# Genetic parameters of body weight in japanese quails (*Coturnix japonica* Temminck & Schlegel, 1849) in the Philippines

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# ABSTRACT

Submitted: 24 April 2019 | Accepted: 24 March 2020

The establishment of breeding and selection programs to improve the genetic potential of poultry necessitates estimation of genetic parameters for different production and reproduction traits. Restricted maximum likelihood (REML) software was used to estimate the heritability (h<sup>2</sup>) and genetic correlations (r) of body weights in Japanese quails (C. japonica) from hatch to fifth week of age. A total of 224 Japanese quails composed of 56 males and 168 females arranged in a Completely Randomized Design (CRD) served as the base population. Body weight records, measured weekly from hatch to fifth week, were utilized to estimate the genetic parameters. Heritability estimates were 0.093±0.004, 0.244±0.010, 0.031±0.001, 0.082±0.004, 0.325±0.016 and 0.025±0.001 for body weights at hatch  $(BW_{a})$ , first week  $(BW_{1})$ , second week  $(BW_{2})$ , third week  $(BW_{3})$ , fourth week  $(BW_{4})$  and fifth week (BW<sub>5</sub>), respectively. Low heritability estimates depict a decrease in additive genetic variance as the generations progressed. Negative genetic correlation was found between BW<sub>0</sub> and BW<sub>4</sub> (r=-0.027). The significant positive genetic correlations of BW<sub>0</sub> with BW<sub>1</sub> (r=0.271); BW<sub>1</sub> with BW<sub>2</sub> (r=0.270), BW<sub>3</sub> (r=0.294), BW<sub>4</sub> (r=0.255), and BW<sub>5</sub> (r=0.243); BW<sub>2</sub> with BW<sub>3</sub> (r=0.561), BW<sub>4</sub> (r=0.649), and BW<sub>5</sub> (r=0.503); BW<sub>3</sub> with BW<sub>4</sub> (r=0.726), and BW<sub>5</sub> (r=0.551); and BW<sub>4</sub> with BW<sub>5</sub> (r=0.689) are expected to bring correlated responses in the other traits.

Keywords: Japanese quail, heritability, genetic correlation, body weight

# INTRODUCTION

Awareness on Japanese quail raising particularly on meat production is beginning to gain the interest of farmers in the Philippines. But most producers find it difficult to establish an outstanding breeding program. The design of breeding

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programs requires knowledge on genetic parameters for improving economically important traits determined under specific environmental conditions. Genetic parameters are necessary to predict the amount of improvement that can be achieved by direct and indirect selection (Harvey & Bearden 1962).

Body weights are affected by genetic and non-genetic factors such as year and season of production, sex, nutrition, adaptability, climatic conditions and management (Hafez 1993). Estimation of heritability and correlations for weekly body weight in Japanese quails were extensively estimated by numerous researchers (Marks 1996, Kumari et al 2009, Narinc et al 2010, Zerehdaran et al 2012). Studies on the heritability of traits are essential for understanding how individual characteristics change from one generation to another in response to selection (Falconer & Mackey 1996). Moreover, the genetic and environmental variations are described by the genetic parameters and vary among population and environments (Khaldari et al 2010).

The studies on genetic parameter estimation of quails in the Philippines if ever available are lacking and mostly focused on egg production. Hence, this study was geared towards estimating heritability and genetic correlations on weekly body weights in Japanese quails (*C. japonica*) from hatch to fifth week of age.

#### MATERIALS AND METHODS

The study was conducted at the University Animal Farm, Los Baños, Laguna, Philippines from April 2017 to December 2017. A total of 224 Japanese quails composed of 56 males and 168 females were arranged in a Completely Randomized Design (CRD) and served as the base population. The foundation stocks or base population placed inside double-tier battery-type cages served as treatment groups. A total of 56 families (1 sire: 3 dams) served as replicates.

The base population is part of the original random-bred population of Japanese guails that was purchased from Drguail Farm, Sariaya, Quezon. At the time of full egg production stage, eggs collected daily were identified based on sire families, and stored at room temperature. After seven days, all accumulated pedigreed eggs were properly sorted and set in setting trays based on sire families, artificially incubated at 37.5°C temperature and 65% relative humidity with automatic turning every three hours. At the end of the 14<sup>th</sup> day of incubation, eggs were set in pedigree baskets in the egg hatcher. Immediately after hatching, the chicks were weighed and leg-banded according to their sire families, and artificially brooded for 21 days using 100-watt electric bulb as source of heat. The experimental quails (Generation 1) were fed with commercial chick starter mash with  $\leq 24\%$  crude protein (CP) and 2800Kcal per kg metabolizable energy (ME) as recommended by Dafwang (2006). The feed and water were supplied ad libitum during the entire duration of the study. Similarly, the brooding-rearing procedures were repeated on the quails of the next generation. Superior quails of generation 1 were selected as the parents of the second generation, and mated randomly at a mating ratio of 1 sire: 3 dams. The guails were weighed on a weekly interval from hatch to fifth week. On the fifth week of age, the birds were transferred to laying cages.

