GENETIC PARAMETERS OF GROWTH, CARCASS, AND LAYING TRAITS IN TWO LINES OF UKRAINIAN QUAIL

Jameela Hairan Salih
Lecturer
Department of Animal Production, Coll. Agric. Engine. Sci. University of Duhok
jameela.hairan@uod.ac

ABSTRACT

The estimation of genetic parameters of certain productive characters in different lines of quail is very important to make a breeding schedule for such lines of quail in the future. This study was carried out for three generations to estimate the response to selection, selection deferential, genetic, and phenotypic correlation between studied traits (growth and laying performance) and heritability estimates in two lines of Ukrainian quail (*Coturnix coturnix coturnix*). A total of 120 Ukrainian quails from (500) quail birds (base population), were selected as parent generation for both lines and also 120 offspring birds specified for the third generation. The selection was based on body weight which was carried out on the 20th day of age. The results showed that the selection can improve breast weight, leg weight, carcass%, and live body weight in both lines. However, the realized heritability has moderate values for 42-day age body weight for both lines; but the dark line recorded a higher genetic correlation between body weight and weight gain compared to the white line. The highest phenotypic correlation estimates between body weight and egg weight were recorded for the white line; in addition, the same line receded better estimates for the studied genetic parameters in all other studied characteristics. It could be concluded that the selection based on the genetic parameters for growth and laying traits was effective for improving it through the three generations.

Keywords: Genetic and phenotypic correlation, response to selection, selection deferential, heritability, quail.

المعالم الوراثية لصفات النمو والذبيحة وإنتاج البيض في خطين من السمان الأوكراني

جميلة حيران صالح
مدرس
قسم الإنتاج الحيواني، كلية علوم الهندسة الزراعية، جامعة دهوك

المستخلص

إن تقدير المعالم الوراثية لبعض الصفات الكمية في مختلف خطوط السمان مهمة جداً لتخطيط استراتيجيات التربية والتحسين الوراثي لها في المستقبل. أجريت هذه الدراسة لثلاثة أجيال بغية تقدير الاستجابة للإنتخاب و الفارق الإنتخابي والإرتباط المظهري والوراثي لصفات الدراسة (أداء النمو وإنتاج البيض) وكذا تقدير المكافئ الوراثي لخطين من السمان الأوكراني (*Coturnix coturnix coturnix*). إجمالي عدد 120 طائراً من السمان الأوكراني من أصل 500 طائر (كعشيرة قاعدية) تم انتخابها كآباء لكلا الخطين، وكذا أختير عدد 120 طائرا لدراسة الجيل الثالث. تم إجراء الانتخاب على أساس وزن الجسم الحي في عمر 20 يوماً. أظهرت النتائج أن الانتخاب قد حسن من وزن صدر الطيور ووزن ارجلها وتصافي الذبيحة % ووزن الجسم ككل في كلا الخطين. على أية حال، فإن المكافئ الوراثي المحقق قدر قيمته كقيم وسطى من أجل وزن جسم الطيور في عمر 42 يوماً لكلا الخطين، بينما سجلت أفراد الخط الداكن معامل ارتباط وراثي عالي بين صفتي وزن الجسم الحي والزيادة الوزنية مقارنة بالخط الأبيض اللون. بينما سجلت أعلى قيم معاملات الارتباط المظهري بين الصفتين السابقتين في الخط الأبيض، كما أن الخط الأخير نفسه سجلت تقديرات أفضل لباقي المعالم الوراثية مقارنة بالبني. يمكن الإستنتاج أن الإنتخاب اعتماداً على المعالم الوراثية لصفات النمو وانتاج البيض كان فعالاً في تحسينها من خلال الأجيال الثلاثة.

الكلمات المفتاحية: الارتباط الوراثي والمظهري، الاستجابة للإنتخاب، الفارق الإنتخابي، المكافئ الوراثي، السمان.

