Genetic evaluation for some productive traits in Japanese quail by used Animal Model

Ramzy, A. A.

Department of Animal Production, Faculty of Agriculture, Al-Azhar University, Nasr City, Egypt.

ABSTRACT:

The present study aimed to estimate Japanese quail's productive traits' genetic markers by used animal model. BW_0, BW_2, BW_4 and BW_6 were 9.32, 64.78, 142.23 and 213.50 gram respectively, while average daily increase. ADI_{0-2}, ADI_{2-4}, ADI_{4-6} and ADI_{0-6} were 3.96, 5.53. 5.09 and 4.86 gram respectively. The additive genetic ($\sigma^2 a$), remainder ($\sigma^2 e$), phenotypic variances ($\sigma^2 p$) and heritability (h^2) are 10.4, 4.2, 14.6 and .71 for **BW_0** while and they were 195, 96, 291 and .67 for **BW_2.** And 715, 432, 1147 and .62 for **BW4** and 1950, 1500, 3450 and 0.57 for **BW6**.The Minimum of breeding of BW_0, BW_2, BW_4 and BW6 were 7.05, 46.73, 119.21 and 192.66 while Maximum of breeding of BW_0, BW_2, BW_4 and BW_6 were 11.44, 79.41, 171.62 and 237.85. **The** minimum of breeding value of ADI_{0-2}, ADI_{2-4}, ADI_{4-6} and ADI_{0-6} were -0.832, -2.37, -1.35 and -0.338 while maximum of breeding value of ADI_{0-2}, ADI_{2-4}, ADI_{4-6} and ADG_{0-6} were 0.73, 1.356, 1.326 and 0.403.In the end, we notice the superiority of the resulting offspring in terms of their educational value of body weights over the generation of parents, and also superiority in the rate of daily gain increase. Therefore, it is recommended to use these offspring in basic clans for the selection of useful body weights and the rate of daily gain increase because it is one of the important productive characteristics and the establishment of a line for the production of meat.

KEYWORDS: Genetic Evaluation, productive Traits, quail, Animal Model

1. INTRODUCTION:

The Japanese quail is one of the most productive bird species. They have a significant effect on the industrial poultry sector due to their high egg and meat output. (**Boni et al., 2010**). Additionally, the advantages they have for breeding include a short generational gap, a small area of floor, high reproductive effectiveness, early sex maturity, quick growth, and useful disease resistance. (**Alkan et al., 2013**). The Japanese quail was a great example for selection programmes because of all these qualities. The primary goal of the poultry industry is to create animals with exceptional genetics and high yield of meat and eggs.

The most crucial instrument is studies on selecting processes for obtaining genetic gain in quail, have been conducted in two directions such as the first focused on developing characteristics of egg production, In most chicken breeding programs, genetic analyses of economic variables like BW and BWI at various Interest in ages is high. (**Silva et al., 2013**). Therefore, estimates of genetic factors for growth features have served as the foundation for the majority of selection programmes. (**Karami et al., 2017**). According to several research, Japanese quail's BW showed positive selection responses when growth qualities were selected for based on genetic criteria. (**Shahraki, et al. (2023)**. Various approaches were employed in selection studies to estimate the selection response. Regression analysis was one of these techniques used to estimate breeding values over generations. This method is dependent on the model and the genetic factors. To the best of the authors' knowledge, most genetic perspectives were ignored in selection research, including genetic patterns, reactions connected with selection, and BLUP estimations.

2. MATERIALS AND METHODS:

Data of the present study were collected on the flock of Japanese quail (Coturnix coturnix japonica) maintained by the Department of Animal Production, Faculty of Agriculture, Al-Azhar University, Cairo, Egypt, during the period from January 2021 until May 2021.

Breeding plan and management:

A total number of offspring 1505 birds at 5 weeks of age resulting from marriage (110 male and 220 female) were taken at random from the flock under consideration of the present study. The mating system in the base population was in a ratio of one male to two females avoiding full and half-sib mattings. Feed and water were provided *ad-libitum.* The experimental diet contained 28% protein and 2920 k cal-ME/Kg until 2 weeks of age and 25% protein with 2850 k cal-ME/Kg during 3-6 weeks of age, then changed to a ration contained 20% protein with 2820 k cal-ME/Kg during the laying period. The minerals and vitamins were adequately supplied to cover the requirements according to **N R C, (1994).** The Temperature started at 37.5°C for the first week after hatching, then decreased 2-3°C weekly to 26-28°C in the fourth week of age till the end of brooding period. No vaccination and/or beak trimming programs were carried out to the breeding stocks.

