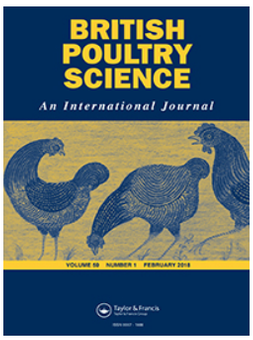

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Genetic parameters for the prediction of abdominal fat traits using blood biochemical indicators in broilers

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ABSTRACT

1. Excessive deposition of body fat, especially abdominal fat, is detrimental in chickens and the prevention of excessive fat accumulation is an important problem. The aim of this study was to identify blood biochemical indicators that could be used as criteria to select lean Yellow-feathered chicken lines.
2. Levels of blood biochemical indicators in the fed and fasted states and the abdominal fat traits were measured in 332 Guangxi Yellow chickens. In the fed state, the genetic correlations (r_g) of triglycerides and very low density lipoprotein levels were positive for the abdominal fat traits ($0.47 \le r_g \le 0.67$), whereas total cholesterol, high-density lipoprotein cholesterol (HDL-C) and low-density lipoprotein cholesterol (LDL-C) showed higher negative correlations with abdominal fat traits ($-0.59 \le r_g \le -0.33$). Heritabilities of these blood biochemical parameters were high, varying from 0.26 to 0.60.
3. In the fasted state, HDL-C:LDL-C level was positively correlated with abdominal fat traits ($0.35 \le r_g \le 0.38$), but triglycerides, total cholesterol, HDL-C, LDL-C, total protein, albumin, aspartate transaminase, uric acid and creatinine levels were negatively correlated with abdominal fat traits ($-0.79 \le r_g \le -0.35$). The heritabilities of these 10 blood biochemical parameters were high ($0.22 \le h^2 \le 0.59$).
4. In the fed state, optimal multiple regression models were constructed to predict abdominal fat traits by using triglycerides and LDL-C. In the fasted state, triglycerides, total cholesterol, HDL-C, LDL-C, total protein, albumin and uric acid could be used to predict abdominal fat content.
5. It was concluded that these models in both nutritional states could be used to predict abdominal fat content in Guangxi Yellow broiler chickens.

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Abdominal fat; blood biochemical traits; genetic correlation; genetic parameter estimation; Guangxi Yellow chicken; heritability; regression

Introduction

Decades of intensive genetic selection have resulted in increased growth rate and chicken production. Unintended effects include excessive fat deposition, especially of abdominal fat, which is harmful (Wang et al. 2012; Huang et al. 2015a; Han et al. 2016). As an important commercial chicken species in China, the production of Yellow-feathered broilers has reached 3 billion annually (Wang et al. 2009; Tang et al. 2012). Yellow-feathered broilers also face the same problem of excessive abdominal fat deposition that fat generally affects feed efficiency and increases the burden of processors and consumers (Mallard and Douaire 1988; Huang et al. 2015b). Therefore, the selection of lean chicken lines has become a prime objective for producers of broiler breeders.

Previous studies have indicated that abdominal fat weight (AFW) and thickness could be used to predictively reduce abdominal fat deposition in chicken lines (Pym and Thompson 1980). However, a contrary report showed that abdominal fat thickness was not an accurate predictor of body fat (Sonaiya 1985). So, in order to reduce abdominal fat deposition in broilers, research has focused on the relationship between blood biochemical parameters and abdominal fat traits. In chickens, the plasma level of very low density lipoprotein (VLDL) has been successfully used to select for a decrease in abdominal fat deposition (Griffin et al. 1982; Whitehead and Griffin 1984; Pym 1987). Lean and fat broiler lines were also developed by using plasma VLDL concentration and abdominal fat percentage (AFP) as selection criteria (Guo et al. 2011). However, no studies have established whether other blood biochemical parameters could be used to predictively reduce excessive abdominal fat deposition in Yellow-feathered broilers.

The Guangxi Yellow chicken is an important commercial native breed with high nutritional value and reasonable prices in China. In the current study, in order to better study the relationship between blood biochemical parameters and abdominal fat traits, the levels of blood biochemical parameters in the fed and fasted states were measured in Guangxi Yellow chickens and the genetic parameters of these blood biochemical indicators were estimated in both states. The objective was to construct optimal linear regression models in the two nutritional states to predict more accurately abdominal fat traits in order to select lean chicken lines.