Received:26/7/2022, Accepted:16/10/2022

INTRODUCTION

European and Far Eastern Japanese quails (Coturnix *Coturnix Spp)*, have been considered as different, however, closely related as two subspecies: The Common quail *Coturnix coturnix coturnix* and the Japanese quail *Coturnix coturnix japonica* Barilani (7). The common quail (*Coturnix coturnix coturnix*) is an abundant and widespread Palearctic bird species (Cramp and Simmons (8). The common quail is registered in Annex II/2 of the EU Birds directive and is one of the most important game species in Europe. Among the different types of poultry farms, *Coturnix coturnix spp* is widely used in the agricultural sector for the production of eggs and meat (14,15,20,35). Quail is a common bird model in numerous fields of research because of its small body size, short generation interval (3-4 generations per year), resistance to many common avian diseases, high egg production, wonderful laboratory experimental bird, less feed consumption and easy maintenance (2,40). To establish a breeding program, it must estimate genetic parameters for improving the traits (16) reported that the efficiency level of production and reproductive traits are affected by both genetic and environmental factors. Genetic parameters and the phenotypic relationship between body weight, carcasses, and organ parameters of quail were estimated by (17,18,39) who reported that the carcass traits of heavy quail line under introgression with the roux gene. Most of the investigations related to *Coturnix* Japanese while other lines were less studied. Other researchers reported the genetic correlations between traits assuming major importance to improve correlated traits (6,21,36). However, it should not be neglected the role of phenotypic correlations and accessibility of records, pedigree information, and reputable pedigree information is necessary to design a breeding program, but dependable pedigree information is not often available in quail production systems Sari (30). Although genetic and phenotypic correlations between body weight and egg production traits were negative (13,36) the greater impact on body weights has resulted in lower egg production and vice versa. Therefore, partitioning the quails into egg- or meat-producing types based on their capability of producing egg or meat at the earlier stages would be helpful for quail production investment. Nevertheless, genetic or phenotypic correlations between early body weights and slaughter weight are weak, which may be due to the nature of the growth pattern in quails Barbieri (6). However, genetic or phenotypic selection of the birds based on early growth performances (as correlated traits) does not lead to improvement in slaughter weight. This may be due to the nonlinear nature of the growth pattern of the birds or the presence of maternal effects, which are not inherited at older ages (1,5). The basic tool for improving the productive potential of birds is selection. Different selection strategies have been working throughout the world comprising mass selection to full pedigree selection (9,23). Selection programs improve economic traits in broilers, growth rate, and carcass characters have improved 2.4-fold and the feed conversion ratio has improved 0.025% per year. Selection experiments provide background information on the inheritance of complex traits and allow the evaluation of hypothetical predictions by comparing observations and expectations Szwaczkowski (38). This study was aimed, at the selection of European quail for body weight at six weeks of age, egg production and carcass traits were carried out for three generations to estimate the response to selection, selection deferential, genetic and phenotypic correlation between traits, and heritability estimates in two lines of Ukrainian quail (*Coturnix coturnix coturnix*).

MATERIALS AND METHODS

Birds management: This study was performed at the poultry farm of the animal production department, College of Agricultural Engineering Sciences, University of Duhok during (1/4/2021-20/8/2021). A selection experiment was carried out for three generations for two lines of Ukrainian quail (white and dark lines). In this experiment, both lines used a total number of 500 Ukrainian quail as the base population. A total of 120 quail were selected as parents for the second generation, and 120 hatched offspring were used as new parents for the third generation. During the breeding period, the diet was composed of 26% crude protein and 2,950 Kcal of metabolizable energy per kg, and for the laying period, the birds were fed commercial feed containing 20% CP and 2,650 kcal ME/kg, During the experimental period, the feed and water were given ad libitum. Lighting programs were 24 hours per day for 3 days and then, from the 4^{th} day to the 42-day old, the birds were provided with 23 hours per day. However, lighting programs for the egg production period were 16 hours per day, and it was kept constant until the end of the experiment. The temperature of the birds' rearing house gradually decreased from 36 ℃ in the first three days to 24℃ in the 4^{th} week. Afterward, it was maintained between 24 and 20℃ until the end of the experimental period. Birds from both lines were housed in group cages with three replications and 20 birds for each replication. Selection based on body weight was performed at the 20^{th} day of age, where 120 unsexed quail with higher body weight for two lines were selected, from a base population, corresponding to about 24% of selected birds These procedures were repeated in every generation for determining some genetic parameters.

Studied traits: The selection was done according to the high body weight and egg production traits. Selected birds were weighted weekly for live body weights (g) individually using a sensitive balance until the 42-day-old, weight gain (g) was computed as the difference between the next and previous body weight, and feed conversion ratio was measured as the ratio of feed intake (g) to weight gain (g), for each line within each generation. In addition, at 42-day age, four males were slaughtered to determine the carcass characteristic within each group. The carcass dissections were determined as a percentage of pre-slaughtered live body weight for each generation. However, at 45 days of age for egg production, the birds were sexed and re-distributed on cages with three replicates for each line separately as families (10 females with 3 males), for 5 successive weeks (From 45 days old up to 177 days of age). At 45 days old, the both exterior and interior quality of the egg were measured. Exterior quality included egg weight, shell weight, shell thickness, and egg index, and interior quality included albumen index, yolk index, and HU. Egg and shell weight were measured using digital scales. Shell thickness was obtained by caliper. Data was calculated using the following formula:

