Direct and correlated responses from selection for early sexual maturity in Japanese quail

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Abstract

Base population after third generation of selection conclude total number of 788 birds at 6 weeks of age were used in this study and randomly assigned to two mating groups. First groupe was selected for early age at sexual maturity (EASM) and the second was as a control line (RBC) to study the direct and correlated responses for this direct of selection. The results can be summarized as follow:

1. EASM was highly significantly (P≤0.01) decreased from 39.54 days to 35.23 days.
2. The actual and the expected selection differentials were 2.52 and 2.29g / generation.
3. The actual response to selection in the (EASM) line was1.46g /generation.

a- Heritability of EASM estimated ranged from 0.29 to 0.35

b- The realized heritability ranged from 0.44 to 0.79.

c- Correlated responses for EASM were as follow:

d- BW_0, BW_2, BW_4, and BW_6 increased significantly (P≤0.05) from 9.95, 40.58, 98.84 and 170.47g to 10.47, 47.01, 101.87 and 181.42g.

e- Egg weight (EW) was decreased (P≤0.05) from 10.74g to 10.04g. But Body weight at sexual maturity (BWSM) was increased from 136.32 g to 139.32 g. Total egg weight at first ten week (TEN_{10}) decreased from 55.25eggs to 54.25egg.

f- Fertility (FR %) was increased (P≤0.05) from 80.58% to 80.90%. and Hatchability (HA %) were increased (P≤0.05) from 70.42% to 70.92%.

g- Meat, dressing and giblets % were increased significantly (P≤0.05) from 42.33, 62.04 and14.27% to 43. 76%, 63.99 and 14.99%.

Keywords: selection, early sexual maturity, direct response, correlated response, Japanese quail.

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1. Introduction

Selection experiments provide the framework for studying the inheritance of complex traits and allow the evaluation of theoretical predictions by testing observations against expectations. Depending on the time scale, short-term experiment can be used to estimate genetic variances and covariances to test their consistency from different sources of information and estimate the magnitude of the initial rates of response to selection (Varkoohi and Kaviani, 2014). The usefulness of selection procedures to increase either productive or reproductive traits depends not only upon the direct response itself, but also upon the associated changes in other economically or biologically important traits caused by correlated response to selection. However, selection for a certain trait may indirectly affect other traits not considered in the program due to the fact that the improved trait is correlated with these traits. Correlated responses were thourally discussed by Falconer (1954), Marks (1971) and Nestor *et al.* (1983). Japanese quail, despite their small body size, have an important place in commercial production because of their high egg and meat production capacity. They are generally reared for egg production in the Far East and Asian countries, and primarily for meat production in European and American countries (Minvielle, 2004). On The other hand, early sexual maturity promotes poultry production by increasing laying performance of the females and reducing the cost to produce males for semen Production. If there is a genetic correlation between characters under selection, the overall response to selection will change according to the

heritability of the traits examined and the strength and sign of the genetic covariance among them (Jensen *et al.*, 2003). The present work was designed to estimate the direct responses to selection for early sexual maturity and correlated responses with some productive and reproductive traits from generation zero to generation four of selection, as well as, to estimate the heritability of sexual maturity and to study the genetic and phenotypic correlations between early sexual maturity and each of growth, egg production, reproductive and carcass traits.

2. Materials and methods

Data of the present study were collected on the flock of Japanese quail (*Coturnix japonica*) maintained by the Department of Animal Production, Faculty of Agriculture, Al-Azhar University, Cairo, Egypt, during the period from May 2017 until September 2018.

