

Genetic evaluation for growth performance in Japanese quail line selected for fast growth rate across eight generations

E.A. El-Full B.Y.F. Mahmoud, D.A.M. Semida, A.M. Emam

Poultry Production Department, Faculty of Agriculture, Fayoum University, Fayoum 63514, Egypt

(Accepted November 5, 2024)

The world is suffering from a protein shortage due to population growth and increased food demand, increasing the pressure on poultry breeders to boost production. Additionally, Japanese quail (JQ), with their small size, rapid growth, short generational interval, and high egg production, offer a promising solution to address this challenge. A ten-generation study conducted at Fayoum University Poultry Research Center involved 17,806 JQ chicks, which were divided into two lines: one was selected for fast growth rate from 1-21 days (FGR1-21), and the other line was the control line (CL). It aimed to investigate the consequences of selection, evaluate selection effectiveness for increased early growth rate (GR1-21). All studied growth traits were significantly influenced by generation, line, and sex effects, except for body weight at hatch (BW1) and GR1-21, where sex had an insignificant effect. The interaction effect between generation and line significantly affected all studied traits, favoring the FGR1-21 line in the 8th selected generation. The cumulative response based on two different methods was in the desired direction for all studied growth traits, except for BW1. This was based on breeding values. The GR1-21 was found to be positively correlated, either genetically or phenotypically, with all correlated traits except for BW1. All studied growth traits had moderate heritability (h^2) estimates ranging from 0.18 to 0.32. It can be concluded that continuous selection for high growth rate has resulted in a well-established paternal line of JQ specialized in meat production, which can be proposed as a sustainable solution to address food security problems.

KEY WORDS: genetic parameters / fast growth rate / direct response /
correlated response / Japanese quail

*Corresponding author: ame04@fayoum.edu.eg

Protein shortage is a major concern in the world today, as the global population continues to grow and demand for food increases, putting great emphasis on poultry breeders to improve and increase the production of their stocks [Katz-Rosene *et al.* 2023]. One potential solution to this problem is through selective breeding for economic traits, which can further increase the efficiency and sustainability of poultry production. Japanese quail (JQ: *Coturnix coturnix japonica*) are small-sized poultry birds with fast growth rates, short generation intervals, significant egg production, and high-quality meat [Mahmoud *et al.* 2015, Farahat *et al.* 2018, Semida 2020]. Due to these advantages, JQ can be proposed as a model animal in numerous studies on various productive indices [Abou Khadiga *et al.* 2018, Emam *et al.* 2023, Mahmoud *et al.* 2023, Akbarimehr *et al.* 2023]. As JQ meat gains consumer interest, producers struggle to obtain superior parental lines. Selectively breeding JQ parent stocks for high early growth potential could help address protein shortages through improved fast-growing birds [Baylan 2017]. In this regard, selection for increased body weight at fixed ages has been associated with negative effects like excessive fatness [Decuypere *et al.* 2003]. In contrast, early growth rate has moderate heritability and can be rapidly improved through selection, with desirable genetic correlations to other growth traits [Semida 2020]. Moreover, for the sake of higher accuracy, the existing genetic evaluation is planned to be conducted through different estimation methods to evaluate the effectiveness of the applied selection program.

Therefore, this study aimed to investigate the consequences of long-term selection for FGR₁₋₂₁ (fast growth rate from 1-21 days) on growth performance and evaluate the effectiveness of the applied selection program and to establish a nucleus for a paternal line, motivated by the fact that there is a scarcity of specified JQ lines in Egypt.

Material and methods

This multi-generational selection experiment was conducted at the Poultry Research Center, Faculty of Agriculture, Fayoum University, Egypt, with approval from the Institutional Animal Care and Use Committee (FU-IACUC) (approval no. AEC2219). It included a pre-base population, a base population, and eight generations of selection for increased early growth rate (1-21 days) in Japanese quail (JQ).

Experimental design and population structure of the selection study

Throughout the selection experiment, a total of 1,300 birds were used in the pre-base population, 1,726 in the base population, 10,609 quail for the FGR₁₋₂₁ line (selected for fast growth rate from 1-21 days), and 4,171 quail for the control line (CL). The inbreeding coefficient was estimated as a by-product while calculating the heritability estimates by restricted maximum likelihood (REML) procedures using the WOMBAT program software [Meyer 2007]. The inbreeding coefficient ranged from 0.000 to 1.423%. As the generation number increased, inbreeding significantly increased by 0.232 ($P \leq 0.001$), as shown in Table 1.

