

Mixed Model Genetic Analysis of Japanese Quail Data After Two Generations of Divergent Selection for Four Week Body Weight

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Abstract: The present study was carried out to evaluate the changes in body weight and Shank length traits after two generations of selection for 4-wk body weight. BLUP values were extrapolated and discussed. Generations exerted significance effect on body weights in both high line (HL) and low line (LL). Effect of incubation period (up to 17 days, *U-17* vs. more than 17 days, *M-17*) on body weight was found to be significant for both lines favoring early hatched group (*U-17*). The significance and persistent inferiority of body weight in the *M-17* could be attributed to a longer period of evaporation and/or consumption of preserved nutritive materials (mainly from yolk) resulting in reduced hatch weight of later hatched chicks. Significant generation effect on right Shank length (RSL_6 and RSL_8) of the HL was detected at 6 and 8 wk of age. However, the trend of progress in selection response in the HL was found to be vague especially in the second generation. Conversely, in case of the LL this trend appears to be fairly comprehensible. Females show general significant superiority as compared to males, in body weights and Shank length especially at later ages which may be due to the development of sex organs. Birds hatched after 17 days of incubation found to have significant heavier body weight and more elongated Shank length than those hatched later. However, base population has a greater percentage of those individuals who are possessing positive parent transmitting values, which may be due to consumption of the additive genetic variance in later generations consequently revealed in reduced ranges of BLUP values. Results revealed a clear trend of enhancement (positively in HL and negatively in LL) through the selected generations.

Keywords: Japanese quail, Divergent selection, Body weight, Shank length, BLUP, Parent transmitting values

INTRODUCTION

The breeding value of an individual is an aggregate expression of the information relative to a performance trait premeditated to predict its genetic potential as accurately as feasible. The genetic merit of an individual transmits to his offspring and therefore valid evaluation of traits' breeding values is fundamental information to be utilized in constructing breeding programs and managerial decisions (Chapman, 1985). From a genetic point of view improvement in animal breeding is expected to be achieved merely via accurate detection of the best animals as parents for the next generation (Chyr *et al.*, 1979).

Nevertheless; the existence of positive genetic relationship between skeletal dimensions and growth (Chambers, 1990) resulted in using the former to evaluate economic traits without the need to slaughter the birds. Garwood *et al.* (1989) found that the high density selected line had a longer Shank length than that in the low one.

Unlike long-term responses to selection, Short-term effects of selection for quantitative traits in birds and animals have been found to be in general agreement with theoretical expectations; (Clayton and Robertson, 1957; Yoo, 1980). Nevertheless, Marks and Lepore (1968) and Marks (1978) reported that initial selection responses for high 4-wk body weight in Japanese quail also follow theoretical expectations.

During their studies of divergent selection for body weight in Japanese quail Darden and Marks (1988a, b); Marks (1995); Nestor and Bacon (1982); Anthony *et al.* (1986); Nestor *et al.* (1996) and Moritsu *et al.* (1997) confirmed that high line was heavier than that selected for low body weight. Moreover, Nestor and Bacon (1982); Anthony *et al.* (1986); Moritsu *et al.* (1997) and

Okamoto *et al.* (1990) each one of them reported females' preponderance on males in body weight for all the selected lines.

BLUP under different procedures has found widespread usage in genetic evaluation of domestic animals because of its desirable statistical properties (Where it takes into consideration both fixed and random effects simultaneously). The properties of BLUP methodology developed by Henderson (1949) are similar to those of the selection index besides it maximizes the correlation between true breeding value (a) and the predicted one (\hat{a}) or minimizes prediction error variance (PEV) ($\text{Var}(a - \hat{a})$). Linear- predictors are linear functions of observations. Unbiased- estimation of realized values for a random variable such as animal breeding values and of estimable functions of fixed effects are unbiased ($E(a | \hat{a}) = \hat{a}$) and Prediction- involves prediction of true breeding values. Also Van der Werf *et al.* (1994) reported that prediction of breeding values using BLUP procedure has the property of minimizing the error variance.

MATERIALS AND METHODS

Experimental Birds were produced and raised at the experimental farm of the College of Agriculture, Suez Canal University, Al-Ismailia, Egypt. The Japanese quail base population (Derived from four hatches of a random mated flock) was used for subsequent divergent selection to produce the next two generations (G_1 and G_2). Eggs were collected daily and marked according to their respective pen number (Applying the biosecurity procedure). Healthy hatched chicks were leg banded. At 4 wk of age leg tags were replaced by wing bands. Feeds were allowed *ad libitum* in a mash form (diet with

24% and 20 % crude protein for growing and layer diets, respectively).

Selection and mating methods:

The topmost 2/3 ranked birds for 4-wk body weight was considered the high body weight line while the lowest 1/3 ranked ones was considered the low body weight line. At 5 wk of age, each female was assigned at random to a non-sib male from the same line.

Studied traits and statistical analysis:

Individual body weights (BW) were recorded at hatch, 2, 4, 6, 8 wk of age. However, right Shank length was measured only at 6 and 8 wk of age. Hatched chicks was assembled into two classes, the first (*U-17*) was for those chicks hatched up to the end of the 17th day of incubation process while the second one (*M-17*) was for those hatched after more than 17 (till 19 days from the beginning of incubation process).