Egg index (%) =egg width (mm)/egg length (mm) x 100

2. Eggshell weight (%) = Eggshell weight (g)/Egg weight (g) x 100

3. Yolk Index =yolk height (mm)/yolk diameter (mm) x 100

4. Albumen Index =albumen height (mm)/average of albumen length and width (mm)x 100

5. HU = 100 log [(albumen height (mm) + 7.57) – (1.7 x egg weight (g)$^{0.37}$]

6-Albumen%= Albumen weight (g)/egg weight (g) x100

7-Yolk %= Yolk weight(g)/ egg weight (g) x100

8-shell%= shell weight (g)/ egg weight(g) x100

The main estimated parameters for the studied traits were:

- Selection differentials, which were computed as the difference between the selected parent mean and the base population mean: S=m1-m0

-Response to selection was calculated as the difference between the offspring mean and the base population mean; R=M2-M0

-Realized heritability was estimated by dividing response to selection on the selection differential for each trait. h^2 =R/S

-Genetic correlations between some growth traits and egg production traits were estimated from the covariance between two traits according to the equation of geometric method (Falconer and Mackay, 1996):

$$r_g = \sqrt{(CovZ2X1 * Cov\ Z1X2)} / \sqrt{(CovZ1X1 * Cov\ Z2X2)}.$$

Where:

1 and 2: characters.

Z: observations of selected parents.

X: observations of progeny.

- Phenotypic correlation = Cov xy \ sx*sy

Cov xy = covariance between x & y

Sx; sy = variances of both studied characters.

Statistical analysis: The results were statistically processed using the MS Excel software, to evaluate selection responses, and realized heritability and correlation coefficient were calculated; hence, line means in each generation were calculated. The calculation of line and generation, specific means was done by the following model within SAS, SAS (32):=

$$Y_{ijk}= \mu +L_i+G_j+e_{ijk}$$

Where: Y_{ijk} observed trait; μ overall mean; L_i fixed effect of it line; G_j fixed effect of jt generation; e_{ijk} random error.

RESULTS AND DISCUSSION

Response to selection for 42-day body weight and weight gain after the selection has been significantly improved (18.41 and 6.47 gm., respectively) and for white line and dark line (15.38 and 9.83, respectively) which is shown in Table 1. This means that the white line has a greater response for body weight than the dark line and less weight gain.

Table 1. Genetic correlation, selection differential, response to Selection, and realized heritability (h^2) for 42-day body weight and weight gain in two lines of common quail

Lines	Traits	Genetic parameters	
	B.W	S	34.04
White		R	18.41
		h^2	0.54
	W.G	S	11.43
		R	6.47
		h^2	0.57
G. correlation	0.69		
	B.W	S	24.81
Dark		R	15.38
		h^2	0.62
	W.G	S	15.61
		R	9.83
		h^2	0.63
G. correlation	0.72		

S; selection differential, R; response to selection, h^2; heritability, B.W; body weight and W.G; weight gain

However, the results showed that the realized heritability had moderate values for 42-day age body weight and weight gain after selection which were different for white and dark lines (0.54-0.57), (0.62-0.63), respectively. This is in agreement with that of (3,24,3019), who found that the estimation of heritability for body weight at 4 - 8 weeks of age ranges between (0.47 to o.74). Method of estimation, population, or sample size perhaps causes the differences in heritability value in a different line. However, the differences in heritability are affected by gene action, environmental effects, estimation method, line and sampling error caused by sample size Prado-Gonzalaez(28) Regarding to genetic correlation between body weight and weight gain, the highest genetic correlation estimate was (0.72) for the dark line which surpassed the white line (0.69)

Table 2. Genetic correlation and phenotypic correlation coefficients for carcass traits within studied lines of 42-day ages of common quail

Traits	Line	l.b.w	Legs	Breast	carcass%
l.b.w	W	-	0.79**	0.86**	0.53*
	D	-	0.56*	0.73**	0.79**
Legs	W	0.64*	-	0.73**	0.67*
	D	0.89**	-	0.44	0.26
breast	W	0.46	-0.58*	-	0.63*
	D	0.83**	-0.77**	-	0.24
carcass%	W	0.61*	0.28	0.62*	-
	D	0.66*	0.47	0.94**	-

Phenotypic correlation above the diagonal and genetic correlation coefficients below the diagonal. *=significant at (*P<0.05*). **=significant at (*P<0.01*).