Table 1. Population size, selection intensity and inbreeding coefficient % over the experimental period (Pre base+ base + eight generations of selection)

Generation	Selection intensity	Inbreeding coefficient %	Line	Sires	Dams	Progeny	Total
Pre-base			-	-	-	1300	1300
Base			-	200	400	1726	1726
The selected generations							
1 st	1.259	0.000	CL FGR ₁₋₂₁	70 89	139 178	454 1359	1813
2 nd	1.928	0.0008	CL FGR ₁₋₂₁	48 86	96 172	456 1138	1594
3 rd	1.295	0.0853	CL FGR ₁₋₂₁	40 90	80 180	472 1296	1768
4 th	1.400	— 0.3530	CL FGR ₁₋₂₁	68 88	136 176	440 1383	1823
5 th	1.428	0.6071	CL FGR ₁₋₂₁	40 87	80 174	632 1641	2273
6 th	1.489	0.9694	CL FGR ₁₋₂₁	48 92	96 184	730 1494	2224
7 th	1.590	— 1.342	CL FGR ₁₋₂₁	45 72	90 144	540 1220	1760
8 th	1.400	1.4233	CL FGR ₁₋₂₁	46 81	92 162	447 1078	1525
Total numbers of sires and dams from 1 st to 8 th generations							
Total		b (SE):0.232 (0.039), P<0.001		1090	2179	17806	17806

CL – the control line and FGR₁₋₂₁ – the selected line for high growth rate during the period from one to 21 days of age, *b* – regression coefficient, SE – standard error and P – probability.

Management and housing

Newly hatched chicks were tagged and housed on chaff litter floors until 35 days old. They were fed ad libitum a starter diet with 24% CP, 2900 Kcal/ME and water offered. Once laying began, breeders were fed a breeder diet with 20% CP, 2900 Kcal/ME, 2.51% calcium and 0.47% available phosphorus according to NRC [1994].

Selection program

Aggregated breeding values of a selection criterion were estimated in two lines of JQ that were simultaneously bred. The FGR₁₋₂₁ line was individually selected for high growth rate during 1-21 days of age according to the estimated aggregated breeding values for eight successive generations, while a CL line was kept under random mating without selection.

Selection criterion

Growth rate during the period from 1-21 days of age (GR₁₋₂₁) was calculated according to Brody [1945] as the following formula:

$$GR = [BW_2 - BW_1 / 1/2 (BW_2 + BW_1)]$$

where:

BW_1 – the weight at the beginning;

BW_2 – the weight at the end of the period.

Body weights at different ages

Body weights at hatch, seven, 14, 21, 28 and 35 days of age (BW_1 , BW_7 , BW_{14} , BW_{21} , BW_{28} and BW_{35} , respectively) were individually recorded to the nearest gram.

Growth rates during different periods of growth

Also, growth rates per chick during the periods: 1-7, 1-14, 1-28 and 1-35 (GR_{1-7} , GR_{1-14} , GR_{1-28} and GR_{1-35}) were calculated according to Brody [1945].

Statistical analyses

The recorded data of the growth traits (BWs and GRs) were analyzed by PROC MIXED [SAS, 2011] to calculate the generation, line and gender-specific means using the following model:

$$Y_{ijklm} = \mu + F_i + L_j + G_k + (F \times L)_{ij} + (F \times G)_{ik} + (L \times G)_{jk} + (F \times L \times G)_{ijk} + a_l + e_{ijklm}$$

where:

Y_{ijklm} – the observation for a trait μ : is the overall mean;

F – the effect of i^{th} generation;

L – the effect of j^{th} line;

G – the effect of k^{th} gender;

$(F \times L)_{ij}$ – the effect of interaction of the i^{th} generation with the j^{th} line;

$(F \times G)_{ik}$ – the effect of interaction of the i^{th} generation with the k^{th} gender;

$(L \times G)_{jk}$ – the effect of j^{th} line with the k^{th} gender;

$(F \times L \times G)_{ijk}$ – the effect of interaction of the i^{th} generation with the j^{th} line with the k^{th} gender;

a – the random additive genetic effect of the l^{th} animal;

e_{ijklm} – the random error term; the random variable was the birds within line.

Means of generation x line were compared using multiple range test [Duncan 1955].

The generation by line interactions were presented to be used in the estimation of the selection response (direct and correlated) for the studied traits.