Statistical analysis of variance was performed using LSMLMW program of Harvey (Harvey, 1990) to obtain Best Linear Unbiased Prediction (BLUP) of random effects, (i.e. quail parent); Best Linear Unbiased Estimators of fixed effects (BLUE) and Henderson III variance components using least squares procedure. Data were corrected for hatch effect by fitting least squares constants (Harvey, 1979). All factors affecting traits studied were analyzed using model (3) of Mixed Model Least Squares and Maximum Likelihood procedure (Harvey, 1990). Mean separation due to hatches or generations were applied by Duncan's multiple rang test (Duncan, 1955) utilizing SAS (1998). The following general model was used with few modifications according to the application:

$$Y_{ijkl} = \mu + L_i + S_j(L)_{ij} + F_k + e_{ijkl}$$

Where:

- Y_{ijkl} = The observation on $ijkl^{\text{th}}$ bird.
- μ = The overall mean for the trait under consideration.
- L_i = The fixed effect of the i^{th} line effect ($i=1, 2$ for high and low body weight selected lines, respectively).
- S_j = The random effect of the j^{th} parent quail nested within the fixed effect L_i
- F_k = The combined fixed effect of the k^{th} generation; hatch and incubation period.
- e_{ijkl} = The random error of observations.

The base linear parent model in matrix notation was as follows:

$$Y = X\beta + Zs + e$$

Where: Y denotes $n \times 1$ vector of observations of body weights (BW) at certain age where n epitomizes number of observations; β denotes $(p \times 1)$ column vector of unknown fixed effects of the combined generation, selection direction (Lines) and incubation period; at which p symbolizes the number of levels for fixed effects; s denotes $(q \times 1)$ column vector of unknown pair of parents random effect at which q indicates the number of levels for random effects; X denotes $(n \times p)$ known incidence matrix for fixed effects; Z denotes $(n \times q)$ known incidence matrix for random effects; e denotes

$(n \times 1)$ column vector of non-observable residual effects, which includes random environmental and non-additive genetic effects, assuming that these effects are normally and independently distributed $(0, \sigma^2_e)$.

Best Linear Unbiased Prediction (BLUP) values:

Though of its shortcoming, application of a sire model implies that only sires are evaluated, using progeny records. Most early applications of BLUP for the prediction of breeding values, especially in dairy cattle, were based on this model. The main advantage with a sire model is that the number of equations is reduced compared with an animal model since only sires are evaluated. It is the only applicable approach in monogamies birds and animals especially if reproduction requires some sort of courtship like that happening in pigeon and wild avian. However, with a sire model, the genetic merit of the mate (dam of progeny) is not accounted for. It is assumed that all mates are of similar genetic merit and this can result in bias in the predicted breeding values if there is preferential mating.

Spearman correlation coefficient between ranks was calculated to get the realized genetic correlation between the BLUP ranks extrapolated for different studied traits according to the following formula.

$$r_s = 1 - \left(\frac{6 \cdot \Sigma d^2}{n(n^2-1)} \right)$$

Where: d is the difference between each rank of corresponding values of x and y , and n is the number of pairs of values

RESULT AND DISCUSSION

Body weight (BW):

From Table (1); Generations exerted significance effect on body weights in both high line (HL; $P \leq 0.0001$) and low line (LL; $P \leq 0.01$, $P \leq 0.001$ or $P \leq 0.0001$). There was a general enhancement in HL body weight at all ages from hatch to 8 wk of age through base, G_1 and G_2 generations (Table 2). However; in the LL (Table 3) the trend was not very clear trend; though it appears to decrease in succeeding generations. Yet; the decrease in the second generation of the HL may be due to environmental conditions where the growing period of first generation was during winter while for the second generation was during relatively hot summer season. The enhancement in body weights (positively in HL and negatively in LL) especially in the first generation might be expressing the enhancement in genetic background of the populations as a response to selection.

As its expected in quails, females were found to have a significant ($P \leq 0.01$ or $P \leq 0.0001$; Table 1) higher body weights than males at most ages except that at earlier ages of life for both high and low body weight lines (Tables 2 & 3), especially when they approaching sexual maturity. Similar bisexual differentiation was also confirmed by Bahie El-Deen (1994 & 1999); Moritsu *et al.* (1997); Omran (1993); Caron *et al.* (1990) and Shebl *et al.* (1996). This sexual dimorphism in body weight with privilege to female in quails was

parallel with the development of sex organs and may be hormonally mediated.

Effect of incubation period was found to be significant (Table 1; $P \leq 0.01$ or $P \leq 0.0001$ for HL and $P \leq 0.01$, $P \leq 0.05$ or $P \leq 0.0001$ for LL) on body weight favoring early hatched group (*U-17*). The significant and persistent inferiority of *M-17* body weight could be attributed to a greater period of evaporation and/or consumption of preserved nutritive materials (mainly from yolk) resulting in reduced hatch weight of later hatched chicks. The superiority of body weight of *U-17* group may be a reflection of a pre-hatch higher embryonic growth rate; which seemed to continue after hatch.

Right Shank length (RSL):

Results in Table (4) revealed presence of significant ($P \leq 0.01$, $P \leq 0.001$, $P \leq 0.0001$, $P \leq 0.05$) generation effect on right Shank length (RSL_6 and RSL_8) of the HL. However; the trend of progress in selection response in the HL was found to be vague especially in the second generation, (Table 5). Conversely; in case of the LL this trend appears to be fairly comprehensible.

Significant sex effect ($P \leq 0.0001$ for HL and $P \leq 0.05$, $P \leq 0.01$ for LL) was assigned on RSL (Table 4), females was found to have longer shanks compared to males at 6 and 8 wk of age (Table 5). Nonetheless; RSL was found to be significantly higher in *U-17* group of HL at 6 wk of age, while incubation period exerted none significant effect at all studied ages for LL (Table 5).

