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Original Article

Genetic parameters of some carcass and meat quality traits in Betong chicken (KU line)

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ABSTRACT

Carcass and meat quality are important traits in poultry production. A breeding plan which emphasizes these traits should be considered to increase production. The objectives of this study were to estimate heritability and genetic correlations of some carcass and meat quality traits and to compare multiple-trait animal models with zero (Zero Model) and non zero (Non-zero Model) additive genetic covariances among traits in Betong chicken (KU line). Pedigree information and performance data of the Betong chicken (KU line) population were used to estimate variance components and genetic parameters using multiple-trait animal models. Two models were employed in this study, where fixed effects were classified as hatching batch and sex. The random effects were assumed to be additive genetic and residual effects. From the Non-zero Model, heritability estimates of body weight at age 16 wk (BW16) and breast meat weight (BMW) were 0.47 and 0.58, respectively. Heritability estimates of meat quality traits ranged from 0.15 to 0.33 with large standard errors. Genetic and phenotypic correlations between BW16 and BMW were high and positive (0.63 and 0.68, respectively). Genetic correlations among meat quality traits had large standard errors. BW16 and BMW may not be associated with meat quality traits. These results indicated that BW16 and BMW can be improved using genetic selection as a criterion in this population. Selection emphasizing increased BW16 and BMW may not have any adverse effect on the other meat quality traits in Betong chicken (KU line).

Introduction

Indigenous chicken meat has been popular among consumers in Thailand, Hong Kong, Southern China, and Japan due to its unique taste and texture, and particularly its low-fat content (Wattanachant et al., 2004). In niche markets, it has two or three times the selling price of commercial broiler meat (Wattanachant et al., 2004). Indigenous chickens can be easily raised in tropical climates and show more resistance to disease; however, they have a low growth rate and farmers have to raise them for 6–7 mo to reach market size (Sopannarath and Bunchasak, 2015; Jaturasitha et al., 2016). One of the strategies to solve these shortcomings is to use a selection program that targets growth and carcass traits (Le Bihan-Duval et al., 1999). However, improving growth and carcass traits needs to consider the effect on meat quality traits as well. One of the well-known indigenous chicken meats suitable for boiling and grilling in Thai cuisine is obtained from Betong chicken, mostly found in the southern part of Thailand (Wangtaweesukkamol et al., 2013). A line of Betong was later developed by Kasetsart University, Bangkok, Thailand which was called Betong chicken (KU line) (Sopannarath and Bunchasak, 2015). Betong chicken (KU line) was developed emphasizing growth performance in a closed flock while maintaining the characteristic gold color of feathers and slow feathering rate of the Betong chicken (Sopannarath and Bunchasak, 2015). Previous studies found that the body weight of the Betong chicken (KU line) can reach the market size at age 16 wk (Putsakul et al., 2010; Wangtaweesukkamol et al., 2013). Therefore, the next selection targets of this population should simultaneously consider growth and carcass and meat quality traits.

The breeding scheme needs to include the estimates of genetic parameters such as heritability, genetic and phenotypic correlations to monitor the target population. These estimates are very

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important to a reliable breeding plan (Gaya et al., 2011). Heritability estimates for carcass traits were reported to be medium–high (Zerehdaran et al., 2004; Le Bihan-Duval et al., 2008; Chabault et al., 2012), and for meat quality traits, they varied from low to high (Le Bihan-Duval et al., 2008; Gaya et al., 2011; Chabault et al., 2012) in broiler and slow-growing lines. Therefore, the objectives of the current study were to estimate heritability and genetic and phenotypic correlations for some carcass and meat quality traits and to compare multiple trait models with zero (Zero Model) and non zero (Non-zero Model) additive genetic covariance among traits in the Betong chicken (KU line) population. These parameters will be further used in the selection scheme of the Betong chicken (KU line) population.

Materials and methods

Animals and data

Data from this study were obtained from the Betong (KU line) population which was established in 2007. The number of chickens was increased and phenotypic variation was observed in the first 2 yr. Subsequently, male and female chicken were selected based on breed characteristics such as feathering rate, golden brown feather color, and growth performance. Mating of related animals such as full-sib and half-sib were avoided in this closed flock.

Carcass and meat quality traits could not be studied in the breeding flock; thus, progeny testing from two hatching batches was designed for some growth, carcass, and meat quality traits. The offspring were produced from 28 cocks and 97 hens at a poultry farm from October to November 2014 by artificially inseminating hens with the same cock on a weekly basis. The eggs were collected every day and marked according to dam number to identify pedigree information. Before incubation, the collected eggs were disinfected with formaldehyde and were then placed in the incubator for 21 d (18 d in the setter and 3 d in the hatchery). After hatching, chickens were individually weighed and wing-banded when they were one-day old. In total, 529 performance records were collected from the progeny test flocks. The pedigree file included chickens of nine generations ($n = 959$).

