Direct and Correlated Responses from Selection for Lately Sexual Maturity in Japanese Quail

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ABSTRACT

A total of 788 chicks aged 6 weeks were taken from the third generation of the base population. The birds were randomly assigned to one of two mating groups: one that was selected for recent age at sexual maturity (LASM), and the other that was kept as a randomly bred control line (RBC). The findings can be summed up as follows: The selected line (LASM) actual means of recently sexual maturity grew considerably (P<0.01) from 50.24 days at generation zero to 63.23 days at the fourth generation of selection. The actual selection differential in the LASM line, where the average was 3.68 and 2.26 g/generation, agreed well with the expected. The actual responses to selection in the (LASM) line were consistent, averaging 1.48g per generation. After the fourth generation of selection, the realized heritability of LASM was calculated as 0.57, 0.53, 0.35, and 0.30 for the first, second, third, and fourth generations of selection, respectively. When selection for LASM, the following were responses for the researched traits: Growth traits: After four generations of selection, BW0, BW2, BW4, and BW6 rose considerably (P<0.05) from 8.95, 36.58, 92.84, and 160.47g in the first generation to 9.47, 38.55, 95.90, and 172.42g in the first generation. Egg production traits: After four generations of selection, egg weight (EW) rose significantly (P<0.05) from 10.32g in the first generation to 11.62g. After four generations of selection, body weight at sexual maturity (BWSM) increased insignificantly from 136.32 g in the first generation to 145.02 g.

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

INTRODUCTION

The primary purpose of egg production selection trials is to improve production performance by increasing the number of birds reproduced from each hen (Bahie El-Deen et al. 1998).

The comparatively poor reproductive performance of birds selected for faster development rate is a frequent concern in all avian species studied. This poor performance is typically manifested as a reduction in overall egg production as well as an increase in the reproduction of eggs that are unsuited for certain environments, such as soft-shelled membrane and double-yolked eggs (Nestor and Bacon, 1982 and Strong et al., 1978).

Selection experiments provide a framework for studying complicated trait inheritance and allow for the testing of theoretical predictions by comparing observations to expectations.

Short-term experiments can be used to estimate genetic variances and covariance, verify their consistency from various sources of information, and assess the magnitude of initial rates of response to selection, depending on the time scale (Varkoohi and Kaviani, 2014). From generation zero to generation four of selection, the current study aimed to quantify direct responses to selection for early sexual maturity and to connect those responses with specific productive and reproductive qualities. In addition, the genetic and phenotypic relationships between early sexual maturity and each of the attributes of growth, egg production, reproduction, and carcass are being investigated. The poultry sector is particularly interested in growth, and the Japanese quail could be valuable in body weight research. Because growth is age-dependent, genetic control of body weight is expected to change with age. Because the physiological and chronological ages of quail and hens are not the same, Different breeding strategies, like selection, inbreeding, and bridization, can be used to optimize egg production and reproductive features.

MATERIALS AND METHODS

From May 2017 to September 2018, data for this study were collected on a flock of Japanese quail (Coturnix coturnix japonica) kept by the Department of Animal Production, Faculty of Agriculture, Al-Azhar University, Cairo, Egypt.

Breeding plan and management: A total of 788 birds (380 males and 408 females) were selected at random from the flock to serve as the study's parents at the age of six weeks.

In the basic population, the mating pattern was one male to two females, preventing full and half-sib matings. The birds were randomly assigned to one of three mating groups: the first was selected for late age at sexual maturity (LASM), the second was kept as a randomly bred control line, and the third was kept as a random bred control line (RBC). Family selection was done within the chosen line, however lower sexual maturity families (one male and two females) were chosen based on their divergence from the line mean.
Feed and water were freely available. According to N R C (1994), the minerals and vitamins were adequately given to meet the requirements (1994).

For the first week after hatching, the temperature was 37.5°C, then dropped 2-3°C weekly to 26-28°C in the fourth week of life till the end of the brooding period.

The breeding stocks were not subjected to any immunization or beak cutting operations.

**Statistical analysis:**

Harvey's least-squares and maximum likelihood computer programme (Harvey, 1987, model type 5) was used to evaluate data on age at sexual maturity, with each line, generation, and sex as fixed effects and sire and dam within sire as random variables.

It was decided to use the following model:

\[
Y_{ijklm} = \mu + G_i + L_j + S_{x} + k_{l} + e_{ijklm}. \]

Where:

- \(Y_{ijklm}\) = the observation of the th bird.
- \(\mu\) = the overall mean, common element to all observations.
- \(G_i\) = the fixed effect of the ith generation.
- \(L_j\) = the fixed effect of the jth line.
- \(S_{x}\) = the fixed effect of sex.
- \(k_{l}\) = the random effect of the kth sire.
- \(e_{ijklm}\) = the random error term.