Best Linear Unbiased Prediction (BLUP):

Regarding high-body-weight selected group (HL) of the base population and first generation sires' proof (Table 6 and 7; respectively), there was a tendency of

the BLUP values of body weight ranges to get wider as quails advance in age. The same trend was also visible in case of the higher 30% sires (i.e. sires expected to be selected as parents for the next generation), however the percentage of positive records of body weight in the two evaluated population were greater than 45% and 42% in the high- and low-body weight generations; respectively. Conversely, in case of right Shank length RSL at 6 and 8 wk of age the range of BLUP values tends to get smaller as age gets advanced in the high- and low-body weight lines. However, the percentage of positive records of right Shank length RSL in the evaluated population were somewhat greater than 55% and 40% in the high- and low-body weight generations; respectively.

As regard to the low-body-weight selected group (LL) of the base population and first generation sires' proof (Table 6 and 7; respectively), it was found that these values ranged from 3.58 to 35.03g with a tendency of the range to get broader (generally similar to high-body-weight selected group) as birds advance in age till 6 wk of age though these ranges decreased thereafter at 8 wk of age. In the same manner, it appeared that in case of lower 30% sires, the percentage of negative records in the evaluated population was greater than 40% and 44% in the base population and first generation; respectively. On the contrary, in case of right Shank length RSL at 6 and 8 wk of age the range of BLUP values tends to get lower as age gets increased in the high- and low-body weight lines. However, the percentage of positive records of right Shank length RSL in the evaluated population were somewhat greater than 44% and 58% in the high- and low-body weight generations; respectively.

Table (1): Least squares analysis of variance of factors affecting body weights of both selected high and low line Japanese quail from hatch to 8 wk of age for all generations.

Selected high body weight line											
Source of variance	df	BW ₀		BW ₂		BW ₄		BW ₆		BW ₈	
		MS	Prob.	MS	Prob.	MS	Prob.	MS	Prob.	MS	Prob.
Generation (G)	2	30.08	0.0001	3386.53	0.0001	45422.56	0.0001	38483.79	0.0001	12352.20	0.0001
Parent: Generation	335	2.51	0.0001	114.25	0.0001	610.19	0.0001	969.81	0.0001	988.30	0.0001
Sex (S)	1	0.09	0.5428	1.42	0.8613	2075.42	0.0082	28465.47	0.0001	249082.24	0.0001
Incubation period (I)	1	58.58	0.0001	5573.95	0.0001	19899.55	0.0001	11611.17	0.0001	3679.81	0.0028
(GxS) Interaction	2	0.08	0.7337	116.64	0.0821	260.88	0.4140	503.32	0.3272	815.94	0.1372
(GxI) Interaction	2	9.01	0.0001	849.82	0.0001	3779.89	0.0001	3207.00	0.0008	1181.75	0.0564
(SxI) Interaction	1	0.09	0.5550	53.50	0.2840	199.43	0.4116	546.28	0.2709	199.38	0.4858
Remainder	1346	0.25		46.57		295.63		450.20		410.18	
Selected low body weight line											
Source of variance	df	BW ₀		BW ₂		BW ₄		BW ₆		BW ₈	
		MS	Prob.	MS	Prob.	MS	Prob.	MS	Prob.	MS	Prob.
Generation (G)	2	1.76	0.4763	1084.62	0.0001	5093.21	0.0002	8311.70	0.0001	5521.43	0.0015
Parent : Generation	209	2.37	0.0001	113.83	0.0001	555.62	0.0001	898.20	0.0001	819.70	0.0001
Sex (S)	1	0.27	0.2983	37.70	0.4175	771.91	0.1122	3458.31	0.0076	20154.86	0.0001
Incubation period (I)	1	6.86	0.0001	583.43	0.0015	2533.09	0.0041	2554.37	0.0216	307.58	0.3874
(G x S) Interaction	2	0.58	0.1020	39.57	0.5016	31.63	0.9016	75.05	0.8558	493.73	0.3016
(G x I) Interaction	2	2.19	0.0002	248.92	0.0133	1483.15	0.0080	2080.51	0.0137	73.76	0.8358
(S x I) Interaction	1	0.42	0.2003	57.47	0.3169	73.72	0.6232	22.68	0.8283	0.12	0.9865
Remainder	666	0.25		57.29		305.19		481.70		411.19	

BW₀, BW₂, BW₄, BW₆, BW₈= Body weight at hatch, 2, 4, 6, 8 wk of age, respectively.

Table (2): Least squares means±SE of different factors affecting body weight trait of selected high line Japanese quail from hatch to 8 wk of age for all generations.

