



EFFECTS OF SELECTION FOR INCREASING EARLY GROWTH RATE ON GROWTH AND CARCASS CHARACTERISTICS OF JAPANESE QUAIL**D. A. M. Semida¹, B. Y. F. Mahmoud¹, E. A. El-Full¹ and A. M. Emam^{1,2}**¹ Fac. of Agric., Poult.Prod. Dep.t, Fayoum Uni., 63514 Fayoum, Egypt.² Corresponding author: Ahmed M Emam Email: ame04@fayoum.edu.eg

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ABSTRACT: This study aimed to investigate the effects of selection for high early growth rate during 1-21 days of age (GR_{1-21}) on growth traits, some plasma constituent and carcass characteristics. An experiment was carried out at the farm of the Poultry Research Center, Faculty of Agriculture, Fayoum University and continued for six generations including 10,024 for two lines (the selected line, HGR_{1-21} and the control line, CL) of Japanese quail chicks. The HGR_{1-21} had better BW_{21} , BW_{35} , GR_{1-21} , GR_{1-35} and BWG_{1-35} than the CL. Generation of selection significantly affected all growth traits. Females had significantly higher BW_{21} , BW_{35} , BWG_{1-35} and GR_{1-35} than males. Quails of HGR_{1-21} had lower high density lipoprotein (HDL) and higher triglycerides (TG) than the CL. Females had higher TG and lower HDL than males. Quails of HGR_{1-21} had higher carcass %, dressing %, weights of giblets, heart, gizzard and liver than CL by 3.65%, 2.59, 23.79, 68.42, 13.21 and 23.47%, respectively. Females had higher weights of giblets, gizzard and liver than males by +12.41%, 14.64% and 12.34%, respectively. The HGR_{1-21} had higher ether extract % (+24.28%) and lower moisture% (-4.79%) than the CL. GR_{1-21} showed moderate heritability (h^2) of 0.28 and ranged from 0.20 to 0.29 for growth traits. The GR_{1-21} found to be positively genetic and phenotypic correlated (r_g & r_p) with BW_{21} , BW_{35} , BWG_{1-35} and GR_{1-35} , with r_g ranged from moderate to high (0.24 to 0.70) and r_p ranged from low to medium (0.03 to 0.41), however there were negative r_g and r_p between GR_{1-21} and BW_1 being -0.15 and -0.50, respectively. Genetic response showed superiority of the selected line than the control ($P < 0.05$) for selection criteria (+0.04). Selection for GR_{1-21} had desired genetic gain with all studied growth traits, except BW_1 . Also, carcass traits and vital organs were improved due to selection for GR_{1-21} .

Key words: selection, early growth rate, carcass characteristics, genetic gain and Japanese quail.

INTRODUCTION

Selection for increasing body weight increased feed consumption, rate of metabolism and leads to higher O₂ demand, augmented muscle mass (especially breast muscle) has not been correlated with a relatively increment in vital organs such as the heart and lungs (Havenstein *et al.*, 2003). Moreover, increasing incidence of ascites syndrome arises from consecutive high body weight selection programs in broilers failing to meet the accelerating demand for O₂ in their bodies due to imbalance between cardiopulmonary system output and the requires of the body (Druyan *et al.*, 2007). Several problems, such as skeletal abnormalities, massive fat deposition and sudden death syndrome occurred due to intensive application of genetic improvement for body weight and slaughter characteristics of poultry (Narinc and Aksoy, 2012). Growth rate is a biometric trait of moderate to high heritability and can be rapidly improved through selection (Anthony *et al.*, 1991). Either short or long term selection for growth rate resulted in increasing overall body weight at marketing age, body weight at sexual maturity, body protein and skeletal muscles (Reddish, 2004). Selection for growth is associated with change in hormone concentration such as growth hormone and thyroxin (Peebles and Marks, 1991) due to physiological role of leptin in growth regulation by controlling food intake and thermo genesis through actions on hypothalamic centers as well as its role in energy expenditure and maturity (Tartaglia *et al.*, 1995). There were positive genetic correlations among growth rate and both body weights at different ages and growth rate during different periods of growth, therefore indirect selection could be used

to enhance these traits (Abdel Fattah, 2006 and Manaa *et al.*, 2015). Several selection investigates have been conducted on live body weight in Japanese quail, however few studies examining early growth rate therefore this study aimed to investigate the influence of selection for early high growth rate of quail on body weight, carcass and some blood constituents.