Statistical analysis:

Data were analyzed using repeatability single-trait animal model of litter traits using MTDFREML programs of **Boldman et al. (1995).** Variances obtained by REML method of VARCOMP procedure **(SAS, 2003)** were used as starting values for the estimation of variance components. Analyses were done according to the general model:

The second on developing growth traits. (**Durmus et al., 2017**). (**Ayatollahi Mehrgardi, 2013**). The most crucial criterion for selection in the second route was weight growth.

$y = Xb + Z_a + W_{pe} + e:$

Where y is the vector of phenotypic observations; b is the vector of fixed effects; a is the vector of random additive genetic effects of doe; pe is the vector of random permanent environmental effects of doe; e is the vector of residual effects; and X, Z, and W are incidence matrices relating the phenotypic observations to fixed, random additive genetic, and permanent environmental effects, respectively. It was assumed that random effects are independent and normally distributed:

$a \sim N(0, A \sigma_a)$, $pe \sim N(0, I \sigma^2_{pe})$ and $e \sim N(0, I \sigma_e)$,

Where A is the numerator relationship matrix, I is the identity matrix, σ is the direct additive genetic variance, σ^2_{pe} is the random permanent environmental variance, and σ_e is the residual variance

- Phenotypic variance was calculated as $\sigma^2_p = \sigma^2_a + \sigma^2_{pe} + \sigma^2_e$

- Heritability (h^2_a) was calculated as $h^2_a = \frac{\sigma 2a}{\sigma 2p}$, where σ^2_a and σ^2_p are the variances due to effects of additive genetic and phenotypic, respectively.

Genetic and rank correlation:

Genetic correlation among progeny predicted breeding values (PBV) (using Best Linear unbiased predictor (BLUP) estimated by MTDFREML of **Boldman et al. (1995),** as well as spearman rank correlation among ranks of (PBV) according to **Spearman (1904)** were estimated by (**SAS, 2003**).

3. RESULTS AND DISCUSSION:

Since the study was carried out descriptive statistics of live weight and body weight gain and presented in (Table, 2)
BW_0, BW_2, BW_4, BW_6 were 9.32, 64.78, 142.24, and 213.50 gram respectively. While ADI_{0-2}, ADI_{2-4}, ADI_{4-6}, ADI_{0-6}, were 3.96, 5.53, 5.1, 4.86. **Aggrey and Cheng** (1994) reported BW_0, BW_7, BW_{14}, BW_{21} BW_{28} days were 7.9, 36.2, 82.3, 129.4 and 179.3 gm. and body weight gain 0-7, 7-14, 14-21 and 21-28 are 28.3, 46.2, 46.8 and 50.1gram. When selection was made for increased egg weight produced during the first 10 weeks of laying, **Farzin, and Seraj,. (2022).** estimated BW_0 ranged between 8.48 and 9.38g among the selected line. Additionally, for lines chosen for high body weight, **Oguz et al. (2001)** reported higher estimates for this trait as 9.3g. BW0 was estimated **by Abdel-Fattah (2006)** to be 7.05g for both sexes combined.

For two weeks body weight (BW_2), **Shalan (2003)** reported estimates for this trait ranging between 35.8 and 63.2g in males and between 36.0 and 63.9g in females for lines selected for high body weight. Higher estimates for this feature were reported by **Abdel-Fattah (2006)** as 54.06 and 54.80g for males and females, respectively.

According to **Shalan (2003)**, estimations for four-week body weight (BW_4) for lines chosen for high body weight ranged from 88.4 to 131.6 g for males and from 91.4 to 137.1 g for females. Higher estimations for this feature were provided by **Abdel-Fattah (2006)** and were 127.25 and 132.17g for males and females, respectively.