2.1 Breeding plan and management

A total number of 788 birds (380 males and 408 females) at 6 weeks of age were taken at random from the flock under consideration as the parents of the present study. The mating system in the base population was in a ratio of one male to two females avoiding full and half-sib matings. The birds were randomly assigned to three mating groups; the first group were established by selection for early age at sexual maturity the second group was maintained as a randombred control line. Family selection was carried out within the selected line, however

lower families in sexual maturity (one male and two females) were selected according to their deviation from the line mean. Feed and water were provided *ad-libitum.* The experimental diet contained 28% protein and 2920 k cal-ME/Kg until 2 weeks of age and 25% protein with 2850 k cal-ME/Kg during 3-6 weeks of age, then changed to a ration contained 20% protein with 2820 k cal-ME/Kg during the laying period. The minerals and vitamins were adequately supplied to cover the requirements according to N R C, (1994). Temperature started with 37.5°C for the first week after hatching, then decreased 2-3°C weekly to 26-28°C at the fourth week of age till the end of brooding period. No vaccination and/or beak trimming programs were carried out to the breeding stocks.

2.2 Statistical analysis

Data of age at sexual maturity was analyzed by using Harvey's least-squares and maximum likelihood computer program (Harvey, 1987, model type 5) including each of line, generation, and sex as a fixed effects and sire and dam within sire as a random effect. The following model was adopted:

$$Yijmkln = \mu + Gi + Lj + Sxm + Sk + Dlk + eijmkln$$

Where, Yijmkln = the observation of ijmkln th bird. μ = the overall mean, common element to all observations. Gi = the fixed effect of ith generation. Lj = the fixed effect of jth line. Sxm = the fixed effect of mth sex. Sk = the random effect of kth sire. Dlk = the random effect of lth dam nested within a random effect of kth

sire. eijmkln = the random error term. Henderson Method 3 (Henderson, 1953) was utilized to estimate the genetic variance components for the different traits studied.

3. Results and Discussion

3.1 Direct response

The actual means of early sexual maturity among four generations of selection in the selected and control lines are presented in (Table 1). Early age at sexual maturity (EASM) was highly significantly (P≤0.01) decreased in the selected line (EASM) from 39.54days at generation zero to 35.23days at the fourth generation of selection. On the other hand, age at sexual maturity in the control line fluctuated randomly from generation to another, as early sexual maturity decreased in the EASM line, the C.V% of this trait increased from 38.04% at generation zero to 40.65% at the fourth generation, respectively (Table 1). The corresponding estimates obtained in the random bred control line (RBC) line were 38.04 and 43.03%. The change in C.V% from generation zero to generation four in EASM and RBC lines were significant (P≤0.01), the averages were 37.71% and 38.09% for EASM and RBD lines, respectively. These results agree with that of Abou Khadiga *et al.* (2016), Kaye *et al.* (2016) and Al-Tikriti, (2018), and not in agreement with those reported by Inal *et al.* (1996).

Table (1): Actual means, standard deviations (S.D) and coefficients of variation (C.V %) for early age at sexual maturity (d) in the selected and control lines among generations of selection.

Line/ Generation	EASM Mean ± S.D	C.V%	RBC Mean ± S.D	C.V%
0	39.54±15.04	38.04	39.54±15.04	38.04
1	38.78±13.87	35.77	38.62±13.92	36.04
2	36.90±13.61	36.88	37.25±13.14	35.28
3	35.50±13.21	37.21	36.14±13.76	38.07
4	35.23±14.32	40.65	35.84±15.34	43.03
Average	37.19±13.51	37.71	37.48±13.82	38.09

EASM = Early age at sexual maturity, RBC = Random bred control line.

The least-square means, their standard errors and test of significance for factors affecting early sexual maturity are presented in tables (2 and 3). Results obtained in Table (2) indicated that among EASM line, age at sexual maturity decreased significantly (P≤0.05) from 37.08 days at the zero generation to 35.75days at the fourth generation. On the other hand, the age at sexual maturity in the RBC line fluctuated randomly from generation to another; however there was no significant increase and/or decrease between the mean of the zero and the fourth generation of selection (Table 2). The least-square means for factors affecting EASM varied significantly (P≤0.05) among generations, lines and sex, while the sire and the dam had non-significant effect on this trait (Table 3). The dam variance component in EASM were higher than the sire components of variance and consequently percentage of variations due to dam effect were larger than that of the sire effects obtained the non-genetic effects, primarily dominance and maternal, (40.88 and 27.73% vs 3.73 and 3.64%), respectively as shown in (Table 4).

