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Heritability Estimates of, Genetic and Phenotypic Correlations among Some Selected Carcass Traits of Japanese Quail (*Coturnix coturnix japonica*) Raised in a Sub-humid Climate

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Abstract

This study was conducted to evaluate some selected carcass traits in Japanese quails as well as provide estimates of their heritability, genetic and phenotypic correlations among them. A total of 389 quails were slaughtered at 8 weeks of age. Sex significantly ($P<0.05$) influenced most carcass traits evaluated. The Japanese quails dressed at an average dressing percentage of 72.36. The heritability estimates of carcass traits derived from the sire variance components varied from low to high. All the carcass traits (carcass weight, front half of carcass weight, Rear half of carcass weight, breast weight, thigh weight, liver weight, heart weight, gizzard weight and dressing percentage) studied were positively genetically correlated to pre-slaughter live weight. Phenotypic correlations between pre-slaughter live weight and other carcass traits followed the same trend as for genetic correlation. It was concluded that Japanese quail have high efficiency of meat production and indirect selection could be used to improve the carcass traits studied.

Keywords: Japanese quail, carcass traits, Heritability, Genetic correlation.

1. Introduction

Japanese quail is the smallest avian specie farmed for meat and egg production (Panda and Singh, 1990) and it has assumed world-wide importance as a laboratory animal (Baumgarther, 1993). Both quail meat and eggs are characterized by high nutritive value that is low in fat and cholesterol (Garwood and Diehl, 1987) which is of particular importance considering the increasing cases of cardiovascular diseases. Diversification into production of quail with short generation interval will be a viable tool in ameliorating shortage of animal protein among the populace in developing countries (NVRI, 1994).

Carcass traits are important in determining the income from meat production because the profitability of a quail enterprise depends largely not only on the number of birds per female, but also on the weight and quality of carcasses the birds produced. Carcass parts of Japanese quail have been studied by several investigators (Ayorinde, 1994; El-Full, 2000, El-Full *et al.*, 2001 and Odunsi and Kehinde, 2009). Dressing percentage is a trait of prime interest to the poultry industry and Japanese quail may serve a useful role in studies involving dressing percentage. This trait determines the net out-put of carcass relative to either live body weight or empty body weight. The most important factors affecting dressing percentage are breed, body size, age at slaughter, sex, nutrition during the growing period and the processing procedures (Carlson *et al.,* 1975).

This study was conducted to estimate the genetic parameters of some carcass traits and to estimate the genetic and phenotypic correlations among the traits in Japanese quail.

2. Materials and Methods

The experiment was carried out at the poultry unit of the Teaching and Research farm of the Faculty of Agriculture, Kogi State University, Anyigba, Nigeria. The house used for the research consists of an open sided building divided into 12 pens (each pen measuring 366x221cm) on either side of a central walk way. The same building was used for mating, brooding and rearing of the quails. A total of 389 pedigree hatched day-old chicks were produced in three hatches using 30 sires, each mated to three females in the breeding cages. At hatching, the chicks were leg banded with small plastic bands to indicate individual and sire identities. The chicks were brooded on a floor pen with wood shavings as litter materials. Brooding temperature started with 37.5^{O}C for the first weak after which the temperature was reduced by 2-3^{O}C weekly until the end of 3 weeks of age when the birds were transferred to rearing pens. In the rearing pens, birds were managed on deep litter from the 4th week to 8 weeks of ages using standard management procedures. Chicks were fed diet containing 24% crude protein and 2741kcal/kg of feed from hatch to 5 weeks of age, thereafter; the birds were fed diet containing 18% crude protein and 2707kcal/kg of feed as recommended by Dafwang (2006). Both feed and water were provided *ad libitum*.

At 8 weeks of age, Japanese quails to be used for carcass evaluation were kept off feed for 12 hours but allowed access to water. Thereafter, they were individually weighed to the nearest 0.1g using a sensitive digital scale and slaughtered by severing the jugular vein. After bleeding each quail was dipped in a water bath at 60^{O}C for 2 minutes and feathers were removed by hand. After de-feathering, the quails were weighed individually to obtain the New York dressed weight. After the removal of head and legs, carcasses were eviscerated manually and carcass weights were obtained. The carcasses were then cut into parts (front half with wings, Rear half, beast thigh). The weights were recorded at each processing step. The heart, liver and gizzard weights were also recorded. In order to reduce variation in the cutting procedure, all dissections were carried out by one operator.

Dressing percentage (D.P) was calculated using the formula;

$$D.P = \frac{\text{Carcass weight}}{\text{Pre-slaughter live weight}} \times \frac{100}{1}$$

2.1 Analytical procedures

Data obtained on carcass traits were analyzed by SPSS 14.0 (2004) using the following model:

$Y_{ijk} = \mu + S_i + B_j + (SB)_{ij} + e_{ijk}$

Where

Y_{ijk} = Individual phenotypic observation
μ = Population mean
S_i = Effect of sex
B_j = Effect of hatch
$(SB)_{ij}$ = Interaction effect of sex and hatch
e_{ijk} = Residual random error.