	Effects	No. Obs	Traits						
			BW ₀	BW ₂	BW ₄	BW ₆	BW ₈		
Overall Means	MU	1691	8.44±0.06	34.42±0.36	95.20±0.81	164.68±1.03	204.34±1.05		
	Generation (G)	B.P.	705	8.18 ^c ±0.10	35.18 ^b ±0.62	89.95 ^b ±1.42	161.20 ^b ±1.80	199.28 ^a ±1.82	
		G ₁	524	8.39 ^b ±0.09	36.88 ^a ±0.55	106.82 ^a ±1.25	175.24 ^a ±1.58	209.93 ^a ±1.62	
		G ₂	462	8.76 ^a ±0.11	31.20 ^c ±0.68	88.83 ^b ±1.55	157.59 ^c ±1.96	203.80 ^b ±2.00	
	Sex (S)	Female	878	8.45 ^a ±0.06	34.46 ^a ±0.41	96.58 ^a ±0.95	169.78 ^a ±1.19	219.44 ^a ±1.19	
		Male	813	8.43 ^a ±0.06	34.39 ^a ±0.42	93.82 ^b ±0.98	159.57 ^b ±1.24	189.24 ^b ±1.24	
	Incubation period (I)	U-17	1207	8.74 ^a ±0.06	37.38 ^a ±0.41	100.78 ^a ±0.95	168.94 ^a ±1.19	206.74 ^a ±1.19	
		M-17	484	8.14 ^b ±0.06	31.47 ^b ±0.49	89.61 ^b ±1.16	160.41 ^b ±1.45	201.93 ^b ±1.44	
	Interaction Means	B.P.	Female	378	8.17 ^a ±0.09	35.61 ^a ±0.67	91.98 ^a ±1.58	167.08 ^a ±1.98	213.80 ^a ±1.98
			Male	327	8.18 ^a ±0.10	34.76 ^a ±0.70	87.92 ^b ±1.63	155.32 ^b ±2.05	184.76 ^b ±2.05
G x S interaction		G ₁	Female	257	8.41 ^a ±0.10	37.13 ^a ±0.67	108.39 ^a ±1.55	180.81 ^a ±1.95	226.68 ^a ±1.96
			Male	267	8.36 ^a ±0.09	36.64 ^a ±0.65	105.24 ^b ±1.52	169.67 ^b ±1.91	193.18 ^b ±1.92
G ₂		Female	243	8.77 ^a ±0.10	30.64 ^a ±0.73	89.35 ^a ±1.69	161.45 ^a ±2.13	217.83 ^a ±2.14	
		Male	219	8.75 ^a ±0.12	31.75 ^a ±0.81	88.30 ^a ±1.90	153.73 ^b ±2.38	189.77 ^b ±2.40	
G x I interaction		B.P.	U-17	602	8.24 ^a ±0.08	35.92 ^a ±0.61	90.61 ^a ±1.43	160.89 ^a ±1.79	200.02 ^a ±1.79
			M-17	103	8.12 ^b ±0.14	34.44 ^b ±1.05	89.30 ^a ±2.46	161.51 ^a ±3.09	198.54 ^a ±3.09
		G ₁	U-17	259	8.76 ^a ±0.11	41.46 ^a ±0.76	115.15 ^a ±1.77	181.08 ^a ±2.23	211.21 ^a ±2.24
			M-17	265	8.01 ^b ±0.11	32.31 ^b ±0.75	98.49 ^b ±1.75	169.39 ^b ±2.21	208.65 ^a ±2.22
G ₂	U-17	346	9.23 ^a ±0.10	34.75 ^a ±0.72	96.60 ^a ±1.69	164.86 ^a ±2.12	208.98 ^a ±2.13		
	M-17	116	8.29 ^b ±0.15	27.64 ^b ±1.07	81.06 ^b ±2.48	150.33 ^b ±3.12	198.62 ^b ±3.14		
S x I interaction	Female	U-17	615	8.74 ^a ±0.06	37.65 ^a ±0.47	102.61 ^a ±1.11	174.79 ^a ±1.38	222.29 ^a ±1.37	
		M-17	263	8.16 ^b ±0.07	31.27 ^b ±0.58	90.54 ^b ±1.40	164.77 ^b ±1.75	216.58 ^b ±1.71	
	Male	U-17	592	8.74 ^a ±0.06	37.11 ^a ±0.47	98.95 ^a ±1.11	163.09 ^a ±1.38	191.19 ^a ±1.37	
		M-17	221	8.12 ^b ±0.07	31.66 ^b ±0.63	88.69 ^b ±1.54	156.05 ^b ±1.91	187.29 ^b ±1.86	

BW₀, BW₂, BW₄, BW₆, BW₈= Body weight at hatch, 2, 4, 6, 8 wk of age, respectively.

B.P. = Base population, G₁= The first generation, G₂= The second generation.

U-17= the class of incubation period for those chicks hatched up to the end of the 17 days from the beginning of the incubation process.

M-17= the class of incubation period for those chicks hatched till 19 days from the beginning of the incubation process.

For the main effects: any three generation or two means of sex or incubation period without a common superscript are significant different (P< 0.05).

For the interaction effects: any two sexes means within generation or any two periods means within generation or any two periods within sex without a common superscript are significant different (P< 0.05).

These results make clear that selection for BW traits in the evaluated population is quite possible and there is correlated selection response in case of the right shank length of the Japanese Quail selected population.

When comparing the two evaluated populations (i.e. base versus 1st generations) and in case of the high-body-weight selected line; it was found that apart from ages, ranges of body weights BLUP values were generally higher in the 1st generation as compared to the base ones. However, there is a general tendency of the base population to have a greater percentage of those individuals who are possessing positive Parent transmitting values. The previous results may reveal that selection in the base population has resulted in some reduction (consumption) of the additive genetic variance consequently revealed in reduced ranges of BLUP values. The greater percentage of individuals having positive BLUP values may normally support this

conclusion of a greater variability and therefore greater relative numbers to choose from.

As regard to the low-body-weight selected line; it was found that ranges of body weights' BLUP values were reordered to what happened with the high-body-weight selected line, and generally higher in the base population as compared to the 1st generation, meanwhile, percentage of individuals having negative parent transmitting values were somewhat greater the 1st generation. However, combining the results of the spearman's correlation coefficients with the ranges of BLUP values, it seemed that phenotypic selection didn't consume a lot of the additive genetic variance which in turn didn't rationally change the ranges of BLUP estimates. Nevertheless, Spearman's studies revealed the low and insignificant relationships between the phenotypic and genetic ranks in both generations which might prevent from the exploitation of the present additive genetic variance; (Table 6).