Progeny from the two hatching batches received the same feeding management and diet. From one-day to age 4 wk, they were raised on a litter floor with brooders using incandescent lighting (24 h light:0 h darkness). After age 4 wks, chickens were transferred to a slat floor barn and fluorescent lighting (23 h light:1 h darkness) was arranged until age 16 wk. Chickens were assigned to separate groups by sex. Feed and fresh water were provided *ad libitum*. The feed was formulated according to the recommendation of Putsakul et al. (2010) without the antimicrobial agent. From one-day to age 4 wk, all chicks were fed a starter diet containing 21% crude protein (CP) and 3050 kcal/kg metabolizable energy (ME). After age 4 wk until age 16 wk, chickens were provided with grower feed containing 18% CP and 3000 kcal/kg ME. Sanitary management and cleaning of the premises were regularly practiced. Approval (ID# ACKU60-AGR-003) was issued by the Kasetsart University Institutional Animal Care and Use Committee and the animal use protocol was in accordance with the guidelines for animal care under the Ethical Review Board of the Office of National Research Council of Thailand for conducting scientific research.

Traits

All chickens were weighed at age 16 wk (BW16); generally, three birds were randomly sampled within a full-sib family to measure carcass and meat quality traits. Chickens were slaughtered at age 16 wk having been fasted overnight before slaughtering. The process of slaughtering for ante-mortem and post-mortem sampling was in accordance with the good manufacturing practices for poultry abattoirs (Thai Agricultural Standard, 2006). Carcasses were dissected into the different cutting parts according to the standards for chicken meat (Thai Agricultural Standard, 2005). Breast meat weight (BMW), which included the breast and fillet muscles, was measured in this step.

Both sides of the pectoralis major muscle were used to determine meat quality traits, namely pH, color, drip loss (DL), and shear force (SF). The pH immediately post-mortem (pH0) and the pH at 24 h post-mortem (pH24) were measured by inserting a probe directly into the left side of pectoralis major muscle as described by Allen et al. (1997). The drip loss percentage was measured from the left side of the pectoralis major muscle. The sample was weighed and suspended in a plastic bag. All samples were hung on a shelf and stored in a 4 °C room for 24 h. Afterward, each sample was removed from the plastic bag, excess surface fluid blotted and the sample weighed to evaluate DL (Northcutt et al., 1994). Color values, namely lightness (L*), redness (a*), and yellowness (b*), were measured after drip loss on the left side of the breast at the surface of the pectoralis major muscle using a Hunter Lab colorimeter (Reston, Virginia, USA), and reported in accordance with the complete International Commission on Illumination system (CIE, 1978). The shear force was measured from the right side of the pectoralis major muscle, which was cooked for 15 min at 95 °C in steam. The size of the sample was 2.0 cm (wide), 1.0 cm (long), and 1.5 cm (high). Shear force values were tested using a Lloyd Texture analyser with a Warner-Bratzler blade attachment (Bognor Regis, West Sussex, UK). The crosshead speed of the machine was set to 80 mm/min (Saláková et al., 2009).

Statistical analysis

Descriptive statistics of performance traits (BW16, BMW, pH0, pH24, DL, SF, L*, a*, and b*) were calculated using the UNIVARIATE procedure in SAS® University Edition (SAS Institute Inc, 2017). The significance of the hatching batch and sex was examined using the PROC GLM procedure of SAS® University Edition (SAS Institute Inc, 2016). The statistical model was $y_{ijk} = \mu + H_i + S_j + e_{ijk}$ where y_{ijk} is the individual performance for BW16, BMW, pH0, pH24, DL, SF, L*, a*, and b*, μ is the overall mean, H_i is the fixed effect of hatching batch i ($i = 1$ and 2), S_j is the fixed effect of sex j ($j =$ male and female) and e_{ijk} is the random residual effect ~ NID $(0, \sigma_e^2)$.