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Materials and methods

Ethics statement

All experiments were performed in accordance with 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).

Experimental populations, nutrition constituents, measurement of abdominal fat traits and blood collection

A total of 332 male birds from line N414 of Guangxi Yellow chicken were used that were obtained from Guangdong Wens Nanfang Poultry Breeding Co., Ltd. The nutritional constituents of the experimental diet are described in Table 1. At age 122 and 124 d, about 1.2 ml blood samples for each bird were collected from the wing vein of 332 fed birds into tubes containing EDTA. Then at age 125 d, the same 332 birds were deprived of feed for 12 h before being killed by decapitation and about 4 ml blood samples for each bird collected without anticoagulant. Body weight (BW) before slaughter and AFW after slaughter were measured. AFP was calculated as the ratio of AFW to BW (AFP = AFW/BW). Plasma in the fed state and serum in the fasted state were separated from whole blood by centrifugation at 3000 *g* for 10 min at room temperature and stored in 1.5-ml centrifuge tubes at −20°C for later biochemical analyses.

Measurement of blood biochemical metabolites

Thirteen blood biochemical parameters, namely triglycerides (mmol/l), total cholesterol (mmol/l), high-density lipoprotein cholesterol (HDL-C, mmol/l), low-density lipoprotein cholesterol (LDL-C, mmol/l), total bile acid (μmol/l), total protein (g/l), albumin (g/l), glucose (mmol/l), aspartate transaminase (AST, U/l), alanine transaminase (ALT, U/l), γ-glutamyl transpeptidase (GGT, U/l), uric acid (μmol/l) and creatinine (μmol/l) in fed and fasted states were measured using standard commercial kits (Roche Diagnostics GmbH, Sandhofer Strasse, Germany), using an Architect C8000 Automatic Biochemical Analyzer (Abbott, Inc., Chicago, IL). Globulin (g/l) concentration in the blood was calculated as the difference between total protein and albumin. The ratios of HDLC:LDLC (%), albumin:globulin (%) and AST:ALT (%) were calculated. Concentrations of plasma VLDL (Abs) in the fed state were measured using the turbidimetric method (Griffin et al. 1982).

Statistical analysis

The phenotypic data and the levels of blood biochemical indicators of Guangxi Yellow chicken were calculated using Microsoft Excel.

The genetic parameters of blood biochemical indicators in the fed and fasted states, including the heritabilities (h^2) of blood biochemical indicators, and the genetic (r_g) and phenotypic (r_p) correlations between these blood biochemical indicators and abdominal fat traits (AFW and AFP) were both estimated using ASReml 3.0 software (Gilmour et al. 2009). A bivariate animal model was used to estimate the heritabilities and the genetic and phenotypic correlations between blood biochemical indicators and abdominal fat traits. The following model was used to analyse the data:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$$

where $\mathbf{y}$ is an n-dimensional vector of observed values for the traits, $\mathbf{X}$ is an $n \times p$ matrix of the fixed effects, $\mathbf{b}$ is a p-dimensional vector of the fixed effects, $\mathbf{Z}$ is an $n \times q$ matrix of the random effects, $\mathbf{u}$ is a q-dimensional vector of the random effects and $\mathbf{e}$ is recognised as an n-dimensional vector of the random residual effects.

JMP version 7.0 was used to construct the best linear regression models by mixed stepwise regression.

Results

Genetic parameter estimations of blood biochemical indicators in the fed state

The phenotypic data of BW, AFW and AFP are expressed as mean value ± SE (Table 2). In the fed state, the h^2 of the 18 blood biochemical parameters and the genetic and phenotypic correlation between each of the blood biochemical values and abdominal fat traits (AFW and AFP) were estimated. Eight blood biochemical indicators (HDL-C, GGT, total cholesterol, total protein, globulin, LDL-C, HDL-C: LDL-C and uric acid) had high heritabilities ($0.46 \le h^2 \le 0.65$). The heritabilities of creatinine, VLDL, albumin, AST, triglycerides and albumin:globulin ranged from 0.23 to 0.39, which were moderate. The heritabilities of the remaining traits including total bile acid, AST:ALT, ALT and glucose, were low ($0 \le h^2 \le 0.13$; Table 3).

