



## Effect of plumage colour and estimation of variance components of bi-weekly growth traits in Japanese quail (*Coturnix coturnix japonica*)

SHAKTI KANT DASH<sup>1</sup>, SWAYAMPBABHA NAIK<sup>2</sup>, PREM PRAKASH DUBEY<sup>3</sup>, PUNEET MALHOTRA<sup>4</sup> and BALJINDER KUMAR BANSAL<sup>5</sup>

Guru Angad Dev Veterinary and Animal Sciences University, Ludhiana, Punjab 141 012 India

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### ABSTRACT

The present investigation was undertaken in black and white quails for studying the effect of plumage colour, estimating genetic parameters and fitting non-linear regression model to growth curve in white and black Japanese quails. White quails were significantly heavier in comparison to black quails across age groups indicating association of plumage colour with growth rate. The body weight variables measured at bi-weekly intervals when considered as a single variable had low repeatability indicating they were genetically not identical variables. Paternal half-sib estimates of heritability indicated higher additive variance in white quails in comparison to black quails. Phenotypic correlation estimates between bodyweights at 2, 4, 6, 8 and 10 weeks of age, ranged from medium to high indicating favourable correlated response in bodyweight variables. Gompertz curve had very good fit with the data (99.6%) and similar curve parameters were estimated in both quail varieties. Point of inflection (IPT) was similar in both quail varieties and was 3.46 (black) and 3.44 weeks of age (white). The estimates of different growth parameters indicated the favourable effect of selection in these quail lines. Results indicated that growth curve estimates can be used for developing future breeding strategies in quails.

**Key words:** Non-linear, Plumage, Parameters, Point of inflection

Growth being the function of genetics, nutrition and management determines the performance of an individual with respect to economical traits. Efficient growth rate of the stock would result in early returns for the farm. Measurement of growth at regular intervals is important for making nutritional and managerial interventions on the basis of growth curve analysis. Japanese quails (*Coturnix coturnix japonica*) are well known for their fast growth rate, higher egg production potential and easy management. Interactions of number of genes specific mutations or combination of mutations are chief cause of varying plumage colours in quails (Bed'hom *et al.* 2012). Till date several quail varieties have been developed through selection and breeding in closed colonies leading to fixation of specific marker genes for plumage colour. Various reports have attempted to associate the effect of plumage colours with growth traits in Japanese quails (Sezer and Tarhan 2005). Broiler breeding programs are based on estimates of growth traits as these traits are known to possess

appreciable additive variance (Zerehdaran *et al.* 2012). Recent publications also indicate the importance of growth curve analysis in selection experiments as the identification of point of inflexion has gained increasing importance (Narianc *et al.* 2014). Association studies on growth performance and plumage are limited in quails in comparison to other poultry species (Inci *et al.* 2015). The present investigation aims for comparative assessment of genetic parameters of growth traits and growth curve parameters estimates in white and black plumage Japanese quail varieties.

### MATERIALS AND METHODS

The present investigation was carried out on 268 black and 704 white quails maintained at the quail section of poultry breeding farm of Directorate Livestock Farms, GADVASU, Ludhiana. Parental population was reared in individual breeder cages (0.30 inch<sup>2</sup>/bird) up to 32 week of age. One male was allotted to 3 females and when the birds were 12-weeks-old pedigreed hatch of the quails was taken at the university hatchery under optimum biosecurity conditions. Eggs were saved for 10 days in cold room of the hatchery at 18°C and hatch was taken during winter. All birds had *ad lib.* access to feed during the period of study.

The body weight of the quails was recorded at 0, 2, 4, 6, 8 and 10 weeks of age and genetic parameter estimates were obtained separately for white and black quails.

Present address: <sup>1</sup>Assistant Professor (shaktikant07@gmail.com), <sup>2</sup>M.V.Sc. Scholar (swayampbabhanaik@gmail.com), <sup>3</sup>Assistant Scientist (prakashagb@gmail.com), <sup>4</sup>Dairy Manager (dr.puneetmalhotra@rediffmail.com), <sup>5</sup>Director and Head (baljinderbansal@rediffmail.com), Directorate of Livestock Farms and Department of Animal Genetics and Breeding, College of Veterinary Science.

