

ISSN 1682-8356  
ansinet.org/ijps



INTERNATIONAL JOURNAL OF  
**POULTRY SCIENCE**

**ANSI***net*

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## Genetic Parameters of Body and Some Carcass Traits in Two Quail Strains

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**Abstract:** In order to estimate genetic parameters for body weights and carcass yield of 2 strains of quails; 32 pairs of Japanese quail (*Coturnix japonica*) and 26 pairs of range quail (*Coturnix ypsilophorus*) randomly were selected from the base populations of parents. Produced progenies (650 birds) were used to estimate the genetic parameters of body weights and carcass characteristics traits. Body weights at 35, 42 and 49 days of ages were significantly different, while there was no significant difference for body weights at 63 days of age ( $p > 0.05$ ). Carcass weight, carcass percent, breast weight and thigh percent were significantly affected by strain source of variations ( $p < 0.1$ ). Estimated heritabilities for different traits were from  $0.030 \pm 0.090$  for breast weight of *Coturnix japonica* to  $0.787 \pm 0.406$  for thigh weight of *Coturnix ypsilophorus*. Genetic correlation among body weights at 35, 42, 49, 63 days of age and among carcass traits (carcass weight, breast weight and thigh weight) were all positive and high, while genetic correlation for breast percent, and carcass percent were low. Genetic correlation of thigh percent with the other considered traits was negative except body weight at 42 days of age, which tended to be low.

**Key words:** *Coturnix ypsilophorus*, *Coturnix japonica*, heritability, Genetic correlation, carcass traits, quail

### Introduction

In order to establish a breeding program, it is essential to estimate genetic parameters for improving the traits. The scale of the genetic parameters could show the amount of improvement by selection. Some of the estimated genetic parameters for various traits of domestic Japanese quail were reported by several workers (Kawahara and Saito, 1976, Toelle *et al.*, 1991 and Minvielle *et al.* 1999, 2000). Kawahara and Saito (1976) reported the genetic parameters of different organs and body weights in the Japanese quail. Toelle *et al.* (1991) estimated genetic and phenotypic relationships between body weight, carcass and some of the organ parameters. Minvielle *et al.* (2000) reported the carcass characteristics of a heavy Japanese quail line under introgression with the roux gene. Most of the investigations on quails are with *Coturnix japonica* while other strains were less considered. The objectives of this study were to estimate genetic parameters of body and some carcass traits in Range quail (*Coturnix ypsilophorus*) and Japanese quail (*Coturnix japonica*).

### Materials and Methods

Thirty two pairs of Japanese quails (*Coturnix japonica*) and 26 pairs of Range quails (*Coturnix ypsilophorus*) were randomly selected from the base populations (the base population were included 500 *Coturnix japonica* and 500 *Coturnix ypsilophorus*). One male and one female quail in an individual one-tier cage (50×50×70cm) performed the mating. All the birds were wing banded according to the cage number. The temperature in house was around 20°C and the light

was given 15 hr per day (from 6:00 AM until 9:00 PM). Diet contained 20% crude protein and 2650 kcal/kg metabolizable energy. Food and water were available *ad libitum* (waterier plason type and feeder from trough type). The eggs were collected for 50 days. Every afternoon the collected eggs were marked according to cage number. Collected eggs were stored in the room with temperature of 12°C and humidity of 70%. Every 10 days the collected eggs were antiseptitized with formaldehyde, and then set in the setter for 14 days and 2 days in hatcher. The setter and hatcher were equipped with separate box which marked according to cage number in order to pedigreed chicks. The wing banded Chickens were transferred to a house with 35°C temperature. The temperature was decreased 20°C on the weekly bases. After the 4<sup>th</sup> week, supplemental heating was disconnected. The chicks had access to continuous lighting for the first 48 hours. At 2 days of age, the daily light was reduced to 15 hours (6:00 AM until 9:00 PM) and was maintained for the rest of the experiment. A starter diet was contained 24% crude protein and 2750 kcal/kg metabolizable energy. Food and water were available *ad libitum*. Sums of 669 chickens from two strains were recorded for body weights at 42, 49 and 63 days of age with a digital balance with accuracy 0.1 gr. In addition, sums of 313 quails at 49 or 63 days of age were killed for carcass measurements. They were fasted for 10 to 15 hours before they were slaughtered, bled and plucked. Evisceration was performed by hand. Carcass weight and carcass parts (breast and thigh) were recorded for each chicken. Variance components of body weights

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Table 1: Description of data for body and carcass weights and percent for strains, (cot) coturnix quail, (ran) Range quails