Aboul-Hassan (2000 & 2001) assessed the Brown strain's BW6 to be 148.1, 140.2g for men and 154.1, 156.0g for females, while the White strain's BW6 was estimated to be 144.1, 140.2g for males and 149.9, 156.0g for females.   Higher estimates for this feature were reported by **Abdel-Fattah (2006)** as 171.40 and 182.27g for males and females, respectively. while **Ramzy(2019)** traits correlated with estimated body weight gain in the EASM line Average daily increase from 0 to 2 weeks old, 2-4 weeks old, 4-6 weeks old, and 0 to 6 weeks old (ADI_{0-2}, ADI_{2-4}, ADI_{4-6}, and ADI_{0-6}) all increased significantly (P 0.05) from 2.43, 5.40, 1.52 and 3.62g/day in the first generation to 2.92, 5.98, 1.90 and 4.04g/day soon after a total of four generations of selection and this results were reported by **Abou-Khadiga et al., (2016) and Aboul-Hassan et al.,(2016).**

Heritability estimates for body weight traits:

Estimation of variance components, as well as direct (h^2a), remainder, phenotypic variance and total (h^2t) heritability estimated by animal model for the considered traits are presented in (Table, 2)

Additive genetic (σ^2a) estimates for all body weight studied traits were moderate. They were from 10.4, 195, 715 and 1950 forBW_0, BW_2, BW_4 and BW_6 however phenotypic variance estimates for all body weight studied traits were moderate. Estimates for both they were 14.6, 291, 1147 and 3450. For BW0, BW2, BW4 and BW6 While estimtes heritability for both BW0, BW2, BW4 and BW6 were 0.71, 0.67, 0.62 and 0.57.

This results was in agreement with **Aggrey and cheng (1994)** they estimated

heritability by animal model for BW_0, BW_7, BW_{14}, BW_{21} BW_{28} days as .12, .31, .12 and .44., Resende, At zero, seven, fourteen, twenty-one, and thirty-eight days old, respectively**,** According to **Resende et al. (2005)**, The mother's environment variance components' anterior means were 0.23, 1.29, 2.76, 4.12, and 5.16. The residual variance components were 0.084, 6.43, 22.66, 31.21, and 30.85, and the mean values of the additive genetic variance components were 0.15, 4.18, 14.62, 27.18, and 32.68.The later means of heritability were, in that order, 0.33, 0.35, 0.36, 0.43, and 0.47 at ages 0; 7, 14, 21, 28, and 38 days. El-Attrouny *et al* (2020) determined the heritability for age progression in Japanese quails. BW0's h2 (0.42) was roughly twice as high as BW6 weeks' (0.22)**.** The trend findings were consistent with other research (**Silva et al., 2013; Ebrahimi et al., 2019; Mohammadi-Tighsiah et al 2018**).

Heritability estimates for body weight increase traits:

Estimation of variance components, as well as additive genetic (σ^2a), remainder (σ^2e), phenotypic variance (σ^2p) and total (h^2_t) heritability estimated by animal model for the considered traits are presented in (Table, 4)

Additive genetic (σ^2a) estimates for all body weight increase studied traits were moderate. They were 1.56, 1.3, 1.17 and 1.3 for ADI_{0-2}, ADI_{2-4}, ADI_{4-6} and $ADI_{0-6.}$ However phenotypic variance estimates for all body weight increase studied traits were moderate. They were 336, 3.1, 3.27 and 3.52 for ADI_{0-2}, ADI_{2-4}, ADI_{4-6} and ADI_{0-6} .While estimtes heritability for both ADI_{0-2}, ADI_{2-4}, ADI_{4-6} and ADI_{0-6} were 0.46, 0.42, 0.36 and 0.37. This result was in agreement with

Aggrey and cheng (1994) they estimated heritability by animal model for body weight gain 0-7, 7-14, 14-21 and 21-28 were 0.17, 0.42, 0.33 and 0.45. **El-Attrouny et al (2020)** found that the estimated h2 for BWG at various ages was typically low, ranging from 0.18gram for (BWG $_{4-6}$) to 0.23gram for (BWG $_{0-6}$). For BWG, estimates of the genetic and phenotypic correlations ranged from 0.12 to 0.72 and 0.17 to 0.60, respectively, for different ages (0 to 2, 2 to 4, 4 to 6, 0 to 6). The calculated genetic association was 0.72 between BWG$_{2-4}$ and BWG0-6, and 0.12 for younger ages. (Between BWG$_{0-2}$ and BWG$_{2-4}$). According to **Caetano et al. (2017),** h^2 for BWG$_{0-3}$ weeks in a population of meat-type quail was estimated to be 0.15. Additionally, the estimations of h2 for BWG$_{0-5}$ weeks and BWG15–20 weeks were 0.08 and 0.10, respectively, in the study of **Mohammadi-Tighsiah et al. (2018).**which, at different times, were less than the current projections. At zero, seven, fourteen, and twenty-eight days old, respectively, Resende, According to **Resende et al. (2005),** the subsequent means of the mother's environment variance components were 0.23, 1.29, 2.76, 4.12, and 5.16, the posterior means of the residual The mean values of the genetic additive variance components were 0.15, 4.18, 14.62, 27.18, and 32.68, and the variance components were 0.084, 6.43, 22.66, 31.21, and 30.85. The second-order heritability measure at ages zero, seven, fourteen, twenty-one, and eighty were, in that order, 0.33, 0.35, 0.36, 0.43, and 0.47.