The phenotypic and genetic correlation estimates for live body weight (l.b.w), carcass%, breast, and legs that were measured in the study are presented in Table 2. Genetic correlations of l.b.w with other studied traits were positive and its value was moderate to high in both lines, except the correlation coefficient between l.b.w and breast % in the white line (0.46). However, the genetic correlation between l.b.w and other traits showed that the selection for l.b.w would increase carcass%, breast, and leg weight in the dark line. In addition, estimates of genetic correlation for legs with breast weights were negative for white (-0.58) and dark lines (-.77), but the correlation coefficients between leg weight and carcass percentage had a positive low value (0.28- 0.47) in white and dark lines respectively. Also, correlation coefficients of breast weight with carcass% were (0.62 and 0.94) in white and dark lines of quails, respectively. In general, these results showed that the selection has increased breast weight, leg weight, carcass%, and l.b.w weights in both lines, but the dark line has more response than the white line. Regarding, phenotypic correlations the results showed that all correlation coefficients were positive and most of them were medium to strong (Table 2). The phenotypic correlation estimates for l.b.w. with legs and breast weight had high coefficients (0.79 and 0.86) in the white line, and (0.56 and 0.73) in the dark line. Phenotypic correlation estimates between breast and leg weight in the two lines were (0.73 and 0.44), also the phenotypic correlation estimates between carcass% and both legs and breast have higher values in the white line compared to the dark line. Generally, poultry breeders have focused on selection for the highest breast yield and carcass percentage for the consumers' demand for processed poultry products Zerehdaran (42).

Table 3. Heritability, genetic correlation, and phenotypic correlation coefficients for egg production traits within studied lines of common quail

Traits	Line	BW.42	FCR	E.N	E.W
BW.42	**W**	**0.54**	**-0.49**	**-0.97****	**0.77****
	D	**0.62**	**-0.44**	**-0.90****	**-0.59***
FCR	**W**	**0.88****	**-0.72**	**0.70****	**0.93****
	D	**NE**	**-0.87**	**0.22**	**0.98****
E.N	**W**	**NE**	**0.30**	**0.69**	**-0.91****
	D	**NE**	**NE**	**0.54**	**-0.39**
E.W	**W**	**NE**	**0.59***	**0.96****	**0.81**
	D	**0.88****	**EN**	**0.98****	**0.76**

Phenotypic correlation above the diagonal, Heritability on the diagonal, and genetic correlation coefficients below the diagonal. *=significant at (*P<0.05*); NE = Non-estimated due to the extreme replication

Heritability, Genetic, and phenotypic correlations were estimated for five successive weeks in the early laying period and were shown in Table 3. The highest phenotypic correlation estimate between body weight and egg weight was recorded for the white line (0.77) which was significant at (P<0.01) compared to the dark line (-0.59). In addition, phenotypic correlations for white and dark lines (0.93 and 0.98) were estimated for feed conversion ratio with egg weight. This result showed that the white line has a better FCR in the laying period. The negative phenotypic correlation coefficients were recorded for EW with EN in both lines (-0.91 and -0.39), respectively. Regarding, the genetic correlation in laying periods for FCR*BW was significant (0.88) at the white line, but it was not estimated for the dark line, also the genetic correlation was not estimated between EN*BW for both lines. The sample size of replication or estimated method may affect the previous results. Moreover, the genetic correlation between studied traits ranged from 0.30 to 0.98 for laying hens, these results are in agreement with that found by (25,33), who computed the genetic correlation between the same traits ranging from 0.83 to 0.96 for egg-type quails. (41), reported that the highest correlations among estimated records were due to similar gene action over time, also they mentioned that the early laying periods have been more affected by genes related to age at sexual maturity. The present results are similar to those found by (13,36), who reported that the negative correlations were between BW and egg production traits, they showed that highest body weights lead to lower egg production and vice versa. Heritability values were computed for white and dark lines as shown in Table 3. BW, FCR, EN, and EW heritability estimates were (0.54 and 0.62), (0.72 & -0.87), (0.69 & 0.54), and (0.81 & 0.76) in white and dark lines, respectively. The present results contrasted with that found by Pereira (27), who mentioned that egg production traits have low values of heritability because of the effect of environment on trait variation. In addition, low heritability could be observed due to homozygosity for special traits leading to the lowest genetic variance. On the other side, the high value of heritability indicates the increasing additive genetic variance among generations Falcorner (10).

