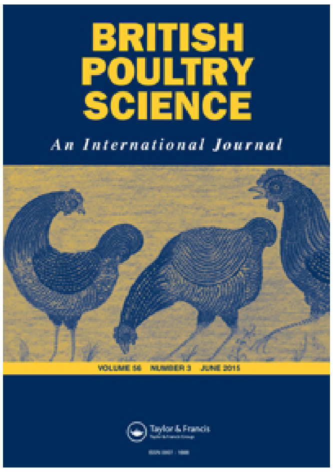

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Genetic evaluation of carcass traits in Japanese quail using ultrasonic and morphological measurements

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Abstract 1. A study was conducted to evaluate the carcass composition of 1083 live birds using ultrasonic and morphological measurements and to estimate the genetic relationship between predicted and dissected carcass composition in Japanese quail.

2. Birds were reared for 35 d, and morphological measurements consisting of the length and width of breast muscle were recorded for all birds using a digital caliper. After slaughtering, the weight and percentage of carcass traits were measured on chilled carcasses. The dimensions of breast muscle were measured in 638 birds with an ultrasound scanner before slaughter at 35 d of age.

3. Genetic parameters from univariate and bivariate analyses were obtained by restricted maximum likelihood using ASREML software.

4. Genetic correlations between body weight at 35 d (BW35) and the percentage of carcass traits were low. Therefore, selection for BW35 may not effectively improve the yield of carcass components in Japanese quail.

5. High genetic correlations between carcass traits and ultrasonic measurements compared to morphological measurements suggest that the ultrasonic technique is a better method to improve breast weight and yield in Japanese quail.

INTRODUCTION

The profitability of poultry meat production is determined by considering the possibilities of the increase in the prime parts, especially breast muscle, and decrease in abdominal fat (Griffin, 1996). In birds, carcass meatiness is greatly dependent on breast muscle percentage. Breast is the most valuable cut in the carcass of poultry and yield of breast has become critical to processors (Young *et al.*, 2001). Several studies reported that particular attention should be paid to the measurement of breast muscle in meat type poultry (Michalik *et al.*, 1999; Rymkiewicz and Bochno, 1999; Berri *et al.*, 2005; Duclos *et al.*, 2006; Strakova *et al.*, 2006; Farhat, 2009).

The main problem with traditional carcass evaluation methods is that birds usually have to be slaughtered to measure carcass traits. Consequently, selection of sires and dams for carcass traits is based only on information recorded on relatives and not on their own performance. Selection based on information of relatives would increase the correlation between estimated breeding values of relatives, resulting in a higher rate of inbreeding (Burrows, 1984; Bijma *et al.*, 2001). A range of indirect measurement methods is available: Some of them use simple, inexpensive methods, whereas others require sophisticated, expensive equipment (Latshaw and Bishop, 2001).The use of non-destructive methods devised to estimate breast meat in live birds on the basis of the measurement of morphological traits such as length, width and depth or breast muscle angle gives unsatisfactory results (Grashorn and Komender, 1990). Non-invasive methods such as

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ultrasonography are the most promising methods to investigate the carcass composition of live animals. Ultrasound is a modern tool used for non-destructive carcass evaluation and meat processing. Ultrasonic scanners provide video images, which make sensor positioning easier. This technique has been used with some livestock such as broiler, swine, horse and cattle to evaluate carcass composition and reproductive status (Michalik *et al.*, 1999; Remignon *et al.*, 2000; Wolcott and Allen, 2005). These studies have demonstrated that ultrasonic measurement is a useful tool for changing carcass composition.

There are few studies presenting the relationships of genetic parameters between ultrasonic and dissected carcass measurements. The aim of the present study was to evaluate the carcass composition of live birds using ultrasonic and morphological measurements and to estimate the genetic relationship between predicted and dissected carcass composition in Japanese quail.