The positive genetic correlation between the various growth traits under investigation **(Table, 5)** ranged between 0.220 and 0.574. For BW at different ages (0, 2, 4, and 6 weeks), **El-Attrouny et al (2020)** estimated genetic and phenotypic correlations; they were positive and ranged from 0.31 to 0.92 and 0.05 to 0.65, respectively. Additionally, they noted that the estimated genetic correlations between the various study age groups were greater than the corresponding phenotypic correlations. Between BW$_4$ and BW$_6$, the genetic correlation was estimated to be at its highest point (0.92), while between BW$_0$ and BW$_2$, it was at its lowest point (0.31). Genetic correlations tended to get stronger with age, with the exception of BW$_0$ correlations with BW in different weeks. Additionally, there was a higher than average correlation between adjacent closet BWs. **Karadavut. (2023)** estimated genotypic correlation in the study was between the 1st and 2nd weeks, with a value of 0.956 (0.980). This was followed by a correlation between 2 and 4 weeks with a value of 0.912. Considering the phenotypic correlations, it was observed that it was higher at the 5th and 6th weeks compared to the others.

Predicted breeding values of progeny (PBV$_S$):

Predicted breeding values of body weight traits for Japanese quail estimated using single trait animal model **(PBVS),** the minimum and the maximum estimates of **PBVS,** their ranges and percent for positive record of PBVS are present in (Table, 6).

The minimum progeny breeding value for BW$_0$, BW$_2$, BW$_4$ and BW$_6$ are ($_7$.05, 46.73, 119.21 and192.66) and the maximum progeny were (11.4, 79.41, 171.6and237.85).respectively.

The present results showed that the ranges of estimated breeding values (EBVs) for quail.

The minimum progeny breeding value for ADI_{0-2}, ADI_{2-4}, ADI_{4-6}, and ADI_{0-6} were (-0.832, -2.37, -1.35 and - 0.33) and the maximum progeny breeding value were (0.73, 1.356, 1.326 and 0.403) respectively. **El-Attrouny (2020)** estimations were with each generation, the BLUP for BW0, BW2, BW4, and BW6 gradually grew until they reached 0.07, 1.17, 3.90, and 6.60 g, respectively. Indicating a similar genetic trend for BWG, the BLUP calculates for BWI_{0-2}, BWI_{2-4}, BWI_{4-6}, and BWI_{0-6} all gradually increased.

The evaluation of breeding programmes required the estimation of genetic trend. The present findings were in agreement with those of **Hussain et al. (2014)**, who noted a linear increase in BW at three weeks old in a few populations as the generations went on. Contrarily, **Narinc et al. (2017)** discovered that the mean of the calculated BLUP values for the BW in the flocks of the starting population, first, and secondly selected generations were determined to be 0.13, 0.20, and 0.13 correspondingly.

CONCLUSION:

This study recommends using the resulting offspring in meat production lines because of the superiority of the offspring in body weight and average daily gain increase by Calculating the educational value for them.

Table (1) Composition of the study diets.

Ingredients	Starter ration	Layer ration
Ground yellow corn	36.35	62.3
Soybean meal	40.5	20.5
Corn gluten meal	3	2.05
Meat meal	10	10
Fat vegetable	5	-
Limestone	2	2
Dicalcium phosphate	2.5	2.5
Salt	0.4	0.4
Vitamin premix	0.25	0.25
Total Kg	**100**	**100**
Crude protein	28.4%	21.3%
ME/Kg. Kcal	2886	2835

Table (2): Actual means and standard deviations (S.D) for different growth traits

Traits	N	Means	S D	CV%
BW0	186	9.3263	1.21735	13.05287
BW2	186	64.7837	11.59886	17.90398
BW4	186	142.2380	21.25650	14.94432
BW6	186	213.5049	20.90473	9.791218
ADI_{0-2}	186	3.9612	.77700	19.61527
ADI_{2-4}	186	5.5324	1.46002	26.39035
ADI_{4-6}	186	5.0905	1.39422	27.38867
ADI_{0-6}	186	4.8614	.48938	10.06665

W_0: weight at hatch; W_2, W_4, W_6: weights at 2, 4 and 6 weeks of age
ADI: average daily increase at (0-2, 2-4, 4-6, 0-6) weeks of age

Table (3): Estimates of additive genetic (σ^2_a), remainder (σ^2_e) and phenotypic variances (σ^2_p) and heritability (h^2) for body weight in Japanese quail.

