INHERITANCE OF BODY WEIGHT, GROWTH RATE AND SOME FITNESS TRAITS IN JAPANESE QUAIL

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Abstract*: A total of 480 males and 480 females derived by randomly mating of 61 sires with 122 dams in one hatch were used to estimate the heritability, genetic and phenotypic correlations of body weights (BW) growth rates (GR) during different periods of growth and fitness traits to determine the best effective selection criteria for future genetic improving in Japanese quail.*

The following results were obtained: *Females were significantly (P≤0.001) heavier than males at 28,35 and 42 days of age. The differences between sexes were 2.64, 4.92, 6.45 and 10.87g at 21, 28, 35 and 42 days of age, respectively. Similar trends of significant sex effects favoring females were found for growth rate during the periods from 1-21, 22-42 and 1-42 days of age (171.6, 63.6 and 182.7% for females vs 171.2, 60.9 and 182.1% for males, respectively). Generally, BW' heritability estimates showed a wider range of variability than GR regardless of sex or method of estimation (0.02 to 0.95 vs 0.01 to 0.71, respectively). GR for male's progeny during all periods of growth had similar trend to BW which had higher dam component heritability (h^2_D) than sire component heritability (h^2_S) due to non-additive effects. Fertility% was influenced by sex-linked effects due to higher h^2_S than their corresponding h^2_D estimates. Heritability estimates of hatchability and survivability had higher h^2_D than h^2_S estimates, which may be due to maternal effects. All phenotypic and genetic correlation estimates between weights at different ages were positive with the magnitude generally decreasing as the interval between weighings increased. Phenotypically, either GR_{1-21} or GR_{1-42} in males and females were positively correlated with BW at different ages except at hatching day ranging from 0.33 to 0.75 and 0.02 to 0.38. Most of genetic correlations among GR separated by several days were high. Therefore, either BW_{42} or GR_{1-42} can be used as criteria of selection to improve growth performance of Japanese quail since they had considerably*

higher heritabilities and genetic correlations with other traits of growth and lower standard errors than others.

INTRODUCTION

In spite of the small body size of Japanese quail, its meat and eggs are widely consumed all over the world. Moreover, Japanese quail has recently become a subject of biological research because it is resistant to diseases, easy to manage and has a short reproductive cycle of only 35 days **(Ernst, 2000)**.

The heritability of a metric character is one of the most important properties of a population. Its predictive role has an important function in the genetic study of metric characters expressing the reliability of the phenotypic value as a guide to the breeding value. Heritability estimates differ according to the character. The characters with the lowest heritabilities are those most closely connected with reproductive fitness, while the characters with the highest heritabilities are those that might be judged on biological grounds to be the least important as determinants of natural fitness **(Falconer, 1989)**.

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. A wide range of heritability estimates for body weight has been cited by many researchers **(Caron *et al*., 1990, Farahat, 1998, Abdel Fattah, 2001**, **Vali *et al.*, 2005 and Saatci *et al*., 2006)**. These studies normally used body weight at different ages and often used different methods to estimate the heritability. **Minvielle (1998)** reviewed that heritability estimates for body weights of Japanese quail at four and eight weeks of age ranged from 0.47 to 0.74. Lower estimates of weekly body weight were estimated by **(Vali *et al.* 2005** and **Saatci *et al*., 2006)**.

The heritability estimates literatured for body weight would be expected to differ in diverse genotypes and under different environments. Therefore, discrepancies between heritability estimates for a particular trait should be considered the norm rather than the exception. Although these estimates indicate considerable variation, heritabilities for BW in Japanese quail appear to fall well within the range of heritabilities found for body weight in chickens **(Siegel and Dunnington, 1987** and **Saatci *et al.,* 2002**).

It is also equally clear that there is a very large negative genetic and phenotypic correlations between early exponential growth rate and

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subsequent linear phase of growth, regardless of species **(Barbato, 1991 and 1992)**.

The goal of the present study was to estimate the heritability, genetic and phenotypic correlations of body weights at different ages, growth rates during different periods of growth and fitness traits which needed to determine the effective selection criteria for future genetic improving in Japanese quail.

MATERIALS AND METHODS

The present study was conducted at the Poultry Research Center, Faculty of Agriculture, Fayoum University. A total of 480 males and 480 females were randomly derived by mating 61 sires with 122 dams in one hatch. The breeders were housed in breeding cages (one male and two females per cage) with sloping floor for collecting the eggs. Eggs were collected twice daily in a pedigree system for each family when production rate reached about 70%, where females were 11 to 14 weeks of age. The eggs of each family (one sire and two dams according to their discrete colored, tinted botched egg shells) were incubated in chicken egg type incubators with egg trays modified to hold quail eggs. The setter and hatcher temperatures were maintained at 37.5°C and at 37.2°C respectively. The relative humidity of the setter and the hatcher were maintained at 56 and 64.5%, respectively. Since the quail egg shells were colored, tinted and botched, accurate assessment of the condition of the embryo by candling during incubation was not possible. Therefore, after taking out all the hatched chicks from the hatcher trays and pedigree boxes, the unhatched eggs were broken open on the hatch day under bright sunlight to identify infertile eggs.