MATERIALS AND METHODS

Pre-slaughter measurements

The experiment was conducted on 1083 pedigree birds (574 males and 509 females) which were generated from 60 sires and 60 dams. The care and use of birds were in accordance with laws and regulations of Gorgan University of Agricultural Sciences and Natural Resources (GUASNR) of Iran. The birds originated from a base population of Japanese quail in the Research Center of GUASNR. More details on base population and pedigree structure are available in the study of Lotfi *et al.* (2011). All birds were kept under the same management conditions. According to the National Research Council (NRC, 1994), a diet containing 240 g crude protein/kg and 12.1 MJ of ME/kg is recommended during the growth period. Feed and water were supplied *ad libitum* and lighting was available for 24 h throughout the experiment. Because of technical limitations, only 638 birds (332 males and 306 females) were measured with an ultrasound scanner at 35 d of age. Pre-slaughter ultrasound measurements were obtained on the right side of breast muscle in each bird. A 7.5 MHz linear probe attached to a CTS900 v ultrasound scanner stand-off block was used to scan the right breast muscle interface. For ultrasonic measurement of the external dimension of breast muscle including length (ULBM, mm), area (UABM, mm^2) and depth (UDBM, mm), a multipurpose ultrasound gel was used as a contact agent on the skin of the right breast muscle. During the ultrasonic measurements, the probe was placed perpendicularly to the breast muscle. Once a satisfactory image had been obtained, it was captured on a printer for image analysis. Anatomically, breast depth refers to the distance between the skin that covers the thoracic pectoral muscle (*Musculus pectoralis thoracicus*) and the origins of this muscle, and the supracoracoideus (*M. supracoracoideus*) on the breast bone. Area of the breast refers to the image plane of the muscles that have been used to measure the depth. In order to measure the depth and surface of breast, the probe was aligned with the breastbone crest and 2 cm to one side, contacting cranially with the collarbone (Melo *et al.*, 2003).

Body weight and carcass measurements

All 1083 birds were weighed, and individual morphological measurements for breast muscle consisting of length (LBM, mm) and width (WBS, mm) were recorded on all birds using a digital caliper. Birds were slaughtered after ultrasonic scanning at 35 d of age. After slaughtering and removing feathers, carcass traits including carcass weight and percentage (CW, CARP), breast meat weight and percentage (BMW, BMP) and thigh weight and percentage (TW, TP) were measured in chilled carcasses. The percentages of carcass traits were expressed relative to BW35.

Statistical analysis

Descriptive statistics, including the test for normality and significance of fixed effects, were obtained using the univariate and general linear model (GLM) procedures of SAS software (SAS Institute, 2001). The following model was used:

$$Y_{ijk} = \mu + s_i + h_j + e_{ijk}$$

where Y_{ijk} is the individual observation for the *k*th trait, μ is the value of the mean, s_i is the fixed effect of the *i*th sex ($i = 1$ for female and 2 for male), h_j is the fixed effect of the *j*th hatch ($j = 1, 2\ldots4$) and e_{ijk} is the random residual effect.

Genetic parameters from univariate and bivariate analysis were obtained by restricted maximum likelihood using ASREML software (Gilmour *et al.*, 2000).

$$Y_{ijkl} = \mu + s_i + h_j + a_k + e_{ijkl}$$

where Y_{ijkl} is the performance of the *l*th bird, μ is the value of the mean, s_i is the fixed effect of the *i*th sex ($i = 1$ for female and 2 for male), h_j is the fixed effect of the *j*th hatch ($j = 1, 2\ldots4$), a_k is the random direct genetic effect of the *k*th individual and e_{ijkl} is the random residual effect.

