

## Short Communication

# Estimation of Heritability and Genetic Correlations of Body Weight in Different Age for Three Strains of Japanese Quail

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## ABSTRACT

In this study genetic parameters of body weight were estimated for three commercial strains of Japanese quail (White, Canadian wild & Brown). Live body weight at 14, 28 and 42 days of age on approximately 900 quail of both sexes from 55 each of sires and dams in each strain were utilized to estimate genetic parameters. The chicks hatched of each sire and dam identified by the same color, and at 10 days of age they were wing-tagged with an aluminum plate. The first weighing was done at 14 days and repeated at 28 and 42 days of age. Analysis was carried out with the records on 900 quails in three strains. Data were analyzed using restricted maximum likelihood (REML) with relationship matrix. The moderate to high heritability for most study traits suggested that selection to increase or decrease these traits will be successful. The genetic correlations of body weight (BW) at different ages, measurements were positive and tended to be moderate to high. These results showed that selection for weight at early ages will have a positive effect on weight at later ages.

**Key Words:** Japanese quail; Body weight; Heritability; Genetic correlation

## INTRODUCTION

Quail is used as pilot animals for research usually done with chickens and turkeys, because they require less time and space, are easier to handle and have low feed requirements, more rapid growth, earlier sexual maturity (six weeks), greater laying ability and shorter time of hatching as compared with chickens (Sadjadi *et al.*, 1980). The main advantages of Japanese quail are the short generation interval (four or more generations per year) and the similarity of the genetic parameters with domestic fowl.

There are a few reports about performance and less about the genetic variability and genetic parameters of Japanese quail in Iran. In order to establish breeding programs, it is necessary to estimate the heritability of traits to be improved, because the degree of heritability allows us estimate the amount of improvement by selection. Therefore, higher the heritability of the trait, the higher the response to selection. Heritability has been estimated for a number of Japanese quail traits. However, for correct estimates, it is necessary to determine the heritability not only for the trait but also for the population and the environmental conditions surrounding the animals (Falconer, 1981). Estimation of genetic parameters is necessary for breeding programs, prediction of response to selection and determination of selection procedure. Since heritability depends on genetic and environment variation, it is better to estimate it in each environmental condition.

Researchers have reported the heritability of body

weight in Japanese quail to be between 0.30 and 0.72 at different ages. Caron *et al.* (1990) explained the importance, in the context of selection programs of genetic parameters estimates for production traits of Japanese quail. Genetic parameters of body weight in Japanese quail were calculated by Kawahara and Saito (1976) but not using Restricted Maximum Likelihood REML procedure. Although Toelle *et al.* (1991) used a REML procedure, they did not use one to one sire and dam records for each animal. In the studies of Kocak *et al.* (1994) and Aggrey and Cheng (1994), birds from known sires and dams were used but they had an extensive pedigree file for the analyses.

In addition to heritability, genetic correlations between economic traits are important for breeding programs especially for selection program. The purpose of the experiment reported in this paper was to estimate the genetic parameters of live weight in three strains of Japanese quail using animal models.

## MATERIALS AND METHODS

The Japanese quail population used for the present study was reared in the poultry research station of agriculture and natural resources research center of Yazd. Fifty one each of males and females of each strain were randomly selected from the base population and one male with one female were located in individual cage for accurate pedigree identification. Each individual was wing-tagged with an aluminum plate numbered. When the eggs were

collected, the sire and dam number was registered on them.

The chicks hatched of each sire and dam, were identified by the same color and at 10 days of age they were wing-tagged with an aluminum plate. The first weighing was done at 14 days and repeated at 28 and 42 days of age. Analysis was carried out with the records on 900 quails in three strains.

The chicks brooded on the floor under heat of lamps until they were 28 days of age. At this time, they were sexed and transfer in cage. Feed consisted of a NRC (National Research Council, 1999) formula, which contained 24% protein and 3200 kcal ME kg<sup>-1</sup>. Feed and water were provided for *ad libitum* consumption and lighting was continuous. Temperature was maintained at 95°F during the 1<sup>st</sup> week and was decreased 5°F every coming week till it reached 85°F (Hameed *et al.*, 2002). Twelve hour prior to weighing, feed, but not water, was removed.