The newly hatched chicks were pedigreed by small size wing plastic bands, which were replaced by wing metal bands at seven days of age. Wing bands were reviewed and quail chicks were visually sexed at 21 days of age. All chicks were brooded in floor brooded until ten days of age, at that time the young birds were transferred to an intermediate battery brooders. Chicks were placed in individual decks of five-deck electric quail battery brooders. From hatch to six weeks of age, all quails had access *ad libitum* to a starter diet containing 24% CP and 2900 K cal/ME and to water. A breeder diet containing 20% CP, 2900 K cal/ME 2.25% calcium and 0.43% available phosphorous was supplied. The minerals and vitamins were adequately supplied to cover the requirements according to **NRC (1994).**

The Following Criteria Were Measured Or Calculated:

1. Body weight at hatch, 7, 14, 21, 28, 35, and 42 days of age (BW_1, BW_7, BW14, BW_{21}, BW_{28}, BW_{35}, and BW_{42}, respectively) were individually recorded to the nearest 0.01g.

2. Growth rates during the periods from 1-21, 22-42, and 1-42 days of age (GR_{1-21}, GR_{22-42}, and GR_{1-42}, respectively) were calculated according to **Brody (1945).**

using the following formula:

$$\mathbf{GR = 100*[W_2 - W_1 / {}^1/_2 (W_2 + W_1)]}$$

where: $\mathbf{W_1}$ **is** the weight at the beginning and $\mathbf{W_2}$ is the weight at the end of the period**.**

3. Fertility% and hatchability (calculated as a percentage of total egg (hatchability (TE) %) and as a percentage of fertile egg (hatchability (FE) %), respectively).

4. Mortality data were collected and defined as the time from hatch to the date the bird died to calculate the survivability during the periods from 1-21(survivability (3W) %) and 1-42 days of age (survivability (6W) %), respectively.

Statistical Analyses

All percentages data were transformed to their corresponding angles for statistical analysis.

Performance of the traits: Data were subjected to one- way analysis of variance to test sex effect using the following models according to **Steel and Torrie (1980)**:

$$\mathbf{Y_{ij} = \mu + S_i + e_{ij}}$$

where: $\mathbf{Y_{ij}}$ is the observed value of the ith sex on the jth chick, $\boldsymbol{\mu}$ is the common mean, $\mathbf{S_i}$**:** sex effect (i = 1 and 2) and $\mathbf{e_{ij}}$ is the residual error.

Genetic And Phenotypic Parameters

According to **Becker (1985),** data were computerized using the hierarchical analyses of variance and covariance procedure of **SAS (2000)** to compute the genetic and phenotypic parameters. The following random model was fitted, for all studied traits to calculate the genetic parameters:

$$\mathbf{Y_{ijk} = \mu + S_i + D_{ij} + e_{ijk.}}$$

where**: Y_{ijk}** is the observation on the **ijk^{th}** bird, **μ** is the overall mean, **S_i** is the effect of the **i^{th}** sire, **D_{ij}** is the effect of the **j^{th}** dam mated to the **i^{th}** sire, and **e_{ijk}** is the error term accounted for the **k^{th}** bird of the **j^{th}** dam and **i^{th}** sire.

Heritability estimates were calculated according to **Becker (1985)** as follows:

$$h^2_S = 4\sigma^2_S / \sigma^2_S + \sigma^2_D + \sigma^2_W$$

$$h^2_D = 4\sigma^2_D / \sigma^2_S + \sigma^2_D + \sigma^2_W$$

$$h^2_{S+D} = 2\sigma^2_{S+D} / \sigma^2_S + \sigma^2_D + \sigma^2_W$$

where: σ^2_S is the sire component of variance, σ^2_D is the dam component of variance and σ^2_W is the remainder of the genetic variance plus the environmental variance. Also, standard errors for heritabilities were calculated according to **Swiger *et al.* (1964)** as follows:

$$Var\ (\sigma^2_g) = 2/k2 * \Sigma_g\ MS_g / f_g + 2$$

$$S.E\ (\sigma^2_g) = SQRT\ Var\ (\sigma^2_g)$$

where: **K** is the coefficient of the variance component being estimated, **MS_g** is the gth mean square used to estimate the variance component, **f_g** is the degrees of freedom of the gth mean square.