Table 1. Descriptive statistics of bi-weekly body weights of different strains of quails

Strain	Trait	Mean±SE	Standard deviation	CV%	Skewness±SE	Kurtosis±SE
Black	BWT0	7.87±0.06*	0.99	12.58	-0.23±0.14	0.41±0.29
	BWT2	41.25±0.74*	9.48	22.98	0.60±0.19	2.74±0.37
	BWT4	109.35±2.21*	25.25	23.09	-0.22±0.21	-0.02±0.42
	BWT6	193.55±2.95*	33.31	17.21	-0.38±0.21	0.54±0.42
	BWT8	230.47±2.93	32.37	14.05	-0.004±0.21	0.25±0.43
	BWT10	239.32±2.93*	32.43	13.55	0.03±0.21	0.17±0.43
White	BWT0	9.01±0.06*	1.68	18.65	1.79±0.09	8.86±0.18
	BWT2	43.54±0.53*	12.83	29.47	0.18±0.10	-0.41±0.20
	BWT4	115.44±1.27*	28.47	24.66	-0.15±0.10	-0.08±0.21
	BWT6	198.43±1.78*	39.23	19.77	-0.42±0.11	0.20±0.22
	BWT8	241.11±1.42	30.38	12.60	0.10±0.11	0.29±0.22
	BWT10	247.82±1.31*	27.93	11.27	-0.10±0.11	2.18±0.23

CV, Coefficient of variation; SE, standard error. \*Indicates significant difference between the means at  $P < 0.05$ .

Repeatability, phenotypic and genetic correlations estimates were obtained for body weight performance measured at different time points. Paternal half-sib method was used for estimation of heritability by the statistical model  $Y_{ij} = m + s_i + e_{ij}$ , where,  $Y_{ij}$ , observation of the  $j^{\text{th}}$  progeny of the  $i^{\text{th}}$  sire;  $m$ , overall mean;  $s_i$ , effect of the  $i^{\text{th}}$  sire;  $e_{ij}$ , random error  $\sim \text{NID}(0, \sigma_e^2)$ . The data were utilized to study the growth curve of black and white plumage quails and the following Gompertz nonlinear regression model was fitted;

$$y_t = \beta_0 e^{(-\beta_1 e^{-\beta_2 t})}$$

where  $y_t$  is weight at age  $t$ ,  $\beta_0$  is the asymptotic (mature) weight parameter,  $\beta_1$  scaling parameter (constant of integration),  $\beta_2$  instantaneous growth rate (per day) parameter. The coordinates of the point of inflection (IPT) and weight at inflection point (IPW), were obtained as  $\text{IPT} = \ln(\beta_1)/\beta_2$  and  $\text{IPW} = \beta_0/e$  (Rizziet al. 2013). Further the absolute growth rate (AGR) at 6 weeks of age; relative growth rate at 6 week of age (RGR) were estimated from following equations;

$$\text{AGR} = \beta_0 \beta_1 \beta_2 e^{(-\beta_1 e^{-\beta_2 t})} e^{(-\beta_2 t)}$$

$$\text{RGR} = \beta_2 [\ln(\beta_0) - \ln(y_t)]$$

Unit increase in BW per unit of time. Parameter estimations will be performed by the NLIN procedure of SAS 9.3 software (SAS Institute Inc., Cary, NC).

## RESULTS AND DISCUSSION

Descriptive analysis and t-test results revealed that white quail was significantly ( $P < 0.05$ ) heavier than the black strain across age groups. Standard deviation estimates indicated greater variation in body weight variables measured at 4, 6, 8 and 10 weeks of age in both quail varieties, which indicates uniform expression of genes related to body weight in older quails. The variation estimates of 0 and 2 weeks body weight traits were markedly low and differed greatly from other body weight variables. Approximately symmetric data was observed for most of the body weight variables in both strains as the skewness estimates ranged between  $\pm 0$ . In black quails the BWT2 had moderate skewness (i.e. between  $\pm 0.5$  to  $\pm 1$ ) and high skewness (i.e.

$> \pm 1$ ) were observed in BWT0 of white quail chicks. The Z-values were estimated by dividing the estimate with its standard error. The Z-value (considering medium sample size 50 to 300) of kurtosis estimate was higher in BWT2 for black quails and absolute value of kurtosis (considering sample size  $> 300$ ) was high in BWT0 in white quails (Table 1). The observations with respect to BWT variables of the present study were superior to those were reported by Saatci *et al.* (2003) and lesser in comparison to Sezer and Tarhan (2005) and Narianc *et al.* (2010) in Japanese quails.