Genetic parameters

Both univariate and bivariate linear animal models used to estimate heritabilities (h^2) of studied traits and correlations. [REML procedures by WOMBAT the program software, Meyer, 2007] as follows:

The univariate model to estimate direct h^2 was:

$$y = Xb + Za + e$$

The bivariate model between selection criterion and other studied traits was:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} x_1 & 0 \\ 0 & x_2 \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \end{bmatrix} + \begin{bmatrix} z_1 & 0 \\ 0 & z_2 \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

where: for trait i ($i = 1, 2$), y_i = vector of observations, b_i = vector of fixed effects (i.e., generation, and line, a_i = vector of random direct genetic effects, e_i = vector of random residual effects, and X_i and Z_i are incidence matrices relating the observations to the respective fixed and direct genetic effects. Breeding value (Za) for studied traits were estimated by the WOMBAT program software [Meyer 2007].

Evaluation of the Selection program

Realized response (Direct and correlated) was obtained according to Henderson [1973] depending on breeding value

Through a mixed model method by determining the difference between the averages of the breeding values of the first and the last generation within each line, separately:

$$\text{Realized response} = (SL_{BV8} - SL_{BV1}) - (CL_{BV8} - CL_{BV1})$$

where: SL_{BV1} and SL_{BV8} are the breeding values of the selected line at the 1st and 8th generation, CL_{BV1} and CL_{BV8} are the breeding values of the control line at the 1st and 8th generation.

2- Guill and Washburn [1974] depending on least square means

$$\text{Realized response} = (SL_t - SL_{t-1}) - (CL_t - CL_{t-1})$$

where: realized response due to selection in the t^{th} generation and SL and CL least square means performance of the selected and the control lines.

Selection intensity (i)

The Proportion of selected animals for breeding (Selected proportion = the number of selected birds / number of all population) was used to acquire the expected theoretical values of selection intensity for varying extents of coefficients according to Falconer and Mackay [1996].

Realized heritability (Rh²)

Realized heritability estimates of the selection criterion were obtained after eight generations of selection as the ratio of cumulative realized response to cumulative selection differential [Falconer and Mackay 1996].

Cumulative selection differential

Mean of the selected individuals minus the population mean for GR_{1-21} depending on breeding value and least square means.

Results and discussion

Generation x line interaction effects on studied growth traits

Generation, line, and gender significantly influenced all growth traits except hatch weight and early growth rate (GR_{1-21}), which were not affected by gender (Tables 2 and 3). There were significant effects due to generation x line interaction on all measured growth traits. The FGR_{1-21} line had the highest body weights at 7, 14, 21, 28, and 35 days, as well as the fastest growth rates at all ages in the 8th generation. This can be attributed to response of intensive selection which aimed at enhancing the performance potential in the selected line. Semida [2020] found significant generation x line interaction effects on BWs and GRs from hatch to 35 days of age. Enhanced growth through selection is attributed to moderate to high heritability [Narinç *et al.* 2014] and hormone changes [Peebles and Marks 1991]. The role of leptin in regulating growth, food intake, thermogenesis, and energy expenditure is also influential [Tartaglia *et al.* 1995].

Table 2. Least square means and (SE) of body weights (BW's) at different ages as affected by generation x line interaction