Genetic correlation (r_g) between any two traits were calculated using the sire, the dam and combined components of variance and covariance as follows:

$$r_g = cov_{xy}\ / SQRT\ (\sigma^2_{(x)} * \sigma^2_{(y)})$$

where: **r_g** is the genetic correlation coefficient, **cov_{XY}** is the genetic covariance between traits X and Y, σ^2_X is the variance component of trait X and σ^2_Y is the variance component of trait Y. Approximate standard errors of the genetic correlation were calculated according to **Robertson (1959)** as follows:

$$S.E\ (r_g) = ((1 - r_g^2) / SQRT\ 2) * SQRT\ (S.E_{h^2X} * S.E_{h^2Y} / h^2_X * h^2_Y)$$

where: **r_g** the genetic correlation. **$S.E\ h^2_X$** and **$S.E\ h^2_y$** the standard errors of the heritability estimates of traits X and Y and **h^2_X and h^2_y** the heritability estimates of traits X and Y.

Phenotypic correlations (r_p) between any two traits were estimated according to **Becker (1985)** as follows:

$$r_p = cov_p\ / SQRT(\sigma^2_{p(x)} * \sigma^2_{p(y)})$$

where: **Cov$_P$ is** the total covariance between x and y traits. Standard errors for phenotypic correlations were calculated according to **Becker (1985)** as follows:

$$S.E\ r_p = 1 - r^2{}_p\ /\ SQRT\ (N)$$

where: $r^2{}_p$ is the square of phenotypic correlation and **N** is the total number of progeny.

RESULTS AND DISCUSSION

Performance Of Growth And Fitness Traits

Means of growth traits during different periods of growth for males and females are presented in Table 1. Females were significantly (P≤0.001) heavier than males at 28,35 and 42 days of age. Thereafter, sex differences increased being 2.64, 4.92, 6.45 and 10.87g at 21, 28, 35 and 42 days of age, respectively. However, opposite results were reported by **Soltan et al. (1987)** for hatch weight and **Oguz et al. (1996)** for body weights from seven up to 42 days of age. Also, lower ratios of females to males BW were cited by **Soltan et al. (1987), Oguz et al. (1996) and Aggrey et al. (2003)**. However, higher ratios for BW at 28, 35 and 42 days of age were cited by **Yalcin et al. (1995), Yannakopoulos et al. (1995), Farahat (1998)** and **Bahie El Deen (2003)**. Similar trends of significant sex effects favoring females were found for growth rate during the periods from 1-21, 22-42 and 1-42 days of age (171.6, 63.6 and 182.7% for females vs 171.2, 60.9 and 182.1% for males, respectively). Sex differences for growth rate increased from 0.4 to 2.7?% from 1-21 to 22-42 days of age. The highest sex difference for growth rate was found during the period from 22 to 42 days of age (1.044, P≤0.001) as shown in Table 1. Higher growth rates were cited by **Badawy et al. (1997).** However, **Farahat (1998), Shalan (1998)** and **Abdel Fattah (2001)** found lower growth rates during 1- 14, 14-28 and 28-42 days of age.

Means of fertility%, hatchability% (calculated as a percentage of total egg and as a percentage of fertile egg), survivability% (after first three weeks of age and after six weeks of age) were 80.53, 60.28, 74.86, 95.56 and 89.64%, respectively as shown in table 3.

Heritabilities Of Growth And Fitness Traits

Heritability estimates of growth traits during different periods of growth, based on paternal, maternal half-sib and full-sib correlations ($h^2{}_S$, $h^2{}_D$ and $h^2{}_{S+D}$, respectively) are presented in Table 2. All estimates of

heritability for BW or GR showed considerable variations throughout different ages or periods of growth, regardless of the estimation method.

Data presented in Table 2 showed that heritability estimates of BW at hatch, 7, 14, 21, 28, 35 and 42 days of age ranged from 0.02 to 0.95 in males and 0.08 to 0.86 in females regardless of the estimation method. The h^2_S estimates of hatch weight of male were much higher than the h^2_D (0.95 vs 0.39) whereas, the h^2_D of female's hatch weight was higher than the h^2_S (0.86 vs 0.42) as shown in Table 2, indicating the presence of a large maternal effect, due to the fact that hatch weights of the full-sibs were similar since eggs produced from the same dam are similar in weights **(El Gindy, 1984)**. The h^2_{S+D} estimates for male progeny weights were higher than those for female progeny weights, at hatch, 7, 14 and 21 days of age, which may be due to sex-linked effects. Similar trends were observed by **El Gindy (1984)** that males showed higher heritability estimates than females. However, these estimates for males were lower than those for females at 28, 35 and 42 days of age. **Marks (1971)** found that females had higher estimates than males. The h^2_D based on male and female progeny weights were generally higher than those of the h^2_S estimates, this may be due to the dominance and maternal effects. The sire estimate indicated only the additive genetic variance effect as suggested by **Falconer (1989).**