**Statistical analyses.** The SPSS (SPSS 9.05 release for windows, 1999) statistical package was used for preliminary data analyses. A general linear model (GLM) was applied to examine the relative importance of the factors influencing quail's weights. Data were analyzed using the model:

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

Where  $Y_{ij}$  is the observation of animal weight (14, 28 & 42 days),  $\mu$  is the mean,  $a_i$  is the effect of sex (I = male & female),  $e_{ij}$  is the random error.

Heritabilities and correlations were estimated by MTDFREML (Meyer, 1997) using an animal model with animal's genetic effect as the only random factor. Standard errors (se) of heritability and correlations were calculated. For the univariate analyses, the model was:

$$Y_{ijkl} = \mu + a_i + c_k + e_{ijkl}$$

Where  $Y_{ijkl}$  is the trait,  $\mu$  is the mean,  $a_i$  is the random effect of animal,  $c_k$  is the effect of sex,  $e_{ijkl}$  is the random error.

## RESULTS AND DISCUSSION

Descriptive statistics of live weight is presented in Table I. The effect of sex in three strains is presented in Table II. Sexual dimorphism in Japanese quail, with heavier females, is well documented. In this study male and female body weights were not different since hatch to 28 days of age ( $P < 0.05$ ), but they have significant difference at 42 days of age and females were heavier than males. This may be due to sexual maturity age lower than female (5 weeks vs 6 weeks) and also, because of testosterone hormone that release in this age and causing decrease of growth rate (Hyánková *et al.*, 2001).

**Table I. Descriptive statistics for live weight**

Strain*	Age (day)	N	Mean (g)	SE	Min (g)	Max (g)	CV%
1	14	237	49.2	0.58	25	70	16.95
	28	237	109.2	1.03	56	140	14.35
	42	237	160.2	1.31	107	216	11.65
2	14	412	57.2	0.5	28	86	18.53
	28	412	139.3	0.9	81	192	13
	42	412	197.1	1.15	152	269	9.96
3	14	258	51.2	0.7	19	81	19.28
	28	258	119.2	1.3	62	172	19.09
	42	258	176	1.6	121	255	12.81

N = Number of observations; SE = Standard Error; Min and Max = Minimum and maximum values;

CV% = Coefficient of variation.

\* 1=White, 2= Canadian wild and 3= Brown

**Table II. Effect of sex on live weight in three strain of Japanese quail in different ages**

Strain	Sex	N	14days (g)	28 days(g)	42days (g)
1	Male	120	N.S	N.S	***
			44.6±1.3	109±1.3	150.5±1.1
	Female	117	41.7±1.4	108.5±1.8	169.7±2
2	Male	228	N.S	N.S	***
			54.2±0.9	123±1.9	185.1±1.1
	Female	211	56.8±1	139.1±1.9	209.8±1.6
3	Male	112	N.S	N.S	***
			50.2±1.2	117.5±2.1	162.6±1.6
	Female	146	50.6±1.1	118.1±2.1	186.3±2.2

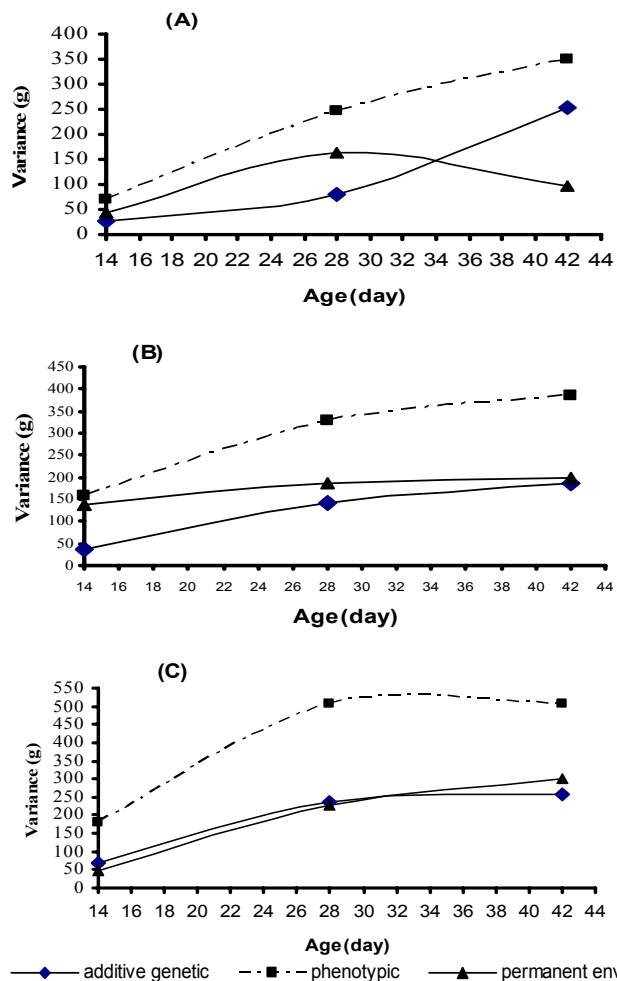
N.S= Not significant (\*\*\*) =  $P < 0.001$