Table (2): Least-squares means and standard errors of early age at sexual maturity in the selected and control lines among generations of selection.

Line/ Items	EASM		RBC	
	No.	Means ± S.E	No.	Means ± S.E
Generation:				
1st	168	37.08±0.28[a]	120	38.08±0.32[a]
2nd	174	35.81±0.36[b]	130	40.81±0.30[a]
3rd	195	34.92±0.26[c]	125	39.65±0.26[a]
4th	175	35.75±0.16[d]	114	41.12±0.38[a]
Sex:				
Male	354	38.19±0.22[a]	230	39.58±0.32[a]
Female	358	41.87±0.30[b]	240	41.32±0.41[b]

EASM = Early age at sexual maturity, RBC = Random bred control line.

Table (3): F- ratios and test of significant for factors affecting early age at sexual maturity.

S.O.V.	d.f	F-ratio
Generation	3	18.83[**]
Sire	226	1.79
Dam :(S)	247	1.54
Line	1	38.08[**]
Sex	1	25.87[**]
Remainder	1231	

Table (4): Variance components (δ^2) and percentage of variation (V %) estimated for random effects on early age at sexual maturity.

Variance components/ Line	Sire		Dam: Sire		Remainder	
	δ^2s	V%[*]	δ^2 D: s	V%[*]	δ^2e	V%[*]
EASM	0.26	3.73	2.85	40.88	3.86	55.39
RBC	0.21	3.64	1.60	27.73	3.96	68.63

These results were in agreement with those obtained by El-Fiky (2005), Aboul-Hassan (2000 a) and Aboul-Seoud *et al.* (2009) when they selected Japanese quail for increased BW6 and BW4, and El-Bourhamy (2004) when he selected Japanese quail for increased feed consumption.

3.2 Selection differential

Selection differential calculated as expected and actual as well as the ratio between the actual and expected selection differentials (Actual/Expected) are presented in Table (5) for EASM line. However, no significant differences were found between the actual and expected selection differentials from generation zero to generation four. This means that the distribution of EASM confirm with the properties of a normal distribution closely enough to allow fairly accurate

prediction. The ratio of actual to expected selection differentials (Table 5) was greater than unity, which suggests that natural selection may had a positive effect on selection for EASM. The same trend was noticed by Aboul-Hassan (2001 b) and El-Fiky (2005) when they selected Japanese quail for high BW_6 and Abu-Mosallam (2014) when he selected Japanese quail for increased feed and water consumption among 3generations of selection. Moreover, Marks and Lepore (1968) among two lines of Japanese quail selected for body weight at 4 weeks of age for six generations. Cumulative (actual and expected) selection differentials are presented in Table (6). The values for cumulative selection differentials (Actual and Expected) were 2.51 and 2.02d at generation zero among the (EASM) line decreased to 2.11 and 1.96 d at generation four. The cumulative actual

selection differential takes into account the effects of natural selection expressed through fertility of selected phenotypes (Falconer, 1954).

Table (5): Actual and expected selection differentials and the ratio of actual to expected selection differentials for early age at sexual maturity.

Generation	Selection differentials		
	Actual	Expected	Actual / Expected
0	2.52±0.18	2.43±0.16	1.04
1	2.61±0.25	2.16±0.18	1.21
2	2.97±0.16	2.62±0.20	1.13
3	2.31±0.05	2.22±0.12	1.04
4	2.18±0.13	2.01±0.12	1.08
Average	2.52±0.15	2.29±0.19	1.10

Table (6): Cumulative (actual and expected) selection differentials for early age at sexual maturity.