Traits	$\sigma^2 a$	$\sigma^2 e$	$\sigma^2 p$	$h^2 \pm SE$
BW_0	10.4	4.2	14.6	.71 ±0.386
BW_2	195	96	291	.67 ± 0.263
BW_4	715	432	1147	.62 ±0.397
BW_6	1950	1500	3450	.57 ±0.707

$\sigma^2 a$= additive genetic variance, σ^2_e = residual variance and σ^2_p = phenotypic variance h^2_a = heritability
For average daily increase at (0-2, 2-4, 4-6, 0-6) weeks of age

Table (4) Estimates of additive genetic (σ^2_a), remainder (σ^2_e) and phenotypic variances (σ^2_p) and heritability (h^2) for body weight increase in Japanese quail.

Traits	$\sigma^2 a$	$\sigma^2 e$	$\sigma^2 p$	$h_t^2 \pm SE$
ADI 0-2	1.56	1.8	3.36	0.46±0.529
ADI 2-4	1.3	1.8	3.1	0.42± 0.299
ADI 4-6	1.17	2.1	3.27	0.36±0.253
ADI 0-6	1.3	2.22	3.52	0.37±0.898

$\sigma^2 a$= additive genetic variance, σ^2_e = residual variance and σ^2_p = phenotypic variance h^2_a = heritability
For average daily increase at (0-2, 2-4, 4-6, 0-6) weeks of age

Table (5): Estimates of genetic correlations between average body weights and average daily gains traits in Japanese quail.

Traits	BW_0	BW_2	BW_4	BW_6	ADG_{0-2}	ADG_{2-4}	ADG_{4-6}	ADG_{0-6}
BW_0	1							
BW_2	.574**	1						
BW_4	.335**	.498**	1	.				
BW_6	.274**	.264**	402**	1				
ADI_{0-2}	.477**	.980**	.455**	.220*	1			
ADI_{2-4}	-.012-	-.181-	.748**	.268**	-.236-*	1		
ADI_{4-6}	-.069-	-.207-*	-.502-**	.563**	-.210-*	-.414-**	1	
ADI_{0-6}	.205*	.049	.349**	.981**	.167	.252*	.622**	1

NS: not significant, *: significant at P<0.05, **: significant at P<0.01

Table (6): Minimum, Maximum, Percentage of accuracy's (%) and Standard errors for body weight estimated by single trait animal model in Japanese quail.

		Traits			
		BW_0	BW_2	BW_4	BW_6
progeny EBVs	Minimum	7.05	46.73	119.21	192.66
	SE	1.71	7.94	15.94	27.43
	Accuracy%	85	82	80	78
	Maximum	11.44	79.41	171.62	237.85
	SE	1.77	14.63	15.39	27.02
	Accuracy%	84	82	82	79
	Range	18.49	126.14	290.83	430.51

Table (7): Minimum, Maximum, Percentage of accuracy's (%) and standard errors for average daily increase estimated by single trait animal model in Japanese quail.

		Traits			
		ADI_{0-2}	ADI_{2-4}	ADI_{4-6}	ADI_{0-6}
progeny EBVs	Minimum	-0.832	-2.37	-1.35	-.338
	SE	0.84	0.81	0.79	0.85
	Accuracy%	74	71	69	67
	Maximum	0.73	1.356	1.326	0.403
	SE	0.86	0.78	0.78	0.81
	Accuracy%	72	73	69	70
	Range	-0.102	-1.014	-0.024	0.065

4. REFERENCES:

Abdel-Fattah, M. H. 2006. Selection for increased body weight and growth rate in Japanese quail. Ph.D. Thesis, Fac. Agric., Fayoum, Univ., Egypt.

Abou- Khadiga, G., Mahmoud, B. Y. F. and El-Full, E. A. 2016, "Genetic evaluation of early egg production and maturation traits using two different approaches in Japanese quail", *Poultry science*, Vol. 95, No. 4, pp. 774-779.