Table (3): Least squares means±SE of different factors affecting body weight trait selected low line Japanese quail from hatch to 8 wk of age for all generations.

Effects	No. Obs	Traits							
		BW ₀	BW ₂	BW ₄	BW ₆	BW ₈			
MU	885	8.01±0.18	30.38±1.13	84.68±2.48	150.11±3.16	191.54±3.04			
Overall Means	Generation (G)	B.P.	705	8.16 ^a ±0.10	35.00 ^a ±0.65	89.71 ^b ±1.41	160.85 ^a ±1.80	199.03 ^a ±1.73	
		G ₁	153	7.95 ^b ±0.18	32.76 ^a ±1.21	95.90 ^a ±2.65	162.08 ^a ±3.37	202.38 ^a ±3.24	
		G ₂	27	7.92 ^b ±0.40	23.37 ^b ±2.77	68.44 ^c ±6.11	127.39 ^b ±7.77	173.20 ^b ±7.43	
	Sex (S)	Female	467	8.06 ^a ±0.18	30.96 ^a ±1.26	87.33 ^a ±2.79	155.71 ^a ±3.54	205.05 ^a ±3.38	
		Male	418	7.96 ^a ±0.19	29.79 ^a ±1.42	82.04 ^a ±3.18	144.51 ^b ±4.03	178.02 ^b ±3.82	
	Incubation period (I)	U-17	749	8.29 ^a ±0.18	32.95 ^a ±1.13	90.04 ^a ±2.47	155.48 ^a ±3.14	193.40 ^a ±3.03	
M-17		136	7.73 ^b ±0.19	27.81 ^b ±1.61	79.33 ^b ±3.63	144.73 ^b ±4.59	189.67 ^a ±4.32		
Interaction Means	G x S interaction	B.P.	Female	378	8.12 ^a ±0.10	35.32 ^a ±0.76	91.75 ^a ±1.69	167.07 ^a ±2.15	213.86 ^a ±2.05
			Male	327	8.19 ^a ±0.11	34.69 ^a ±0.79	87.68 ^b ±1.75	154.64 ^b ±2.22	184.20 ^b ±2.12
		G ₁	Female	73	7.91 ^a ±0.18	32.44 ^a ±1.36	97.82 ^a ±3.03	168.94 ^a ±3.84	219.13 ^a ±3.64
			Male	80	8.00 ^a ±0.19	33.08 ^a ±1.41	93.98 ^a ±3.14	155.22 ^b ±3.98	185.62 ^b ±3.78
	G ₂	Female	16	8.15 ^a ±0.36	25.13 ^a ±2.93	72.43 ^a ±6.57	131.11 ^a ±8.32	182.16 ^a ±7.86	
		Male	11	7.69 ^b ±0.46	21.61 ^a ±3.69	64.46 ^a ±8.28	123.67 ^a ±10.48	164.24 ^b ±9.90	
	G x I interaction	B.P.	U-17	602	8.22 ^a ±0.09	35.73 ^a ±0.64	90.37 ^a ±1.43	160.57 ^a ±1.81	199.80 ^a ±1.72
			M-17	103	8.10 ^b ±0.15	34.27 ^a ±1.11	89.06 ^a ±2.47	161.14 ^a ±3.13	198.26 ^a ±2.98
		G ₁	U-17	125	8.30 ^a ±0.17	37.03 ^a ±1.31	105.10 ^a ±2.92	171.86 ^a ±3.70	205.01 ^a ±3.51
			M-17	28	7.61 ^b ±0.28	28.49 ^b ±2.09	86.70 ^b ±4.66	152.30 ^b ±5.91	199.74 ^a ±5.60
		G ₂	U-17	22	8.35 ^a ±0.27	26.07 ^a ±2.20	74.65 ^a ±4.93	134.02 ^a ±6.24	175.39 ^a ±5.89
			M-17	5	7.49 ^b ±0.55	20.66 ^a ±4.42	62.23 ^a ±9.91	120.76 ^b ±12.55	171.01 ^a ±11.86
S x I interaction	Female	U-17	394	8.37 ^a ±0.18	33.93 ^a ±1.31	93.13 ^a ±2.90	161.33 ^a ±3.68	206.90 ^a ±3.51	
		M-17	73	7.75 ^b ±0.20	27.99 ^b ±1.71	81.53 ^b ±3.86	150.08 ^b ±4.88	203.20 ^a ±4.59	
	Male	U-17	355	8.21 ^a ±0.18	31.96 ^a ±1.33	86.94 ^a ±2.96	149.64 ^a ±3.76	179.90 ^a ±3.58	
		M-17	63	7.72 ^b ±0.21	27.62 ^b ±2.01	77.13 ^b ±4.56	139.38 ^b ±5.75	176.14 ^a ±5.38	

BW₀, BW₂, BW₄, BW₆, BW₈= Body weight at hatch, 2, 4, 6, 8 wk of age, respectively.

B.P.= Base population, G₁= The first generation, G₂= The second generation.

U-17= the class of incubation period for those chicks hatched up to the end of the 17 days from the beginning of the incubation process.

M-17= the class of incubation period for those chicks hatched till 19 days from the beginning of the incubation process.

For the main effects: any three generation or two means of sex or incubation period without a common superscript are significant different (P≤ 0.05).

For the interaction effects: any two sexes means within generation or any two periods means within generation or any two periods within sex without a common superscript are significant different (P≤ 0.05).

Table (4): Least squares analysis of variance of factors affecting right shank length for the selected high and low lines of all generations (base population, 1st, and 2nd generation) of Japanese quail at 6 and 8 wk of age.