generation	Item line	Generation x Line interaction					
		BW ₁ (g)	BW ₇ (g)	BW ₁₄ (g)	BW ₂₁ (g)	BW ₂₈ (g)	BW ₃₅ (g)
1	CL	8.38 ^{de} (0.07)	32.20 ^a (0.50)	66.05 ⁱ (1.57)	115.04 ⁱ (1.23)	150.86 ^g (1.58)	188.78 ^{ef} (1.32)
	FGR_{1-21}	7.64 ^g (0.04)	34.16 ^a (0.29)	70.79 ^h (0.98)	125.79 ^g (0.87)	154.07 ^g (0.84)	190.84 ^c (1.41)
2	CL	8.80 ^b (0.07)	30.46 ^b (0.37)	60.35 ^j (1.16)	103.41 ^k (1.22)	155.13 ^f (1.66)	181.46 ^g (1.61)
	FGR_{1-21}	8.89 ^b (0.04)	33.95 ^b (0.19)	72.21 ^g (0.59)	117.70 ^h (0.63)	167.37 ^g (0.86)	187.84 ^g (0.84)
3	CL	9.31 ^a (0.10)	30.28 ^b (0.52)	62.73 ^j (1.15)	100.30 ^j (1.55)	161.93 ^f (1.70)	180.57 ^g (1.59)
	FGR_{1-21}	9.37 ^a (0.06)	35.97 ^a (0.32)	79.12 ^f (0.65)	128.47 ^f (0.89)	175.05 ^e (1.02)	190.48 ^c (0.91)
4	CL	7.62 ^g (0.06)	31.16 ^a (0.29)	67.56 ⁱ (1.48)	107.82 ⁱ (1.43)	166.39 ^g (1.51)	188.42 ^{ef} (2.07)
	FGR_{1-21}	8.04 ^f (0.03)	38.07 ^f (0.21)	84.59 ^c (0.73)	140.00 ^c (0.64)	183.08 ^b (0.72)	209.58 ^c (1.03)
5	CL	8.72 ^b (0.05)	38.44 ^f (1.30)	84.24 ^c (1.93)	132.19 ^c (1.85)	166.66 ^g (1.98)	214.80 ^b (2.14)
	FGR_{1-21}	8.52 ^c (0.03)	41.51 ^d (0.95)	90.04 ^{cd} (1.58)	140.06 ^c (1.43)	180.81 ^b (1.52)	220.12 ^a (1.61)
6	CL	8.31 ^{de} (0.06)	36.80 ^a (1.34)	80.38 ^f (1.30)	123.07 ^a (1.96)	165.77 ^f (1.92)	203.51 ^d (1.99)
	FGR_{1-21}	8.43 ^{cd} (0.03)	42.30 ^a (0.16)	91.91 ^c (1.25)	137.14 ^d (1.49)	188.65 ^f (1.60)	217.34 ^{ab} (1.71)
7	CL	8.23 ^e (0.06)	40.30 ^a (1.86)	87.93 ^d (1.31)	135.50 ^a (1.98)	174.18 ^e (1.21)	202.50 ^{de} (1.95)
	FGR_{1-21}	8.34 ^{de} (0.04)	47.08 ^b (0.72)	101.24 ^b (1.14)	151.00 ^b (1.63)	189.08 ^e (1.18)	217.97 ^{ab} (1.70)
8	CL	8.29 ^{de} (0.04)	32.95 ^a (0.96)	75.37 ^{fg} (1.01)	121.26 ^{gh} (1.75)	152.28 ^f (1.41)	180.92 ^g (1.97)
	FGR_{1-21}	8.41 ^{cd} (0.04)	53.88 ^a (0.82)	107.06 ^a (1.24)	154.70 ^a (1.63)	190.10 ^a (1.12)	220.15 ^a (1.75)
Probability							
generation (F)		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
line (L)		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
gender (G)		0.7592	0.0001	0.0001	0.0001	0.0001	0.0001
F x L interaction		0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
F x G interaction		0.0473	0.0050	0.1420	0.0001	0.0001	0.0001
L x G interaction		0.0104	0.3632	1.000	1.000	1.000	1.000
F x L x G interaction		0.4473	1.000	1.000	1.000	1.000	0.9957

Means having different superscripts in the same column are significantly differed at specified probability, SE – stander error; FGR_{1-21} – the selected line for high growth rate during 1-21 days of age; CL – the control, BW₁, BW₇, BW₁₄, BW₂₁, BW₂₈ and BW₃₅: body weights at hatch, 7, 14, 21, 28 and 35 days of age, respectively.

Evaluation of direct selection response by different estimating methods

Positive cumulative selection responses were observed depending on both least square means and breeding values, exhibiting a favorable trend (Tab. 4). Comparable

Table 3. Least square means and (SE) of growth rates (GR's) during different periods of growth as affected by generation x line interaction