Table 4. Genetic correlation for egg quality traits within studied lines of common quail

Line	EW-HU	EW-YP	EW-ALP	EW-ShP	YP-ALP
White	-0.89 **	-0.79*	0.52*	0.87**	0.72*
Dark	-0.78*	-0.65*	0.64*	0.65*	0.69*

EW: egg weight, HU: Haugh unit, YP: yolk percentage, ALP: albumen percentage, ShP: shell percentage

Table 4, shows the genetic correlation coefficients of external and internal egg quality traits in white and dark lines of common quail. Commonly, genetic correlations between studied traits in both lines were high. A high and negative genetic correlation was recorded between egg weight and the Haugh unit in the white line (-0.89) which surpassed the second studied line (-0.78), however, the Haugh unit is an important scale to evaluate egg quality, based on albumen height of the egg. These results contrasted with those recorded by Sari and Saatci (31) who mentioned the genetic correlation between EW-HU unit was (-0.06), EW-ALP (0.06), and EW-ShP (-0.15). (37) reported that the new eggs, albumen height of eggs was the highest and decreased with increasing storage time. Also, high and negative correlations were found between egg weight and yolk percentage (-0.79 and -0.65) in white and dark lines, respectively. Additionally, moderate and positive genetic correlations were found between egg weight and albumin percentage, and was for the white line as (0.52), and also positive and high correlation recorded for the dark line (0.64). The correlation between egg weight with shell percentage and between yolk % and albumen % was strong and high. The genetic correlations can be used to improve egg quality by selection according to the yolk and albumen ratio. On the other hand, a selection for egg weight occurs by making a selection on yolk percentage because yolk percentage is a proportion of yolk weight and egg weight. These results are in agreement with that found by (22,31), they showed a high and positive genetic correlation between egg weight and shell weight (0.85 and 0.75) respectively.

Table 5. Phenotypic correlation for egg quality traits in the dark line of common quail

Traits	E.W	E.S	Y.H	Y.W	Y.D	YI	AL.W	AL.H	Al.D	AL.I	Sh. W	HU	YP	Al.P	Sh.P
E.W	1														
E.S	-0.01	1													
Y.H	0.30	0.43	1												
Y.W	0.89**	-0.16	0.38	1											
Y.D	-0.09	0.19	0.05	-0.08	1										
Y.I	0.32	0.29	0.88**	0.39	-0.43	1									
AL.W	0.94**	0.02	0.22	0.71**	-0.14	0.28	1								
AL. H	-0.18	-0.19	-0.20	-0.18	0.44	-0.40	-0.21	1							
Al. D	0.13	0.18	0.17	0.08	0.34	0.00	0.17	-0.19	1						
AL.I	-0.22	-0.22	-0.23	-0.19	0.18	-0.30	-0.25	0.88**	-0.63*	1					
Sh. W	0.79**	0.23	0.17	0.70**	0.12	0.11	0.65*	0.06	0.06	0.01	1				
H.U	-0.32	-0.18	-0.24	-0.30	0.45	-0.43	-0.33	0.99**	-0.19	0.87**	-0.07	1			
Y.P	0.05	-0.35	0.25	0.49	-0.03	0.23	-0.25	-0.04	-0.10	0.01	0.03	-0.05	1		
Al.P	-0.03	0.11	-0.17	-0.41	-0.12	-0.09	0.31	-0.12	0.14	-0.15	-0.31	-0.10	-0.87**	1	
Sh.P	-0.03	0.40	-0.10	-0.03	0.30	-0.23	-0.19	0.32	-0.09	0.29	0.58*	0.29	-0.01	-0.48	1

E.W: egg weight, E.S: egg shape, YH: yolk height, YW: yolk weight, Y.D: yolk diameter, YI: yolk index, AL.W: albumen weight, AL.H: albumen height, AL.D: albumen diameter, AL.I: albumen index, Sh.W: shell weight, H.U: haugh unit, Y.P: yolk percentage, AL.P: albumen percentage, Sh.P: shell percentage.

The phenotypic correlation between the external and internal quality characteristics of eggs in the dark common quail line (*Coturnix coturnix coturnix*) is illustrated in Table 5. The phenotypic correlations between egg weight with the following characteristics -yolk weight was (0.89), albumen weight was (0.94), and shell weight was (0.79) - which were high and positive; and with other traits, the correlations were low to moderate. High levels of positive correlations were shown between yolk high and yolk index (0.88) and between yolk weight and shell weight (0.7). The phenotypic correlation of albumen high with albumen index and albumen high with Hugh unit were positive and high (0.88 and 0.99), respectively. Moderate and negative correlation was estimated between albumen percentage with shell percentage (-0.48). Low and negative correlations were found between egg weight and shell percentage. These results are similar to that found by another researcher (4,22).