Variance and covariance components

The information from pedigree and performance data was used to estimate genetic (co)variance components. Multiple trait animal models with zero (Zero Model) and non zero (Non-zero Model) additive genetic covariances among traits were determined in these data. The fixed effects were hatching batch and sex. The random effects were additive genetic and residual effects. Variance and covariance components for BW16, BMW, pH0, pH24, DL, SF, L*, a*, and b* were estimated using single trait analyses. 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, 2016). The prior values of (co)variance in a multiple trait analysis were obtained and modified from the results of single trait analyses in the same dataset. The mixed linear animal model for multiple traits is shown in Equation (1):

$$y = Xb + Za + e \tag{1}$$

where y is the vector of the observations for BW16, BMW, pH0, pH24, DL, SF, L*, a*, and b*, b is the vector of fixed effects including hatching batch and sex for BW16, BMW, pH0, pH24, DL, SF, L*, a*, and b*, a is the vector of random additive genetic effect for BW16, BMW, pH0, pH24, DL, SF, L*, a*, and b*, X is the incidence matrix of fixed effect that related animal records to element of b, Z is the incidence matrix of random effect that related animal records to element of a and, e is the vector of random residual effect for BW16, BMW, pH0, pH24, DL, SF, L*, a* and b*. From the model, the assumption of mean and variance is presented in Equation (2):

$$E[y] = Xb \text{ and } \mathrm{var}\begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} G \otimes A & 0 \\ 0 & R \otimes I \end{bmatrix} \qquad (2)$$

where A is the numerator relationship matrix, I is the i identity matrix, G is the variance matrices of additive genetic with zero and non-zero additive genetic covariances among traits for the Zero Model and the Non-zero Model, respectively and R is the (co) variance matrices of residual error with zero and non-zero residual error covariances among traits for the Zero Model and the Non-zero Model.

The most appropriate model was chosen based on the log likelihood ratio test. The reduction in −2logL was calculated by logL from WOMBAT software. The difference between the −2logL for both models was tested against the chi-square distribution, with the degrees of freedom being the difference in the number of variance and covariance components in the models. The model that had the lowest −2logL was the best fit model (Dobson, 1990).

Estimation of the genetic parameters

Estimates of heritability were computed from the variance components with the two models. Estimates of (co)variance components from the Non-zero Model were used to calculate genetic correlation and phenotypic correlation using the equation of Falconer and Mackay (1996).

Results and discussion

Phenotypic variability

Descriptive statistics of some carcass and meat quality traits are reported in Table 1. Means of BW16 and BMW in Betong (KU line) chicken were higher than those determined in Betong chicken by Gongruttananun and Chotesangasa (2001) and in black chicken lines by Sungkhapreecha et al. (2015). In the current study, Betong chicken (KU line) could reach a body weight 1.93 kg by age 16 wk as in previous reports by Putsakul et al. (2010) and Wangtaweesukkamol et al. (2013). The averages of pH0 and pH24 were 6.70 and 5.95, respectively. These values were somewhat above the ranges for pH at 0 h and 24 h post-mortem found in crossbred native chicken (Chee; 6.38–6.54 for pH0 and 5.58–5.80 for pH24; Promket et al., 2016). The mean of DL in Betong (KU line) chicken was 2.32%, which agreed with the findings in native chicken by the Chiang Mai Livestock Breeding and Research Center (Leangwunta et al., 2003). Honikel and Hamm (1994) suggested that DL within 24 h should be less than 3%. The current results for pH0, pH24, and DL in Betong chicken (KU line) were within the ranges for normal meat. The meat of Betong chicken (KU line) had a high water-holding capacity and was suitable for chilled meat.

Table 1
Descriptive statistics for carcass and meat quality traits.

Trait[a]	Number	Mean ± SD	Minimum	Maximum
Growth and carcass				
BW16 (g)	526	1931.58 ± 376.28	962.00	2949.00
BMW (g)	252	275.55 ± 42.98	159.00	399.00
Meat quality				
pH0	251	6.70 ± 0.39	5.43	7.68
pH24	252	5.95 ± 0.18	5.33	6.56
DL (%)	249	2.32 ± 0.71	0.77	4.35
SF (N)	252	29.80 ± 12.31	14.98	90.92
L*	251	62.01 ± 2.82	51.57	67.63
a*	251	5.57 ± 0.95	3.30	9.47
b*	251	17.60 ± 2.47	11.18	23.06

[a] SD = standard deviation; BW16 = body weight at age 16 wk; BMW = breast meat weight; pH0 = pH immediately post-mortem; pH24 = pH at 24 h post-mortem; DL = drip loss; SF = shear force; L* = lightness; a* = redness; b* = yellowness.

Meat color is an important factor, which can influence purchasing decisions by customers (Jaturasitha et al., 2008). Breast meat colors, described by L*, a* and b*, were higher than those of several indigenous chicken breeds (Wattanachant et al., 2004; Chabault et al., 2012). Moreover, the SF can refer to meat tenderness. Meat with a higher SF is tougher than meat with a lower SF (Cavitt et al., 2004). The mean of SF in Betong chicken (KU line) was 29.80 N, which was similar to the SF in native chicken at age 12 wk (31.75 N; Jaturasitha et al., 2002). However, the mean of SF in Betong chicken (KU line) was lower than that of indigenous chicken from a local farm in southern Thailand at age 16 wk (40.11 N; Wattanachant et al., 2004) and black-boned chicken and Thai native chicken at age 16 wk (36.10 and 44.30 N, respectively; Jaturasitha et al., 2008). The different values of breast meat color parameters (L*, a*, and b*) and the SF in the chicken meat were probably due to the different strains of indigenous chicken breeds in Thailand.