Henderson Method 3 (Henderson, 1953) was utilized to estimate the genetic variance components for the different traits studied.

**RESULTS AND DISCUSSION**

1. **Direct response:**

In this paper, we describe the real methods of LASM for four generations of selection in the selected and control lines (Table, 1). Sexual maturity in the selected line (LASM) has recently grown, from 50.24 days at zero generation to 63.23 days in the fourth generation of selection. With a duration of 57.33 days on average. This outcome was in line with expectations.

| Generation | Actual | Expected | Actual / Expected |
|------------|--------|----------|-------------------|
| 0          | 3.22±0.11 | 3.03±0.20 | 1.06              |
| 1          | 3.68±0.15 | 3.18±0.28 | 1.16              |
| 2          | 3.90±0.19 | 3.32±0.20 | 1.17              |
| 3          | 3.71±0.15 | 3.46±0.19 | 1.07              |
| 4          | 3.88±0.19 | 3.31±0.15 | 1.17              |
| Average    | 3.68±0.85 | 3.26±0.20 | 1.13              |

2. **Selection response:**

In this table, the actual and cumulative selection responses are shown (Table 3). During the four generations of selection, the real response to selection in the line (LASM) declined from generation to generation.

Following the first generation of selection, the estimated response to selection was 1.82 days, then rapidly decreased as selection progressed to 1.62, 1.38, and 1.10 days after the second, third, and fourth generations of selection among the LASM line. With a 1.48-second average.

| Generation | Actual | Cumulative |
|------------|--------|------------|
| 0-1        | 1.82±0.45 | 1.82       |
| 1-2        | 1.62±0.34 | 3.46       |
| 2-3        | 1.38±0.40 | 4.82       |
| 3-4        | 1.10±0.67 | 5.92       |
| Average    | 1.48±0.42 | -----      |

This regularity of the selection response has been found in a number of published selection experiments. After four generations of selection, the cumulative response to selection in the LASM line was 5.92d.

**Heritability estimates for late age at sexual maturity:**

**Components of variance:**

The LASM line has heritability estimates for age at sexual maturity determined from components of variation, i.e. sire (paternal half-sibs), dam within sire (maternal half-sibs), and sire plus dam (full-sibs) (Table 4). The dam component, on the other hand, is likely
to be bigger in magnitude due to dominance deviations and maternal effects. Among the four generations of selection, heritabilities computed from the sire component (h^2s) varied from 0.11 to 0.19, whereas those computed from the dam components (h^2D) are often greater than those computed from the sire components, ranging from 0.26 to 0.33. This could be due to the substantial dam variance components obtained, as well as non-genetic influences such as dominance and maternal, which often cause h^2D estimates to be much bigger than h^2S estimates. Heritabilities calculated from full-sibs components (h^2S+D) were moderate to high in magnitude (0.23 - 0.26). Debes (2004), Melky (2007), Abou Kandiga, et al. (2016), and Kaye, Joshua, et al. (2016) all noted the same tendency (2016). With a few exceptions, estimations of heritability based on female progeny weights were often greater than those based on male progeny weights. The estimated dam heritability estimates (h^2D) are significantly bigger than the estimated sire heritability estimates, according to the unweighted mean of heritability estimates for male or female progeny weights (h^2S).

Table 4. Heritability estimates computed from sire, dam, sire plus dam components of variance and realized heritability for lately age at sexual maturity.

| Generation | Heritability | Sires h^2S±SE | Dams: Sires h^2D±SE | Full-sibs h^2S+D±SE | Realized h^2S±SE |
|------------|--------------|---------------|---------------------|---------------------|-----------------|
| 1          | 0.19±0.83    | 0.26±0.53     | 0.23±0.14           | 0.57±0.96           |                 |
| 2          | 0.13±0.78    | 0.33±0.72     | 0.23±0.26           | 0.53±0.57           |                 |
| 3          | 0.11±0.29    | 0.30±0.69     | 0.26±0.50           | 0.35±0.90           |                 |
| 4          | 0.16±0.47    | 0.29±0.73     | 0.23±0.23           | 0.30±0.64           |                 |

Realized heritability:

The realized heritability was derived from the LASM line and shown every generation as the ratio between response to selection and selection difference (R/S) (Table, 4). The realized heritability estimates for recent age at sexual maturity dropped from 0.57 in the first generation to 0.30 in the fourth. However, he computed Realized heritability differently than Kaye, Joshua, et al., (2016). (0.23). The current estimates were consistent with those reported by Abu-Mosallam (2014), who calculated higher estimates of realized heritability for HFC4-6 when selection was applied, ranging from 0.70 to 0.77, which were higher than those reported by Aboul-Hassan (1997) and El-Fiky (2005), who reported a range of estimates (0.12-0.21) for realized heritability of BW6.