Trait	No. Obs.		Mean (gr)		SE		Min (gr)		Max (gr)		SD		CV	
	cot	ran	cot	ran	cot	ran	cot	ran	cot	ran	cot	ran	cot	ran
BW35	226	122	135.80	127.00	1.68	2.05	67.49	72.94	185.10	174.70	25.30	22.63	18.60	17.83
BW42	223	118	161.20	152.70	1.69	2.36	76.56	60.70	214.20	200.70	25.30	25.65	15.70	16.79
BW49	214	118	181.40	175.80	1.66	2.50	100.70	108.30	238.20	240.70	24.30	27.16	13.40	15.45
BW63	96	52	197.70	193.10	2.57	4.32	147.90	141.90	259.30	257.40	25.20	31.16	12.70	16.13
CW	200	113	125.90	120.90	0.96	1.39	75.83	79.28	171.00	152.20	13.50	14.78	10.70	12.23
CP	200	113	65.81	68.13	0.38	0.70	31.84	52.99	74.89	86.79	5.39	7.31	8.20	10.73
BRW	200	113	50.81	49.17	0.43	0.60	36.41	30.88	63.99	65.94	6.04	7.28	11.90	14.8
BP	200	113	40.41	40.64	0.23	0.26	31.76	32.02	73.98	54.81	3.30	2.79	8.18	6.86
TW	72	41	27.83	27.62	0.36	0.51	20.07	19.57	34.10	33.54	3.01	3.26	10.80	11.82
TP	72	41	22.61	23.47	0.13	0.21	19.68	20.73	25.41	27.07	1.12	1.31	4.97	5.56

BW: body weight days, CW: carcass weight, CP: carcass percent, BRW: breast weight, BP: breast percent, TW: thigh weight, TP: thigh percent, No. Obs: number of observations, SE: standard error of mean, Min: minimum, Max: maximum, SD: standard deviation, and CV: coefficient of variation.

Table 2: Least squares means and standard error for body weight (gr) in quails

Variation sources	BW35	BW42	BW49	BW63
Over all means	133.06± 1.32	158.78± 1.39	179.52± 1.40	196.05± 2.25
Strain Coturnix	135.49± 1.40 <sup>a</sup>	160.81± 1.54 <sup>a</sup>	181.54± 1.62 <sup>a</sup>	198.46± 2.17 <sup>a</sup>
Range	125.95± 1.91 <sup>b</sup>	150.73± 2.10 <sup>b</sup>	172.36± 2.16 <sup>b</sup>	192.81± 2.93 <sup>a</sup>
Sex				
Female	133.32± 1.59 <sup>a</sup>	160.59± 1.75 <sup>a</sup>	187.13± 1.80 <sup>a</sup>	213.32± 2.45 <sup>a</sup>
Male	128.12± 1.75 <sup>b</sup>	150.96± 1.93 <sup>b</sup>	167.78± 2.00 <sup>b</sup>	177.94± 2.66 <sup>b</sup>
Hatch				
1	137.51± 2.74 <sup>b</sup>	155.86± 3.01 <sup>b</sup>	175.13± 3.10 <sup>bc</sup>	195.81± 3.20 <sup>b</sup>
2	123.07± 3.22 <sup>c</sup>	144.99± 3.54 <sup>c</sup>	171.88± 3.74 <sup>bc</sup>	201.11± 3.52 <sup>a</sup>
3	108.43± 2.41 <sup>d</sup>	142.20± 2.65 <sup>c</sup>	168.56± 2.73 <sup>c</sup>	189.98± 2.57 <sup>c</sup>
4	147.47± 2.69 <sup>a</sup>	173.32± 2.95 <sup>a</sup>	191.44± 3.12 <sup>a</sup>	NA
5	137.11± 1.89 <sup>b</sup>	162.48± 2.08 <sup>b</sup>	180.25± 2.14 <sup>b</sup>	NA

BW: body weight days.

<sup>a, b, c, d</sup> Means within each subclass column with different superscript are significantly different (P=0.05), NA: not available.

and carcass traits were estimated using the general linear models procedures of SAS Institute (1998).

Model used was:

$$Y_{ijklm} = \mu + ST_i + HA_j + SA_k + SE_l + e_{ijklm}$$

Where:  $Y_{ijklm}$  was an individual observation for trait Y.  $\mu$  was overall mean for trait  $Y_{ijklm}$ .  $ST_i$  was fixed effect of the  $i^{th}$  strain.  $HA_j$  was fixed effect of the  $j^{th}$  hatch.  $SA_k$  was fixed effect of the  $k^{th}$  slaughter age.  $SE_l$  was fixed effect of the  $l^{th}$  sex.  $e_{ijklm}$  was random error associated with the measurement of each individual.