Heritability estimates for GR during different periods of growth ranged from 0.01 to 0.71 in males, 0.03 to 0.52 in females, regardless of the estimation method as shown in Table 2. Growth rates for male's progeny during all studied periods of growth had similar trend to body weight which had higher h^2_D than h^2_S due to non-additive effects. However, females had higher h^2_S during the periods 1-21 and 1-42 higher than those based on dam component of variance indicating sex-linked effects (Table 2). These estimates are within the range of heritabilities for growth traits estimated by several investigators **(Soltan *et al.* 1987, El Fiky, 1991, Sharaf, 1992, Bahie El Deen, 1994 and 1999, Farahat, 1998, Shalan, 1998, Abdel Fattah, 2001** and **Saatc*i et al.,* 2002)**.

Heritability estimates of fertility, hatchability and survivability are presented in Table 3. Fertility% was influenced by sex-linked effects due to higher h^2_S than their corresponding h^2_D estimates (0.22 vs 0.05). However, opposite trends for hatchability was reported by **Abdel Gawad (1969)** for Dokki-4 and **Shebl (1980)** for Alexandria strain of chickens. Comparable estimates of h^2_S to those obtained in the present study were reported by **El Tahawy (2000)** for Alexandria strain ranged from 0.18 to 0.32. Heritability estimates of hatchability and survivability had higher h^2_D than h^2_S estimates,

which may be due to maternal effects. However, **Hassan (1994)** found opposite trend for hatchability in quail. Also, heritabilities of survivability during the periods 1-21 and 1-42 were influenced by maternal effects since it had higher h^2_D than the h^2_S as shown in Table 3. **El Tahawy (2000)** found similar heritability estimates ranged between 0.12 and 0.26 for the sire component heritability for Alexandria chickens.

Correlations Among Body Weights At Different Ages

All phenotypic correlation estimates between weights at different ages were positive as shown in Tables 4 and 5. Similar trends were reported by **Sharaf (1992), Bahie El Deen (1994), Farahat (1998)** and **Shalan (1998)**. The r_p of males between hatch weight with BW at 7, 14, 21, 28, 35 and 42 were 0.31, 0.30, 0.25, 0.19, 0.16 and 0.15, respectively for males. The genetic correlation estimates for these traits were larger and followed the same trends as the r_p (Table 4). The estimates of r_p between BW_7 with BW's at 14 to 42 days of age were 0.80, 0.58, 0.04, 0.30 and 0.84, respectively. The corresponding estimates of r_g had the same trend of estimates of r_p being positive and larger and ranged from 0.03 to 0.99, regardless the method of estimation. Large positive estimates of r_p for males between BW_{14} with BW's at 21 to 42 days thereafter ranging between 0.44 and 0.79. Similar large positive estimates of r_p and with large estimates of r_g were found for each of BW at 28, 35 and 42 days of age with other BW's at various ages. The estimates of r_p had higher values than 0.56, and the estimates of r_g ranged from 0.29 to 0.99. However, BW at 35 days of age showed negative estimates of r_g of -0.50 with BW at 42 days of age. Females' body weights followed the same general trend for either phenotypic or genetic correlations as the males. The estimates of r_p ranged from 0.19 to 0.84 and the estimates of r_g were positive and had larger range from 0.02 to 0.99, regardless of the estimation method, except the r_{gS} between body weights at hatch and 35 days and r_{gD} between BW at seven and 42 days of age being -0.33 and -0.31, respectively, as shown in Table 5. In general, as birds advanced in age the r_p correlation estimates among body weights tended to be higher than at the earliest ages as shown in Tables 4 and 5 for males and females, respectively. Similar trend for estimates of r_g in Japanese quail was cited by **Abdel Fattah (2001)**.

Correlations between body weights and growth rates at different ages and periods of growth

Phenotypically, either GR_{1-21} or GR_{1-42} in males and females were positively correlated with body weights at different ages from 7 up to 42 days of age, except at hatch, ranging from 0.33 to 0.75 and 0.02 to 0.38.

These estimates are in harmony with the cited estimates of correlations between GR_{1-42} and body weights at different ages, except at hatch, and BW_{14} in males, females and combined sexes ranged from 0.12 to 0.63 as reported by **Abdel Fattah (2001)**. However, GR_{21-42} was negatively correlated with BW from hatch up to 35 days of age ranging from -0.07 to -0.74, whereas positively correlated with BW_{42} being 0.14 and 0.25 for males and females, respectively as shown in Table 6.