Item		Generation x Line interaction				
generation	line	GR ₁₋₇	GR ₁₋₁₄	GR ₁₋₂₁	GR ₁₋₂₈	GR ₁₋₃₅
1	CL	1.19 ^a (0.01)	1.53 ⁱ (0.01)	1.69 ^c (0.002)	1.79 ^c (0.03)	1.79 ^a (0.002)
	FGR ₁₋₂₁	1.26 ^c (0.01)	1.60 ^g (0.01)	1.72 ^{de} (0.001)	1.80 ^c (0.03)	1.80 ^{de} (0.001)
2	CL	1.07 ⁱ (0.01)	1.51 ⁱ (0.01)	1.67 ^a (0.005)	1.78 ^f (0.03)	1.80 ^{de} (0.003)
	FGR ₁₋₂₁	1.15 ⁱ (0.01)	1.59 ^c (0.003)	1.73 ^{de} (0.002)	1.80 ^d (0.03)	1.82 ^{cd} (0.001)
3	CL	1.05 ⁱ (0.01)	1.51 ⁱ (0.01)	1.68 ^{ef} (0.004)	1.78 ^f (0.03)	1.80 ^{de} (0.003)
	FGR ₁₋₂₁	1.14 ⁱ (0.01)	1.61 ^h (0.004)	1.75 ^c (0.003)	1.81 ^c (0.03)	1.83 ^{bc} (0.002)
4	CL	1.25 ^f (0.01)	1.54 ^b (0.01)	1.69 ^c (0.005)	1.79 ^c (0.03)	1.81 ^{cd} (0.002)
	FGR ₁₋₂₁	1.35 ^c (0.01)	1.68 ^b (0.004)	1.77 ^{bc} (0.004)	1.83 ^a (0.03)	1.85 ^a (0.003)
5	CL	1.26 ^c (0.02)	1.62 ^c (0.03)	1.70 ^a (0.005)	1.81 ^c (0.03)	1.80 ^{de} (0.04)
	FGR ₁₋₂₁	1.31 ^d (0.02)	1.64 ^d (0.03)	1.78 ^{bc} (0.07)	1.83 ^a (0.03)	1.85 ^a (0.04)
6	CL	1.26 ^c (0.02)	1.62 ^c (0.03)	1.70 ^a (0.07)	1.81 ^c (0.03)	1.84 ^{ab} (0.04)
	FGR ₁₋₂₁	1.30 ^{de} (0.02)	1.65 ^c (0.03)	1.79 ^{bc} (0.07)	1.82 ^b (0.03)	1.85 ^a (0.04)
7	CL	1.35 ^c (0.02)	1.67 ^b (0.03)	1.72 ^{de} (0.07)	1.82 ^b (0.03)	1.84 ^{ab} (0.04)
	FGR ₁₋₂₁	1.39 ^b (0.02)	1.69 ^a (0.03)	1.82 ^b (0.07)	1.83 ^a (0.03)	1.85 ^a (0.04)
8	CL	1.18 ^b (0.02)	1.60 ^g (0.03)	1.72 ^{de} (0.07)	1.79 ^c (0.03)	1.82 ^{cd} (0.03)
	FGR ₁₋₂₁	1.46 ^a (0.02)	1.70 ^a (0.03)	1.83 ^a (0.07)	1.83 ^a (0.03)	1.85 ^a (0.03)
Probability						
generation (F)		0.0001	0.0001	0.0001	0.0001	0.0001
line (L)		0.0001	0.0001	0.0001	0.0001	0.0001
gender (G)		0.0026	0.0001	0.6065	0.0001	0.0069
F x L interaction		0.0002	0.0001	0.0001	0.0001	0.0001
F x G interaction		0.006	0.0013	0.4536	0.0265	1.000
L x G interaction		0.0001	0.0037	1.000	0.1253	1.000
F x L x G interaction		0.6971	1.000	0.4781	0.8830	0.8716

Means having different superscripts in the same column are significantly differed at specified probability. SE – stander error; FGR₁₋₂₁ – the selected line for high growth rate during 1-21 days of age; CL – the control line, GR₁₋₇, GR₁₋₁₄, GR₁₋₂₁, GR₁₋₂₈ and GR₁₋₃₅: growth rates during the periods from 1-7, 1-14, 1-21, 1-28 and 1-35 days of age, respectively.

Table 4. Heritabilites (h²) and evaluation of direct selection responses for GR₁₋₂₁ by different estimating methods after eight generations for the combined sex

Item	Estimate
Direct h ²	0.25
Cumulative selection differential (breeding value)	0.20
Cumulative selection differential (least square means)	0.22
Cumulative selection response depending on breeding value	0.051
Cumulative selection response depending on least square means	0.071
Realized h ² (breeding value)	0.26
Realized h ² (least square means)	0.32

findings for cumulative direct selection responses in growth traits were reported by Baylan *et al.* [2009] and El-Attrouny *et al.* [2020]. The cumulative selection response based on least square means [Guill and Washburn, 1974] was higher (+0.019) than that based on breeding values [Henderson, 1973] which is consistent with the higher selection differential observed for least square means. However, breeding values are considered more accurate for estimating genetic responses as they account solely for