In order to estimate variance components and genetic parameters, data were analyzed using derivative-free maximum likelihood method applying DFREML 3.0.0 software (Meyer, 1998) by the simplex way.

$$Y = X\beta + Z\alpha + e$$

Where:  $y$  is the vector of observations,  $\beta$  is the vector of fixed effects (including strain, sex and hatch effects for overall data, and including sex and hatch effects for analyses performed for each strain solely),  $\alpha$  is the vector of random direct additive genetic effects.  $X$  and  $Z$  are the incidence matrices for  $\beta$  and  $\alpha$  respectively. The above model was run in both single trait and multi traits ways by DFUNI and DXMUX procedures of DFREML

software (Meyer, 1998), respectively. All the correlation coefficients (including genetic, environment, and phenotypic) among the studied traits were estimated using multi traits analysis.

## Results and Discussion

Description and statistical parameters of different traits for both strains are shown in Table 1. Least-squares means and standard errors by strain, sex, hatch for body weight is shown in Table 2.

Body weights of two strains at 35, 42 and 49 days of age were significantly different ( $p < 0.01$ ), but there were not any significant difference at 63 days of ages ( $p > 0.05$ ). Sex was a significant source of variation for body weights at 35, 42, 49 and 63 days of ages ( $p < 0.01$ ). Females showed a higher body weight than males, which was agreed with previous studies (Kawahara and Saito, 1976; Caron and Minvielle, 1990; Toelle *et al.*, 1991; Bumgartner, 1994; Minvielle *et al.*, 2000). Results obtained for body weight in coturnix Japanese are agreed or higher than the previous studies, which were unselected, but it was lower than selected group (Bacon *et al.* 1986; Marks, 1993; Syed Hussien *et al.*, 1995,

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Table 3: Least squares means and standard error for carcass traits in quails

Variation sources	carcass (gr)	carcass % <sup>1</sup>	Breast (gr)	Breast % <sup>2</sup>	Thigh (gr)	Thigh % <sup>2</sup>
Over all means	124.09±0.80	66.63±0.35	50.21±0.37	40.49±0.18	27.75±0.29	22.92±0.12
Strain Coturnix	127.12±1.01 <sup>a</sup>	65.92±0.37 <sup>b</sup>	51.19±0.45 <sup>a</sup>	40.34±0.21 <sup>a</sup>	27.99±0.36 <sup>a</sup>	22.66±0.14 <sup>b</sup>
range	121.36±1.34 <sup>b</sup>	68.89±0.50 <sup>a</sup>	48.78±0.60 <sup>b</sup>	40.18±0.28 <sup>a</sup>	27.30±0.49 <sup>a</sup>	23.47±0.19 <sup>a</sup>
Sex						
Female	126.59±1.12 <sup>a</sup>	64.23±0.41 <sup>b</sup>	52.52±0.50 <sup>a</sup>	41.55±0.23 <sup>a</sup>	28.56±0.40 <sup>a</sup>	23.19±0.15 <sup>a</sup>
Male	121.89±1.24 <sup>b</sup>	70.58±0.46 <sup>a</sup>	47.45±0.55 <sup>b</sup>	38.98±0.26 <sup>b</sup>	26.72±0.46 <sup>b</sup>	22.94±0.18 <sup>a</sup>
Hatch						
1	126.07±2.04 <sup>ab</sup>	66.88±0.75 <sup>c</sup>	50.07±0.91 <sup>a</sup>	39.70±0.42 <sup>bc</sup>	NA	NA
2	128.97±2.31 <sup>a</sup>	70.43±0.85 <sup>a</sup>	51.01±1.03 <sup>a</sup>	39.46±0.48 <sup>c</sup>	NA	NA
3	122.10±1.68 <sup>bc</sup>	67.84±0.64 <sup>bc</sup>	49.56±0.75 <sup>a</sup>	40.52±0.35 <sup>abc</sup>	NA	NA
4	124.04±1.89 <sup>abc</sup>	65.62±0.70 <sup>c</sup>	50.11±0.84 <sup>a</sup>	40.72±0.39 <sup>ab</sup>	NA	NA
5	120.02±1.31 <sup>c</sup>	66.25±0.48 <sup>c</sup>	49.18±0.58 <sup>a</sup>	40.91±0.27 <sup>a</sup>	27.64±0.30	23.06±0.12
Slaughter age						
49 days	121.70±1.09 <sup>b</sup>	66.24±0.40 <sup>b</sup>	49.64±0.48 <sup>a</sup>	40.84±0.22 <sup>a</sup>	27.67±0.29	23.03±0.11
63 days	125.06±1.15 <sup>a</sup>	68.23±0.43 <sup>a</sup>	50.10±0.51 <sup>a</sup>	40.20±0.23 <sup>a</sup>	NA	NA

<sup>a, b, c, d</sup> Values within a column and classification (strain or sex or hatch) with no common superscript are significantly different (P=0.01). NA: not available. <sup>1</sup> Relative to body weight, <sup>2</sup> Relative to carcass weight.