MATERIALS AND METHODS

This work was carried out at the farm of the Poultry Research Center, Faculty of Agriculture, Fayoum University. An experiment was continued for six generations (pre-base, base and four selected generations) including 10,024 Japanese quail (*Coturnix coturnix japonica*) chicks. The selected breeders were housed (two females were randomly assigned to each male) in breeding cages. Matings of close relatives were avoided to decrease the rate of inbreeding depression. Eggs were daily collected in a pedigree system for each family depending on the shell color and patterns of each female when ages of females were 11–14 weeks of age. The newly hatched chicks were wing banded using small size plastic bands, chicks were brooded on the floor until 35 days of age. According to NRC (1994), all quails from hatch to 35 days of age were fed *ad libitum* on a starter diet containing 24% crude protein and 2900 K Cal ME and . All chicks were weekly individually weighed to calculate growth rate. From 42 days of age to the end of the study, a breeder diet containing 20% crude protein, 2900 K Cal ME, 2.25% calcium and 0.43% available phosphorous was supplied. Birds were in continuous light during the first 35 days of age and then reduced to 16 h of light per day thereafter. Birds were kept under the

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same managerial hygienic and environmental conditions. At the fourth generation, a slaughter test was performed at 35 days of age using 25 chicks per sex within each line, which were randomly selected for whole body carcass analysis and all giblets were separately weighed. Carcass composition was analyzed in the Laboratory of the Poultry Production Department, Faculty of Agriculture, Fayoum University. Lipid content was measured by ether extraction. Protein content was determined as by N Kjeldahl x 6.25. About three cm³ of blood samples from each chick were collected during slaughtering into dry clean centrifuge tubes containing one drop of heparin and immediately centrifuged at 3000 rpm for 20 minutes. The clear plasma samples were carefully drawn and transferred to dry, clean, small glass bottles and stored at -20 °C in a deep freezer until the time of chemical analyses. Plasma samples were assayed for total cholesterol (mg/dl), high density lipoprotein (HDL, mg/dl), low density lipoprotein (LDL, mg/dl) and triglycerides (TG, mg/dl) by enzymatic colorimetric tests using commercial kits (STANBIO) according to the manufacturer's recommendations.

Selection Program

Aggregated breeding values of a selection criterion were estimated in two lines of Japanese quail that were simultaneously bred. The selected line for high growth rate during 1-21 days of age (HGR₁₋₂₁) was selected according to the estimated aggregated breeding values for four successive generations, while a control line (CL) was kept under random mating without selection.

Studied Traits

Selection criteria:

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

$$GR = [W_2 - W_1 / 1/2 (W_2 + W_1)]$$

where: w₁: the weight at the beginning and w₂: is the weight at the end of the period.

Also, Growth rate during the period from 1-35 days of age (GR₁₋₃₅) was calculated.

Body weight at different ages:

Body weight at hatch, 21 and 35 days of age (BW₁, BW₂₁ and BW₃₅, respectively) were individually recorded to the nearest 0.01g.

Body weight gain during the period from 1-35 days of age (BWG₁₋₃₅):

According to the following formula BWG₁₋₃₅ was calculated.

$$BWG_{1-35} = BW_{35} - BW_1$$

Slaughter traits:

Carcasses%: (100 X Carcass weight / BW₃₅).

Dressing % was determined: ((Carcass weight + Giblets) / BW₃₅) X 100.

BLM % : ((Carcass weight - bones weight) / BW₃₅) X 100

Statistical analyses

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

$$Y_{ijklm} = \mu + a_i + G_j + L_k + S_l + G_j \times L_k + G_i \times S_l + L_k \times S_l + G_j \times L_k \times S_l + e_{ijklm}$$

where:

Y_{ijklm}: is the observation for a trait μ : is the overall mean, a: is the random additive genetic effect of the ith animal, G: the effect of jth generation, L: the effect of kth line, S: the effect of lth sex, G_j x L_k: the effect of interaction of the jth generation with the kth line, G_j x S_l: the