The carcass data were also subjected to genetic analysis using the mixed model least squares and maximum likelihood computer programme of Harvey (1990). The reduced sire model (Becker, 1992) was used to fit the data.

$Yij = \mu + a_i + e_{ij}$

Where

Y_{ij} = observation on the jth progeny of the ith sire
μ = population mean
a_i = Random effect of the ith sire (i = 1,…30).
e_{ij} = Residual random error.

The Harvey programme computed estimates of genetic and phenotypic correlation as well as heritability estimates of traits from sire variance components.

3. Results and Discussion

Table 1 presents the effect of sex on carcass traits. Sex had very highly significant ($P<0.001$) effect on pre-slaughter live, carcass, front half of carcass, rear half of carcass, breast, thigh, liver and gizzard weights. However, sex, hatch and sex × hatch interaction had no significant ($P>0.05$) effect on heart-weight and dressing percentage. Female quails had significantly higher ($P<0.05$) pre-slaughter, carcass, rear half of carcass, breast, liver and gizzard weights than the males but showed no significant ($P>0.05$) differences in heart weight and dressing percentage. The significant effect of sex on most carcass traits studied agrees with the results of Yalcin *et al.* (1995) and Sharaf (1996) who reported significant sex effect on carcass characteristics. Male quails had heavier thigh than females. A similar observation was made by Odunsi and Kehinde (2009). The males had significantly ($P<0.05$) heavier front half of carcass than the females which contradicts the report of EL-Full (2000) who reported no significant difference in both front and rear half of carcass of male and female Japanese quail. Although male quails had higher dressing percentage than the females, the difference was not significant ($P>0.05$). This agrees with the finding of Joseph *et al.*

(1992), but disagrees with EL-full (2000) who reported that female quails have significantly ($P<0.05$) higher dressing percentage than males. The pre-slaughter live weight (for sexes combined) reported in this study closely agrees with the findings of Singh *et al.* (1981) who reported 134.4g for Live weight of Japanese quail at slaughter age of 8 weeks. Pre-slaughter live weight is important because it has been found that carcass weight and all carcass composition are influenced by live body weight (Bacon and Nestor, 1983). The dressing percentage of 72.36 for the sexes combined in this study is lower than the value of 77% and 78.7% reported by Jones *et al.* (1979) and EL-full (2002). It is however comparable to the values of 71% and 72% reported by Hay and Marion (1973) and Dobson (1969) for dressing percentages in broiler chicken and turkey, respectively. Consequently, the high efficiency of Japanese quail for meat production could be established by comparing the estimates reported for the dressing percentage of quail with those reported for broiler chicken and turkey.

Heritability estimates of carcass traits derived from the sire variance components in Japanese quail is presented in Table 2. The estimate ranged from 0.11±0.10 for heart weight to 0.42±0.03 for carcass weight. The carcass traits were lowly to highly heritable. The h^2 estimates for heart and liver weights (0.11±0.10 and 0.25±0.08) were similar to those (0.11 and 0.27) reported by Ledur *et al.* (2006) but diverged from those found by Kawahara and Saito (1976) and EL-Full *et al*. (2001). The heritability estimate for breast weight (0.34±0.10) was similar to that reported by Singh and Trehan (1994) and Gaya *et al.* (2006) but differed from those reported by Vali *et al*. (2005) and Rance *et al*. (2002).

The heritability estimate for dressing percentage (0.21±0.06) reported in this study is in chose agreement with that found by EL-Full *et al*. (2001). Nether the less, the heritability estimates for carcass and thigh weights (0.42±0.03 and 0.39±0.02) were different from those reported by Vali *et a*l. (2005). Heritability estimate for gizzard weight was similar to that reported by Gaya *et al.* (2006) but differed from the values reported by Kawahara and Saito (1976) and Rance *et al*. (2002). Differences in heritability estimates could be attributed to different methods of estimation, breed, environmental effects and sampling error due to small data set or sample size (Prado-Gonzalez *et al*., 2003). Based on estimated heritability values for pre-slaughter live, carcass, front half of carcass, rear half of carcass, breast, thigh, liver and gizzard weight and dressing percentage, it appears that direct selection would be effective in improving these traits. In order words, considerable direct additive genetic effects seem to exist in the expression of these carcass traits based on their heritability estimates.

Table 3 shows the genetic (below diagonal) and phenotypic (above diagonal) correlation among carcass traits in Japanese quail. All carcass traits were positively genetically correlated to pre-slaughter live weight. Unrealistic genetic correlation estimates (>1) were obtained between pre-slaughter live weight and carcass weight (1.26) and also between thigh weight and dressing percentage (1.44) due to small sample size. Phenotypic correlations among carcass traits ranged from -0.01 to 0.98 with most of the estimates being positive. Dressing percentage showed the weakest non-significant ($P>0.05$) relationship with other carcass traits.