**Table III. Heritabilities (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) with their ( $\pm$  SE)**

Strain	Age (day)	14	28	42
1	14	<b>0.37±0.12</b>	0.92±0.06	0.84±0.05
	28	0.64	<b>0.33±0.12</b>	0.98±0.09
	42	0.6	0.46	<b>0.72±0.12</b>
2	14	<b>0.24±0.07</b>	0.96±0.02	0.94±0.03
	28	0.62	<b>0.43±0.09</b>	0.99±0.04
	42	0.45	0.48	<b>0.48±0.1</b>
3	14	<b>0.38±0.13</b>	0.78±0.08	0.60±0.12
	28	0.81	<b>0.46±0.12</b>	0.97±0.01
	42	0.54	0.7	<b>0.50±0.12</b>

The values for heritability, genetic and phenotypic correlations for liveweights were similar to that reported by others (Table III). Saatci *et al.* (2002) reported lower  $h^2$  than that found in this study for 14, 28 and 42 days of age, but Marks (1996) estimated it 0.32 - 0.42 for 28 days weight of Japanese quail, which is higher than the value found for strain 1 and 2 in this study (Table III). Heritability estimated in the current study for 42 days weight was similar to another report (Akbas *et al.*, 2004). In this study heritability of body weight in three strains were increased by the increment of age that this similar to the results of Akbas *et al.* (2004). This finding may be explained by the changes of genetic variances for weight over ages. The change of phenotypic and permanent environmental variances for weight over ages was increased by the increment of age but permanent environmental variance was considerably less increased over time than the genetic counterparts. The

**Fig. 1. Estimates of additive genetic, phenotypic and permanent environmental variances for weight at different ages in strain1 (A), strain 2 (B) and strain3 (C)**



changes in genetic, phenotypic and permanent environmental variances for weight over ages are shown in Fig. 1. In this study, all correlations among weights were found positive. Moreover, genetic correlations were higher than phenotypic correlations. Within the same interval, genetic correlations slightly decreased with time. The genetic correlations were all positive, which suggested that selection for weight at an early age will have a positive effect on weight at a later age. Akbas *et al.* (2004) reported a genetic correlation between 2-weeks weight with 4-weeks weight and for 2-weeks with 6-weeks and 4-weeks with 6-weeks as 0.84, 0.8 and 0.87, respectively. These values were lower than those in the present study. In three strains the genetic correlation between 2 and 4-weeks weight (in strain 1, 2 & 3 were 0.92, 0.96 & 0.78, respectively) was higher than the estimate (0.76) by Aggrey and Cheng (1994).

Kocak *et al.* (1994) reported a weak phenotypic correlation (0.11) between 38 days weight and 58 days weight of Japanese quail. The phenotypic correlations between traits at different ages in this study were significantly higher than those reported by Kocak *et al.* (1994). Genetic correlations were higher than phenotypic correlation as expected and reported by Brah *et al.* (1997) for 2, 4 and 6 weeks live weights of Japanese quail. Because of high heritability for body weights and genetic correlations between them and weight recorded at later ages, selection on the basis of early body weights is feasible.

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