Correlation analysis showed that triglycerides, total bile acid and VLDL had high and positive genetic correlations with abdominal fat traits (AFW and AFP) ($0.47 \le r_g \le 0.67$). High and negative genetic correlations ($-0.59 \le r_g \le -0.33$) were observed between HDL-C, total cholesterol and LDL-C levels and abdominal fat traits. The phenotypic correlations between triglycerides, LDL-C, HDL-C:LDL-C, total bile acid, albumin, globulin, albumin: globulin, creatinine and VLDL levels and abdominal fat traits reached significance level ($P < 0.05$).

Genetic parameter estimation of blood biochemical indicators in the fasted state

Estimations of genetic parameters for blood biochemical indicators in the fasted state are shown in Table 4. GGT, total

Table 1. Nutrition constituents of the experimental ration.

Ingredient	Content
ME (MJ/kg)	11.9
CP (g/kg)	204
Calcium (g/kg)	8.5
Phosphorus (g/kg)	6.3
Methionine (g/kg)	3.9
Lysine (g/kg)	8.6

Table 2. Phenotypic data of Guangxi Yellow chicken (n = 332).

Trait	Mean ± SE
BW (g)	1853.8 ± 10.93
AFW (g)	35.22 ± 1.498
AFP (%)	1.83 ± 0.072

BW: body weight; AFW: abdominal fat weight; AFP: abdominal fat percentage.

Table 3. Genetic parameter estimates of blood biochemical indicators in the fed state[a].

Parameter	Mean ± SE	Heritability	Genetic correlation		Phenotypic correlation	
			AFW	AFP	AFW	AFP
Triglycerides (mmol/l)	1.07 ± 0.020	0.39 ± 0.16	0.48 ± 0.22*	0.47 ± 0.21*	0.31 ± 0.05**	0.31 ± 0.05**
Total cholesterol (mmol/l)	2.46 ± 0.024	0.57 ± 0.17	−0.43 ± 0.23*	−0.46 ± 0.23*	−0.07 ± 0.06	−0.05 ± 0.06
HDL-C (mmol/l)	1.38 ± 0.015	0.46 ± 0.17	−0.55 ± 0.25*	−0.59 ± 0.25**	−0.04 ± 0.06	−0.03 ± 0.06
LDL-C (mmol/l)	0.71 ± 0.010	0.60 ± 0.15	−0.33 ± 0.20*	−0.33 ± 0.20*	−0.16 ± 0.06**	−0.15 ± 0.06**
HDL-C:LDL-C (%)	2.04 ± 0.030	0.62 ± 0.17	0.22 ± 0.22	0.21 ± 0.21	0.13 ± 0.06*	0.13 ± 0.06*
Total bile acid (μmol/l)	8.54 ± 0.182	0	0.55 ± 16.61	0.55 ± 18.89	0.12 ± 0.06*	0.11 ± 0.06*
Total protein (g/l)	45.98 ± 0.263	0.57 ± 0.16	−0.07 ± 0.23	−0.06 ± 0.22	−0.06 ± 0.06	−0.04 ± 0.06
Albumin (g/l)	14.96 ± 0.082	0.34 ± 0.14	0.10 ± 0.27	0.06 ± 0.26	0.15 ± 0.06**	0.16 ± 0.06**
Globulin (g/l)	31.02 ± 0.234	0.58 ± 0.17	−0.10 ± 0.23	−0.08 ± 0.22	−0.11 ± 0.06*	−0.10 ± 0.06*
Albumin:globulin (%)	0.49 ± 0.004	0.39 ± 0.16	0.15 ± 0.26	0.09 ± 0.26	0.19 ± 0.06**	0.18 ± 0.06**
Glucose (mmol/l)	12.24 ± 0.042	0.13 ± 0.12	−0.01 ± 0.40	−0.01 ± 0.39	0.05 ± 0.06	0.04 ± 0.06
AST (U/l)	175.36 ± 1.442	0.38 ± 0.15	−0.02 ± 0.26	−0.04 ± 0.25	0.04 ± 0.06	0.04 ± 0.06
ALT (U/l)	4.31 ± 0.045	0.04 ± 0.13	0.31 ± 0.92	0.28 ± 0.63	0.02 ± 0.06	0.01 ± 0.06
AST:ALT (%)	44.44 ± 0.719	0.01 ± 0.10	−0.32 ± 1.72	−0.07 ± 1.09	−0.03 ± 0.06	−0.04 ± 0.06
GGT (U/l)	26.11 ± 0.304	0.49 ± 0.16	0.01 ± 0.24	0.02 ± 0.24	0.06 ± 0.06	0.06 ± 0.06
Uric acid (μmol/l)	274.81 ± 4.197	0.65 ± 0.20	0.07 ± 0.24	0.11 ± 0.23	0.10 ± 0.06	0.09 ± 0.06
Creatinine (μmol/l)	4.40 ± 0.037	0.23 ± 0.15	0.22 ± 0.32	0.26 ± 0.31	0.11 ± 0.06*	0.11 ± 0.06*
VLDL (Abs)	0.13 ± 0.003	0.26 ± 0.14	0.67 ± 0.24**	0.65 ± 0.24**	0.30 ± 0.05**	0.30 ± 0.05**