Paternal half-sib estimates of heritability in black quails had higher standard errors. Very high additive genetic variance was observed in white quails across body weight variables considered at different age groups (Table 2). Magda *et al.* (2010) observed high heritability estimates of 0.77 and 0.90 in the first and second generations of random bred quails at 2 weeks of age, moderate estimates were observed for 4 and 6 weeks of age. Narinc *et al.* (2014) estimated heritability for body weight at 5 week of age as 0.36; similar estimates were also reported by Sari *et al.* (2011) using REML procedure. Resende *et al.* (2002) observed heritability estimates for body weight of 0.33, 0.35, 0.36, 0.44 and 0.48 at hatch, 7-, 14-, 21- and 28-day-old Japanese quails, respectively, by variance partitioning using linear model approach. Daikwo *et al.* (2014) observed decreasing heritability with advancement of age; heritability estimates of weekly body weight of Japanese quail ranged between  $0.12 \pm 0.02$  at 42 days of age and  $0.91 \pm 0.11$  at 0 day of age. Kaye *et al.* (2017) observed that heritability estimates ranged between 0.48 and 0.34 in male Japanese

Table 2. Paternal half-sib heritability estimates of body weight traits at different ages of black and white strains of quail

Trait	N	Black	N	White
BWT0	267	0.28±0.18	701	0.76±0.15
BWT2	163	0.37±0.28	581	0.69±0.16
BWT4	130	0.40±0.33	499	0.59±0.17
BWT6	127	0.06±0.30	482	0.93±0.19
BWT8	122	0.13±0.32	454	0.89±0.20
BWT10	122	0.14±0.32	450	0.74±0.19

quails and 0.57 and 0.83 in female Japanese quails from 5 to 8 weeks of age.

The estimates of repeatability of body weight considered as a single variable for both the quail strains were low and negative, (0.04±0.01 and 0.05±0.01 in black and white respectively) which is due to the fact that these body weight traits might be affected differently at different ages of the bird (0, 2, 4, 6, 8, 10 weeks) by both genetics and temporary environment leading to higher within individual variance. Further the assumptions for repeatability estimation such as the observations on the same individual recorded at different times should be genetically the same and different measurements should have the same variance with their components in the similar proportions, did not apply well for the present study leading to unnatural repeatability estimates.

All correlation estimates between bodyweights at 2, 4, 6, 8 and 10 weeks of ages ranged from medium to high. However the correlation estimates of BWT0 with other BWT variables were low for white quail varieties indicating the set of genes which expresses during incubation up to hatching were mostly different from the set of genes that regulate the post hatch growth and development of the bird (Table 3). In contrast to the present study Daikwo *et al.* (2014) reported strong and positive phenotypic and genetic correlations between BWT variables across all age groups from day 0 to 7 weeks of age and discussed that the same genes were controlling the body weight traits at different ages with increasing expressivity. Genetic correlation between 2 and 4 weeks and 4 and 6 weeks of age were reported to be 0.76 and 0.99 (Brah *et al.* 1997). The high genetic correlation in various studies indicated that the heavier birds carry their weight into succeeding ages thus making selection at early body weight highly effective (Saatci *et al.* 2003, Narinc *et al.* 2010).

Growth curve analysis indicated similar growth curves having very good fit with the data of black and white quails (Table 4). The curve parameters for white and black quails indicated similar expression pattern of growth related genes in both the quail varieties. The estimate of asymptotic limit of the weight ( $\beta_0$ ) of growth curve, when age (t) approaches infinity were 257.55 and 268.28, for black and white quails, respectively. Alkan *et al.* (2009) have reported  $\beta_0$  parameter in the range of 295 and 306 as their data were obtained from population selected for body weight.  $\beta_0$  parameter was 233.12 in a similar study by Narinc *et al.* (2014). Selection for body weight alters the growth of quails and their growth curve parameters. The  $\beta_2$  parameter representing the instantaneous growth rate had an estimate of 0.45 (black) and 0.44 (white), which was similar to 0.47 reported by Alkan *et al.* (2009) and higher to 0.08 observed by Narinc *et al.* (2014) in Japanese quail. Change between sequential weeks was estimated by AGR and RGR is the ratio of the rate of change in body weight to the achieved growth at a given age. The AGR in black (26.88 g/week) was lower in comparison to white quails (27.75 g/week), whereas RGR was 0.13% for both the quail varieties. The average values

Table 3. Estimates of phenotypic correlation between body weight traits (above diagonal black quail and below diagonal white quail)

Trait	BWT0	BWT2	BWT4	BWT6	BWT8	BWT10
BWT0		0.36	0.16	0.18	0.21	0.34
BWT2	0.04		0.82	0.40	0.16	0.27
BWT4	0.10	0.63		0.53	0.19	0.23
BWT6	0.02	0.32	0.61		0.69	0.58
BWT8	0.03	0.35	0.41	0.55		0.79
BWT10	0.07	0.26	0.29	0.44	0.67	