Results presented in Table 7, showed that GR_{1-21} in males was genetically correlated with body weights from 7 up to 42 days of age with r_{gS+D} estimates ranged from 0.29 to 0.54 and r_{gD} ranged from 0.60 to 0.91. However, GR_{22-42} and GR_{1-42} were negatively correlated with BW at all ages studied ranging from -0.05 to -0.99. Females showed similar trend of negative r_{g}s for GR_{22-42} with all weights at different ages. Positive estimates of r_g were found in female GR_{1-42} with BW at 35 and 42 days of age, the latter revealed higher estimates than the former (0.16 and 0.19). Negative or low r_gs based on dam components of variance and covariance was found for GR_{21-42} with body weights at all ages studied in males ranged from -0.09 to -0.99. Whereas, inconsistent trend of low or negative r_gs from dam components was shown in Table 7. Similar trends for r_{gS} and r_{gS+D} correlations in quail were reported by **Abdel Fattah (2001)**.

Correlations among growth rates during different periods of growth

Based on S+D components, GR during the period 1-42 revealed positive r_ps ranged from 0.02 to 0.73. The r_gs were large and ranging from 0.48 to 0.88 as shown in Table 8. However, GR_{1-21} in either males or females were negatively correlated with GR_{21-42} based on sire or dam components (Table 8). Most of r_gs among growth rates separated by several days were high. Lower values tended to involve among growth rates taken only a fewer days apart. These results are in agreement with those reported by **Chambers (1990) in chickens** and **Abdel Fattah (2001) in** quail.

It can be concluded that either BW_{42} or GR_{1-42} can be used as criteria of selection to improve growth performance of Japanese quail since they had considerably higher heritabilities and genetic correlations with other traits of growth and lower standard errors than others.

Table 1. Means ± SE for body weights in grams (BW, g) and growth
rate in percentage (GR,%) for Japanese quail.

Trait	Age or period (days)	Males (M)	*Females (F)*	F-M	F/M	Significance of ratio
BW	1	7.01±0.06	7.09±0.06	0.08	1.011	P≥0.05
	7	25.07±0.03	25.29±0.31	0.22	1.009	P≥0.05
	14	54.06±0.52	54.80±0.57	0.74	1.014	P≥0.05
	21	91.65±0.78	94.29±0.79	2.64	1.029	P≤0.01
	28	127.25±1.01	132.17±1.02	4.92	1.039	P≤0.001
	35	154.16±0.84	160.61±1.05	6.45	1.048	P≤0.001
	42	171.40±0.88	182.27±1.13	10.87	1.063	P≤0.001
GR	1-21	171.2±3.00	171.6±0.30	0. 40	1.002	P≥0.05
	22-42	60.9±0.50	63.6±0.60	2.70	1.044	P≤0.001
	1-42	182.1±0.10	182.7±0.20	0.60	1.003	P≤0.001

Table 2.. Heritability estimates ± SE from sire, dam and sire + dam
components of variance for growth traits at different ages of
Japanese quail.

Trait	Age or period, days	Male			Female		
		Base of estimate			Base of estimate		
		S	D	S+D	S	D	S+D
BW	1	0.95±0.29	0.39±0.21	0.67±0.18	0.42±0.26	0.86±0.29	0.64±0.19
	7	0.23±0.17	0.17±0.22	0.20±0.14	0.12±0.16	0.18±0.23	0.15±0.14
	14	0.15±0.19	0.48±0.26	0.32±0.16	0.24±0.18	0.23±0.23	0.24±0.14
	21	0.14±0.20	0.55±0.27	0.35±0.17	0.23±0.20	0.43±0.25	0.33±0.16
	28	0.29±0.20	0.37±0.24	0.33±0.15	0.08±0.21	0.74±0.30	0.41±0.18
	35	0.02±0.16	0.33±0.25	0.18±0.15	0.27±0.20	0.45±0.25	0.36±0.16
	42	0.29±0.16	0.36±0.25	0.33±0.15	0.30±0.20	0.43±0.25	0.37±0.16
GR	1- 21	0.01±0.20	0.71±0.30	0.36±0.18	0.41±0.20	0.18±0.21	0.30±0.14
	22-42	0.02±0.15	0.27±0.24	0.15±0.14	0.03±0.01	0.43±0.20	0.23±0.12
	1- 42	0.17±0.17	0.23±0.23	0.19±0.14	0.52±0.23	0.45±0.24	0.49±0.17

S: Sire component, D: Dam component, S+D: sire+dam components, BW: body weight and GR:

Growth rate.

Table 3. Means ± SE and heritability estimates ± SE from sire, dam, and sire+dam components of variance for fitness traits in Japanese quail.

