PREDICTION OF GENETIC GAIN IN JAPANESE QUAIL POPULATION SELECTED FOR HIGH FOURTH WEEK BODY WEIGHT

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Abstract: The selection programme for high 4-week body weight yielded satisfactory improvements in body weights strains. The traits studied had the heritabilities ranging from low to high indicating the scope for their further genetic improvement by selection coupled with optimum management. The expected response to selection in body weight at 4-weeks age in Black, Brown and Black random bred male Japanese quails were 3.62, 6.06 and 6.91g, respectively and the corresponding response in females were 1.11, 2.13 and 12.79 g.
Keywords: Japanese Quail, Selection, Genetic gain, Heritability, Body weight.

Introduction

In chicken dominated poultry industry, Japanese Quail (*Coturnixcoturnix japonica*) provides better means of diversification. It has unrivalled ability to produce luscious meat and eggs faster, in greater quantity. Moreover, quail meat is preferred over chicken meat because of its taste and delicacy, less fat content (low calorific value) but more of phospholipids and less cholesterol.

The research work had carried out on Black and Brown strains of selected lines (undergone 10 Generation of selection) and random bred Black strain CARI of Japanese quails population, which were maintained at Poultry Experimental Station (PES), College of Veterinary Science, Rajendranagar, Hyderabad. Forecasting the outcome of research program is very essential to understand and predict the direction and amount of response in the genetic improvement through selection program

Materials and Method

The strains pertaining to the study initially undergone selection for high 6 week body weight during first four generations followed by selection for high 4 week body weight which has been continued till tenth generation. The random bred Black strain was procured from Central Avian Research Institute (CARI), Izatnagar. Tenth generation birds were used as parent stock for 11th generation Black and Brown strain birds. A total of 57 and 50 dam

families of G_{10} Black and Brown strains respectively were housed in individual cages. The first generation random bred Black strain was produced from 122 sire families of random bred base population. A total of 526 Black and 296 Brown chicks were obtained from 10 pedigree hatches and in the case of Black random bred, 1395 chicks were produced from 5 pedigree hatches. The hatches were taken at weekly interval during April 2008 to June 2008. The chicks of all 3 strains were wing banded at day-old and body weight was recorded and they were immediately transferred to brooder house. The chicks of 3 strains were reared together and maintained in brooder house in deep litter system until 4 weeks of age. At 4 weeks of age, individual birds were selected and were housed in cages

Individual's own 4-week body weight was considered and mass selection was practiced. From each hatch and strain, about 25-30 per cent of the top ranking males and about 50-60 per cent of top ranking females in G_{11} population and about 14 per cent males and 27 per cent females in random bred Black strain were selected.Concentrate feed mash and fresh water were made available *ad-libitum* to all the experimental birds.

Statistical Analysis

The data on body weight were included for all the birds which survived until four weeks of age. The data recorded on various body weights were subjected to least squares analysis (Harvey, 1979) using the following fixed effects linear model to study the influence of genetic and non-genetic effects.

$$Y_{ijkl} = \mu + h_i + S_j + Sx_k + e_{ijkl}$$

Where, Y_{ijkl} is measurement of a trait j^{th} bird belonging to k^{th} sex, j^{th} strain and i^{th}hatch, μ is overall mean, h_i is effect of ith hatch (i = 1 to 10), S_j is effect of jth strain (j = 1, 2 and 3, Black, Brown and Black random bred, respectively), Sx_k is effect of k^{th}sex (k = 1 and 2, male and female, respectively), e_{ijkl} is random error assumed to be normally and independently distributed with mean zero and variance $\sigma^2 e$

The differences between various hatches and strains were tested for significance byDuncan's Multiple Range Test (D.M.R.T)as modified by Kramer (1957).

Heritability estimates were computed for body weight traits studied based on the data adjusted for the effects of hatch by using paternal half-sib correlation method as per Becker (1985). The statistical model used in this analysisis

$$Y_{ij} = \mu + S_i + e_{ij}$$

Where, Y_{ij} is measurement on j^{th} quail belonging to i^{th} sire, μ is overall mean, S_i is effect of ith sire, e_{ij} is random error assumed to be distributed normally and independently with meanzero and variance $\sigma^2 e$.