additive genetic effects, minimizing the influence of environmental factors. After eight selection generations, the realized heritability for GR_{1-21} was 0.26, slightly higher than the directly estimated heritability of 0.25. This suggests that a substantial portion of the phenotypic variation in this trait is attributable to additive genetic effects. This indicates that selection for GR_{1-21} can lead to genetic improvement in early growth rate. A similar pattern was noted by Baylan *et al.* [2009] in their calculations of heritability using an animal model and realized heritability from breeding values. The results revealed higher realized heritability with least square means compared to breeding values, agreeing with Semida [2020]. Direct selection responses from all estimation methods were consistently positive, indicating the selection program was accurate and can continue successfully for more generations with considerable responses. The results suggest that the selection program for GR_{1-21} was effective in achieving genetic improvement, as indicated by the positive cumulative selection response and the consistency between the direct and realized heritability estimates based on breeding values. However, it is important to note that breeding values are considered more accurate for estimating genetic parameters and responses, as they account solely for additive genetic effects and minimize the influence of environmental factors.

Evaluation of correlated selection responses by different estimating methods:

Cumulative responses for correlated traits were higher using least square means based on Guill and Washburn [1974] versus breeding values according to Henderson [1973] method, this is because least square means incorporate both genetic and environmental effects, while breeding values depend solely on the additive genetic effect, as shown in Table 5.

Table 5. Correlated selection responses, heritability, genetic and phenotypic correlations and (SE) between GR_{1-21} and body weights at different ages and growth rate traits during different periods of growth

Trait	Correlated selection responses		h^2 (SE)	rg (SE)	rp (SE)
	Henderson [1973]	Guill and Washburn [1974]			
BW ₁	-0.083	0.86	0.22(0.027)	-0.16(0.006)	-0.19(0.002)
BW ₇	4.93	18.97	0.21(0.002)	0.17(0.004)	0.25(0.001)
BW ₁₄	11.03	26.95	0.24(0.001)	0.19(0.003)	0.27(0.001)
BW ₂₁	13.056	22.69	0.25(0.001)	0.41(0.002)	0.42(0.001)
BW ₂₈	6.65	34.61	0.24(0.005)	0.33(0.002)	0.40(0.001)
BW ₃₅	14.62	37.17	0.25(0.001)	0.35(0.001)	0.42(0.001)
GR ₁₋₇	0.048	0.210	0.18(0.001)	0.20(0.003)	0.24(0.001)
GR ₁₋₁₄	0.031	0.030	0.19(0.001)	0.18(0.006)	0.20(0.002)
GR ₁₋₂₈	0.006	0.057	0.22(0.006)	0.33(0.006)	0.37(0.002)
GR ₁₋₃₅	0.017	0.030	0.23(0.007)	0.40(0.004)	0.41(0.001)

BW₁, BW₇, BW₁₄, BW₂₁, BW₂₈ and BW₃₅ – body weights at hatch, 21 and 35 days of age, respectively, GR₁₋₇, GR₁₋₁₄, GR₁₋₂₁, GR₁₋₂₈ and GR₁₋₃₅ – growth rates during the periods from 1-7, 1-14, 1-21, 1-28 and 1-35 days of age, respectively, h^2 : heritability, SE: stander error, rg: genetic correlation, rp – phenotypic correlation.

The cumulative response obtained from the two different estimating methods was in the desired direction for all studied growth traits except for BW₁ based on breeding

values. This indicates that selection for GR resulted in favorable genetic changes in these correlated traits. Similar trends have been observed in many studies [Baylan *et al.* 2009, Khaldari *et al.* 2010 and El-Attrouny *et al.* 2020]. The positive correlated responses for most traits suggest that selection for GR₁₋₂₁ can lead to simultaneous improvements in growth performance. The differences in selection responses among experiments arise from differences in selection intensity, precision, and genetic diversity in the studied populations. Earlier studies indicated a continuous increase in body weight and growth across generations due to the selection for higher body weight.

The effectiveness and accuracy of the selection program were supported by large population, intensive selection, and diverse estimation methods. Notably, methods centered on estimating breeding values are regarded as the most optimal approaches for genetic improvement [Chomchuen *et al.* 2022].

Heritability, genetic and phenotypic correlations between GR₁₋₂₁ and correlated growth traits

As shown in Table 5, heritability (h^2) for body weight (BW) at all studied ages were moderate, ranging from 0.21 to 0.25, indicating that these traits are influenced by both genetic and environmental factors. These estimates agree with those reported by Semida [2020], where h^2 for BWs ranged from 0.25 to 0.29. The h^2 estimates are in line with previous reports for BW₁ [Sezer *et al.* 2006], BW₇ [Saatci *et al.* 2006, Semida 2020], BW₁₄, BW₂₁ [Silva *et al.* 2013], BW₂₈, and BW₃₅ [Semida 2020]. Conversely, h^2 for BW₁ and BW₃₅ were low (0.07 and 0.03) as reported by Saatci *et al.* [2006] and Barbieri *et al.* [2015], and h^2 for BW₃₅ was 0.13 [Saatci *et al.* 2006]. This wide range of estimates could be attributed to differences in populations, estimation methods, statistical models, and selection criteria.