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effect of interaction of the j^{th} generation with the l^{th} sex, $L_k \times S_l$: the effect of k^{th} line with the l^{th} sex, $G_j \times L_k \times S_l$: the effect of interaction of the j^{th} generation with the k^{th} line with the l^{th} sex and e_{ijklm} : is the random error term; the random variable was the birds within line. Means of generation were compared using multiple range test (Duncan, 1955). Data of plasma constituents, carcass characteristics and chemical composition of carcass traits were analyzed by PROC MIXED (SAS, 2011) to calculate the line and sex specific means by the following model:

$$Y_{ijkl} = \mu + a_i + L_j + S_k + L_j \times S_k + e_{ijkl}$$

where:

Y_{ijkl} : is the observation for a trait μ : is the overall mean, a : is the random additive genetic effect of the i^{th} animal, L : the effect of j^{th} line, S : the effect of k^{th} sex, $L_j \times S_k$: the effect of j^{th} line with the k^{th} sex and e_{ijkl} : is the random error term; the random variable was the birds within line.

Genetic Parameters:

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

The univariate model to estimate direct h^2 was:

$$y = Xb + Za + e$$

The bivariate model to estimate correlations between selection criteria trait 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.

Genetic gain:

Genetic gain evaluation depending on breeding values (EBV's) for the studied traits through a mixed model method (Henderson, 1973), by determining the difference between the averages of the EBV's of the first and the last generation within each line separately.

RESULTS AND DISCUSSION

Selection criteria

Generation effect:

Selection criterion (GR_{1-21}) significantly increased as generation number increased, the G_4 had the fastest whereas, the G_1 showed the slowest GR_{1-21} (1.77 vs 1.70) indicated that G_4 surpassed the G_1 by +4.118% (Table 2). Also, Abdel Fattah (2006) recorded the same trend of GR 's which increased after three generations of selection for high GR during the period from one to 42 days of age.

Line effect:

Line significantly affected GR_{1-21} ($P < 0.0071$) favoring the selected line which exceeded the CL by +0.05 (+2.941%) as shown in Table 2. This improvement of growth by selection may be due to moderate to high estimates of heritability for GR (Narinc *et al.*, 2014 and Manaa *et al.*, 2015), association with alteration in hormone concentration such as growth hormone and thyroxin due to physiological role of leptin in growth regulation by controlling food intake and thermo genesis through actions on hypothalamic centers as well as its role in energy expenditure and maturity (Peebles and Marks, 1991 and Tartaglia *et al.*, 1995). Regardless of selection criteria,

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calculated averages for GR₁₋₂₁ of selected line GR₁₋₄₂ were 1.71, 1.68, 1.69 and 1.70 vs 1.71, 1.66, 1.69 and 1.69 in CL at base, first, second and third generation, respectively (Abdel Fattah, 2006).

Sex effect:

Sex affected GR₁₋₂₁ ($P \leq 0.8208$) favoring males which surpassing females by +0.02 (+1.156%) as shown in Table 2. This may be due to higher metabolic rate in males or occurred as a result of performance of male sexual activities due to hormonal change (Selim *et al.*, 2006). Conversely, calculated GR₁₋₂₁ indicated that females had faster GR₁₋₂₁ than males (Abdel Fattah, 2006).

Performance of growth traits:

Generation effects on growth traits:

Generation of selection significantly affected all growth traits. The 4th generation of selection had the best BW₂₁, BW₃₅, BWG₁₋₃₅ and GR₁₋₃₅ except for BW₁. The 1st generation had the lowest BW₁ (7.84g), the 2nd generation showed lower BW at 35 days of age and Gain₁₋₃₅ being 186.45g and 177.74, respectively whereas the lowest BW₂₁ and GR₁₋₃₅ were obtained for the 3rd generation (Table 2). Similarly there were significant differences due to generation effect for BW's from hatching up to 21 days (Emam, 2015 and Meabed, 2015).

Line effects on growth traits:

The effect of short-term selection (4 generations) for GR₁₋₂₁ on all growth traits was found significant. The HGR₁₋₂₁ line had better performance for BW₂₁, BW₃₅, GR₁₋₃₅ and BWG₁₋₃₅ than the CL, whereas the CL had heavier BW₁ than HGR₁₋₂₁ line. Also, there were significant higher BW's favoring the selected line, however, the selected line had significantly higher BW₁ than the CL (Narendra Nath *et al.*, 2011). Regardless of generation, selected lines for BW had

significantly heavier BW₃₅ than the control line (Taskin *et al.*, 2017).