The levels of significance for hatching batch and sex are summarized in Table 2. Significant ($p < 0.01$) differences between hatching batches were recorded for BW16, BMW, pH0, pH24, and DL. The BW16 and BMW of hatching batch 1 were heavier than those of hatching batch 2. Although hatching batch 1 had the same feeding and management as hatching batch 2, some other environmental effects could have caused the difference in performance. The meat of hatching batch 2 had higher pH0 than hatching batch 1; however, the meat of hatching batch 2 had a slightly lower pH24 than hatching batch 1. The meat of hatching batch 2 had higher DL than hatching batch 1 but the effect of hatching batch was not significantly ($p > 0.05$) different for the SF, L*, a* and b* parameters. The effect of sex was significant ($p < 0.01$) for the BW16, BMW, pH24, DL, SF and b* parameters. Males had heavier BW16 and BMW than females. The meat of females had lower pH24 and higher DL, SF and b* values than the meat of males.

Variance components and heritability estimates

Variance components and heritability estimates for some carcass and meat quality traits from the two models are shown in Table 3. The value of −2logL of the Non-zero Model was significantly lower than that of the Zero Model. It confirmed that the model with non zero covariances among traits was the better fit model. Therefore, heritability estimates of those traits from the Non-zero Model were more suitable than those from the Zero Model. Heritability estimates of those traits from the Non-zero Model were higher than those from the Zero Model, as well as having a smaller SE.

Heritability estimates for BW16 and BMW were high in both models. Based on the Non-zero Model, the heritability estimate for BW16 (0.47) was similar to a previous report regarding Betong chicken (KU line) by Wangtaweesukkamol et al. (2013), but higher than reported in Black Hmong chicken (0.10; Sungkhapreecha et al., 2015). The heritability estimate of BMW in the current study was

Table 2
Least squares mean ± SE and level of significance of fixed effect for carcass and meat quality traits.

Trait[a]	Hatching batch[b]			Sex[b]		
	1	2	*p*-value	Male	Female	*p*-value
BW16 (g)	2033.85 ± 10.28^{a}	1874.64 ± 9.80^{b}	<0.0001	2282.63 ± 10.32^{a}	1625.86 ± 9.76^{b}	<0.0001
BMW (g)	287.65 ± 2.64^{a}	262.31 ± 2.62^{b}	<0.0001	303.24 ± 2.60^{a}	246.72 ± 2.66^{b}	<0.0001
pH0	6.59 ± 0.03^{b}	6.81 ± 0.03^{a}	<0.0001	6.65 ± 0.03	6.74 ± 0.03	0.0573
pH24	6.09 ± 0.01^{a}	5.82 ± 0.01^{b}	<0.0001	5.97 ± 0.01^{a}	5.93 ± 0.01^{b}	0.0067
DL (%)	1.97 ± 0.05^{b}	2.68 ± 0.05^{a}	<0.0001	2.08 ± 0.05^{b}	2.57 ± 0.05^{a}	<0.0001
SF (N)	29.06 ± 1.08	30.65 ± 1.07	0.2943	27.08 ± 1.06^{b}	32.64 ± 1.08^{a}	0.0003
L*	61.92 ± 0.25	62.10 ± 0.25	0.6173	62.15 ± 0.25	61.87 ± 0.26	0.4450
a*	5.59 ± 0.09	5.55 ± 0.08	0.7481	5.65 ± 0.08	5.48 ± 0.09	0.1490
b*	17.67 ± 0.19	17.60 ± 0.19	0.7889	16.33 ± 0.19^{b}	18.93 ± 0.19^{a}	<0.0001

[a] BW16 = body weight at age 16 wk; BMW = breast meat weight; pH0 = pH immediately post-mortem; pH24 = pH at 24 h post-mortem; DL = drip loss; SF = shear force; L* = lightness; a* = redness; b* = yellowness.

[b] Least squares means within a row with different lowercase superscript letters differ at $p < 0.05$.

Table 3
Variance component and heritability estimate (h^2) ± SE from multiple trait analysis for carcass and meat quality traits in the models with zero (Zero Model) and non-zero (Non-zero Model) additive genetic covariance among traits.