Trait	Means ± SE	S	D	S+D
Fertility %	80.53±1.27	0.22±0.01	0.05±0.01	0.13±0.01
Hatchability (TE) %	60.28±1.53	0.20±0.01	0.37±0.02	0.29±0.01
Hatchability (FE) %	74.86±1.45	0.12± 0.01	0.22±0.01	0.17± 0.01
Survivability (3W) %	95.56±0.30	0.18±0.01	0.37±0.02	0.28±0.01
Survivability (6W) %	89.64±0.97	0.13± 0.01	0.25± 0.01	0.19±0.01

S: Sire, D: Dam, S+D: Sire+dam components, Hatchability (TE): calculated as a percentage of total egg, Hatchability (FE): calculated as a percentage of fertile egg, Survivability (3W) and (6W): calculated during the first three and six weeks of age respectively.

Table 4. Genetic (above diagonal) and phenotypic (below diagonal) correlations ± SE for males from sire, dam and sire+dam components of variance among body weights at different ages of Japanese quail.

Trait	Base of estimates	BW_1	BW_7	BW_{14}	BW_{21}	BW_{28}	BW_{35}	BW_{42}
BW_1	S		0.230.57±	0.090.89±	0.270.65±	0.260.43±	#	#
	D		0.150.86±	0.310.42±	0.220.63±	0.350.42±	0.340.50±	0.390.30±
	S+D		0.67±0.17	0.180.57±	0.180.55±	0.210.41±	0.250.51±	0.200.63±
BW_7	S			0.050.03±	0.100.91±	0.060.94±	0.870.25±	0.060.53±
	D			0.140.11±	0.200.17±	0.140.11±	0.280.77±	0.070.95±
	S+D	0.040.31±		0.020.07±	0.020.90±	0.010.71±	0.040.04±	0.060.94±
BW_{14}	S				0.270.84±	0.050.08±	0.570.46±	0.90±0.67
	D				0.030.96±	0.130.83±	0.160.79±	0.100.99±
	S+D	0.040.30±	0.020.80±		0.050.93±	0.020.67±	0.100.68±	0.010.99±
BW_{21}	S					0.270.19±	0.050.08±	0.340.94±
	D					0.100.88±	0.090.88±	0.250.69±
	S+D	0.040.25±	0.030.58±	0.020.79±		0.050.93±	0.010.95±	0.210.73±
BW_{28}	S						0.540.26±	0.710.96±
	D						0.130.84±	0.090.88±
	S+D	0.040.19±	0.020.71±	0.030.63±	0.030.95±		0.140.66±	0.010.95±
BW_{35}	S							0.38±0.50
	D							0.120.11±
	S+D	0.040.16±	0.030.55±	0.040.30±	0.030.80±	0.020.74±		0.060.05±
BW_{42}	S							
	D							
	S+D	0.040.15±	0.010.84±	0.040.44±	0.030.56±	0.030.65±	0.01±0.85	

S: sire component, D: dam component, S+D: sire+dam components, BW: body weight and #: unrealistic values(> 1).

Table 5. Genetic (above diagonal) and phenotypic (below diagonal) correlations ± SE for females from sire, dam and sire+dam components of variance among body weights at different ages of Japanese quail.

Trait	Base of estimates	BW1	BW7	BW14	BW21	BW28	BW35	BW42
BW1	S		0.650.02±	0.460.20±	0.510.11±	0.870.21±	0.43±0.33-	0.09±0.46
	D		#	0.160.77±	0.140.74±	0.200.48±	0.160.69±	0.250.43±
	S+D		0.180.73±	0.220.52±	0.200.53±	0.220.41±	0.230.33±	0.230.30±
BW7	S			0.400.66±	0.300.78±	0.200.52±	#	#
	D			0.340.75±	0.240.78±	0.500.08±	0.600.05±	0.55-0.31±
	S+D	0.040.26±		0.270.71±	0.190.78±	0.320.25±	0.270.64±	0.340.50±
BW14	S				0.070.93±	0.900.88±	0.490.39±	0.290.25±
	D				0.110.90±	0.350.46±	0.460.35±	0.480.29±
	S+D	0.040.24±	0.020.81±		0.010.91±	0.110.80±	0.130.80±	0.170.28±
BW21	S					0.980.88±	0.010.99±	0.030.97±
	D					0.190.67±	0.210.70±	0.290.54±
	S+D	0.040.24±	0.030.65±	0.010.84±		0.130.77±	0.120.80±	0.160.70±
BW28	S						0.130.76±	0.120.79±
	D						0.250.52±	0.200.63±
	S+D	0.040.24±	0.030.54±	0.020.69±	0.020.79±		0.120.96±	0.290.88±
BW35	S							0.060.94±
	D							0.07±0.91
	S+D	0.040.22±	0.040.47±	0.030.53±	0.030.59±	0.020.69±		0.050.92±
BW42	S							
	D							
	S+D	0.040.19±	0.040.36±	0.040.44±	0.030.52±	0.030.62±	0.010.84±	

S: sire component, D: dam component, S+D: sire+dam component, BW: body weight and #: unrealistic values (>

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Table 6. Phenotypic correlations ±SE between body weight and growth rate estimated from sire+dam components of Japanese quail.