Aboul–Hassan, M. A. 2000. Comparative study of growth traits in two strains of Japanese quail. Fayoum J. Agric . Res.&Dev. 1

Aboul–Hassan, M. A. 2001. Crossbreeding effects on some growth and egg production traits among two strains of Japanese quail. Al-Azhar. J. Agric . Res . 34:41-57.

Aboul-Hassan, M. A., El-Fiky, F. A., Aboul-Seoud, D. I. and Ramzy, A. A 2016, "Direct and Correlated Responses from Long–Term Selection for Water Consumption in Japanese quail", *Middle East Journal of Applied Science*, Vol. 7, PP. 126-134.

Aggrey, S. E. and Cheng, K. M. 1994. Animal model analysis of genetic (co) variances for growth traits in Japanese quail. *Poultry Science*, *73*(12), 1822-1828.

Hussain, J., Akram, M., Ahmad, S., Rehman, A., Lohani, F., Munir, A. & Noshahi, H. 2014. Comparative study on production performance, egg geometry, quality and hatching traits in four close-bred stocks of Japanese quail. *Agric. Adv*, *3*(1), 13-18.

Alkan, S., T. Karsli, K. Karabağ and A. Galiç 2013. The effects of selection and season on clutch traits and egg

production in Japanese quails (Coturnix coturnix japonica) of different lines. Süleyman Demirel Üniversitesi Ziraat Fakültesi Dergisi, 8: 71-77.

Ayatollahi Mehrgardi, A., 2013. Divergent selection for four-week bodyweight in Japanese quail (Coturnix coturnix japonica): Response to selection and realized heritability. J. Livest. Sci. Technol. 1, 57-59.

Boldman, K. G.; Kriese, A.; Van Vleck, L. D.; Van Tassell, C. P. and Kachman, S. D. 1995. A manual for use of MTDFREML. A set of programs to obtain estimates of variances and covariances [DRAFT]. U.S. Department of Agriculture, Agricultural Research Service, USA.

Boni, I., Nurul, H., & Noryati, I. 2010. Comparison of meat quality characteristics between young and spent quails. *Int Food Res J*, *17*(3), 661-6.

Caetano da Costa, G., Mota, R. R., da Silva, D. A., de Oliveira, H. R., Viana, J. M. S., de Siqueira, O. H. G., ... & e Silva, F. F. 2017. Bayesian estimation of genetic parameters for individual feed conversion and body weight gain in meat quail. *Livestock Science*, *200*, 76-79.

Narinc, D., Durmus, I., Alkan, S., Karabag, K. & Karsli, T., 2017. Effects of mass selection on egg production on some reproductive traits in Japanese quail. Europ. Poult. Sci. 1, 81.

Ebrahimi, K., Dashab, G. R., Faraji-Arough, H., & Rokouei, M. 2019. Estimation of additive and non-additive genetic variances of body weight in

crossbreed populations of the Japanese quail. *Poultry science*, *98*(1), 46-55.

El-Attrouny, M. M., Manaa, E. A., & Ramadan, S. I. 2020. Genetic evaluation and selection correlated response of growth traits in Japanese quail. *South African Journal of Animal Science*, *50*(2), 325-333.

Farzin, N., and Seraj, A. 2022. Genetic parameters of weekly egg production using random regression models in two strains of Japanese quails. Journal of Applied Genetics, 63(4), 763-769.

Karadavut, U.2023. Determination of Heritability and Genotypic-Phenotypic Correlations According to Yield Traits in Japanese Quails. *Türk Tarım ve Doğa Bilimleri Dergisi*, *10*(2), 465-472.

Karami, K., Zerehdaran, S., Tahmoorespur, M., Barzanooni, B. & Lotfi, E., 2017. Genetic evaluation of weekly bodyweight in Japanese quail using random regression models. Br. Poult. Sci. 58, 13-18. https://doi.org/10.1080/00071668.2016.1236362.

Shalan MH, Kosba MA, El-Deen MB. 2003. Long-term selection for body weight in Japanese quail under Egyptian conditions. 3-Correlated response of some egg production traits. Egyptian Poultry Science Journal; 23: 961-975.

Mohammadi-Tighsiah, A., Maghsoudi, A., Bagherzadeh-Kasmani, F., Rokouei, M., & Faraji-Arough, H. 2018. Bayesian analysis of genetic parameters for early growth traits and humoral immune responses in Japanese quail. *Livestock Science*, *216*, 197-202.