Generation	Selection differentials	
	Cumulative (Actual)	Cumulative (Expected)
0	2.51	2.02
1	2.04	1.76
2	1.85	1.92
3	1.90	2.11
4	2.11	1.96
Average	2.08	1.95

3.3 Selection response

The actual and cumulative selection responses are presented in Table (7). The actual response to selection in the line EASM decreased or/ increased from generation to another through the four generations of selection. The estimated response to selection after the first generation of selection was 1.42 day, then it decreased and increased gradually as the selection continued to 1.28, 1.32 and 1.82day after the second, the third and the fourth generation of selection among EASM line. This regularity of the selection response had been observed in many selection experiments reported in the literature. The cumulative response to selection in the EASM line was 5.84 day after the fourth generation of selection. However, El-Fiky (2005) reported that the actual response to selection for HBW_6 was 2.58g after the first generation of selection and fluctuated to be 1.82g after the fourth generation of selection. Moreover, Aboul-Seoud *et al.* (2009) reported that the actual response to selection in the line (HBW_4) was decreased from generation to another through the three generations of selection. Abu-Mosallam (2014) when he selected Japanese quail for increased feed

consumption among three generations of selection found that the actual response to selection in the line (HWC$_{4-6}$) was decreased from generation to another through the three generations of selection. On the other hand, Falconer (1954) have shown that the irregularity in response to selection might have been due to many causes of genetically or environmental nature. Differences in natural selection differential, fertility and/or genetic-environment interaction on BW might cause such irregularity in selection response especially in such small numbers of generations as it was the case in the present study.

Table (7): Actual and cumulative selection responses for early age at sexual maturity.

Generation	Selection responses	
	Actual	Expected
0-1	1.42±0.85	1.42
1-2	1.28±0.54	2.70
2-3	1.32±0.47	4.02
3-4	1.82±0.67	5.84
Average	1.46±0.92	-----

3.4 Heritability estimates

3.4.1 Components of variance

Heritability estimates for early age at sexual maturity calculated from components of variance *i.e.* sire (paternal half-sibs), dam within sire (maternal half-sibs) and sire plus dam (full-sibs) among the EASM line are presented in Table (8). However, the dam component is expected to be larger in magnitude by the variances due to the dominance deviations and maternal effects. Heritabilities computed from the sire component (h^2$_S$) ranged between 0.18 and 0.23 among the four generations of selection and that computed from the dam components (h^2$_D$) are generally higher than those computed from the sire components, it ranged between 0.29 and 0.39. This may be due to the large dam variance components obtained and the non-genetic effects, primarily dominance and maternal,

normally result in the h^2$_D$ estimates being considerably larger than h^2$_S$ estimates. While, heritabilities computed from full-sib components (h^2$_{S+D}$) ranged between moderate and high in magnitude (0.20-0.28). The results are in agreement with the corresponding values reported by Debes (2004), Meky (2007), Abou Khadiga *et al.* (2016) and Kaye *et al.* (2016).

3.4.2 Realized heritability

The realized heritability estimated for early age at sexual maturity. As the ratio between response to selection and selection differential (R/S) calculated from the EASM line presented per generation in Table (8). The estimates of the realized heritability for early sexual maturity increased from 0.56 at the first generation to 0.79 at the fourth generation.

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Table (8): Heritability estimates computed from sire, dam, sire plus dam components of variance and realized heritability for early age at sexual maturity.

Heritability / Generation	Sires $h^2_S \pm S.E$	Dams: Sires $h^2_{D:S} \pm S.E$	Full-sibs $h^2_{S+D} \pm S.E$	Realized $h^2 \pm S.E$
1	0.23±0.43	0.30±0.58	0.27±0.45	0.56±0.22
2	0.20±0.38	0.35±0.75	0.23±0.66	0.49±0.31
3	0.21±0.52	0.29±0.65	0.20±0.58	0.44±0.26
4	0.18±0.40	0.39±0.78	0.28±0.78	0.79±0.38

3.5 Correlated responses

Selection for EASM had consequences for some other traits. The weights and/or the weight gains recorded at different ages and growth periods, egg production, reproductive traits and the carcass traits may be changed. The actual means of the correlated traits associated with selection for EASM are presented in Tables (9 to 11).