The positive genetic correlations between pre-slaughter live weight and all other carcass traits were similar to the observations of Vali *et al*. (2005) and Gaya *et al*. (2006) who reported positive genetic correlation between live weights and most carcass traits considered. The phenotypic correlation between pre-slaughter live weight and other carcass traits followed the same trend as for genetic correlation. Heart weight appeared to be negatively, genetically correlated with gizzard weight and dressing percentage. Liver weight showed negative genetic correlation with gizzard weight and dressing percentage. Also, gizzard weight expressed negative genetic correlation with dressing percentage. These results were in agreement with the findings of EL-Full *et al*. (2001). The corresponding phenotypic correlations followed a similar trend.

Where genetic correlations between carcass traits were positive, it indicates that such traits might be controlled by the same group of genes or closely linked genes. Where correlations were positive and varied from moderate to high, it implies that selection for one carcass trait may lead to a concomitant increase in the other, although not in the same proportion. The reverse is the case where correlations were negative.

4. Conclusion

In this study, Japanese quails dressed at an average dressing percentage of 72.36. This dressing percentage is high and comparable to values obtained for broiler chickens and turkeys and this indicates high efficiency of meat production from quail birds. Carcass traits, although with moderate to high heritability may not be selected for directly because they are slaughter traits. Indirect selection such as family or pedigree selection could be used to improve this category of traits.

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Table 1: Effect of sex on least-squares means ± SEM of carcass traits in Japanese quail.

Traits	Sex	Mean	Combined sexes
Pre-slaughter Liveweight	Male	126.49±1.29^b	
	Female	149.83±2.14^a	133.76±1.32
Carcass weight	Male	87.96±0.99^b	
	Female	92.45±1.64^a	90.01±0.81
Front half of carcass weight	Male	54.93±0.71^a	
	Female	51.80±1.18^b	54.78±0.58
Rear half of carcassweight	Male	33.03±0.34^b	
	Female	40.64±0.57^a	35.24±0.38
Breast weight	Male	28.82±0.38^b	
	Female	33.04±0.63^a	29.73±0.34
Thigh weight	Male	6.62±0.10^a	
	Female	5.64±0.17^b	6.44±0.09
Liver weight	Male	2.06±0.09^b	
	Female	2.84±0.15^a	2.37±0.08
Heart weight	Male	1.13±0.02	
	Female	1.17±0.03	1.15±0.01
Gizzard weight	Male	2.45±0.04^b	
	Female	3.31±0.06^a	2.67±0.04
Dressing Percentage	Male	73.31±6.18	
	Female	61.77±10.23	72.36±4.82

a,b = means within sex – subgroup with different superscripts are significantly different ($P<0.05$)

Table 2: Heritability estimates of carcass traits from sire variance components in Japanese quail.

Parameter	h^2
Pre-slaughter live weight	0.27±0.10
Carcass weight	0.42±0.03
Front half of carcass weight	0.38±0.06
Rear half of carcass weight	0.29±0.10
Breast weight	0.34±0.10
Thigh weight	0.39±0.02
Liver weight	0.25±0.08
Heart weight	0.11±0.10
Gizzard weight	0.36±0.30
Dressing percentage	0.21±0.06

Table 3: Genetic (Below diagonal) and Phenotypic (above diagonal) correlations among carcass traits in Japanese quail.

	LW	CW	BR	TH	LR	GZ	HR	FH	RH	DP
LW		0.83***	0.73***	0.32***	0.44***	0.72***	0.39***	0.52***	0.98***	0.01
CW	1.26		0.65***	0.71***	0.11	0.42***	0.49***	0.90***	0.76***	0.26
BR	0.46	0.51		0.18*	0.26***	0.56***	0.34***	0.43***	0.71***	0.01
TH	0.32	0.12	0.34		-0.20*	-0.10	0.34***	0.86***	0.21*	0.10
LR	0.40	0.30	0.04	0.01		0.36***	-0.06	-0.14	0.44**	-0.06
GZ	0.19	0.21	0.06	-0.14	-0.13		0.22***	0.08	0.76***	-0.04
HR	0.26	0.09	0.03	0.32	0.48	-0.03		-.46***	0.33***	0.09
FH	0.52	0.63	0.68	0.41	0.01	0.06	0.07		0.40***	0.14
RH	0.43	0.51	0.44	0.78	0.04	0.03	0.09	0.74		-0.01
DP	0.77	0.75	0.58	1.44	-0.72	-0.16	-0.26	0.66	0.72	

* = ($P < 0.05$) ** = ($P < 0.01$) *** ($P < 0.001$)
LW – Pre-slaughter live weight, CW – Carcass weight, BR – Breast weight,
TH – Thigh weight, LR – Liver weight, GZ – Gizzard weight, HR – Hear weight,
FH – Front half of carcass weight, RH – Rear half of carcass weight,
DP – Dressing percentage

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