Sex effects on growth traits:

Females had significantly higher BW₂₁, BW₃₅, BWG₁₋₃₅ and GR₁₋₃₅ than males. On the other hand, BW at hatch and GR₁₋₂₁ insignificantly favored males regardless of line and generation of selection as shown in Table 2. Results of Narinc *et al.* (2014) and Elkomy *et al.* (2019) indicated that females were consistently heavier than males for BW at different ages. In addition, there was significant sexual dimorphism of Japanese quail BW favoring females than its counterpart males which occurred as a result of male sexual activities due to the hormonal change. Similarly, Taskin *et al.* (2017) indicated that sex was a significant source of variation for BW at all the ages across selection generations. Similarly, calculated GR₁₋₃₅ indicated that females had faster GR than males (Daikwo *et al.*, 2014).

Performance of some plasma constituent traits:

Line effect on plasma constituent traits:

As shown in Table 3, quails of the selected line had significantly and unpreferably lower HDL (good cholesterol) and higher TG whereas both LDL and total cholesterol were insignificantly differed than the CL. Similarly, significant differences due to line effect were found for TG and cholesterol, the longer shank length at 28 days of age had higher concentrations of TG than other lines (Farahat *et al.*, 2018).

Sex effect on plasma constituent traits:

Females had significantly higher TG and lower HDL than males whereas, sex insignificantly affected each of LDL and total cholesterol. Farahat *et al.* (2018) found that sex had insignificant effects on

TG and cholesterol. Moreover, a high level of lipids in the plasma is also an indicator of the great needs of the growing oocytes for yolk lipids (Sato *et al.*, 2004).

Performance of some carcass traits:

Line effect on carcass traits:

Quails of the selected line significantly had higher carcass %, dressing %, weights of giblets, heart, gizzard and liver (+3.65%, +2.59, 23.79, 68.42, 13.21 and 23.47% respectively) than the CL as shown in Table 4. Similar trend of significant line effect on carcass% was reported by Mahmoud *et al.* (2018). However, Khaldari *et al.* (2010) reported insignificant differences due to lines for carcass%. Similarly, Alkan *et al.* (2010) reported that line insignificantly affected carcass%. Selection for high BW₄₂ and GR₁₋₄₂ significantly improved carcass%, dressing% and boneless meat % of Japanese quail, also the HGR₁₋₄₂ line had higher carcass%, dressing% and BLM% than other lines as reported by Mahmoud (2006). Mahmoud *et al.* (2018) found significant differences due to lines for dressing%.

Sex effect on carcass traits:

Females had higher weights of giblets, gizzard and liver than their counterparts males by +12.41%, +14.64% and +12.34% whereas, BLM insignificantly affected by sex (Table 3). Males had significantly higher carcass% and dressing %, (+4.00 and +2.87%, respectively). Similarly, there were significant effects on carcass% due to sex (Alkan *et al.*, 2010 and Pourtorabi *et al.*, 2017). This may be due to anatomical differences (sexual organs) between males and females that increase as they approach the age of sexual maturity (early in Japanese quail).

Performance of chemical composition of carcass traits:

Line effect on chemical composition of carcass traits:

Unfortunately, the selected line had higher ether extract % (+24.28%) whereas, had lower moisture% (-4.79%) than the CL (Table 5). Similarly, there were significant effects on ether extract % due to line whereas, insignificantly affected protein% as reported by Mahmoud (2006).

Sex effect on chemical composition of carcass traits:

Sex had no significant effect on all chemical composition of carcass traits. Similarly, Mahmoud (2006) reported that sex insignificantly affected Ether extract% and protein%.

Genetic parameters for the studied growth traits:

Heritability (h²) of selection criteria GR₁₋₂₁

The GR₁₋₂₁ had medium h² 0.28 (Table 6). The results of h² are in agreement with those reported by Abdel Fattah (2006) who found that h² estimates of GR₁₋₂₁ were 0.21, 0.19 and 0.20 based on sire, dam and sire + dam variance component in base population, respectively.