Table 1. *Descriptive statistics of direct carcass traits, ultrasonic and morphological measurements of breast muscle at 35d of age.*

Trait	*N*	Mean	Sex			Hatch				
			Male	Female	SEM	1	2	3	4	SEM
BW_{35} (g)	1083	186.2	183.3^{b}	189.3^{a}	2.81	179.0^{c}	192.5^{a}	184.6^{b}	187.6^{b}	2.14
CW (g)	1083	121.6	119.2^{b}	124.3^{a}	1.84	115.8^{c}	128.4^{a}	118.8^{bc}	123.3^{b}	1.95
CP (%)	1083	65.0	64.7^{b}	65.3^{a}	0.23	64.7	66.7	64.4	65.7	0.27
BMW (g)	1083	46.6	45.5^{b}	47.8^{a}	0.97	42.9^{b}	48.0^{a}	47.0^{a}	48.2^{a}	1.56
BMP (%)	1083	24.7	24.6^{b}	24.9^{a}	0.13	24.0	24.9	25.5	25.7	1.08
TW (g)	1083	28.3	27.9^{b}	28.7^{a}	0.37	26.9^{b}	29.2^{a}	28.5^{a}	27.9^{ab}	0.67
TP (%)	1083	15.1	15.1	15.1	0.28	15.0	15.2	15.5	14.9	0.37
LBM (mm)	1083	58.1	57.6	58.6	0.86	56.6^{b}	60.2^{a}	58.0^{b}	59.6^{a}	0.71
WBM (mm)	1083	29.1	28.8	29.3	1.26	27.7	30.6	29.0	28.9	1.81
ULBM (mm)	638	48.3	47.9	48.0	0.27	46.9	49.1	47.3	48.2	1.55
UABM (mm)	638	63.4	63.0	63.0	0.39	62.0^{b}	65.7^{a}	63.3^{ab}	62.4^{b}	0.93
UDBM (mm)	638	24.1	24.0	24.0	0.21	23.0^{b}	25.1^{a}	24.2^{ab}	23.8^{b}	0.51

BW35 = BW at 35 d of age; CW = carcass weight; CP = carcass percentage; BMW = breast muscle weight; BMP = breast muscle percentage; TW = thigh weight; TP = thigh percentage; LBM = length of breast muscle (measured by caliper); WBM = width of breast muscle (measured by caliper); ULBM = ultrasonic length of breast muscle; UABM = ultrasonic area of breast muscle; UDBM = ultrasonic depth of breast muscle.

Means with different letters in each row shows significant differences ($P < 0.05$).

RESULTS

Description of traits

The overall means and significance of the fixed effects for recorded traits are summarised in Table 1. Average values for BW35, weight and percentage of carcass traits (CW, CP, BMW, BMP and TW) were significantly higher in females compared with males ($P < 0.05$), although TP did not differ between sexes. The effect of sex was not significant for dimensions of breast muscle measured by either ultrasound (ULBM, UABM and UDBM) or caliper (LBM and WBM).

Hatch influenced most of the traits. Birds from the second hatch generally had higher BW and carcass traits compared to the first and the 4th hatch ($P < 0.05$).

Genetic parameters

Genetic parameters of BW35 and direct carcass traits at 35 d of age are presented in Table 2. The heritability estimates for BW35 and weights of carcass traits were higher (from 0.49 for BW35 to 0.61 for BMW) than percentages of carcass traits (from 0.17 for CP to 0.37 for BMP). High genetic correlations were found between BW35 and weight of carcass traits (from 0.89 to 0.95), while genetic correlations of this trait with percentage of carcass traits were moderate to low (from 0.11 to 0.20). Similarly, CW, BMW and TW showed high genetic correlations with each other, while their genetic correlations with CP, BMP and TP were lower. Phenotypic relationships among all traits were similar to genetic correlations and confirm these relationships. Genetic parameters of ultrasonic and morphological measurements of breast muscle at 35 d of age are presented in Table 3. The heritability estimates for these traits were moderate, ranging from 0.18 to 0.34.

There were moderate genetic correlations between ultrasonic and morphological measurements of breast muscle. Genetic correlations of LBM with ULBM, UABM and UDBM were from 0.21 to 0.41. Similarly, positive and moderate genetic correlations were observed between

Table 2. *Estimated heritability (bold, diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations with their standard error for direct carcass traits of Japanese quail at 35 d of age.*