Trait	Sex	GR		
		1- 21	22- 42	1- 42
BW1	M	-0.41±0.04	-0.17±0.04	-0.61±0.03
	F	-0.47±0.04	-0.11±0.05	-0.64±0.03
BW7	M	0.34±0.04	-0.46±0.04	0.02±0.05
	F	0.60±0.03	-0.43±0.04	0.06±0.05
BW14	M	0.55±0.03	-0.60±0.03	0.02±0.05
	F	0.56±0.03	-0.57±0.03	0.06±0.05
BW21	M	0.75±0.02	-0.74±0.02	0.27±0.04
	F	0.70±0.02	-0.68±0.02	0.21±0.04
BW28	M	0.64±0.03	-0.44±0.04	0.15±0.04
	F	0.55±0.03	-0.36±0.04	0.14±0.05
BW35	M	0.54±0.03	-0.07±0.05	0.27±0.04
	F	0.38±0.04	0.04±0.05	0.21±0.04
BW42	M	0.49±0.03	0.14±0.04	0.38±0.04
	F	0.33±0.04	0.25±0.04	0.28±0.04

M: males and F: females, BW: body weight and GR: growth rate.

Table 7. Genetic correlations ±SE of males and females between body weight and growth rate from sire, dam and sire+dam components of Japanese quail.

Trait	Base of estimate	Male			Female		
		GR_{1-21}	GR_{22-42}	$_{42-1}GR$	GR_{1-21}	GR_{22-42}	$_{42-1}GR$
BW_1	S	0.08±-0.89	0.10±0.31	0.20±-0.23	0.18±-0.74	0.11±-0.29	0.07±-0.88
	D	0.49±-0.09	0.27±-0.67	0.33±-0.62	0.37±-0.42	0.24±-0.51	0.08±-0.81
	S+D	0.21±-0.52	0.30±-0.41	0.04±-0.54	0.19±-0.54	0.26±-0.45	0.05±-0.84
BW_7	S	0.59±-0.06	0.83±0.31	0.37±-0.63	0.40±0.54	0.13±0.67	0.45±-0.21
	D	0.16±0.89	0.10±-0.09	0.81±-0.05	0.39±-0.74	0.15±0.11	0.28±-0.42
	S+D	0.39±0.42	0.06±-0.05	0.45±-0.33	0.48±-0.03	0.40±-0.54	0.24±-0.34
BW_{14}	S	0.42±-0.67	0.54±-0.79	0.45±-0.25	0.27±0.60	0.12±0.30	0.44±-0.25
	D	0.09±0.91	0.17±-0.81	0.49±0.31	0.73±0.12	0.10±-0.09	0.28±-0.03
	S+D	0.35±0.39	0.10±0.89	0.42±-0.21	0.32±-0.40	0.25±-0.08	0.24±-0.10
BW_{21}	S	0.77±-0.22	0.60±0.81	0.40±-0.72	0.28±0.62	0.10±-0.52	0.42±-0.08
	D	0.21±0.74	.14±0.84	0.50±0.09	0.54±0.24	0.19±-0.74	0.29±-0.14
	S+D	0.32±0.44	0.08±0.82	0.41±-0.15	0.28±0.41	0.23±-0.66	0.24±-0.12
BW_{28}	S	0.55±0.14	0.84±0.37	0.43±-0.52	0.20±0.87	0.25±0.18	0.57±0.05
	D	0.16±0.84	0.01±-0.99	0.58±0.14	0.47±0.11	0.31±-0.33	0.28±-0.04
	S+D	0.28±0.54	0.09±-0.68	0.41±-0.15	0.30±0.28	0.36±-0.29	0.25±-0.01
BW_{35}	S	0.15±-0.52	0.60±-0.71	0.25±-0.59	0.12±0.85	0.74±-0.68	0.42±-0.10
	D	0.37±0.60	0.52±-0.30	0.46±0.52	0.57±0.04	0.41±-0.04	0.30±0.34
	S+D	0.46±0.37	0.24±-0.49	0.30±0.28	0.26±0.45	0.38±-0.14	0.26±0.16
BW_{42}	S	0.17±-0.71	0.14±-0.99	0.12±-0.88	0.29±0.52	0.11±-0.33	0.35±-0.14
	D	0.22±0.78	0.44±-0.47	0.36±0.64	0.53±0.26	0.40±0.17	0.26±0.49
	S+D	0.47±0.29	0.13±-0.89	0.50±-0.29	0.28±0.39	0.38±0.07	0.24±0.19

S: Sire component, D: Dam component, S+D: sire+dam components, BW: Body weight and GR: Growth rate.