Table 4: Heritability estimates single-trait method in quails

Traits	Coturnix	Range	Overall
BW35	0.295±0.133	0.413±0.244	0.325±0.107
BW42	0.245±0.127	0.457±0.231	0.289±0.110
BW49	0.114±0.107	0.409±0.222	0.195±0.094
BW63	0.121±0.158	0.472±0.243	0.452±0.209
CW	0.438±0.155	0.327±0.180	0.413±0.120
CP	0.084±0.085	0.060±0.119	0.082±0.071
BRW	0.482±0.160	0.404±0.194	0.483±0.125
BP	0.030±0.090	0.215±0.184	0.142±0.095
TW	0.278±0.239	0.787±0.406	0.505±0.241
TP	NA	NA	0.266±0.188

BW: body weight days, CW: carcass weight, CP: carcass percent, BRW: breast weight, BP: breast percent, TW: thigh weight, TP: thigh percent. N.A: not available

1996, 1999). There were significant differences (p<0.01) of body weights among hatches as well.

Least-squares means and standard errors by strain, sex, hatch and slaughter ages for carcass traits are shown in Table 3. Carcass weight, carcass percent, breast weight and thigh percent were significantly affected by strain source of variations (p<0.01), while breast percent and thigh weight for two strains were not significantly different (p>0.05).

A significant difference (P<0.01) for all carcass traits except thigh percent were between sexes. Carcass weight, breast weight, breast percent and thigh weight of females showed higher figures than males, which are consistent with other reports (Caron and Minvielle, 1990; Toelle *et al.*, 1991; Minvielle *et al.*, 1999, 2000). Males showed higher percentage of carcass weight than females, which supported the earlier studies results (Minvielle *et al.*, 2000; Caron and Minvielle, 1990). There were no significant difference (P>0.05) in the breast weight and breast percent between slaughter ages, but carcass weight and carcass percent were significantly different (P<0.01). From the results obtained, it could be

concluded that, slaughter at 63 days of age compared to 49 days slaughter increased carcass weights over this period but breast weight and breast percentage were not affected (Table 3).

Genetic parameters estimates for body weights and carcass traits for two strains are presented in Table 4. Heritability estimates seems to be different for two strains, and generally higher for Range quails. The lowest and highest heritability in Coturnix quails were for the breast percent and breast weight, respectively, and in Range quails were carcass percent and thigh weight, respectively (Table 4). A wide range of heritability estimates for body weights has been reported by different researchers (Kawahara and Saito, 1976; Strong *et al.*, 1978, Nestor *et al.*, 1982, Caron and Minvielle, 1990; Toelle *et al.*, 1991 and Minvielle, 1998).

These studies normally used body weights at different ages and often used different methods to estimate the heritability. Minvielle (1998) who reviewed reports from several studies stated that the heritability estimations for body weights at 4 and 8 weeks of ages ranges from 0.47 to 0.74. Toelle *et al.*, 1991 reported heritability estimations from sire, dam and sire plus dam components unadjusted for body weight 0.49±0.13, 0.70±0.14, and 0.59±0.8 respectively. It seems differences in heritability estimates might be attributed to method of estimation, strain, environmental effects and sampling error due to small data set or sample size (Prado-Gonzalez *et al.*, 2003). The definition of the correct model is important, because the more complex the model, the larger the time needed for solution. This is even more important with large amount of data and in multi-trait analysis, because CPU time is a function of the number of variance and covariance components to be estimated (Prado-Gonzalez *et al.*, 2003).