Selected high body weight line						
Source of variance	RSL ₆			RSL ₈		
	df	MS	Prob.	df	MS	Prob.
Generation (G)	2	57.37	0.0012	2	101.25	0.0000
Parent : Generation	335	8.37	0.0000	328	7.75	0.0000
Sex (S)	1	149.04	0.0000	1	186.40	0.0000
Incubation period (I)	1	7.23	0.0700	1	0.99	0.4368
(G x S) Interaction	2	2.32	0.3483	2	1.73	0.3484
(G x I) Interaction	2	1.59	0.4847	2	1.26	0.4629
(S x I) Interaction	1	2.03	0.3367	1	1.97	0.2725
Remainder	1346	2.20		1284	1.64	
Selected low body weight line						
Source of variance	RSL ₆			RSL ₈		
	df	MS	Prob.	df	MS	Prob.
Generation (G)	2	10.35	0.3041	2	13.92	0.1943
Parent : Generation	209	8.65	0.0000	198	8.43	0.0000
Sex (S)	1	11.75	0.0261	1	8.89	0.0329
Incubation period (I)	1	1.08	0.5000	1	1.26	0.4207
(G x S) Interaction	2	2.41	0.3611	2	2.33	0.3019
(G x I) Interaction	2	1.61	0.5056	2	1.10	0.5670
(S x I) Interaction	1	14.98	0.0120	1	8.76	0.0342
Remainder	666	2.36		627	1.94	

RSL₆, RSL₈=Right shank length at 6, 8 wk of age, respectively.

Table (5): Least squares means \pm SE of different factors affecting right shank length for the selected high and low lines of all generations (base population, 1st, and 2nd generation) of Japanese quail at 6 and 8 wk of age.

Effects	Traits								
	HL			LL					
	No. Obs	RSL ₆	RSL ₈	No. Obs	RSL ₆	RSL ₈			
MU		1691	40.45 \pm 0.10	40.93 \pm 0.10	885	39.78 \pm 0.33	40.19 \pm 0.33		
Overall Means	Generation (G)	B.P.	705	40.25 ^b \pm 0.17	40.68 ^b \pm 0.17	705	40.23 ^a \pm 0.19	40.65 ^a \pm 0.19	
		G ₁	524	40.19 ^b \pm 0.15	40.57 ^b \pm 0.16	153	39.92 ^a \pm 0.34	40.10 ^b \pm 0.34	
		G ₂	462	40.90 ^a \pm 0.19	41.53 ^a \pm 0.10	27	39.19 ^b \pm 0.76	39.82 ^b \pm 0.76	
	Sex (S)	Female	878	40.82 ^a \pm 0.11	41.35 ^a \pm 0.10	467	40.11 ^a \pm 0.35	40.48 ^a \pm 0.34	
		Male	813	40.08 ^b \pm 0.11	40.50 ^b \pm 0.11	418	39.46 ^b \pm 0.37	39.90 ^b \pm 0.36	
	Incubation period (I)	U-17	1207	40.55 ^a \pm 0.11	40.89 ^a \pm 0.10	749	39.67 ^a \pm 0.33	40.06 ^a \pm 0.33	
		M-17	484	40.34 ^a \pm 0.12	40.97 ^a \pm 0.12	136	39.89 ^a \pm 0.40	40.32 ^a \pm 0.39	
	Interaction Means	B.P.	Female	378	40.70 ^a \pm 0.18	41.14 ^a \pm 0.17	378	40.57 ^a \pm 0.20	41.03 ^a \pm 0.20
			Male	327	39.80 ^b \pm 0.18	40.23 ^b \pm 0.18	327	39.89 ^b \pm 0.21	40.27 ^b \pm 0.21
		(G x S)	G ₁	Female	257	40.55 ^a \pm 0.18	41.04 ^a \pm 0.18	73	40.06 ^a \pm 0.36
Male			267	39.84 ^b \pm 0.17	40.09 ^b \pm 0.17	80	39.78 ^a \pm 0.37	39.97 ^a \pm 0.38	
G ₂		Female	243	41.21 ^a \pm 0.19	41.88 ^a \pm 0.19	16	39.69 ^a \pm 0.74	40.18 ^a \pm 0.72	
		Male	219	40.59 ^b \pm 0.22	41.18 ^b \pm 0.21	11	38.69 ^a \pm 0.94	39.46 ^a \pm 0.91	
B.P.		U-17	602	40.34 ^a \pm 0.16	40.73 ^a \pm 0.15	602	40.32 ^a \pm 0.17	40.69 ^a \pm 0.17	
		M-17	103	40.16 ^a \pm 0.27	40.63 ^a \pm 0.26	103	40.15 ^a \pm 0.30	40.61 ^a \pm 0.29	
(G x I)		G ₁	U-17	259	40.22 ^a \pm 0.20	40.51 ^a \pm 0.20	125	39.78 ^a \pm 0.34	39.87 ^a \pm 0.47
		M-17	265	40.17 ^a \pm 0.20	40.63 ^a \pm 0.20	28	40.06 ^a \pm 0.55	40.32 ^a \pm 0.59	
G ₂		U-17	346	41.09 ^a \pm 0.19	41.42 ^a \pm 0.19	22	38.92 ^a \pm 0.56	39.61 ^a \pm 0.54	
		M-17	116	40.70 ^b \pm 0.28	41.64 ^a \pm 0.27	5	39.47 ^a \pm 1.12	40.03 ^a \pm 1.09	
(S x I)		Female	U-17	615	40.97 ^a \pm 0.12	41.36 ^a \pm 0.11	394	40.20 ^a \pm 0.35	40.50 ^a \pm 0.36
			M-17	263	40.67 ^b \pm 0.14	41.35 ^a \pm 0.13	73	40.02 ^a \pm 0.42	40.45 ^a \pm 0.41
	Male	U-17	592	40.14 ^a \pm 0.12	40.41 ^a \pm 0.11	355	39.14 ^b \pm 0.36	39.61 ^b \pm 0.36	
		M-17	221	40.02 ^a \pm 0.15	40.59 ^a \pm 0.14	63	39.77 ^a \pm 0.47	40.19 ^a \pm 0.45	

RSL₆, RSL₈=Right shank length at 6, 8 wk of age, respectively. B.P. = Base population, G₁= The first generation, G₂= The second generation. Incubation period: U-17= incubation period of 17 days, M-17= incubation period of 18 or 19 days.