3.5.1 Correlated responses

Body weights for the EASM line (BW_0, BW_2, BW_4 and BW_6) increased significantly (P≤0.05) from 9.95, 40.58, 98.84 and 170.47g in the first generation to 10.47, 47.01, 101.87 and 181.42g after four generations of selection (Table 9). However, body weight gain traits among the EASM line Average daily gain from 0-2 weeks of age, Average daily gain from 2-4 weeks of age, Average daily gain from 4-6 weeks of age and Average daily gain from 0-6 weeks of age (ADG_{0-2}, ADG_{2-4}, ADG_{4-6} and ADG_{0-6}) increased significantly (P≤0.05) from 2.43, 5.40, 1.52 and 3.62g/day in the first generation to 2.92, 5.98, 1.90 and 4.04g/day after four generations of selection. Similar results were reported by Silva *et al.* (2013), Abou-Khadiga *et al.* (2014), Mahmoud *et al.* (2014), Saima *et al.* (2014), Aboul- Hassan *et al.* (2016) and El-Fiky *et al.* (2016).

Table (9): Actual means and standard deviations (S.D) for growth traits studied in both sexes for lines and generations of selection when selection was applied for early age at sexual maturity.

Line Gen Trait	Early age at sexual maturity				Random bred control line			
	1	2	3	4	1	2	3	4
BW_0	9.95±0.60	10.57±0.62	10.75±0.43	10.47±0.62	9.85±0.82	9.64±0.74639	9.59±0.85	10.00±0.62
BW_2	40.58±4.22	42.05±4.24	47.01±5.32	42.85±4.26	40.25±4.72	41.80±4.24	40.66±4.86	42.05±0.29
BW_4	98.84±14.56	101.87±15.40	101.45±17.62	100.87±15.48	96.52±12.55	97.22±14.57	98.58±16.17	87±15.40
BW_6	170.47±16.41	178.02±17.18	182.42±16.15	179.02±17.58	165.78±17.20	162.54±16.10	164.05±11.85	168.02±14.18
ADG_{0-2}	2.43±0.34	2.82±0.33	2.89±0.44	2.92±0.37	2.44±0.40	2.32±0.589	2.42±0.67	2.52±0.30
ADG_{2-4}	5.40±0.66	5.88±0.62	5.90±0.62	5.98±0.69	5.65±0.45	5.35±0.61	5.48±0.40	5.58±0.90
ADG_{4-6}	1.52±0.31	1.70±0.52	1.81±0.61	1.90±0.57	1.55±0.30	1.52±0.45	1.52±0.60	1.60±0.92
ADG_{0-6}	3.62±0.50	3.84±0.93	3.90.42	4.04±0.63	3.74±0.48	3.60±0.30	3.65±0.38	3.71±0.93

Table (10): Actual means and standard deviations for egg production and reproductive traits studied in females for lines and generations of selection when selection was applied for early age at sexual maturity.