The selection differential (S) was estimated as the mean superiority of selected parents (P_S) over the population mean (P).The response to selection (S) was estimated as the product of intensity of selection (i), heritability (h^2) and phenotypic standard deviation (σ_P).

$$S = P_S - P \text{ and } R = ih^2\sigma_P$$

Results and Discussion

The proportion of population selected for the propagation of next generation was 32.02, 33.33 and 13.48 percent males respectively in Black, Brown and Black random bred Japanese quails, whereas the corresponding proportions in females were 50.18, 60.53 and 25.56 percent (Table.1). These percentages were in accordance with the studies of Ajay kumar (2001, 2002), in which 20 to 33.33 percent of the population was selected to be the parents of next generation. Feroz Mohammed *et al*. (2006) applied selection pressure of 9.39 to 22.01 percent for males and from 22.37 to 28.81 percent for females in two generations of selection.

The population means (P), selected parent mean (P_S), selection differential (S), heritability (h^2) and intensity of selection along with response to selection (g) in body weights of Black, Brown and Black random bred Japanese quails are presented in Table 2.

In the Black, Brown and Black random bred strains of Japanese quails, the selection differentials of 13.40, 6.00 and 29.54 g, respectively could be attained in males while, the corresponding selection differentials in females were 6.71, 3.09 and 24.61 g in 11th generation of selection. The intensities of selection (i) were 0.53, 0.26 and 1.27, respectively in Black, Brown and Black males and 0.24, 0.11and 1.11, respectively in females (Table 2).

Sreenivasulu (1997) reported selection differentials ranging from 13.59 to 17.92 g among the three meat type Japanese quails lines at 5-weeks of age, while Metodiev and Drbohlav (1998) recorded the selection differentials ranging from 4.59 to 28.66 g among four generations of selection for 5-week body weight. The selection differentials observed in the present study were similar to those reported by above authors.

In the study, the males and females of 11th generation Black and Brown strain were selected based on individual's own body weight at 4 weeks age, information on dam's AFE and dam' egg production up to 16 weeks of age, while in Black random bred strain, the parents were selected based on their 4-week body weight, since this was the first generation

after pedigree was setup, for further propagation of the flock. The selection criteria in 11th generation birds might have resulted in variation in body weight in the population.

In conclusion, the populations had genetic variation ranging from low to high for body weight in 11th generation (Black and Brown) strain and in Black random bred strain. Which, indicating that the genetic variation is more in the selected population has a scope for their further genetic improvement by selection coupled with optimum management. Response to selection is high in black random bred population, it indicated that the male black random bred population had high phenotypic standard deviation (σ_P), high heritability (h^2) and the population subjected to high selection indencity (i).

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Table 1. Proportion of males and females selected

Strain	Population		Selected number		Proportion selected (%)	
	Males	Females	Males	Females	Males	Females
Black	253	273	81	137	32.02	50.18
Brown	144	152	48	92	33.33	60.53
Black Random bred	675	720	91	184	13.48	25.56
Total	1072	1145	220	413	20.52	36.07

Table 2. Selection differential (S) and Response to selection (R) in body weights

Males							
Black :	$\overline{P}$	$\overline{P}_S$	S	σ_P	I	h^2	R
BW0	8.10	8.11	0.01	0.95	0.01	£	£
BW2	65.70	74.97	9.27	17.11	0.54	0.61	5.61
BW4	152.90	166.30	13.40	25.16	0.53	0.27	3.62
Brown :							
BW0	8.30	8.60	0.30	0.97	0.31	£	£
BW2	58.30	62.57	4.27	14.37	0.30	0.46	1.97
BW4	138.10	144.10	6.00	23.52	0.26	1.01	6.06
Black random bred :							
BW0	7.40	7.51	0.11	0.97	0.11	£	£
BW2	51.20	64.17	12.97	12.51	1.04	0.29	3.79
BW4	128.00	157.54	29.54	23.33	1.27	0.23	6.91
Females							
Black :	P	P_S	S	σ_P	I	h^2	R
BW0	8.20	8.29	0.09	0.89	0.10	£	£
BW2	65.90	70.11	4.21	17.70	0.24	0.17	0.72
BW4	155.40	162.11	6.71	27.69	0.24	0.17	1.11
Brown :							
BW0	8.10	8.20	0.10	0.96	0.10	£	£
BW2	59.00	61.78	2.78	15.73	0.18	0.75	2.09
BW4	139.40	142.49	3.09	27.03	0.11	0.69	2.13
Black random bred :							

BW0	7.42	7.66	0.24	0.82	0.30	£	£
BW2	53.61	65.81	12.20	13.77	0.89	0.45	5.49
BW4	133.96	158.57	24.61	22.16	1.11	0.52	12.79

[£] Not estimable; $\overline{P}$, $\overline{P}_S$, S and R are in grams