However, the trend of reducing the BLUP values in the successive generations, revealed in body weights, is reversed in case of right shank length (RSL). In this case, it seems that RSL as a conformational trait is not subjected to transitional natural selection as it is in the traits related with the bird fitness (*i.e.* bird's weight). It appears that phenotypic selection didn't utilize a lot of the additive genetic variance which in turn didn't practically change the ranges of BLUP values. On the other hand, Spearman's coefficients exposed the low to intermediate insignificant relationships between the phenotypic and genetic ranks in both generations which might prevent from the exploitation of the present additive genetic variance; (Tables 6 & 7).

When considering the spearman correlation coefficient between phenotypic and genetic ranks of the sires, results in Table (6) revealed that- apart from positive or negative sign- correlation gets higher as birds advance in age with a general tendency of these figures to range from low to moderate. However, the greater correlation value between ranks being in the same direction between phenotypic and genetic ranks was at 8th wk of age. Negative figures at med-ages (e.g. 2nd and 4th wk of age) means that phenotypic selection will not accompanied with the desired genetic gain.

Considering the spearman correlation coefficient of the low-body-weight selected group of the base

population (Table 6), it was found that the correlation values (neglecting the sign) get higher as birds advance in age till 6 wk of age then it dramatically decreased with the significance being at 6 and 8 wk of age ($P \leq 0.05$). What's more, correlation figures ranged from low to moderate values and the greater and significant correlation values between ranks being at 6 wk of age. The negative figures appeared but insignificantly only at hatch.

For the high- body- weight selected line of the first generation, the spearman correlation coefficient between phenotypic and genetic ranks (Table 7), was found to get higher as birds advance in age with a higher significant correlation value between phenotypic and genetic ranks being in the same direction at 4th and 8th wk of age. Ultimately, the spearman correlation coefficient of the low-body-weight line of the sires of the first generation, shown in Table 7, revealed that the correlation values had no obvious trend, the higher and the only significant correlation value of ranks being in the same direction between phenotypic and genetic ranks was only in the second week of age.

The pervious results indicate that if selection is to be made on phenotypic values it should be later in life as possible to get reliable result from selection. In this respect, the latest conclusions set great advantage on using genetic values to select individuals with an extra

economic benefit of reducing the generation interval. Therefore, if selection is meant to be made at earlier ages to get the desired genetic gain and reduce the

generation intervals and selection cost, parent transmitting values should be used for this task or function.

Table (6): Minimum, maximum estimates and the range of sire Transmitting abilities (STV) of the base population individuals along with STV of the superior (for HL*) and inferior (for LL*) 30% sires and the number, percentage of sires that possess positive (for HL) and negative (for LL) SBV according to the direction and spearman correlation coefficients between phenotypic and genetic ranks for respective body weight traits of Japanese quail from hatch to 8 wk of age.

High body weight line (Base population)								
Traits	Minimum	Maximum	Range	Upper 30%		Positive records		Spearman Correlation
				Min	Range	Number	%	
BW ₀	-1.33	1.96	3.30	0.23	1.74	45	48.91	0.023 ^{ns}
BW ₂	-6.55	8.56	15.12	1.49	7.07	46	50.00	-0.197 ^{ns}
BW ₄	-17.79	17.03	34.82	3.64	13.39	50	54.35	-0.103 ^{ns}
BW ₆	-20.46	17.32	37.78	4.36	12.96	42	45.65	0.201 ^{ns}
BW ₈	-19.65	24.63	44.28	3.77	20.86	50	54.35	0.451 [*]
RSL ₆	-1.233	1.5819	2.8144	0.2518	1.3301	51	55.435	0.242 [*]
RSL ₈	-1.337	1.3893	2.7261	0.2784	1.1109	51	55.435	0.332 [*]
Low body weight line (Base population)								
Traits	Minimum	Maximum	Range	Lower 30%		Negative records		Spearman Correlation
				Max	Range	Number	%	
BW ₀	-1.19	2.39	3.58	-0.28	0.9	16	53.33	-0.081 ^{ns}
BW ₂	-5.92	6.37	12.29	-1.13	4.79	16	53.33	0.037 ^{ns}
BW ₄	-11.7	13.67	25.36	-3.67	8.03	17	56.67	0.077 ^{ns}
BW ₆	-17.42	17.61	35.03	-4.7	12.72	13	43.33	0.399 [*]
BW ₈	-16.88	17.47	34.35	-4.46	12.42	12	40.00	0.373 [*]
RSL ₆	-1.133	0.9122	2.0447	-0.179	0.9534	12	40	0.170 ^{ns}
RSL ₈	-1.032	0.746	1.7783	-0.37	0.6624	12	40	0.250 ^{ns}

* HL and LL = the lines selected for high and low 4 wk of age body weight, respectively.

BW₀, BW₂, BW₄, BW₆, BW₈= Body weight at hatch, 2, 4, 6, 8 wk of age, respectively.