Genetically, GR₁₋₂₁ was positively correlated (rgs: 0.17-0.41) and phenotypically (rps: 0.25-0.42) with body weights during the period from 7 to 35 days, indicating that selection for GR₁₋₂₁ can indirectly improve overall growth performance, except for BW₁ which showed negative genetic (-0.16) and phenotypic (-0.19) correlations. Phenotypic correlations were higher than genetic correlations, similar to trends reported by Semida [2020]. The h^2 of GR₁₋₂₁ (0.25) surpassed h^2 's during other growth periods (0.18-0.23). Phenotypic correlations (rp 0.20-0.41) between GR₁₋₂₁ and other growth rates exceeded the corresponding genetic correlations (rg 0.18-0.40). Nariñç *et al.* [2014] reported higher h^2 (0.29) for GR₁₋₃₅. Positive but lower rg (0.24) and rp (0.26) were found between GR₁₋₂₁ and GR₁₋₃₅. Higher rp compared to rg may be due to phenotypic correlations involving both additive genetic and non-additive genetic effects, as well as environmental influences [Hadfield *et al.* 2007]. The correlation between traits can result from genes influencing both, pleiotropy, or linkage disequilibrium between genes. Pleiotropy leads to permanent correlations, while those from disequilibrium are temporary, arising from population crossings or introgressions [Hill 2013].

Conclusion

Selection responses across various estimating methods consistently exhibited desirable trends, indicating the accuracy of the applied program. Continuous selection for fast growth rate has resulted in a well-established paternal line with high growth potential of JQ which can be proposed as a sustainable solution for food security problem.

REFERENCES

1. ABOU KHADIGA G., MAHMOUD B. Y. F., EL-FULL, E. A., 2018 - Modelling of growth alteration in Japanese quail after a selection experiment for body weight at 4 weeks of age. *The Journal of Agricultural Science*, 156, 1153-1159]
2. AKBARIMEHR M., SOLKA M., NOSRATI M., RASOULI B., VAHABI-ASIL O., SEIDAVIA., HOSSEINTABAR-GHASEMABAD B., MARCHEWKA J., SZTANDARSKI P., JASZCZYK A., HORBAŃCZUK K., PETRYKOWSKI S., SIWIEC D., HORBAŃCZUK J.O., 2023 - Multi-strain probiotic improved feed conversion ratio and selected health indicators in Japanese quail. *Animal Science Papers and Reports* 41, 345-358.
3. BARBIERI A., ONO R.K., CURSINO L.L., FARAH M.M., PIRES M.P., BERTIPAGLIA T.S., PIRES A.V., CAVANI L., CARREÑO L.O.D., FONSECA R., 2015 - Genetic parameters for body weight in meat quail. *Poultry Science*, 94, 169-171.
4. BAYLAN M., 2017 - Effects of different selection methods using body weight on egg yield parameters in Japanese quail. *Brazilian Journal of Poultry Science*, 19, 623-628.
5. BAYLAN M., CANOGULLARI S., SAHIN A., COPUR G., BAYLAN M., 2009- Effects of different selection methods for body weight on some genetic parameters. *Journal of Animal and Veterinary Advances* 8, 1385–1391.
6. BRODY S., 1945- Bioenergetics and growth. Reinhold Publishing Corp., New York, NT.
7. CHOMCHUEN K., TUNTIYASAWASDIKUL V., CHANKITISAKUL V., BOONKUM W., 2022 - Genetic evaluation of body weights and egg production traits using a multi-trait animal model and selection index in Thai native synthetic chickens. *Animals* 12 (3), 335.
8. DECUYPERE E., BRUGGEMAN V., BARBATO G.F., BUYSE J., 2003 - Growth and reproduction problems associated with selection for increased broiler meat production. Pp: 13-28. In: Poultry Genetics, Breeding and Biotechnology, edited by Muir. W. M. and Aggrey, S. E, CABI Publishing, London.
9. DUNCAN D.B., 1955- Multiple range and multiple F-tests. *Biometrics* 11, 1-42.
10. 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, 325-333.
11. EMAM A.M., ELNESR S.S., EL-FULL E.A., MAHMOUD B.Y., ELWAN H., 2023- Influence of improved microclimate conditions on growth and physiological performance of two Japanese quail lines. *Animals* 13(6), 1118]
12. FALCONER D. S., MACKAY T. F. C., 1996 - Introduction to quantitative genetics. 4th Ed. Longman, London.
13. FARAHAT G. S., MAHMOUD B. Y., EL-KOMY E. M., EL-FULL E. A., 2018 - Alterations in plasma constituents, growth and egg production traits due to selection in three genotypes of Japanese quail. *The Journal of Agricultural Science* 156, 118-126.
14. GUILL R., WASHBURN K., 1974 - Genetic changes in efficiency of feed utilization of chickens maintaining body weight constant. *Poultry Science* 53, 1146-1154.