Trait[a]	Zero Model[b]				Non-zero Model[b]			
	σ_a^2	σ_e^2	σ_p^2	h^2 ± SE	σ_a^2	σ_e^2	σ_p^2	h^2 ± SE
BW16	12,557.100	15,573.500	28,130.600	0.45 ± 0.12	13,599.400	15,472.700	29,072.100	0.47 ± 0.12
BMW	1000.000	1000.000	2000.000	0.50 ± 0.25	631.081	464.289	1095.370	0.58 ± 0.18
pH0	0.019	0.118	0.137	0.14 ± 0.11	0.025	0.104	0.129	0.19 ± 0.13
pH24	0.001	0.013	0.014	0.10 ± 0.11	0.006	0.019	0.026	0.25 ± 0.21
DL	0.053	0.265	0.318	0.17 ± 0.13	0.072	0.240	0.313	0.23 ± 0.14
SF	18.852	126.492	145.343	0.13 ± 0.12	22.763	124.845	147.608	0.15 ± 0.13
L*	2.067	6.024	8.091	0.26 ± 0.14	2.136	5.926	8.062	0.27 ± 0.14
a*	0.296	0.618	0.914	0.32 ± 0.14	0.301	0.603	0.904	0.33 ± 0.14
b*	0.955	3.526	4.481	0.21 ± 0.12	1.063	3.470	4.533	0.24 ± 0.13
−2LogL			−774.756				−1266.480	

[a] BW16 = body weight at age 16 wk (g); BMW = breast meat weight (g); pH0 = pH immediately post-mortem; pH24 = pH at 24 h post-mortem; DL = drip loss (%); SF = shear force (N); L* = lightness; a* = redness; b* = yellowness.

[b] σ_a^2 = additive genetic variance; σ_e^2 = residual variance; σ_p^2 = phenotypic variance.

close to the value of 0.47 in a previous report on a broiler dam line (Zerehdaran et al., 2004). This indicated that selection based on those traits will result in a high genetic gain for growth performance in the Betong chicken (KU line) population.

The heritability estimates for meat quality traits ranged from low to moderate in both models. Based on the Non-zero Model, the heritability estimates of pH0 and pH24 values in the current study were 0.19 and 0.25, respectively. The heritability estimates of pH0 and pH24 values were lower than those in a slow-growing line chicken (0.34 and 0.48, respectively; Chabault et al., 2012). The heritability estimate of the pH0 value was similar to that described in turkey (0.21; Le Bihan-Duval et al., 2003), whereas the heritability estimate of the pH24 value was lower than that found in sibs from an elite flock of a male line in Brazil (0.31; Gaya et al., 2011). Use of these estimates should be carefully considered in this breeding scheme because the standard errors of these estimates were large.

Heritability estimates of SF in both models were low with large standard errors, which were lower than that of 0.20 in sibs from an elite flock of a male line in Brazil (Gaya et al., 2011) and 0.34 in a male grandparent line of Hubbard chicken (Le Bihan-Duval et al., 2008). The heritability estimate of DL was moderate and was similar to that in a report on a slow-growing line (Chabault et al., 2012). Heritability estimates of colors (L*, a*, and b*) in the current study were moderate. Similar heritability estimates values of colors (L*, a*, and b*) were reported in a male grandparent line of Hubbard chicken (0.35, 0.25 and 0.31, respectively; Le Bihan-Duval et al., 2008). The estimates were slightly lower than those in a slow-growing line (0.44, 0.39 and 0.30, respectively; Chabault et al., 2012). However, the estimate of b* in this population was higher than that of b* (0.12) in sibs from an elite flock of a male line in Brazil (Gaya et al., 2011). As a result of the heritability estimates for meat quality traits, selection based on meat quality traits would be expected to have a lower genetic response than for the growth and carcass traits in the Betong chicken (KU line) population.

Genetic and phenotypic correlations

Genetic and phenotypic correlations were estimated by the Non-zero Model. Genetic and phenotypic correlations are presented in Table 4. The phenotypic correlations between BW16 and BMW for a* and b* were positive (0.68 ± 0.04 and 0.52 ± 0.05, respectively). Phenotypic correlations between BMW and DL, pH0 and a*, pH24 and L*, and L* and a* were negative (−0.22 ± 0.07, −0.24 ± 0.06, −0.28 ± 0.07, and −0.35 ± 0.06, respectively). The phenotypic correlations among other traits were low.