Correlated responses for lately age at sexual maturity:

Other qualities were harnessed as a result of LASM selection. Weights and/or weight gains recorded at various ages and growth phases, as well as egg production, reproductive qualities, and carcass traits, may all be altered. Tables from show the actual means of the relevant qualities associated with LASM selection (5 to 10).

Growth traits:

After four generations of selection, the body weights of the LASM line (BW0, BW2, BW4, and BW6) grew considerably (P<0.05) from 8.95, 36.58, 92.84, and 160.47 g in the first generation to 9.47, 38.55, 95.90, and 172.42 g (Table, 41). Hasson (2000), Debes (2004), El-Fiky et al., (2000), and Abdel-Tawab (2006) noticed the same trend when selecting Japanese quail for increased EW, and Abu-Mosallam (2014) noticed the same trend when selecting Japanese quail for increased feed consumption among the first three generations of selection. Aboul-Hassan et al., 2016; El-Fiky et al., 2016. (2016). When it came to Japanese quail water and feed intake, they chose carefully. Body weight rose considerably (P<0.05) by 0.15, 0.10, and 0.14 g each generation for the RBC line and insignificantly (P>0.10) by 0.14, and 3.42 g/day in the first generation to 2.62, 1.69, and 3.64 g/day in the fourth. However, after four generations of selection, body weight gain features in the LASM line (ADG0-2, ADG4-6, and ADG0-6) increased insignificantly (P>0.05) from 2.32, 1.42, and 3.42 g/day in the first generation to 2.62, 1.69, and 3.64 g/day in the fourth. However, after four generations of selection, body weight gain at (ADG2-4) rose significantly (P<0.05) from 5.20 g/day in the first generation to 5.66 g/day.

Table 5. 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 LASM.

| Line | Gen / Trait | 1 | 2 | 3 | 4 | RBC |
|------|------------|---|---|---|---|-----|
| BW0  | 8.95±0.64  | 9.57±0.65 | 9.75±0.42 | 9.47±0.65 | 8.85±0.89 | 8.64±0.77 | 8.59±0.85 | 8.57±0.65 |
| BW2  | 36.58±4.20 | 38.05±4.28 | 43.01±5.32 | 38.55±4.28 | 36.25±4.74 | 35.20±4.22 | 36.66±4.82 | 37.35±4.28 |
| BW4  | 92.84±14.00 | 95.87±15.47 | 95.45±17.65 | 95.90±15.47 | 90.52±12.55 | 94.22±14.54 | 93.58±16.47 | 95.80±15.47 |
| BW6  | 160.47±16.51 | 168.02±17.11 | 172.42±16.35 | 168.92±17.11 | 155.78±17.24 | 152.54±16.10 | 154.05±11.82 | 159.02±17.11 |
| ADG0-2| 2.32±0.40  | 2.77±0.42 | 2.79±0.54 | 2.62±0.42 | 2.34±0.42 | 2.22±0.54 | 3.2±0.67 | 2.72±0.42 |
| ADG4-6| 5.20±0.66  | 5.48±0.62 | 5.60±0.62 | 5.60±0.62 | 5.16±0.40 | 4.95±0.61 | 5.11±0.44 | 5.48±0.62 |
| ADG0-6| 1.42±0.33  | 1.60±0.55 | 1.71±0.61 | 1.69±0.58 | 1.45±0.39 | 1.49±0.45 | 1.42±0.62 | 1.60±0.55 |
| ADG0-6| 3.42±0.57  | 3.74±0.92 | 3.88±0.92 | 3.64±0.90 | 3.54±0.41 | 3.40±0.35 | 3.55±0.41 | 3.74±0.92 |

The regression coefficients of the growth variables evaluated (weights and gains) on generation number have been used to determine correlated responses in the line chosen for LASM (table 5). Body weights grew by 0.22, 0.18, 0.10, and 0.12 g each generation of selection, respectively, at 0, 2, 4, and 6 weeks of age (P<0.05).