Table 6. Phenotypic correlation for egg quality traits in the white line of common quail

Traits	E.w.	E.S	Y.H	Y. W	Y.D	YI	AL.W	AL. H	Al D	ALI	Sh. W.	HU	YP	AlP	Sh P
E. W.	1														
E.S	-0.13	1													
Y.H	-0.12	0.09	1												
Y. W.	0.87 **	-0.34	-0.18	1											
Y.D	0.17	-0.11	0.25	0.16	1										
YI	-0.23	0.16	0.69	-0.28	-0.53	1									
AL. W	0.84	0.09	-0.01	0.48	0.17	-0.14	1								
AL. H	0.14	-0.16	0.48	-0.02	0.13	0.31	0.19	1							
Al D	0.33	0.03	0.31	0.01	0.14	0.17	-0.05	-0.04	1						
ALI	-0.06	-0.14	0.28	-0.01	0.03	0.21	0.18	0.86**	-0.53*	1					
Sh. W.	0.16	0.14	-0.04	0.24	-0.14	0.06	0.27	0.44	-0.37	0.57*	1				
HU	0.42	-0.16	0.51	-0.19	0.11	0.36	0.02	0.98**	-0.01	0.82	0.36	1			
YP	-0.05	-0.50	-0.20	0.83**	0.14	-0.29	-0.06	-0.18	0.07	-0.18	0.01	-0.26	1		
AlP	0.46	0.42	0.19	-0.66	-0.01	0.18	0.30	0.06	0.05	0.01	-0.28	0.09	-0.90	1	
ShP	-0.27	0.27	0.07	-0.53	-0.31	0.28	-0.51	0.29	-0.26	0.38	0.58	0.39	-0.39	-0.052	1

E.W: egg weight, E.S: egg shape, YH: yolk height, YW: yolk weight, Y.D: yolk diameter, YI: yolk index, AL. W: albumen weight, AL.H: albumen height, AL. D: albumen dimeter, AL. I: albumen index, Sh.W: shell weight, H.U: haugh unit, Y.P: yolk percentage, AL.P: albumen percentage, Sh.P: shell percentage.

Table 6, illustrates the phenotypic correlation coefficients between different internal and external egg quality traits in the white line of common quail (*Coturnix coturnix coturnix*). Phenotypic correlations of egg weight with other study traits ranged from negative -0.05 up to positive and high coefficient 0.87. Correlations of egg shape with yolk percentage and albumen percentage were moderate (-0.50 and 0.42), respectively. In addition, phenotypic correlations between yolk high with yolk index, albumin high, and Hugh unit were (0.69,0.48 and o.51), respectively. Also, the correlation between yolk weight with albumen percentage was (-0.60), and with shell percentage was (-0.53) as negative and moderate. The same coefficients between yolk dimeter with yolk index was (0.53), albumin weight with shell percentage was (-0.51) and with albumin, the percentage was (0.30). The phenotypic correlation between albumen high with each of albumen index, Hugh unit, and shell weight was positive and relatively high to moderate (0.86,0.98 and 0.44), respectively. Moreover, the correlation between albumen diameter with albumen index has a negative and moderate value (-0.53) in the white line of common quail. Phenotypic correlations between albumen index with each of shell weight was (0.57), Hugh unit (0.82) and shell percentage was (0.38); and for shell weight with shell percentage was (0.58), Hugh unit with shell percentage was (0.39). Finally, the correlation coefficient between the yolk percentage and with albumen percentage was negative (-0.90) and with shell percentage was also negative (- 0.39). The current results are in agreement with that reported by Seker (34), who found a similar correlation coefficient between egg shall weight and egg shall percentage. Anyway, eggshell percentage is affected by egg size and egg weight, and there is a high correlation between shell strength and shell thickness Özçelik (26).

CONCLUSIONS

It could be concluded that the selection based on the genetic gain (response to selection) in quail improving breast weight, leg weight, carcass percentage, live body weight, and egg production traits in both lines.

REFERENCES

1. Ahmad, H. A. 2009. Poultry growth modeling using neural networks and simulated data. J. Appl. Poult. Res. (18):440–446.