Genetic correlation between BW16 and BMW was positive (0.63 ± 0.15) according to the estimates of phenotypic correlation between BW16 and BMW. This result was in agreement with genetic correlation between body weight and BMW obtained from broiler chicken (Le Bihan-Duval et al., 1999). Genetic correlations between BW16 and meat quality traits, namely pH0, pH24, DL, SF and color (L*, a*, and b*) ranged from low to high. Genetic correlation between BW16 and SF was negative (−0.45 ± 0.38), whereas genetic correlation between BW16 and b* was highly positive (0.51 ± 0.27). Moreover, genetic correlation between a* and b* values was positive (0.61 ± 0.25).

Table 4

Genetic correlations ± SE (above diagonal), and phenotypic correlations ± SE (below diagonal) from multiple traits analysis for carcass and meat quality traits.

Trait[a]	BW16	BMW	pH0	pH24	DL	SF	L*	a*	b*
BW16	–	0.63 ± 0.15	−0.05 ± 0.35	0.09 ± 0.39	0.00 ± 0.33	−0.45 ± 0.38	−0.29 ± 0.29	0.26 ± 0.27	0.51 ± 0.27
BMW	0.68 ± 0.04	–	0.22 ± 0.38	0.11 ± 0.43	−0.47 ± 0.30	−0.27 ± 0.41	−0.42 ± 0.32	0.17 ± 0.30	0.21 ± 0.33
pH0	0.06 ± 0.07	0.05 ± 0.07	–	−0.14 ± 0.54	−0.08 ± 0.46	0.55 ± 0.48	0.02 ± 0.43	−0.40 ± 0.36	0.12 ± 0.44
pH24	−0.04 ± 0.08	−0.01 ± 0.09	−0.11 ± 0.08	–	0.02 ± 0.53	−0.29 ± 0.57	−0.48 ± 0.44	0.19 ± 0.44	−0.01 ± 0.48
DL	−0.15 ± 0.07	−0.22 ± 0.07	−0.16 ± 0.06	−0.11 ± 0.08	–	0.04 ± 0.52	−0.14 ± 0.42	0.31 ± 0.41	0.11 ± 0.43
SF	−0.08 ± 0.07	−0.06 ± 0.07	0.17 ± 0.06	−0.13 ± 0.08	0.08 ± 0.07	–	−0.08 ± 0.49	0.04 ± 0.46	0.17 ± 0.49
L*	−0.10 ± 0.07	−0.15 ± 0.07	0.16 ± 0.07	−0.28 ± 0.07	0.06 ± 0.07	0.00 ± 0.07	–	−0.42 ± 0.30	0.06 ± 0.40
a*	0.12 ± 0.07	0.11 ± 0.08	−0.24 ± 0.06	0.06 ± 0.08	−0.07 ± 0.07	−0.15 ± 0.06	−0.35 ± 0.06	–	0.61 ± 0.25
b*	0.16 ± 0.07	0.16 ± 0.07	0.15 ± 0.06	−0.17 ± 0.08	−0.03 ± 0.07	0.06 ± 0.07	−0.05 ± 0.07	0.52 ± 0.05	–

[a] BW16 = body weight at age 16 wk; BMW = breast meat weight; pH0 = pH immediately post-mortem; pH24 = pH at 24 h post-mortem; DL = drip loss; SF = shear force; L* = lightness; a* = redness; b* = yellowness.

Genetic correlations of BMW and meat quality traits, namely pH0, pH24, DL, SF and color (L*, a* and b*) ranged from low to high. The estimated genetic correlation between BMW and DL was negative (−0.47 ± 0.30) and similar to that between BMW and L* (−0.42 ± 0.32). Genetic correlations among meat quality traits (pH0, pH24, DL, SF, L*, a* and b*) ranged from low to high. The estimate of genetic correlation between pH0 and pH24 values was low according to the report on the broiler line by Le Bihan-Duval et al. (2001), who indicated that the rate and range of the pH0 and pH24 values may be controlled by different genes. The pH0 value was positively correlated with SF.

The negative genetic correlation was −0.40 ± 0.36 between pH0 and a* in meat, but estimates of the genetic correlation of pH0 with both L* and b* were 0.02 ± 0.43 and 0.12 ± 0.44, respectively. The estimated genetic correlation between pH24 and the L* value of the meat was negative (−0.48 ± 0.44), whereas that of pH24 with both a* and b* was 0.19 ± 0.44 and −0.01 ± 0.48, respectively. Although the standard error of the estimated genetic correlation between pH24 and the L* value in meat was high, the result of this estimate confirmed the highly negative correlation shown in many previous reports, such as that of Le Bihan-Duval et al. (2008) who reported estimates in a male grandparent line of Hubbard chicken (−0.65 ± 0.11), Gaya et al. (2011), who reported on sibs from an elite flock of a male line in Brazil (−0.41 ± 0.10), and Chabault et al. (2012) who reported on a slow-growing line (−0.83 ± 0.07). Therefore, lower pH24 may lead to a higher L* value in meat. Many reports found that L* was correlated with DL, indicating water holding capacity in meat (Chabault et al., 2012; Le Bihan-Duval et al., 2001). However, estimates of the DL and L* values in the current study do not support a claim that they are genetically correlated.