Data on body weight of Japanese quails from hatch to fifth week were analyzed using Statistical Analysis System (SAS) software ver. 9.2 to determine the results of fixed effects on growth values using the linear model presented in Table 1.

Response Variable	Fixed Effects	Random Effects	Covariate	Error
BW <sub>0-5</sub>	Location (1-8)	Generation (n=2)	Generation	е
		Family (n=56)	Family	

Table 1. Linear model used in the analysis of variance of body weight of Japanese quails from hatch to fifth week of age

BW means body weights from hatch to fifth week in grams; e=error

Simple statistics were obtained for body weight of the Japanese quail using the MEANS procedure of SAS (2009). Only significant (p<0.05) fixed effects and covariates were included in the final linear model, and the least square means procedure was used to examine the effect of generation on heritability trait.

The variance components for each body weight were obtained using the Restricted Maximum Likelihood Method (REML) by PROC VARCOMP of SAS 9.3 (SAS Institute Inc., Cary, NC). The heritability (h<sup>2</sup>) expresses the total proportion of the total variance that is attributable to differences of breeding values, and this is what determines the degree of resemblance between relatives (Falconer & Mackay 1996). Heritability was calculated in each generation from sire variance component as (Becker 1985):

$$h^2 = \frac{2\sigma^2 s}{\sigma^2 s + \sigma^2 w}$$

where:

 $\sigma_s^2$  = variance of sire  $\sigma_w^2$  = variance of remainder

Genetic correlation (r) among reproduction traits were calculated using REML by PROC CORR of SAS 9.3 (SAS Institute Inc., Cary, NC).

### **RESULTS AND DISCUSSION**

The data set for body weights contained the following records: 409 for at hatch  $(BW_0)$ , 385 for first week  $(BW_1)$ , 347 for second week  $(BW_2)$ , 334 for third week  $(BW_3)$ , 334 for fourth week  $(BW_4)$  and 330 for fifth week  $(Bw_5)$ .

Japanese quails in Generation 1 were generally heavier than Generation 2. Specifically, body weights at third week (BW<sub>3</sub>) were statistically higher (p<0.01) in Japanese quails at Generation 1 (51.525g±7.915g) than at Generation 2 (35.901g±6.493g) as shown in Table 2. Likewise, Japanese quails at week four (BW<sub>4</sub>) were heavier (p<0.05) at Generation 1 (73.861g±10.100g) than Generation 2 (57.243g±12.280g), see Table 2. Result of this study was in contrast to the results obtained by Varkoohi et al (2011); Grasteau and Minvielle (2003) and Marks (1993) who reported that body weight increases with generation encouraging the application of selection for successive generations.

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Trait	n	Generation 1 (Mean ± SE)	n	Generation 2 (Mean ± SE)
BW <sub>0</sub>	262	6.126±1.041	147	5.952±0.902
$BW_1$	253	18.237±3.348	132	14.068±2.162
$BW_2$	233	32.957±5.275	114	26.921±6.820
BW3**	223	51.525±7.915ª	111	35.901±6.493 <sup>b</sup>
$BW_4^*$	223	73.861±10.100ª	111	57.243±12.280 <sup>b</sup>
$BW_5$	220	90.941±10.302	110	79.273±12.102

Table 2. Weekly body weight (g) of Japanese quails at Generation 1 and Generation 2 from hatch to fifth week of age

BW means body weight, in grams

\*\*Significant at p<0.01; \*Significant at p<0.05

The variance component and heritability estimates for body weights of Japanese guails from hatch to fifth week of age are presented in Table 3. Heritability (h<sup>2</sup>) estimates were 0.093±0.004, 0.244±0.010, 0.031±0.001, 0.082±0.004, 0.325±0.016 and 0.025±0.001 for BW<sub>0</sub>, BW<sub>1</sub>, BW<sub>2</sub>, BW<sub>3</sub>, BW<sub>4</sub> and BW<sub>5</sub>, respectively. The estimated low and moderate heritability values agreed with the results of several studies by different authors (Hussain et al 2014, Sezer 2007, Sezer et al 2006, Resende et al 2005, Akbas et al 2004). However, Kaplan et al (2016) and Aggrey and Cheng (1994) observed higher h<sup>2</sup> values with 0.63 and 0.38, respectively. Estimates obtained for BW<sub>1</sub> (0.244±0.010) and BW<sub>2</sub> (0.031±0.001) were lower compared to the reported values of Kaplan et al (2016) with 0.42 and 0.40, respectively. The  $h^2$  for BW<sub>2</sub> (0.082±0.004) closely agreed to the estimates (0.01-0.18) of Hussain et al (2014) and Akbas et al (2004). Mostly, results of some studies conducted by a number of researchers have relatively higher estimates (0.43 & 0.58) (Resende et al 2005, Saatci et al 2006). At week four age of guails, variable h<sup>2</sup> estimates were recorded by a number of researchers as 0.03, 0.19, and 0.61 by Hussain et al (2014); Saatci et al (2006); and Akbas et al (2004). The heritability estimate at BW<sub>4</sub> (0.325±0.016) conformed to the heritability values of 0.22-0.47 by Varkoohi et al (2011) and Abdullah et al (2011). Meanwhile, heritability of quails at BW<sub>5</sub> (0.025±0.001) was lower than other studies with estimates ranging from 0.35 to 0.55 (Kaplan et al 2016, Narinc et al 2014, Sari et al 2011, Narinc et al 2010, Aksit et al 2003). In this study, the lower h<sup>2</sup> estimates might be due to the small data set involving less number of birds in two generations. Mehrgardi (2012) also estimated lower heritability values in advanced generations of Japanese quail depicting a decrease in additive genetic variance as the generations progressed in long-term selection.