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

Genetically, h² for BW's at different ages showed moderate h² ranged from 0.25 to 0.29. The BW₁ had higher h² of 0.29 whereas, BW₂₁ showed lower h² of 0.25 than other BW's, both GR₁₋₃₅ and BWG₁₋₃₅ had moderate h² of 0.20 (Table 6). Heritability estimates for BWs of this work were in agreement with the reports of other studies concerning BW₁ (Sezer *et al.*, 2006), BW₂₁ (Silva *et al.*, 2013) and BW₃₅ (Barbieri *et al.*, 2015). However, h² estimates of the this study were lower

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than those reported by several authors BW_1 , BW_{21} (Silva *et al.*, 2013) and BW_{35} (Sezer *et al.*, 2006). Conversely, h^2 for BW_1 and BW_{35} were low (0.07 and 0.03, BW_1) as reported by Saatci *et al.* (2006) and Barbieri *et al.* (2015) and h^2 for BW_{35} being 0.13 (Saatci *et al.*, 2006). The results of Narinc *et al.* (2014) found moderate h^2 for GR_{1-35} being 0.29. This wide range of estimates could be due to the differences in populations, method of estimation and statistical models.

The GR_{1-21} found to be positively correlated with BW_{21} , BW_{35} , BWG_{1-35} and GR_{1-35} , with rgs ranged from 0.24 to 0.70 and r_p ranged from 0.03 to 0.41, however there were negative r_g and r_p between GR_{1-21} and BW_1 being -0.15 and -0.50, respectively was found as shown in Table 6. Similarly, r_g and r_p correlations between GR_{1-21} and BW_1 were negative ranged from -0.41 to -0.47 (Abdel Fattah, 2006). Genetic correlations can arise in several ways, they can be caused by pleiotropic gene effect, linkage, pleiotropic occurs when one locus affects multiple traits (Falconer, 1989). Selection based on growth rate, body weights and skeletal measurement traits could increase growth traits of quail (Abdel Fattah, 2006, Emam 2015 and Meabed 2015) due to the expected positive rgs among these traits.

Genetic gain:

Response showed superiority of the selected line than the control ($P < 0.05$) for selection criteria (+0.04). Selection for GR_{1-21} had favorable genetic gain with all growth traits, except BW_1 . Genetic gain estimates indicated insignificant and positive differences for all studied traits whereas, significant differences for BW_1 and BW_{21} were -1.16 and +6.80, respectively. Also, Emam (2015) reported significant genetic gain

for BW from hatch up to 35 days of age which ranged from 0.03 to 4.07 in selected line for BW_3 under normal diet line and from -0.05 to 8.65 in selected line for BW_3 under restricted protein diet line. Meabed (2015) found very highly significant genetic gain for BW_1 , BW_{21} and BW_{35} being +0.37, +14.93 and +12.51. in longer shank length at 28 days of age and -0.12, +15.85 and +18.14, respectively in shorter shank length at 28 days of age. In addition Abdel Fattah (2006) found inconsistent change -0.04 to +0.04% and -0.01 to +0.03% in GR_{1-21} due to selection for high BW_{42} and high GR_{1-42} .

CONCLUSION

Selection for high growth rate during the period from 1 to 21 days of age in Japanese quail improves growth traits especially at marketing age (BW_{35}), carcass characteristics and vital organs (carcass %, dressing %, weights of giblets, heart, gizzard and liver) were improved by the selection for high growth rate. Selection for GR_{1-21} had desired genetic gain with most studied growth traits (BW_{21} , BW_{35} , BWG_{1-35} and GR_{1-35}) and there were positive r_g and r_p correlations between GR_{1-21} and studied growth traits, therefore indirect selection could be used to enhance these traits.

Table (1): Population size over the six generations of the selection experiment.

Generation	Line	Progeny	Sires	Dams	Total
Pre-base	-	1300	200	400	1300
Base	-	1726	132	264	1726
First	Control line	454	70	139	1813
	Selected line	1359	89	178	
Second	Control line	456	48	96	1594
	Selected line	1138	86	172	
Third	Control line	472	40	80	1768
	Selected line	1296	90	180	
Fourth	Control line	440	68	136	1823
	Selected line	1383	88	176	
Total					10,024

Table (2): Least square means \pm SE for the growth traits as affected by generation, line and sex effects.