All standard errors of genetic correlations were larger than those of phenotypic correlations (Table 4). However, it could be inferred that the estimated genetic correlations between those traits were significant from the result of the Non-zero Model being better than for the Zero Model. Low-to-medium genetic correlations between BW16 and meat quality traits were found.

In conclusion, genetic variations of some carcass and meat quality traits were found in the Betong chicken (KU line) population. The model with non-zero additive genetic covariances among traits could improve the heritability estimates by adjusting the covariance components among traits. Heritability estimates of BW16 and BMW were found to be high. Body weight at age 16 wk and BMW can be improved by genetic selection. Selection for increasing BW16 could increase BMW in the Betong chicken (KU line) population. However, selection with an emphasis on BW16 and BMW may not have any effect on meat quality traits, namely pH0, pH24, DL and SF. Selection based on increasing weight gain may lead to redder meat and more yellowness in meat. Estimates of genetic correlations between BMW and DL, BMW and L*, pH0 and SF, pH0 and a*, pH24 and L*, and L and a* were high with large standard errors. Thus, BW16 and BMW should be included in the selection criteria in the breeding program of the Betong chicken (KU line) population. Due to the large standard errors of the estimates for meat quality traits, further investigation is necessary by increasing the number of progeny for meat quality traits.

Conflict of interest

The authors certify that there is no conflict of interest with any financial organization regarding the material discussed in the manuscript.

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References

Allen, C.D., Russell, S.M., Fletcher, D.L., 1997. The relationship of broiler breast meat color and pH to shelf-life and odor development. Poultry Sci. 76, 1042–1046.

Cavitt, L.C., Youm, G.W., Meullenet, J.F., Owens, C.M., Xiong, R., 2004. Prediction of poultry meat tenderness using razor blade shear, allo-kramer shear, and sarcomere length. J. Food Sci. 69, SNQ11–SNQ15.

Chabault, M., Baéza, E., Gigaud, V., et al., 2012. Analysis of a slow-growing line reveals wide genetic variability of carcass and meat quality-related traits. BMC Genet. 13, 90.

CIE, 1978. Recommendations on Uniform Colour Spaces, Colour Difference Equations, Psychometric Colour Terms, vol. 15. CIE, Paris, France (E-1.3.1) 1971/(TO-1.3). Suppl. 15.

Dobson, A.J., 1990. An Introduction to Generalized Linear Models. Chapman and Hall, New York, NY, USA.

Falconer, D.S., Mackay, T.F.C., 1996. Introduction to Quantitative Genetic, fourth ed. Longman House, Harlow, England.

Gaya, L.G., Mourão, G.B., Ferraz, J.B.S., et al., 2011. Estimates of heritability and genetic correlations for meat quality traits in broilers. Sci. Agric. 68, 620–625.

Gongruttananun, N., Chotesangasa, R., 2001. Growth and carcass yields at various ages of Betong chickens raised on floor. In: Proceedings of the 39th Kasetsart University Annual Conference: Animals and Veterinary Medicine, 3–7 February 2001. Kasetsart University, Bangkok, Thailand, pp. 59–66 (in Thai).

Honikel, K.O., Hamm, R., 1994. Measurement of water-holding capacity and juiciness. In: Pearson, A.M., Dutson, T.R. (Eds.), Quality Attributes and Their Measurement in Meat, Poultry and Fish Products. Springer US, Boston, MA, USA, pp. 125–161.

Jaturasitha, S., Leangwunta, V., Leotaragul, A., et al., 2002. A comparative study of Thai native chicken and broiler on productive performance, carcass and meat quality. In: Proceedings of Deutscher Tropentag 2002. International Research on Food Security, Natural Resource Management and Rural Development: Challenges to Organic Farming and Sustainable Land Use in the Tropics and Subtropics. Witzenhausen, Germany, p. 146.

Jaturasitha, S., Srikanchai, T., Kreuzer, M., Wicke, M., 2008. Differences in carcass and meat characteristics between chicken indigenous to northern Thailand (black-boned and Thai native) and imported extensive breeds (Bresse and Rhode Island Red). Poultry Sci. 87, 160–169.

Jaturasitha, S., Chaiwang, N., Kreuzer, M., 2016. Thai native chicken meat: an option to meet the demands for specific meat quality by certain groups of customers; a review. Anim. Prod. Sci. 57, 1582–1587.