*Means significantly different between genetic and phenotypic correlation and abdominal fat traits (AFW and AFP) ($P < 0.05$).
**Means very significantly different between genetic and phenotypic correlation and abdominal fat traits (AFW and AFP) ($P < 0.01$).
[a]Values are expressed as estimates ± SE, $n = 332$.
AFW: abdominal fat weight; AFP: abdominal fat percentage; HDL-C: high-density lipoprotein cholesterol; LDL-C: low-density lipoprotein cholesterol; VLDL: very low density lipoprotein; AST: aspartate transaminase; ALT: alanine transaminase; GGT: gamma-glutamyl transpeptidase.

Table 4. Genetic parameter estimates of blood biochemical indicators in the fasted state[a].

Parameter	Mean ± SE	Heritability	Genetic correlation		Phenotypic correlation	
			AFW	AFP	AFW	AFP
Triglycerides (mmol/l)	0.33 ± 0.004	0.22 ± 0.13	−0.53 ± 0.33*	−0.52 ± 0.32*	0.10 ± 0.06*	0.10 ± 0.06*
Total cholesterol (mmol/l)	2.88 ± 0.030	0.35 ± 0.14	−0.76 ± 0.23**	−0.79 ± 0.23**	−0.20 ± 0.06**	−0.18 ± 0.06**
HDL-C (mmol/l)	1.68 ± 0.018	0.38 ± 0.15	−0.62 ± 0.26**	−0.68 ± 0.25**	−0.08 ± 0.06	−0.07 ± 0.06
LDL-C (mmol/l)	0.89 ± 0.017	0.59 ± 0.15	−0.46 ± 0.19**	−0.44 ± 0.19*	−0.25 ± 0.06**	−0.24 ± 0.06**
HDL-C:LDL-C (%)	2.11 ± 0.050	0.28 ± 0.13	0.38 ± 0.26*	0.35 ± 0.26	0.16 ± 0.06**	0.16 ± 0.06**
Total bile acid (μmol/l)	5.50 ± 0.206	0.10 ± 0.12	−0.38 ± 0.44	−0.31 ± 0.43	−0.13 ± 0.06*	−0.13 ± 0.06*
Total protein (g/l)	43.03 ± 0.305	0.46 ± 0.15	−0.36 ± 0.22*	−0.35 ± 0.22*	−0.15 ± 0.06**	−0.14 ± 0.06**
Albumin (g/l)	15.28 ± 0.098	0.30 ± 0.14	−0.36 ± 0.28*	−0.38 ± 0.28*	0.03 ± 0.06	0.03 ± 0.06
Globulin (g/l)	27.75 ± 0.259	0.51 ± 0.16	−0.31 ± 0.22	−0.29 ± 0.22	−0.19 ± 0.06**	−0.18 ± 0.06**
Albumin:globulin (%)	0.56 ± 0.005	0.54 ± 0.17	0.04 ± 0.24	0.01 ± 0.24	0.19 ± 0.06**	0.19 ± 0.06**
Glucose (mmol/l)	13.91 ± 0.057	0.27 ± 0.14	−0.17 ± 0.30	−0.23 ± 0.29	−0.01 ± 0.06	0.004 ± 0.06
AST (U/l)	252.71 ± 2.372	0.30 ± 0.13	−0.41 ± 0.25*	−0.44 ± 0.24*	−0.03 ± 0.06	−0.04 ± 0.06
ALT (U/l)	2.45 ± 0.043	0.15 ± 0.12	−0.40 ± 0.35	−0.38 ± 0.35	−0.06 ± 0.06	−0.06 ± 0.06
AST:ALT (%)	116.94 ± 3.356	0.18 ± 0.12	0.15 ± 0.33	0.10 ± 0.32	0.06 ± 0.06	0.06 ± 0.06
GGT (U/l)	28.71 ± 0.354	0.40 ± 0.16	−0.11 ± 0.26	−0.13 ± 0.26	−0.001 ± 0.06	−0.01 ± 0.06
Uric acid (μmol/l)	193.83 ± 3.473	0.47 ± 0.16	−0.60 ± 0.20**	−0.57 ± 0.20**	−0.19 ± 0.06**	−0.19 ± 0.06**
Creatinine (μmol/l)	6.57 ± 0.053	0.29 ± 0.14	−0.44 ± 0.27*	−0.42 ± 0.27*	−0.10 ± 0.06*	−0.10 ± 0.06*