2. Akpa, G. N., J. Kaye, I. A. Adeyinka, and M. Kabir. 2008. The relationships between laying age and repeatability of egg quality traits in Japanese quails (*Coturnix coturnix japonica*). Int. J. of Poult. Sci. 7-6. 555 – 559.

3. Aksit, M., I. Oguz, Y. Akbas, O. Altan, and M. Ozdogan. 2003. Genetic variation of feed traits and relationships to some meat production traits in Japanese quail (*Coturnix coturnix japonica*). Arch Geflugelkd. 67-2: 76-82.

4. Alkan, S., K. Karabag, A. Galic, T. Karsli, and M.S. Balcioglu. 2010. Determination of body weight and some carcass traits in Japanese quails (*Coturnix coturnix japonica*) of different lines. Kafkas Univ Vet. Fak. Derg., 16-2: 277-280.

5. Anthony, N. B., D. A. Emmerson, K. E. Nestor, W. L. Bacon, P. B. Siegel, and E. A. Dunnington. 1991. Comparison of growth curves of weight-selected populations of turkeys, quail, and chickens. Poult. Sci. (70): 13–19.

6. Barbieri, A., R. K. Ono, L. L. Cursino, M. M. Farah, M. P. Pires, T. S. Bertipaglia, A. V. Pires, L. Cavani, L. O. Carreno, and R. Fonseca.2015. Genetic parameters for body weight in meat quail. Poult. Sci. (94): 169–171.

7. Barilania, M., S. Deregnaucourte, S.Gallegob, N. Gallic, R. Muccia, M. Piomboc, Puigcerverd, S. Rimondia, D. Rodríguez, S. Teijeirob, Spanòc and E. Randia. 2005. Detecting hybridization in wild (*Coturnix c. coturnix*) and domesticated (*Coturnix c. japonica*) quail populations. Biological Conservation, 126-4: 445-455.

8. Cramp, S., and K. Simmons.1980. The birds of the Western Palearctic, hawks to bustards. Oxford, UK: Oxford University Press. (2): 695.

9. Durmus, I., S. Alkan, K. Narinc, Karabag and T. Karsli. 2017. Effect of mass selection on egg production on some reproductive traits in Japanes quail. Europ. Poult. Sci, (10): 1399/eps.168.

10. Falconer, D. S. 1989. Introduction to quantitative genetics 3rd edition, Longman, London, New York, 160-174.

11. Fuller, R. C., C. F. Baer, and J. Travis. 2005. How and when selection experiments might actually be useful. Integrated Comparative Biology. (45): 391-404.

12. Hill, W. J., T. F. C. Mackay and D. S. Falconer. 2004. Introduction to quantitative genetics. Genetics (167):1529-1536.

13. Kranis, A., P. M. Hocking, W. G. Hill, and J. A. Woolliams. 2006. Genetic parameters for a heavy female Turkey line: impact of simultaneous selection for body weight and total egg number. Brit Poult. Sci. (47): 685–693.

14. Lukanov, H., A. Genchev and P. Kolev. 2019. Egg quality traits in WG, GG and GL Japanese quail populations. Trakia J. Sci. (17): 49-55.

15. Melnyk, V. V., N. P. Prokopenko and S. M. Bazyvolyak. 2019. Poultry farming in Ukraine: poultry and egg and meat production, Modern poultry. 3-4: 2-8 (in Ukrainian).

16. Melnyk, Yu. F., V. P. Kovalenko and A. M. Uhnivenko. 2008. Selection of farm animals. Kyiv. Intas (in Ukrainian).

17. Minvielle, F., E. Hirigoyen; and M. Boulay.1999. Associated effects of the Roux feather colour mutation on growth, carcass traits, egg production, and reproduction of Japanese quail. Pou. Sci. (78): 1479-1484.