The genetic, environmental and phenotypic correlations for all traits measured in the study are shown in Table 5 and 6. Genetic correlation among body weight at 35, 42, 49 and 63 days of ages and also among carcass traits

Table 5: Heritability multi-traits method ( $h^2$ ), genetic ( $r_g$ ) and environmental ( $r_e$ ) correlations and standard errors of various traits<sup>1</sup>

Traits	BW35	BW42	BW49	BW63	CW
BW35	0.263±0.098	0.964±0.037	0.985±0.081	0.799±0.208	0.849±0.140
BW42	0.868±0.020	0.224±0.093	0.975±0.048	0.695±0.227	0.870±0.104
BW49	0.817±0.026	0.861±0.023	0.121±0.083	0.804±0.223	0.894±0.121
BW63	0.415±0.120	0.548±0.120	0.615±0.083	0.374±0.196	0.847±0.106
CW	0.661±0.045	0.679±0.051	0.704±0.045	0.871±0.044	0.273±0.101
CP	-0.044±0.095	0.016±0.084	-0.070±0.081	-0.388±0.117	0.266±0.075
BRW	0.057±0.066	0.698±0.069	0.735±0.061	0.661±0.080	0.871±0.029
BP	0.151±0.090	0.110±0.086	0.151±0.078	0.138±0.129	0.027±0.085
TW	0.763±0.055	0.823±0.041	0.896±0.023	NA	0.874±0.034
TP	-0.347±0.145	-0.249±0.149	-0.247±0.141	NA	-0.315±0.144
Traits	CP	BRW	BP	TW	TP
BW35	0.209±0.444	0.854±0.100	0.218±0.365	0.974±0.082	-0.079±0.466
BW42	0.050±0.570	0.694±0.160	0.020±0.039	0.995±0.610	0.362±0.421
BW49	0.0001±0.660	0.777±0.164	-0.128±0.592	0.994±0.050	-0.366±0.458
BW63	0.004±0.568	1.00±0.083	0.009±0.518	NA	NA
CW	0.457±0.808	0.941±0.042	-0.403±0.373	0.962±0.044	-0.389±0.378
CP	0.119±0.084	-0.034±0.502	-0.108±0.475	0.906±0.401	-0.420±0.543
BRW	0.147±0.089	0.262±0.100	0.013±0.685	0.965±0.066	-0.308±0.389
BP	-0.081±0.078	-0.619±0.060	0.152±0.094	-0.159±0.422	-0.008±0.641
TW	-0.031±0.119	0.778±0.061	0.213±0.118	0.281±0.141	-0.225±0.535
TP	-0.341±0.125	-0.347±0.151	-0.190±0.144	0.004±0.152	0.190±0.164

BW: body weight days, CW: carcass weight, CP: carcass percent, BRW: breast weight, BP: breast Percent, TW: thigh weight, TP: thigh percent, NA: not available. <sup>1</sup>The  $h^2$  on the diagonal,  $r_g$  above and  $r_e$  below the diagonal.

Table 6: Phenotypic correlations among various traits

Traits	BW35	BW42	BW49	BW63	CW	CP	BRW	BP	TW	TP
BW35	1									
BW42	0.890	1								
BW49	0.838	0.882	1							
BW63	0.547	0.592	0.654	1						
CW	0.614	0.733	0.745	0.861	1					
CP	0.037	0.020	-0.062	-0.286	0.273	1				
BRW	0.656	0.683	0.713	0.790	0.876	0.524	1			
BP	0.084	0.093	-0.148	0.104	0.880	-0.082	0.524	1		
TW	0.827	0.871	0.915	NA	0.905	0.140	0.847	0.199	1	
TP	-0.277	-0.279	-0.273	NA	-0.333	-0.351	-0.329	-0.157	-0.049	1

BW: body weight days, CW: carcass weight, CP: carcass percent, BRW: breast weight, BP: breast percent, TW: thigh weight, TP: thigh percent, NE: not available.

(carcass weight, carcass percent, breast weight and thigh weight) were all positive and ranged from 0.995±0.610 to 0.0001±0.660. Genetic correlation among body weight at 35 and 49 days of age with thigh percent, and genetic correlation among carcass trait with thigh percent were negative and ranged from -0.008±0.641 to -0.420±0.543 (Table 5). Correlation estimates among body weight at all ages with carcass, breast and thigh weight were high (Table 5).

Earlier results suggest that selection to body weight would cause increase in carcass and breast weight. In addition, genetic correlation among the various traits measurements are important regarding the traits would

be used in the calculation of the index for selection study (Toelle *et al.*, 1991). In this study, genetic correlation of body weight at 63 days of age with breast weight was 1.00±0.083. Toelle *et al.* (1991) reported the correlation of deboned with total drum and deboned with total thigh were high (around 1.00 or greater). This indicates that selection for total drum and thigh weights would be also effective for increasing leg muscle mass.

**Acknowledgement**

The authors would like to thank the Isfahan University of Technology, Isfahan, Iran for financial support of this research.

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