*Means significantly different between genetic and phenotypic correlation and abdominal fat traits (AFW and AFP) ($P < 0.05$).
**Means very significantly different between genetic and phenotypic correlation and abdominal fat traits (AFW and AFP) ($P < 0.01$).
[a]Values are expressed as estimates ± SE, $n = 332$.
AFW: abdominal fat weight; AFP: abdominal fat percentage; HDL-C: high-density lipoprotein cholesterol; LDL-C: low-density lipoprotein cholesterol; AST: aspartate transaminase; ALT: alanine transaminase; GGT: gamma-glutamyl transpeptidase.

protein, uric acid, globulin, albumin:globulin and LDL-C had high heritabilities ($0.40 \leq h^2 \leq 0.59$). The heritabilities of triglycerides, glucose, HDL-C:LDL-C, creatinine, AST, albumin, total cholesterol and HDL-C varied from 0.22 to 0.38, which showed a moderate level. The heritabilities of the remaining three measured blood biochemical indicators (total bile acid, ALT and AST:ALT) were low ($0.10 \leq h^2 \leq 0.18$).

Higher positive genetic correlation coefficients were found between HDL-C:LDL-C level and abdominal fat traits (AFW and AFP) ($0.35 \leq r_g \leq 0.38$), whereas total cholesterol, HDL-C, uric acid, triglycerides, LDL-C, creatinine, AST, ALT, albumin, total protein and total bile acid levels showed high and negative genetic correlations with abdominal fat traits ($-0.79 \leq r_g \leq -0.31$). The phenotypic correlations between triglycerides, total cholesterol, LDL-C, HDL-C:LDL-C, total bile acid, total protein, globulin, albumin:globulin, uric acid and creatinine levels and abdominal fat traits reached significance level ($P < 0.05$).

Best linear models to predict abdominal fat traits using blood biochemical parameters

For multiple regression analysis, 5 variables were selected (triglycerides, total cholesterol, HDL-C, LDL-C and VLDL) in the fed state whose genetic correlations with abdominal fat traits (AFW and AFP) and heritabilities were high according to the genetic parameter estimations of blood biochemical indicators. The partial regression coefficients of triglycerides and LDL-C were significant. The best models using these two parameters are shown in Table 5.

Similarly, for the multiple regression analysis in the fasted state, 10 variables (triglycerides, total cholesterol, HDL-C, LDL-C, HDL-C:LDL-C, total protein, albumin, AST, uric acid and creatinine) were selected whose genetic correlations with abdominal fat traits (AFW and AFP) and heritabilities were high according to the genetic parameter estimations of blood biochemical indicators. The partial

Table 5. Multiple regression models to predict AFW and AFP using the levels of blood biochemical parameters in the fed state.

	AFW			AFP		
Parameter	Estimate	*P* value	R^2	Estimate	*P* value	R^2
Intercept	30.23	<0.0001	0.13	1.561	<0.0001	0.12
Triglycerides (mmol/l)	23.96	<0.0001		1.133	<0.0001	
LDL-C (mmol/l)	−28.98	<0.001		−1.314	<0.001	

AFW: abdominal fat weight; AFP: abdominal fat percentage; LDL-C: low-density lipoprotein cholesterol.

regression coefficients of triglycerides, total cholesterol, HDL-C, LDL-C, total protein, albumin and uric acid were significant. The best models using these 7 parameters are shown in Table 6.

