33 (male) and 0.38 (female), while at the age of 7 d of 0.37 (male) and 0.40 (female).

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Heritability in the breeding program implies a better opportunity to select native chickens based on body weight characteristics, especially early selection at the end of the grower phase (12 wk). Body weight produces 0.25 heritability, meaning that body weight is influenced by 25 % genetic factors and 75 % non-genetic. The higher the heritability value, the greater the genetic factor determining a trait [45]. Therefore, heritability is an essential genetic parameter in deciding which features are prioritized for selection with faster and more economical results. Traits with economic value that have more influence on genetic factors will be prioritized for selection first.

Table 3 shows a very high genetic correlation (rG) between body weight with body height and body circumference, 0.75 and 0.89, respectively. The genetic correlation between body weight with body length and wing length is high: 0.55 and 0.54, respectively. The genetic correlation between body weight with thigh-shank length and thigh circumference was moderate: 0.45 and 0.39, respectively. Meanwhile, body weight with beak length and head circumference are negative low: -0.03 and -0.16 receptively.

The genetic correlation between body weight and some of these traits differs from the results of a study Adeleke *et al.* [44] examining local Nigerian chickens aged 12 wk. The genetic correlation between body weight and body length was 0.83 (higher), and wing length was 0.05 (lower). Different results were also obtained between body weight with the shank and thigh, which received a genetic correlation of 0.42 and 0.63.

Genetic correlation is essential in breeding programs to determine which traits will be selected, considering other characteristics. Positive genetic correlation means that an increase in the first trait will also increase the second trait and vice versa. Conversely, a negative correlation means that an increase in the first trait will decrease the second trait. Therefore, chickens cannot be selected for several characteristics simultaneously to get optimal results. Thus, genetic correlation information helps us make more efficient selections. Furthermore, a positive genetic correlation is sufficient to select only one trait since it will automatically increase the other characteristics, making the selection program more efficient in time, cost, and effort. On the other hand, caution is needed if there is a negative genetic correlation because an increase in the first trait will negatively affect the other characteristics.

4 Conclusion

Lurik and Wareng male chickens have the potential as genetic sources in crossbreeding and selection programs to produce new native chicken lines with advantages in body size traits. Body weight can be prioritized to be selected first because it has the highest inheritance coefficient compared to other characteristics. Selection to increase body weight can increase body height, body length, body circumference, thigh-shank length, and thigh circumference.

The author would like to thank the Rector of the University of Muhammadiyah Malang, Indonesia, for supporting and permitting this research to be carried out successfully. This research is part of the National Research Priority funded by the Ministry of Research and Technology (now the Ministry of Education, Culture, Research and Technology) through the National Research and Innovation Agency in 2020 with a contract number: 7/EI/II/PRN/2020.

Conflict of interest. The researchers guarantee that everything discussed in this manuscript has no conflict of interest with financial affairs, personal affairs, or other relationships with people or organizations.

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