N R C 1994. National Research Council, Nutrient Requirements of Poultry.9th Ed. National Academy of Sciences, Washington, D.C. USA.

Oguz, I.; Akbas, Y. and Altan, O. 2001. Relationship of body weight at sexual maturity with body weights at various ages in lines of Japanese quail. |, Published online, 219 -223.

Ramzy, A. A. (2019). Selection for sexual maturity in Japanese quail. Ph.D. Thesis, Thesis. Fac. Agric. Al-Azhar Univ. Cairo, Egypt.

Resende, R.O., Martins, E.N., Georg, P.C., Paiva, E., Conti, A.C.M., Santos, A.I., Sakaguti, E.S. & Murakami, A.E., 2005. Variance components for bodyweight in Japanese quails (Coturnix japonica). Braz. J. Poult. Sci. 7, 23-25. https://doi.org/10.1590/S1516-635X2005000100004.

SAS, 2003. Statistical analysis system. SAS Release 9.1.3. For windows, SAS Institute Inc. Cary, NC, USA.

Shahraki, Y., Seraj, A., & Farzin, N. 2023. Estimation of genetic parameters for traits related to external and internal egg quality in wild and white Japanese quails. Animal Production Research, 11(4), 77-89.

Silva, L. P., J. C. Ribeiro, A. C. Crispim, F. G. Silva, C. M. Bonafe, F. F. Silva and R. A. Torres 2013. Genetic parameters of body weight and egg traits in meat-type quail. Livestock Sci., 153: 27-32.

Spearman, C. 1904. The proof and measurement of association between two things. Amer. J. Psychol., 15(1): 72-101 **(**as cited in **Kendall *et al*., 1938).**

اِ التقييم الوراثى لبعض الصفات الانتاجية فى السمان اليابانى باستخدام نموذج الحيوان
أحمد رمزي أحمد عبدالله
قسم الانتاج الحيوانى كلية الزراعة بالقاهرة. جامعة الازهر مدينة نصر مصر

تهدف هذه الدراسة إلى تقدير المقاييس الوراثية لبعض الصفات الإنتاجية في السمان الياباني باستخدام نموذج الحيوان . وكان الوزن عند الفقس و 2 و 4و 6 هى(9.32 و 64.78 و 142.23 و 213.50) جرامًا على التوالى كان معدل النمو اليومى فى فترات النموالمختلفة (صفر -2 و2 – 4 و 4-6 وصفر -6) هى(3.96, 5.53. 5.09 و 4.86)جرام/يوم على التوالى . والتاثير الوراثى التجمعى والتاثير المتبقى والتباين المظهرى والمكافىء الوراثى لوزن الجسم عند الفقس هى (10.4 و4.2 و14.6 و0.71) بينما(195 و96 و 291 و0.67) لوزن الجسم عند الاسبوع الثانى و (715 و 432 و 1147 و 0.62) لوزن الجسم عند الاسبوع الرابع و(1950و1500و 3450و0.57) لوزن الجسم عند الاسبوع السادس .والحد الادنى للقيمة التربوية لوزن الجسم عند الفقس و 2 و 4و 6 (7.05و 46.73 و 119.21 و 192.66) الحد الاقصى لوزن الجسم عند الفقس و 2 و 4و 6 (11.44 و 79.41 و 171.62 و 237.85) الحد الادنى للقيمة التربوية لمعدل الزيادة اليومية عند (0-2 و 2-4 و 4-6 و 0-6) هى (0.832و 2.37و 1.35و 0.338) والحد الاعلى للقيمة التربوية لمعدل الزيادة اليومية عند (0-2 و 2-4 و 4-6 و 0-6) هى (0.73 و 1.356 و 1.326و 0.43) فى النهاية نلاحظ تفوق الابناء فى الاداء الانتاجى من خلال القيمة التربوية لوزن الجسم مقابل الاداء الانتاجى للعشيرة القاعدية والزيادة فى معدل الزيادة اليومية لذلك يوصى باستخدام هذه الابناء لتكوين عشائر اساسية للزيادة فى اوزان الجسم ومعدل الزيادة اليومية لانها من الخصائص المهمة وانشاء خط لانتاج اللحم .

الكلمات المفتاحية : التقييم الوراثى , الصفات الانتاجية , نموذج الحيوان .