Discussion

In this study, blood biochemical parameters of birds were measured in both fed and fasted states whereas in rats, pigs, humans and other species, the determination of blood biochemical parameters has been carried out in the fasting state (Novelli et al. 2007; Pietiläinen et al. 2009; Muñoz et al. 2012; Lin et al. 2014; Arpegård et al. 2015). However, previous studies indicated that plasma VLDL concentration should be measured in the fed state (Li et al. 1999). This is because there was a significant positive phenotypic correlation between abdominal fat traits and plasma VLDL concentration for birds in the fully fed state, yet the correlation decreased or no longer existed for the birds in the fasting state (Li et al. 1999). Therefore, measurement of blood biochemical parameters in both fed and fasted states is essential for exploring the relationship between them and abdominal fat traits in chickens.

In the fed state, the levels of triglycerides, total cholesterol, LDL-C, total protein, albumin, globulin, glucose, AST, ALT and uric acid were all in agreement with the ranges reported in chickens (Yeung et al. 2009; Samanta et al. 2011; Cinar et al. 2014; Ma et al. 2014; Al-Zghoul et al. 2015; Gholami-Ahangaran et al. 2016; Mishra et al. 2016; Griggs et al. 2017). In the present study, HDL-C was higher than reported by Samanta et al. (2011) and Ma et al. (2014) (0.50–1.10 mmol/l), GGT concentration was higher than found by Cinar et al. (2014) (18.37–23.68 U/l) and Al-Zghoul et al. (2015) (9.5–12.5 U/l), whereas creatinine level was lower than in the studies of Mishra et al. (2016) (5.47–5.81 μmol/l) and Wang et al. (2015) (40.7–52.1 μmol/l). In the fasted state, total cholesterol, HDL-C, LDL-C, total protein, albumin, globulin, albumin:globulin, glucose, AST, ALT, GGT, uric acid and creatinine were similar to those reported for chickens (Hosseinzadeh et al. 2014; Jing et al. 2014; Abbasi et al. 2015; Bubel et al. 2015; Dong et al. 2015; Soria et al. 2015; Ghareeb et al. 2016). Conversely, the level of triglycerides was lower than in previous studies in chickens (0.45–1.60 mmol/l; Hosseinzadeh et al. 2014; Akbari and Torki, 2014; Abbasi et al. 2015; Ghareeb et al.2016). Compared with the values reported by Dong et al. (2015), the HDL-C:LDL-C ratio was lower (2.64 and 3.66), and the total bile acid level was higher (1.96 and 4.18 μmol/l), as was the AST:ALT ratio (52.51 and 57.90). The differences between these studies may be associated with differences in chicken breeds and age of chickens (Yeung et al. 2009).

In the fed state, there were high genetic correlations for blood biochemical parameters (triglycerides, total cholesterol, HDL-C, LDL-C and VLDL) and abdominal fat traits (AFW and AFP) as well as high heritabilities. The heritability estimate of triglycerides in this study (h^2 = 0.39) was higher than that reported for chickens by Loyau et al. (2013) (h^2 = 0.02). The heritability of cholesterol of 0.57 here agreed with that reported for chickens by Abdel Latif (2001) (h^2 = 0.43–0.61). Heritabilities of HDL-C and LDL-C have not been reported in chickens. Whilst the heritability estimate of VLDL here (0.26) was close to that reported by Grunder and Chambers (1988), the genetic correlations between VLDL and abdominal fat traits (AFW and AFP) were lower than those found before in chickens (Grunder and Chambers 1988).