Table 8. Genetic (above diagonal) and phenotypic (below diagonal) correlations ± SE among growth rates at different periods of age for males and females of Japanese quail.

Base of estimates	Trait	Male			Female		
		GR$_{1-21}$	GR$_{22-42}$	$_{42-1}$GR	GR$_{1-21}$	GR$_{22-42}$	$_{42-1}$GR
S	GR$_{1-21}$		0.39±0.90	±0.210.94		0.93±0.39	±0.03-0.39
D			0.43±0.57	±0.500.53		0.59±0.04	0.35±0.04
S+D			±0.39-0.56	0.18±0.79		±0.40-0.11	±0.10-0.11
S	GR$_{22-42}$			0.53±0.85			±0.10-0.24
D		0.03±0.51		±0.570.41	±0.04-0.49		±0.160.78
S+D				±0.61-0.41			0.27±0.46
S	$_{42-1}$GR						
D					0.03±0.66		
S+D		±0.020.73	0.04±0.02		0.04±0.25		

S: Sire component, D: Dam component, S+D: sire+dam components and GR: Growth rate.

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الملخص العربى

توريث صفات وزن الجسم ومعدل النمو والموائمة فى السمان اليابانى

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استخدم 480 ذكر و480 أنثى نتجت من التزاوج العشوائى لعدد 61 أب مع 122 أمم فى تفريخـة واحده لتقدير المكافىء الوراثى والارتبـاط الوراثى والمظهرى لـوزن الجسم ومعدلات النمو خلال فترات النمو المختلفة و صفات الموائمة وذلك لتحديد أفضل الصفات الانتخابية للتحسين الوراثى المستقبلى فى ا لسمان اليابانى.

وقد تم التوصل الى النتائج التالية:

كانت الإناث أثقل معنوياً (P≤0.001) من الذكور عند عمر 28و 35و 42 يوم و كانت الفروق بين الجنسين 2.64و 4.92و 6.45و 10.87 جرام عند هذه الأعمار علـى التوالى. نفس الاتجاه لتأثير الجنس المعنوى لصالح الإناث وجد بالنسبة لمعدل النمو خـلال الفترات من 1- 21 و22-42 و1-42 يـوم من العمر (171.6-63.6-182.7% للإنـاث مقابل 171.2-60.9-182.1 % للذكور). أظهرت قيم المكافىء الوراثى لوزن الجسم ومعدل النمو مدى واسع من الاختلافات بغض النظر عن الجنس و طريقة التقدير (0.02- 0.95 لـوزن الجسم مقابل 0.01-0.71 لمعدل النمو) والاتجاه العام فى قيمة المكافىء الوراثى المقدر من مكونات تباين الأم كان أعلى من المقدر من مكونات تباين الأب بالنسبة لمعدل النمو للذكور خـلال جميـع فترات النمو وكذلك وزن الجسم . أيضا كانت قيمة العمق الوراثى لصفة الخصوبة المقدر من مكونات تبـاين الأب أعلى من المقدر من مكونات تباين الأم وعلى العكس من ذلك جـاءت قيم العمق الوراثى لصفات الفقس والحيويـة الذى ربما يرجع إلى التأثيرات الأمية على هذه الصفات. معدل النمو خـلال الفترات من 1-21 و

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Genetic Parameters, Body Weight, Growth Rate, Fitness, Japanese Quail.

1-42 فى الإناث والذكور كان يرتبط مظهريا ارتباط موجب مـع وزن الجسم عند جميـع الأعمـار ماعدا عمر الفقس وتتراوح قيمـة من 0.33-0.75 فى الـذكور و 0.02-0.75 فى الإنـاث. وبشكل عام كانت معظم الارتباطـات الو راثيـة بين معدلات النمو ذات قيم مرتفعـة. لذلك يمكن استخدام صفة وزن الجسم عند عمر 42 يوم أو معدل النمو خلال الفترة من 1-42 يوم من العمر للانتخـاب لتحسين صفات النمو فى السمان اليابانى نظرا لارتفاع قيم المكافىء الوراثى والارتباطات الو راثيـة لهاتان الصفتان مع صفات النمو الأخرى بالإضافة إلـى انخفـاض قيمـة الخطـاء المعيـارى لهمـا عن الصفات الأخرى.