Johnson, D.L., Thompson, R., 1995. Restricted maximum likelihood estimation of variance components for univariate animal models using sparse matrix techniques and average information. J. Dairy Sci. 78, 449–456.

Leangwunta, V., Jaturasitha, S., Leotaragul, A., Phongphaew, A., Kantapanit, C., 2003. The meat and fat quality of native chickens and their crosses. In: Proceedings of 41st Kasetsart University Annual Conference: Animals and Veterinary Medicine, 3–7 February 2003. Kasetsart University, Bangkok, Thailand, pp. 52–63 (in Thai).

Le Bihan-Duval, E., Millet, N., Remignon, H., 1999. Broiler meat quality: effect of selection for increased carcass quality and estimates of genetic parameters. Poultry Sci. 78, 822–826.

Le Bihan-Duval, E., Berri, C., Baeza, E., Millet, N., Beaumont, C., 2001. Estimation of the genetic parameters of meat characteristics and of their genetic correlations with growth and body composition in an experimental broiler line. Poultry Sci. 80, 839–843.

Le Bihan-Duval, E., Berri, C., Baeza, E., et al., 2003. Genetic parameters of meat technological quality traits in a grand-parental commercial line of Turkey. Genet. Sel. Evol. 35, 623–635.

Le Bihan-Duval, E., Debut, M., Berri, C.M., Sellier, N., Sante-Lhoutellier, V., Jego, Y., Beaumont, C., 2008. Chicken meat quality: genetic variability and relationship with growth and muscle characteristics. BMC Genet. 9, 53.

Meyer, K., 2016. WOMBAT a Program for Mixed Model Analyses by Restricted Maximum Likelihood. Animal Genetics and Breeding Unit. University of New England, Armidale, NSW, Australia.

Northcutt, J.K., Foegeding, E.A., Edens, F.W., 1994. Water-holding properties of thermally preconditioned chicken breast and leg meat. Poultry Sci. 73, 308–316.

Promket, D., Ruangwittayanusorn, K., Somchan, T., 2016. The study of carcass yields and meat quality in crossbred native chicken (Chee). Agric. Agric. Sci. Procedia. 11, 84–89.

Putsakul, A., Bunchasak, C., Chomtee, B., Kao-ian, S., Sopannarath, P., 2010. Effect of dietary protein and metabolizable energy levels on growth and carcass yields in Betong chicken (KU line). In: Proceedings of 48th Kasetsart University Annual Conference: Animals, 3–5 February 2010. Bangkok, Thailand, pp. 158–166.

Saláková, A., Straková, E., Válková, V., Buchtová, H., Steinhauserová, I., 2009. Quality indicators of chicken broiler raw and cooked meat depending on their sex. Acta Vet. 78, 497–504.

SAS Institute Inc, 2016. SAS/STAT®14.2 User's Guide. Cary, NC, USA.

SAS Institute Inc, 2017. Base SAS® 9.4 Procedures Guide. 7th Ed. Cary, NC, USA.

Sopannarath, P., Bunchasak, C., 2015. Betong chicken (KU line) or KU Betong chicken. Kasetsart Ext. J. 61, 13–21 (in Thai).

Sungkhapreecha, P., Duangjinda, M., Laopaiboon, B., Boonkum, W., 2015. Estimation of genetic parameters for growth performances in various black chicken lines and crossbred black chicken. Khon Kaen Agr. J. 43, 309–318 (in Thai).

Thai Agricultural Standard, 2005. Chicken Meat (TAS 6700-2005). National Bureau of Agricultural Commodity and Food Standards. Ministry of Agriculture and Cooperatives, Bangkok, Thailand.

Thai Agricultural Standard, 2006. Good Manufacturing Practices for Poultry Abattoir (TAS 9008–2006). National Bureau of Agricultural Commodity and Food Standards. Ministry of Agriculture and Cooperatives, Bangkok, Thailand.

Wangtaweesukkamol, N., Loongyai, W., Chomtee, B., Sopannarath, P., 2013. Genetic parameters for body weights in Betong chicken (KU Line). Agric. Sci. J. 44 (Suppl. 1), 167–170 (in Thai).

Wattanachant, S., Benjakul, S., Ledward, D.A., 2004. Composition, color, and texture of Thai indigenous and broiler chicken muscles. Poultry Sci. 83, 123–128.

Zerehdaran, S., Vereijken, A.L.J., Van Arendonk, J.A.M., Van Der Waaij, E.H., 2004. Estimation of genetic parameters for fat deposition and carcass traits in broilers. Poultry Sci. 83, 521–525.