Item	GR ₁₋₂₁	BW ₁	BW ₂₁	BW ₃₅	BWG ₁₋₃₅	GR ₁₋₃₅
Generation effect (G):						
G ₁	1.70 \pm 0.001 ^d	7.84 \pm 0.06 ^c	121.80 \pm 1.01 ^b	197.11 \pm 1.35 ^b	189.26 \pm 1.34 ^b	1.85 \pm 0.002 ^a
G ₂	1.74 \pm 0.002 ^c	8.71 \pm 0.04 ^b	106.80 \pm 0.71 ^c	186.45 \pm 0.91 ^c	177.74 \pm 0.92 ^c	1.82 \pm 0.001 ^b
G ₃	1.75 \pm 0.002 ^b	9.13 \pm 0.04 ^a	106.44 \pm 0.71 ^c	188.22 \pm 0.91 ^c	179.14 \pm 0.91 ^c	1.81 \pm 0.001 ^c
G ₄	1.77 \pm 0.002 ^a	7.95 \pm 0.05 ^c	132.50 \pm 0.88 ^a	205.46 \pm 1.16 ^a	197.29 \pm 1.15 ^a	1.85 \pm 0.002 ^a
Line effect:						
CL	1.70 \pm 0.003 ^b	8.63 \pm 0.04 ^a	107.63 \pm 0.73 ^b	185.22 \pm 0.96 ^b	176.81 \pm 0.96 ^b	1.81 \pm 0.003 ^b
HGR ₁₋₂₁	1.75 \pm 0.001 ^a	8.51 \pm 0.03 ^b	116.62 \pm 0.41 ^a	194.93 \pm 0.53 ^a	186.33 \pm 0.53 ^a	1.83 \pm 0.001 ^a
Sex effect:						
Female	1.73 \pm 0.001	8.55 \pm 0.03	117.08 \pm 0.64 ^a	198.72 \pm 0.76 ^a	190.19 \pm 0.76 ^a	1.83 \pm 0.001 ^a
Male	1.75 \pm 0.003	8.52 \pm 0.04	111.85 \pm 0.67 ^b	186.27 \pm 0.79 ^b	177.73 \pm 0.79 ^b	1.82 \pm 0.002 ^b
p-value						
Generation	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
Line	0.0071	0.0071	0.0001	0.0001	0.0001	0.0001
Sex	0.8208	0.4621	0.0001	0.0001	0.0001	0.0001
Generation*Line	0.6493	0.0001	0.0015	0.3902	0.0946	0.0001
Generation*Sex	0.5489	0.0801	0.7124	0.0634	0.2468	0.8406
Line*Sex	0.0700	0.3268	0.5106	0.5893	0.5841	0.6123
Generation*Line*Sex	0.5814	0.5163	0.8144	0.7412	0.6541	0.5355

Means having different superscripts within each effect in the same column are significantly differed at specified probability, SE: stander error, BW₁, BW₂₁ and BW₃₅: body weights at hatch, 21and 35 days of age respectively, BWG₁₋₃₅: body weight gain during the periods from 1-35 days of age, GR₁₋₂₁ and GR₁₋₃₅: growth rates during the periods from 1-21 and 1-35 days of age, HGR₁₋₂₁: the selected line for high growth rate during 1-21 days of age, CL: the control line, P: Probability.

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Table (3): Least square means \pm SE for the some plasma constituent traits as affected by line, sex and line x sex effects

Item	HDL, mg/dl	LDL, mg/dl	Total cholesterol, mg/dl	TG, mg/dl
Line effect:				
CL	44.71 \pm 1.20 ^a	116.15 \pm 7.36	193.44 \pm 9.59	179.52 \pm 11.33 ^b
HGR ₁₋₂₁	36.72 \pm 1.22 ^b	135.75 \pm 7.45	214.50 \pm 9.47	256.96 \pm 12.84 ^a
Sex effect:				
Female	38.87 \pm 1.17 ^b	126.50 \pm 7.18	210.38 \pm 9.24	266.04 \pm 12.47 ^a
Male	42.55 \pm 1.24 ^a	124.74 \pm 7.62	196.26 \pm 9.81	169.89 \pm 11.74 ^b
p-value				
Line	0.0001	0.0649	0.1238	0.0001
Sex	0.0366	0.8670	0.2993	0.0001
Line*Sex	0.0394	0.5720	0.3301	0.0001

Means having different superscripts within each effect in the same column are significantly differed at specified probability, SE: stander error, HDL: high density lipoprotein, LDL: low density lipoprotein and TG: triglycerides, HGR₁₋₂₁: the selected line for high growth rate during 1-21 days of age, CL: the control line, P: Probability.