Table (7): Minimum, maximum estimates and the range of sire Transmitting abilities (STV) of the first generation individuals along with STV of the superior (for HL*) and inferior (for LL*) 30% sires and the number, percentage of sires that possess positive (for HL) and negative (for LL) SBV according to the direction and spearman correlation coefficients between phenotypic and genetic ranks for respective body weight traits of Japanese quail from hatch to 8 wks of age.

High body weight line (1 st G)								
Traits	Minimum	Maximum	Range	Upper 30%		Positive records		Spearman Correlation
				Min	Range	Number	%	
BW ₀	-1.49	2.05	3.54	0.16	1.89	33	42.86	0.008 ^{ns}
BW ₂	-6.79	10.46	17.25	1.22	9.24	34	44.16	0.114 ^{ns}
BW ₄	-12.29	17.45	29.74	2.56	14.90	37	48.05	0.266 [*]
BW ₆	-18.63	25.84	44.47	3.98	21.86	39	50.65	0.176 ^{ns}
BW ₈	-27.43	31.68	59.11	4.47	27.21	33	42.86	0.254 [*]
RSL ₆	-1.514	1.7954	3.3091	0.4569	1.3385	45	58.442	0.247 [*]
RSL ₈	-1.685	1.5085	3.1931	0.3574	1.1511	45	58.442	0.295 [*]
Low body weight line (1 st G)								
Traits	Minimum	Maximum	Range	Lower 30%		Negative records		Spearman Correlation
				Max	Range	Number	%	
BW ₀	-0.40	0.43	0.83	-0.23	0.17	5	55.56	0.267 ^{ns}
BW ₂	-2.54	3.40	5.94	-1.28	1.26	5	55.56	-0.780 [*]
BW ₄	-6.84	8.29	15.13	-1.82	5.02	5	55.56	-0.243 ^{ns}
BW ₆	-8.50	10.69	19.19	-2.97	5.53	5	55.56	0.000 ^{ns}
BW ₈	-6.54	5.58	12.12	-3.78	2.76	4	44.44	0.412 ^{ns}
RSL ₆	-0.681	0.5477	1.2282	-0.297	0.3838	5	55.556	0.371 ^{ns}
RSL ₈	-0.581	0.4858	1.0665	-0.209	0.3718	4	44.444	0.486 ^{ns}

* HL and LL = the lines selected for high and low 4 wk of age body weight, respectively.

BW₀, BW₂, BW₄, BW₆, BW₈= Body weight at hatch, 2, 4, 6, 8 wk of age, respectively.

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التحليل الوراثي باستخدام طريقة النموذج المُختلط لبيانات السمان الياباني بعد جيلين من الانتخاب في الاتجاهين المتضادين لصفة وزن الجسم عند عمر ٤ أسابيع

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أجريت هذه الدراسة - بمزرعة كلية الزراعة-جامعة قناة السويس - بغرض التقييم الوراثي لصفات وزن الجسم وطول الساق بعد جيلين من الانتخاب لصفة وزن الجسم عند عمر ٤ أسابيع في الاتجاهين المتضادين (الموجب والسالب)، كما تم تقدير ومناقشة قيم الـ BLUP للسمان الياباني. شملت العوامل المدروسة تأثير كل من الجيل، إتجاه الانتخاب، طول فترة التفريخ، الجنس (ذكر، أنثى). كان تأثير الجيل على صفات وزن الجسم معنوياً في كل من الخطتين المنتخبتين (خط وزن الجسم العالي ووزن الجسم المنخفض)، كما ظهر أيضاً تأثير طول فترة التفريخ على صفات وزن الجسم معنوياً مفضلاً الأفراد التي فقست عند ١٧ يوم من بداية التفريخ وقد تم إرجاع أسباب عدم تفوق الأفراد التي فقست بعد ١٧ يوم من بداية التفريخ إلى احتمالية زيادة معدل البخر (جفاف نسبي)، وإستهلاك المواد الغذائية كالصغار مما أدى إلى إنخفاض وزن الجسم عند الفقس وبعد الفقس. ظهر أيضاً تأثير الجيل معنوياً على صفة طول الساق عند عمر ٦ و ٨ أسابيع في الخط المنتخبتين لوزن الجسم العالي. وعلى أية حال وجد أن الإستجابة للانتخاب في الجيل الثاني كان إلى حد ما مبهمه على العكس من وضوح إتجاه التغير في حالة الخط المنتخبتين لوزن الجسم المنخفض. أظهرت الإناث تفرقاً معنوياً على الذكور في صفات وزن الجسم وطول الساق خاصة في الأعمار الكبيرة (٦ و ٨ أسابيع) والذي قد يكون راجع إلى تطور الأعضاء الجنسية الأنثوية. وجد أن الأفراد التي فقست بعد ١٧ يوم من بداية التفريخ تفوقت بصورة معنوية في وزن الجسم على الأفراد التي فقست بعد هذه الفترة. وجد أن جيل الأساس ضم نسبة عالية من الأفراد التي قامت بالتوريث كأباء وهذا قد يكون راجع إلى إستهلاك التباين الوراثي التجمعي في الأجيال التالية مما أدى إلى إنخفاض المدى بين قيم الـ BLUP. وقد أظهرت النتائج إتجاه واضح ولكن غير متوازى القدر للإستجابة للانتخاب وذلك من خلال التحسن الإيجابي في حالة الخط المنتخبتين لوزن الجسم العالي والتحسن السلبي في الخط المنتخبتين لوزن الجسم المنخفض في كل الأجيال المنتخبة.