Egg production and reproductive traits:

After four generations of selection, egg weight (EW) grew considerably (P<0.05) from 10.32 g in the first generation to 11.62 g, whereas BWSM increased insignificantly (P>0.05) from 136.32 g in the first generation to 145.02 g (Table, 6). TEW10 was considerably raised (P<0.05) from 470.25 g in the first generation to 464.54 g after four generations of selection, while TEN10 was insignificantly lowered (P>0.05) from 54.25 egg on the first generation to 53.34 g after four generations of selection. However, DEM fell from 9.40 g/day in the first generation to 9.30 g/day after four generations of selection (P<0.05) (Table, 6). However, reproductive traits showed a significant decrease (P<0.05) in FR percent from 82.58 percent in the...
first generation to 80.00 percent after four generations of selection, while HA percent decreased insignificantly (P>0.05) from 70.52 percent in the first generation to 68.11 percent after four generations of selection (Table, 6). After four generations of selection, EEM percent grew significantly (P<0.05) from 5.64 percent in the first generation to 6.79 percent. After four generations of selection, the LEM and TEM percents declined dramatically (P<0.05) from 16.35 and 21.99 percent in the first generation to 16.69 and 23.48 percent. Farrag et al., (2008) discovered that fertility percentages in G0, G1, and G2 were 69.92, 64.71, 72.61; 59.87, 61.72, 73.21 percent and 60.58, 64.82, 75.90 percent, respectively. According to Samaha et al., (2010), fertility percents in the base, first, second, and third generation were 94.11, 96.79, 94.05, and 95.34, respectively. Okenyi (2013), reported that fertility percents were 76.29 percent for G0, 70.06 percent for G1, and 65.98 percent for G2 of selection. Furthermore, Aboul-Mosallam (2014) found that egg weight (EW) increased significantly (P<0.05) from 10.32 g in the first generation to 10.96 g after three generations of selection, and ASM increased significantly (P<0.05) from 55.15 day in the first generation to 59.62 day after three generations of selection when he selected Japanese quail for increased feed consumption.

Table 6. 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 LASM.

| Line   | Trait    | LASM | RBC |
|--------|----------|------|-----|
|        | Gen 1    | 2    | 3   | 4    | 1    | 2    | 3   | 4    |
| EW     | 10.32±9.50 | 10.62±9.52 | 10.96±10.02 | 11.62±9.52 | 10.25±10.62 | 10.35±10.48 | 10.10±11.25 | 10.62±9.52 |
| BWSM   | 136.32±18.95 | 143.02±28.05 | 146.35±22.16 | 145.02±28.05 | 138.72±19.65 | 137.72±18.00 | 139.12±16.95 | 143.92±28.09 |
| TEN10  | 54.25±7.25 | 52.54±6.33 | 50.48±7.10 | 53.54±6.35 | 55.65±5.69 | 57.02±5.12 | 56.54±5.62 | 52.74±6.38 |
| TEM4   | 470.25±14.25 | 462.54±16.50 | 458.25±15.65 | 464.54±16.50 | 472.54±15.69 | 474.18±15.03 | 482.04±14.15 | 462.54±16.50 |
| DEM    | 9.40±6.21 | 9.20±5.62 | 9.10±6.58 | 9.30±6.24 | 9.37±5.66 | 9.77±5.66 | 9.70±5.02 | 9.20±5.62 |
| FR%    | 82.58 | 80.65 | 78.69 | 80.00 | 84.25 | 85.01 | 84.96 | 80.65 |
| HA%    | 68.49 | 68.11 | 66.21 | 70.52 | 75.95 | 76.02 | 75.78 | 68.49 |
| EEM%   | 5.64 | 6.65 | 6.95 | 6.79 | 5.72 | 6.14 | 5.45 | 6.65 |
| LEM%   | 16.69 | 16.99 | 17.02 | 16.35 | 15.89 | 15.60 | 15.43 | 16.94 |
| TEM%   | 23.48 | 23.64 | 23.97 | 21.99 | 21.61 | 21.74 | 20.88 | 23.59 |

Carcass traits:

Meat, bone, giblets, and dressing percent attributes in the LASM line grew considerably (P<0.05) from 44.33, 7.57, 13.24, and 60.04 percent in the first generation to 45.41, 8.06, 13.95, and 61.94 percent after four generations of selection in the LASM line (Table, 7). The equivalent values for the control line among carcass qualities studied, on the other hand, were not significant (Table, 7).

Table 7. Actual means and standard deviations for carcass traits studied in both sexes for lines and generations of selection when selection was applied for LASM.

| Trait    | LASM | RBC |
|----------|------|-----|
|          | Gen 1 | 2 | 3 |
| Meat%    | 44.33 | 46.64 | 46.95 |
| Giblets% | 13.24 | 13.84 | 13.95 |
| Bone%    | 7.57 | 7.76 | 8.06 |
| Dressing%| 60.04 | 61.51 | 61.94 |

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