Table (4): Least square means \pm SE for carcass traits as affected by line, sex and line x sex effects

Item	Percentages			Weights			
	Carcass%	Dressing %	BLM%	Giblets, g	Heart, g	Gizzard, g	Liver, g
Line effect:							
CL	67.04 \pm 1.55 ^b	73.70 \pm 1.60 ^b	49.37 \pm 0.87	11.81 \pm 1.13 ^b	1.33 \pm 0.08 ^b	5.22 \pm 0.12 ^b	5.24 \pm 0.27 ^b
HGR ₁₋₂₁	69.49 \pm 1.36 ^a	75.61 \pm 1.42 ^a	50.51 \pm 0.82	14.62 \pm 0.85 ^a	2.24 \pm 0.06 ^a	5.91 \pm 0.16 ^a	6.47 \pm 0.19 ^a
Sex effect:							
Female	67.32 \pm 1.17 ^b	73.91 \pm 1.24 ^b	49.37 \pm 0.82	14.40 \pm 0.88 ^a	1.77 \pm 0.07	5.95 \pm 0.14 ^a	6.19 \pm 0.23 ^a
Male	70.01 \pm 1.74 ^a	76.03 \pm 1.77 ^a	50.51 \pm 0.82	12.81 \pm 1.10	1.79 \pm 0.07	5.19 \pm 0.15 ^b	5.51 \pm 0.24 ^b
p-value							
Line	0.0052	0.0334	0.2984	0.0001	0.0001	0.0012	0.0004
Sex	0.0014	0.0139	0.7579	0.0018	0.8823	0.0004	0.0432
Line*Sex	0.0011	0.0038	0.3409	0.0414	0.7872	0.0132	0.3084

Means having different superscripts within each effect in the same column are significantly differed at specified probability, SE: stander error, BLM: boneless meat, HGR₁₋₂₁: the selected line for high growth rate during 1-21 days of age, CL: the control line, P: Probability.

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Table (5): Least square means \pm SE for chemical composition of carcass as affected by line, sex and line x sex effects

Item	Protein %	Ether extract %	Ash%	Moisture %
Line effect:				
CL	22.74 \pm 0.43	3.13 \pm 0.16 ^b	1.98 \pm 0.10	69.67 \pm 0.50 ^a
HGR ₁₋₂₁	23.78 \pm 0.44	3.89 \pm 0.17 ^a	2.18 \pm 0.11	66.33 \pm 0.52 ^b
Sex effect:				
Female	22.97 \pm 0.41	3.54 \pm 0.17	1.97 \pm 0.11	68.31 \pm 0.52
Male	23.16 \pm 0.44	3.47 \pm 0.16	2.19 \pm 0.10	67.68 \pm 0.51
p-value				
Line	0.2958	0.0016	0.1901	0.0001
Sex	0.7603	0.7592	0.1467	0.3885
Line*Sex	0.7273	0.8605	0.3053	0.8096

Means having different superscripts within each effect in the same column are significantly differed at specified probability, SE: stander error, HGR₁₋₂₁: the selected line for high growth rate during 1-21 days of age, CL: the control line, P: Probability.

Table (6): Heritability, genetic gain, genetic and phenotypic correlations \pm SE of R₁₋₂₁ and some growth traits.

Trait	h ² \pm SE	Genetic gain	rg \pm SE	rp \pm SE
GR ₁₋₂₁	0.28 \pm 0.005	+0.04 \pm 0.01 [*]		
BW ₁	0.29 \pm 0.030	-1.16 \pm 0.03 ^{***}	-0.15 \pm 0.04	-0.50 \pm 0.02
BW ₂₁	0.25 \pm 0.031	+6.80 \pm 0.60 ^{**}	0.47 \pm 0.02	0.41 \pm 0.03
BW ₃₅	0.26 \pm 0.006	+5.47 \pm 0.87 ^{ns}	0.33 \pm 0.10	0.24 \pm 0.03
GR ₁₋₃₅	0.20 \pm 0.004	+0.02 \pm 0.003 ^{ns}	0.70 \pm 0.05	0.03 \pm 0.01
BWG ₁₋₃₅	0.20 \pm 0.004	+4.54 \pm 0.79 ^{ns}	0.24 \pm 0.03	0.26 \pm 0.03