Trait	BW35	CW	CP	BMW	BMP	TW	TP
BW35	**0.49 ± 0.041**	0.95 ± 0.013	0.20 ± 0.091	0.88 ± 0.033	0.14 ± 0.080	0.89 ± 0.024	0.11 ± 0.104
CW	0.89 ± 0.013	**0.50 ± 0.031**	0.44 ± 0.078	0.96 ± 0.014	0.34 ± 0.121	0.95 ± 0.011	0.13 ± 0.081
CP	0.03 ± 0.027	0.38 ± 0.024	**0.17 ± 0.054**	0.58 ± 0.066	0.84 ± 0.063	0.56 ± 0.081	0.76 ± 0.090
BMW	0.82 ± 0.014	0.92 ± 0.010	0.38 ± 0.024	**0.61 ± 0.041**	0.53 ± 0.091	0.84 ± 0.030	0.13 ± 0.011
BMP	0.03 ± 0.033	0.28 ± 0.030	0.75 ± 0.013	0.51 ± 0.024	**0.37 ± 0.051**	0.19 ± 0.133	0.23 ± 0.090
TW	0.84 ± 0.012	0.89 ± 0.014	0.28 ± 0.034	0.82 ± 0.012	0.17 ± 0.033	**0.52 ± 0.020**	0.33 ± 0.122
TP	0.11 ± 0.034	0.15 ± 0.031	0.61 ± 0.010	0.12 ± 0.031	0.43 ± 0.021	0.41 ± 0.032	**0.32 ± 0.042**

BW35 = BW at 35 d of age; CW = carcass weight; CP = carcass percentage; BMW = breast muscle weight; BMP = breast muscle percentage; TW = thigh weight; TP = thigh percentage

Table 3. *Estimated heritability and genetic correlations with their standard error for ultrasonic and morphological measurements of breast muscle at 35 d of age.*

Trait	Heritability	Genetic correlation	
		LBM	WBM
ULBM	0.34 ± 0.052	0.41 ± 0.061	0.35 ± 0.084
UABM	0.27 ± 0.038	0.38 ± 0.034	0.31 ± 0.051
UDBM	0.39 ± 0.054	0.21 ± 0.062	0.24 ± 0.070
LBM	0.22 ± 0.031		
WBM	0.18 ± 0.030		

ULBM = ultrasonic length of breast muscle; UABM = ultrasonic area of breast muscle; UDBM = ultrasonic depth of breast muscle; LBM = length of breast muscle (measured by caliper); WBM = width of breast muscle (measured by caliper).

WBM with ULBM, UABM and UDBM (from 0.24 to 0.35).

Estimated genetic correlations of direct carcass traits with ultrasonic and morphological measurements of breast muscle at 35 d of age are presented in Table 4. The results showed low-to-moderate genetic correlations between CW and CP with ultrasonic (ULBM, UABM and UDBM) and morphological measurements of breast muscle (from 0.14 to 0.39). Genetic correlations between BMW and BMP with ultrasonic (ULBM, UABM and UDBM) and morphological measurements of breast muscle were moderate to high (from 0.32 to 0.71).

DISCUSSION

Sex differences for carcass traits in Japanese quail have been reported previously (Lotfi *et al.*, 2011). However, the present results contrast with the results of other studies that have reported higher carcass percentage in males compared with females in Japanese quail (Minvielle *et al.*, 2000; Vali *et al.*, 2005; Saatci *et al.*, 2006; Shokoohmand *et al.*, 2007; Khaldari *et al.*, 2010; Narinc *et al.*, 2010). The slaughter age could be the reason behind these differences as the birds were slaughtered at 35 d of age before reaching full sexual maturity. In other studies, however, birds were slaughtered after sexual maturity at 42 d of age or older. After sexual maturity, because of the development of reproductive organs, the BW of female birds is higher than that of male birds. Consequently, the average values of carcass traits in males are higher than in females.

Significant hatch effects on carcass traits have been reported by Peebles *et al.* (1999) and Zerehdaran *et al.* (2004) in broilers and Lotfi *et al.* (2011) in Japanese quail. In all of these studies, the mean values of traits in the first hatch were generally lower than later hatches. Hens at first hatch lay smaller eggs that hatch smaller chicks and egg weight and hatching weight are highly correlated to final BW and carcass composition.