15. HADFIELD J.D., NUTALL A., OSORIO D., OWENS I.P.F., 2007 - Testing the phenotypic gambit: Phenotypic, genetic and environmental correlations of colour. *Journal of Evolutionary Biology*, 20, 549-557.
16. HENDERSON C.R., 1973 - Sire evaluation and genetic trends. *Journal of Animal Science (Symposium)* 10-41.
17. HILL W.G., 2013 - Genetic correlation. In 'Brenner's encyclopedia of genetics'. 2nd Ed., (Eds S Maloy, K Hughes) pp: 237-239.
18. KATZ-ROSENE R., HEFFERNAN A., ARORA A., 2023 - Protein pluralism and food systems transition: A review of sustainable protein meta-narratives. *World Development, Elsevier* 161 (C).
19. KHALDARI M., PAKDEL A., YEGANE H. M., JAVAREMI A.N., BERG P., 2010- Response to selection and genetic parameters of body and carcass weights in Japanese quail selected for 4-week body weight. *Poultry Science* 89, 1834-1841.
20. MAHMOUD B.Y.F., ABOU KHADIGA G., EL-FULL E.A., 2015 - Correlated response to selection for some egg performance traits in egg line of Japanese quail. *Animal Production Science* 56, 913-917]
21. MAHMOUD B.Y., SEMIDA, D.A., EL-FULL, E.A., EMAM, A.M. 2023 - Genetic evaluation for survival traits in Japanese quail line selected for fast growth rate. *Animal Biotechnology* 34, 2414-2419.
22. MEYER K., 2007 - WOMBAT: a tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML). *J. Zhejiang Univ. Science* B8, 11, 815-821.
23. N.R.C., 1994- Nutrient requirements of domestic animals. Nutrient Requirements of Poultry, 9th Rev. Ed Washington, DC: National Academy Press.
24. NARINÇ D., KARAMAN E., AKSOY T., FIRAT M.Z., 2014 - Genetic parameter estimates of growth curve and reproduction traits in Japanese quail. *Poultry Science* 93, 24-30.
25. PEEBLES E., MARKS H., 1991 - Effect of selection on plasma thyroxin concentrations in Japanese quail under thiouracil and protein stress. *Poultry Science* 70, 641-650.
26. SAATCI M., OMED H., DEWI I.A.P., 2006 - Genetic parameters from univariate and bivariate analyses of egg and weight traits in Japanese quail. *Poultry Science* 85,185-190.
27. SAS, 2011- SAS/STAT® 9.3 Statistics user's guide. Statistical analytical system. SAS Institute Inc, Carry.
28. SEMIDA D.A.M., 2020- Selection for augmenting early growth rate in Japanese quail. M.Sc. Thesis, Fac., Agric., Fayoum, Univ.
29. SEZER M., BERBEROGLU E., ULUTAS Z., 2006 - Genetic association between sexual maturity and weekly live-weights in laying-type Japanese quail. *South African Journal of Animal Science* 36,142-148.
30. SILVA L.P., RIBEIRO J.C., CRISPIM A.C., SILVA F.G., BONAFÉ C.M., FABYANO F.S., TORRES R.A., 2013- Genetic parameters of body weight and egg traits in meat-type quail. *Livestock Science* 153, 27-32.
31. TARTAGLIA L.A., DEMBSKI M., WENG X., DENG N., CULPEPPER J., DEVOS R., RICHARDS G.J., CAMPFIELD L.A., CLARK C.T., DEEDS J., MUIR C., SANKER S., MORIARTY A., MOORE K.J., SMUTKO J.S., MAYS G.G., WOOLF E.A., MONROE C.A., TEPPER R. I., 1995 - Identification and expression cloning of leptin receptor, OB-R. *Cell* 29, 1263-1271.