h²: heritability, SE: stander error, rg: genetic correlation, rp: phenotypic correlation, BW₁, BW₂₁ and BW₃₅: body weights at hatch, 21and 35 days of age respectively, BWG₁₋₃₅: body weight gain during the periods from 1-35 days of age, GR₁₋₂₁ and GR₁₋₃₅: growth rates during the periods from 1-21 and 1-35 days of age, ns: non-significant, *, **, ***: significant at levels 0.05, 0.01, 0.001 respectively.

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الملخص العربي

تأثيرات الانتخاب لزيادة معدل النمو المبكر على صفات النمو و خصائص الذبيحة في السمان الياباني

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تهدف هذه الدراسة إلى دراسة تأثير الانتخاب لزيادة معدل النمو المبكر خلال الفترة 1-21 يوم من العمر (GR₁) (21 على صفات النمو في السمان الياباني ، و كذلك بعض خصائص مكونات البلازما و صفات الذبيحة. تم إجراء تجربة في مزرعة مركز بحوث الدواجن ، كلية الزراعة ، جامعة الفيوم واستمرت لمدة ستة أجيال متتالية حيث تضمنت على 10,024 طائر من السمان الياباني في خطين (الخط المنتخب، HGR₁₋₂₁ وخط المقارنة ، CL). كان الخط المنتخب أفضل في وزن الجسم عند 21، 35 يوم من العمر وكذلك معدل النمو والزيادة في وزن الجسم في الفترة 1-35 يوم من العمر عن خط المقارنة. كان تأثير الجيل معنوياً على جميع صفات النمو كما كانت الإناث أعلى من الذكور في اوزان الجسم عند 21، 35 يوم من العمر وكذلك معدل النمو والزيادة في وزن الجسم في الفترة 1-35 يوم من العمر. السمان في الخط المنتخب كان اقل في الليبوبروتينات عالية الكثافة و اعلى في الدهون الثلاثية من خط المقارنة. كانت الإناث أعلى من الذكور في الليبوبروتينات عالية الكثافة والدهون الثلاثية. السمان في الخط المنتخب كان أعلى في الذبيحة (%، التصافي % و اوزان الأحشاء، القلب، القانصة والكبد (+3.65%، +2.59%، 23.79%، 68.42%، 13.21%، 23.47 على التوالي) من خط المقارنة. كان للإناث أوزان أعلى في الأحشاء و القانصة والكبد من الذكور بنسبة + 12.41 % و 14.64 % و 12.34 %. كان الخط المنتخب أعلى في المستخلص الأثيري (% + 28.24) و اقل في الرطوبة (% - 4.79) من خط المقارنة. أظهرت صفة معدل النمو في الفترة من 1-21 يوم من العمر معامل توريث متوسط و قيمته 0.28 و تراوحت قيم معامل التوريث لصفات النمو من 0.20 الى 0.29. كان هناك ارتباط وراثي ومظهري موجب بين الصفة المنتخبة و صفات وزن الجسم عند 21، 35 يوم وكذلك الزيادة الوزنية للجسم و معد النمو في الفترة من 1-35 يوم من العمر و تراوحت قيم الارتباط الوراثي من متوسط الى عالي 0.24 الى 0.70 كما تراوحت قيم الارتباط المظهري من منخفضة الى متوسطة 0.03 الى 0.41 بينما تراوحت قيم الارتباط الوراثي والمظهري بين الصفة المنتخبة ووزن الجسم عند عمر يوم -0.15 ، -0.50. الانتخاب لصفة معدل النمو المبكر خلال الفترة من 1-21 يوم من العمر كان له عائد وراثي جيد على كل صفات النمو المدروسة ما عدا وزن الجسم عند عمر يوم كما تحسنت صفات الذبيحة ووزن الاعضاء الحيوية نتيجة الانتخاب لصفة معد النمو خلال الفترة من 1-21 يوم من العمر. الكلمات الدالة: الانتخاب، معدل النمو المبكر، خصائص الذبيحة، العائد الوراثي، السمان الياباني.