The genetic correlations between triglycerides, total cholesterol, HDL-C, LDL-C, HDL-C:LDL-C, total protein, albumin, AST, uric acid, creatinine and abdominal fat traits (AFW and AFP) as well as heritabilities were high in the fasted state. The heritability estimates of triglycerides, total cholesterol, HDL-C, LDL-C and total protein levels were similar to those previously reported in chickens (Hollands et al. 1980; Amira et al. 2009; Dong et al. 2015). However, compared with a previous study in chickens by Dong et al. (2015), the heritability for the HDL-C:LDL-C ratio in the current study was lower, as was the creatinine heritability, whereas heritabilities of AST and uric acid levels were higher. This may be caused by many reasons. The broilers used by Dong et al. (2015) were derived from the Northeast Agricultural University broiler lines divergently selected for abdominal fat content since 1996 compared to the population of Guangxi Yellow chicken in the current study that was a local chicken breed. The population used by Dong et al. (2015) was reared in cages, while Guangxi Yellow chicken was reared on the floor.

The heritability estimate of albumin level was lower than reported by Amira et al. (2009). In the present study, the genetic correlations between triglycerides, HDL-C:LDL-C, total protein, AST, uric acid and abdominal fat traits (AFW

Table 6. Multiple regression models to predict AFW and AFP using the levels of blood biochemical parameters in the fasted state.

	AFW			AFP		
Parameter	Estimate	*P* value	R^2	Estimate	*P* value	R^2
Intercept	40.27	<0.01	0.21	1.946	<0.01	0.21
Triglycerides (mmol/l)	101.67	<0.0001		5.018	<0.0001	
Total cholesterol (mmol/l)	55.94	<0.01		3.141	<0.01	
HDL-C (mmol/l)	−81.49	<0.01		−4.408	<0.001	
LDL-C (mmol/l)	−81.68	<0.001		−4.354	<0.0001	
Total protein (g/l)	−1.33	<0.001		−0.063	<0.001	
Albumin (g/l)	5.65	<0.0001		0.270	<0.0001	
Uric acid (μmol/l)	−0.10	<0.0001		−0.005	<0.0001	

AFW: abdominal fat weight; AFP: abdominal fat percentage; HDL-C: high-density lipoprotein cholesterol; LDL-C: low-density lipoprotein cholesterol.

and AFP) were consistent with the results of Dong et al. (2015). The current study also found that total cholesterol, HDL-C, albumin and creatinine were negatively correlated with abdominal fat traits, whereas Dong et al. (2015) reported that these biochemical parameters were positively correlated with abdominal fat traits. The differences may be attributed to differences in breeds, genetic backgrounds and environments (Dong et al. 2015).

The aim of this study was to identify blood biochemical indicators that could be used to select lean Yellow-feathered chicken lines. For the fed state, two blood biochemical parameters (triglycerides and LDL-C) were selected that could be used to predict abdominal fat traits (AFW and AFP) in chickens. The present findings are similar to a previous study suggesting that the levels of triglycerides reflect the severity of abdominal obesity in humans (Medvedeva et al. 2003). Although lower glucose levels are good indicators of the ability to synthesise and store lipids in chickens (Baéza et al. 2015), the heritability and genetic correlations between glucose and abdominal fat traits were low; so, glucose was not selected for the model. Similarly, in the fasted state, the results implied that an optimal model could be constructed using 7 parameters (triglycerides, total cholesterol, HDL-C, LDL-C, total protein, albumin and uric acid) to predict abdominal fat traits. Some of the blood biochemical parameters detected in the current study were also identified by some other studies to be associated with fatness. Dong et al. (2015) reported that HDL-C and HDL-C:LDL-C levels have the potential to be used as biomarkers for selecting lean broilers. In humans, a previous study documented that uric acid could be used as a risk factor in predicting obesity (Masuo et al. 2003; Kong et al. 2013). In swine, Muñoz et al. (2012) stated that circulating total protein is the best biomarker for early estimation of obesity. To the best of our knowledge, there are no reports regarding the relationship between other blood biochemical parameters and abdominal fat traits.

In conclusion, by estimating genetic parameters for the selection of blood biochemical parameters in fed and fasted states, optimal models were constructed to predict abdominal fat traits (AFW and AFP). In the fed state, triglycerides and LDL-C could be used to predict abdominal fat traits (AFW and AFP). In the fasted state, the results showed that optimal models could be constructed with triglycerides, total cholesterol, HDL-C, LDL-C, total protein, albumin and uric acid to predict abdominal fat traits. The results of the current study may benefit the breeding of lean Guangxi Yellow chicken lines.

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Disclosure statement

No potential conflict of interest was reported by the authors.

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