Trait	Variance Con	Heritability	
	Among Sire	Within Sire	(h <sup>2</sup> ± SE)
BW <sub>0</sub>	0.045	0.922	0.093 ± 0.004
BW <sub>1</sub>	1.113	8.000	0.244 ± 0.010
BW <sub>2</sub>	0.520	33.412	0.031 ± 0.001
BW <sub>3</sub>	2.312	53.748	0.082 ± 0.004
BW <sub>4</sub>	29.950	154.256	0.325 ± 0.016
BW <sub>5</sub>	2.103	167.787	0.025 ± 0.001
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Table 3. Variance component and heritability estimates for body weight of Japanese quailsat from hatch to fifth week of age

In the present study, except for  $BW_0$  with  $BW_4$  the, genetic correlations were positive, ranging from 0.271 to 0.689 (Table 4). Table 4 revealed strong genetic correlations estimated between weekly body weights, except for the correlation between  $BW_0$  with  $BW_2$  (r=0.002),  $BW_3$  (r=0.033) and  $BW_5$  (r=0.016). Negative genetic correlation was found between  $BW_0$  and  $BW_4$  (r=-0.027). The significant (*p*<0.001) positive genetic correlations of  $BW_0$  with  $BW_1$  (r=0.271);  $BW_1$  with  $BW_2$  (r=0.270),  $BW_3$  (r=0.294),  $BW_4$  (r=0.255), and  $BW_5$  (r=0.243);  $BW_2$  with  $BW_3$  (r=0.561),  $BW_4$ (r=0.649), and  $BW_5$  (r=0.503);  $BW_3$  with  $BW_4$  (r=0.726) and  $BW_5$  (r=0.551); and  $BW_4$ with  $BW_5$  (r=0.689) are expected to bring correlated responses in the other traits. The accurate selection for body weight at  $BW_5$  can be achieved based on body weight at  $BW_4$  because the 2 traits show a genetic correlation of 0.689 implying favorable individuals for body weight at  $BW_4$  should also be the most desirable for body weight at  $BW_5$ .

Table 4. Genetic correlations among body weights of	Japanese quails from hatch to fifth week of age

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Trait	BW <sub>0</sub>	$BW_1$	BW <sub>2</sub>	BW <sub>3</sub>	BW <sub>4</sub>	BW <sub>5</sub>	
BW <sub>0</sub>	1.000	0.271***	0.002	0.033	-0.027	0.016	
$BW_1$	1	.000	0.270***	0.294***	0.255***	0.243***	
$BW_2$			1.000	0.561***	0.649***	0.503***	
$BW_3$				1.000	0.726***	0.551***	
$BW_4$					1.000	0.689***	
$BW_5$						1.000	

\*\*\*-significant at p<0.001

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The highest genetic correlation estimate between BW<sub>3</sub> with BW<sub>4</sub> (r=0.726) was slightly lower compared to the findings of Sezer (2007) who disclosed higher genetic correlation values for weekly body weights as  $r_{g1-2}$ =0.89,  $r_{g2-3}$ =0.94,  $r_{g3-4}$ =0.93,  $r_{g4-5}$ =0.92, and  $r_{g5-6}$ =0.96. Similarly, Sezer et al (2006) reported the genetic correlations range from 0.46 to 0.98 between weekly body weights. Akbas et al (2004) reported genetic correlations estimates for weekly body weights between 2-4, 2-6 and 4-6 weeks as 0.84, 0.80 and 0.80, respectively. Although the estimates did not correspond with the published reports (eg, Sezer 2007, Sezer et al 2006, Akbas et al 2004), differences in the on-farm research setting and procedures should not be overlooked.

## ACKNOWLEDGMENT

The author would like to thank the Accelerated Science and Technology for Human Development Program (ASTHRDP) under the Department of Science and Technology (DOST).

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