Table 4. Estimates of curve parameters and model fitness (R<sup>2</sup>) for different strains of quail

Strain	Parameter	Estimate±SE	R <sup>2</sup>
Black	b <sub>0</sub>	257.55±11.84	99.6%
	b <sub>1</sub>	4.76±0.90	
	b <sub>2</sub>	0.45±0.06	
White	b <sub>0</sub>	268.28±12.13	99.6%
	b <sub>1</sub>	4.59±0.81	
	b <sub>2</sub>	0.44±0.05	

for AGR and RGR at 5 weeks of age were 3.56/day and 1.90%, respectively (Narinc *et al.* 2014). Various authors have suggested that RGR as a favourable tool in growth assessment under varied genetic and environmental conditions (Aggrey 2004, Narinc *et al.* 2010). IPT was similar in both quail varieties and was found to occur at 3.46 (black) and 3.44 weeks of age (white). Narinc *et al.* (2014) reported IPT at 17.81 days of age, which was better than that of present study. Pearson correlation estimates between asymptotic limit of the weight ( $\beta_0$ ) and instantaneous growth rate ( $\beta_2$ ) were strong negative indicating that a higher  $\beta_0$  would lead to lower  $\beta_2$  (Table 5). Similar estimates were reported by Akbas and Yaylak (2000) and Narianc *et al.* (2014) who discussed that such strong negative correlation is related to the average rate of maturing.

In conclusion the quail birds had satisfactory growth rate indicating favourable effect of selection in these quail lines in the previous generations. The estimates of heritability indicated that early selection for growth would help in improving the marketable age of meat type quails in both

Table 5. Correlation between curve parameters of different strains of quail

Parameter	b <sub>0</sub>	b <sub>1</sub>	b <sub>2</sub>
<i>Black</i>			
b <sub>0</sub>	1.00	-0.61	-0.82
b <sub>1</sub>	-0.61	1.00	0.91
b <sub>2</sub>	-0.82	.913	1.00
<i>White</i>			
b <sub>0</sub>	1.00	-0.61	-0.83
b <sub>1</sub>	-0.61	1.00	0.91
b <sub>2</sub>	-0.83	0.91	1.00

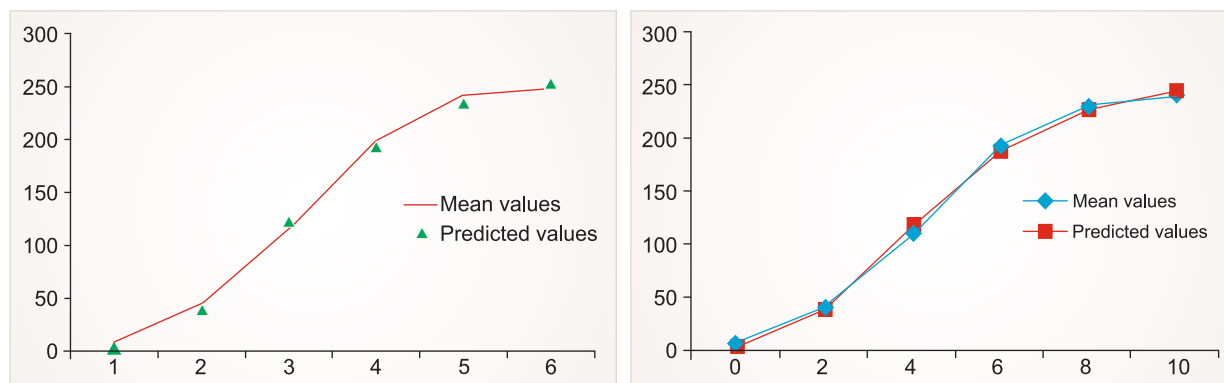


Fig 1. Growth curve of white and black plumage quails with actual and predicted bi-weekly body weight values.

quail varieties. The white quails had superior growth rate in comparison to black quails this created avenue for future studies on effect or interaction of plumage related genes on growth associated genes in Japanese quails. The body weight as a single variable measured at different time points had low repeatability which made it obvious that the BWT variables were not genetically identical. The growth curves were similar for both quail varieties. The Gompertz growth curve analysis helped in identifying the point of inflection and curve parameters, which can be used for developing future strategies of selection based on individual's superior curve parameters.

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