Line Gen Trait	Early age at sexual maturity				Random bred control line			
	1	2	3	4	1	2	3	4
EW	10.64±18.95	10.94±19.52	11.46±10.62	10.74±18.90	10.45±10.60	10.85±10.28	10.70±11.25	10.55±10.28
BWSM	136.32±18.95	143.02±28.05	146.35±22.16	139.32±18.35	138.72±19.65	137.72±18.00	139.12±16.95	137.43±18.06
TEN10	55.25±7.20	53.54±6.31	51.48±7.15	54.25±7.27	55.25±5.69	57.66±5.72	56.50±5.60	57.00±5.75
TEW10	454.25±14.23	460.54±16.44	463.25±13.65	467.25±14.26	462.54±15.60	466.18±15.03	462.64±14.18	466.87±15.13
DEM	9.44±6.29	9.25±6.48	9.10±6.58	9.64±6.69	9.37±4.78	9.77±5.66	9.70±5.02	9.54±5.66
FR%	80.58	79.60	78.60	80.90	82.25	84.51	83.39	84.51
HA%	70.42	68.09	66.61	70.92	73.95	75.02	74.28	75.02
EEM%	5.63	6.64	6.93	5.93	5.71	6.13	5.43	6.10
LEM%	17.00	16.98	16.34	16.34	15.88	15.60	15.41	15.62
TEM%	22.27	23.62	23.93	21.97	21.59	21.73	20.84	21.72

3.5.2 Egg production and reproductive traits

Egg weight (EW) was decreased significantly (P≤0.05) from 10.64g in the first generation to 10.74g after four generations of selection (Table 10). BWSM was insignificantly increased (P≤0.05) from 136.32 g in the first generation to 139.32 g after four generations of selection (Table 10). While TEN_{10}, insignificantly increased (P≤0.05) from 55.25egg in the first generation to 54.25egg after four generations of selection. While TEW_{10} and DEM were significantly increased (P≤0.05) from 454.25g and 9.41 g/day in the first generation to 467.25g and 9.64g/day after four generations of selection (Table 10). However, reproductive traits: Fertility percentage (FR %) was significantly increased (P≤0.05) from 80.58% in the first generation to 80.90% after four generations of selection and hatchability percentage (HA %) were significantly increased (P≤0.05) from 70.42% in the first generation to 70.92% after four generations of selection (Table 10).

While, early embryonic mortality (EEM %) increased significantly (P≤0.05) from 5.63% in the first generation to 5.93% after four generations of selection, and lately embryonic mortality (LEM %), and total embryonic mortality. Total embryonic mortality (TEM %) were decreased significantly (P≤0.05) from 17.00 and 22.27% in the first generation to 16.34 and 21.97% after four generations of selection. The same trend was noticed by Ozdemir and Poyraz (2000), Aboul-Seoud et al. (2009), Abo Samaha et al. (2010), Okenyi et al. (2013), Abu-Mosallam (2014), Dauda et al. (2014) and Faruque Shakila et al. (2016). On the contrary, the corresponding values for the control line among egg production and reproductive traits studied were fluctuated from generation to another with no significant trend (Table 10).

3.5.3 Carcass traits

Meat dressing and giblets (%) were increased significantly (P≤0.05) from 42.33, 62.04 and14.27% in the first

generation to 43.76, 63.99 and 14.99% after four generations of selection. While, bone (%) traits were decreased significantly (P≤0.05) from 9.05% in the first generation to 8.53% after four generations of selection (Table 11).

Table (11): Actual means and standard deviations for carcass traits studied in both sexes for lines and generations of selection when selection was applied for early age at sexual maturity.

Line Gen Trait	Early age at sexual maturity				Random bred control line			
	1	2	3	4	1	2	3	4
Meat %	42.33	48.44	46.05	43.76	44.00	45.38	45.18	44.76
Giblets %	14.27	14.67	14.90	14.99	14.89	14.48	14.39	15.04
Bone %	9.05	8.96	8.70	8.53	8.24	8.57	8.02	8.65
Dressing %	62.04	62.91	63.44	63.99	61.69	60.98	61.39	60.89

The same trend was noticed by Mohammed (1990), Abdel-Tawab (2006), Abu-Mosallam (2014), Aboul-Hassan *et al*. (2016) and El-Fiky *et al*. (2016). On the contrary, the corresponding values for the control line among carcass traits studied were fluctuated from generation to another with no significant trend (Table 11).

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