18. Minvielle, F., J. L. Monvoisin, J. Costa and Y. Maeda. 2000. Long-term egg production and heterosis in quail lines after within-line or reciprocal recurrent selection for high early egg production, Brit. Poult. Sci. (41): 150–157.
19. Minvielle, F. 1998. Genetic and breeding of Japanese quail for production around the world. Proceedings 6th Asian Pacific poultry congress Nagoya, Japan. hal-02764843.
20. Minvielle, F.2004. The future of Japanese quail for research and production. Poult. Sci. (60): 500-507.
21. Mohammadi, T. A., A. Maghsoudi, K. F. Bagherzadeh, M. Rokouei, and A. H. Faraji.2018. Bayesian analysis ofgenetic parameters for early growth traits and humoral immune responses in Japanese quail. Livest. Sci. (216): 197–202.
22. Narinc, D., A. Aygun, E. Karaman, and T. Aksoy.2015. Egg shell quality in Japanese quail: characteristics, heritabilities and genetic and phenotypic relationships. Animal. (9): 1091–1096.
23. Narinç, D., T. Aksoy and T. Kaplan. 2016. Effects of multi-trait selection on phenotypic and genetic changes in japanese quail (*Coturnix coturnix Japonica*). The Journal of Pou. Sci. (53):103-110.
24. Narinc, D., T. Aksoy, and E. Karaman. 2010. Genetic parameters of growth curve parameters and weekly body weights in Japanese quail (*Coturnix coturnix japonica*). J. Anim. Vet. (9): 501-507.
25. ONI., 2007. Genetic and phenotypic relationships between mcnally model parameters and egg production traits. International Journal of Poultry Science. 6-1: 8-12, Available from: <http://docsdrive.com/pdfs/ansinet/ijps/8-12.pdf>.
26. Ozcelik, M. 2002. The phenotypic correlations among some external and internal quality characteristics in quail eggs. Ankara Univ. Vet. Fak. Derg. (49): 67–72.
27. Pereira, J. C. 2004. Melhoramento genético aplicado à produção animal. 4.ed. Belo Horizonte, Fepmvz. 609p.
28. Prado, G. E., A. L. Ramirez and C. J. Segura. 2003. Genetic parameters for body weight of Creole chickens from southeastern Mexico using an animal model. Livestock Research for Rural Development. (15): 1-7.
29. Reddy, R.P. 1996. Symposium: the effects of long term selection on growth of poultry. Introduction. Poult. Sci. (75):1164-1167.
30. Sari, M., M. Tilki, and M. Saatci. 2011. Genetic parameters of slaughter and carcass traits in Japanese quail (*Coturnix coturnix japonica*). Br. Poult. Sci. (52): 169–172.
31. Sari, M., M. Tilki, and M. Saatci. 2016. Genetic parameters of egg quality traits in long-term pedigree recorded Japanese quail. Poult. Sci. (95): 1743–1749. http://dx.doi.org/10.3382/ps/pew118.
32. SAS Institute.2014. Statistical Analysis System (SAS, institute, Inc.), version 9.4. Cary NC, USA.
33. Savegnago, R.P. 2011.Estimates of genetic parameters, and cluster and principal components analysis of breeding values related to egg production traits in a White Leghorn population. Poult.Sci.(90):2174 2188.Availablefrom:<http://ps.oxfordjournals. org/content/90/10/2174. full.pdf+html>. Accessed: Apr. 11, 2016. doi: 10.3382/ps.2011-01474.
34. Seker, I., F. Ekmen, M. Bayraktar and S. Kul. 2004. The effects of parental age and mating ratio on egg weight, hatchability and chick weight in Japanese quail. Journal of Animal and Veterinary Advances. (3): 424-430.
35. Shanaway, M. M. 1994. Quail production systems: a review. Rome, Food and Agriculture Organization of the United Nations. ISBN 92-5: 103384-6.
36. 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. Livest. Sci. (153): 27–32.
37. Silversides, F. G., and T. A. Scott. 2001. Effect of storage and layer age on quality of eggs from two lines of hens. Poult. Sci. (80): 1240– 1245.
38. Szwaczkowski, T. 2003. Use of mixed model methodology in poultry breeding: estimation of genetic parameters. In: Muir WM, Aggrey SE, editor. Poultry genetics, breeding and biotechnology. Wallingford: CAB International. 165-210.

39. Toelle, V. D., G. B. Havenstein, K. E. Nestor and W. R. Harvey. 1991. Genetic and phenotypic relationship in Japamese quail. 1. Body weight, Carcass and organ measurements. Poult. Sci. (70): 1679-1688.
40. Vali, N., M. Edriss, and H. Moshtaghi. 2006. Comparison of egg weight between two quail strains. Int. J. Poult. Sci. (5): 398- 400.
41. Wolc, A. and T. Szwaczkowski. 2009. Estimation of genetic parameters for monthly egg production in laying hens based on random regression models. Journal of Applied Genetics. (50): 41-46. Available from <http://www.livestockscience.com/ article/S1871-1413(13)00070-X/pdf>.
42. Zerehdaran, S., E. Lotfi and Z. Rasouli. 2012. Genetic evaluation of meat quality traits and their correlation with growth and carcass composition in Japanese quail. British Poult.Sci. (53): 756–762.