Heritability estimates for BW and direct carcass traits at 35 d of age were moderate to high. The estimates of heritability for BW (0.49), CW (0.50), BMW (0.61) and TW (0.52) are close to those reported in previously published studies in Japanese quail (Vali *et al.*, 2005; Lotfi *et al.*, 2011). This means that phenotypes of the traits are generally associated with additive genetic effects (Prado-Gonzalez *et al.*, 2003), and improvement in carcass components is feasible through genetic selection. Heritability estimates for BMP and TP (0.37 and 0.32, respectively) were higher than those reported in the research done by Khaldari *et al.* (2010). High genetic correlations were found between BW35 and the weight of carcass components. Previous reports similarly showed high genetic correlations between BW and the weight of carcass components in Japanese quail (Minvielle *et al.*, 2000; Vali *et al.*, 2005; Shokoohmand *et al.*, 2007; Khaldari *et al.*, 2010). Genetic correlations of BW35 with the percentage of carcass components were low. This finding is in agreement with studies of Le Bihan-Duval *et al.* (1998) and Zerehdaran *et al.* (2004), who reported low genetic correlations between BW and BMP in broilers. Despite the fact that selection for BW35 will increase the weight of carcass components, it will not effectively improve the yield of carcass components, e.g. breast in Japanese quail. Therefore, evaluation of carcass components is essential for improving carcass and breast yield.

The main problem with carcass evaluation is that birds have to be slaughtered to measure

Table 4. *Estimated genetic correlations with their standard error of direct carcass traits with ultrasonic and morphological measurements of breast muscle in Japanese quail at 35 d of age.*

Trait	ULBM	UABM	UDBM	LBM	WBM
CW	0.39 ± 0.120	0.34 ± 0.103	0.26 ± 0.094	0.20 ± 0.094	0.23 ± 0.070
CP	0.27 ± 0.105	0.31 ± 0.117	0.29 ± 0.132	0.25 ± 0.067	0.14 ± 0.082
BMW	0.68 ± 0.101	0.71 ± 0.107	0.57 ± 0.101	0.42 ± 0.062	0.37 ± 0.071
BMP	0.54 ± 0.124	0.46 ± 0.131	0.58 ± 0.120	0.32 ± 0.077	0.38 ± 0.101

CW = carcass weight; CP = carcass percentage; BMW = breast muscle weight; BMP = breast muscle percentage; ULBM = ultrasonic length of breast muscle; UABM = ultrasonic area of breast muscle; UDBM = ultrasonic depth of breast muscle; LBM = length of breast muscle (measured by caliper); WBM = width of breast muscle (measured by caliper).

carcass traits. Indirect carcass measurements provide the opportunity to collect information from live birds, and as a result, individual performance information for carcass traits would be available on all birds. In the present study, ultrasonic and morphological measurements of breast muscle were used as indirect methods to evaluate the weight and yield of carcass and breast in live birds. The heritability estimates of ultrasonic and morphological measurements of breast muscle were moderate, which means that genetic improvement is feasible through selection for these traits. Although no estimates of heritability of ultrasonic carcass traits have been published for Japanese quail, moderate-to-high heritability estimates were reported in broilers (Argentão *et al.*, 2002; Gaya *et al.*, 2006). Genetic correlations between ultrasonic and morphological measurements showed that they are different traits for evaluating carcass components. Higher genetic correlations between carcass traits and ultrasonic breast measurements compared to morphological breast measurements showed that the ultrasonic technique is a more accurate method. Grashorn and Komender (1990) demonstrated that using morphological breast muscle measurements as an indirect method to evaluate carcass composition in broilers is not satisfactory. Silva *et al.* (2006) obtained a correlation coefficient of 0.87 between breast weight and its volume measured by an ultrasonic method. High genetic correlations between breast weight and ultrasonic measurements were also found in broilers by Argentão *et al.* (2002) and Gaya *et al.* (2006). The present study demonstrated that ultrasonic measurements of breast muscle may be effectively used to improve breast weight and yield in Japanese quail.

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