Response to Selection And Estimation of Genetic Parameters For 4 wk Body Weight in Quail

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Introduction

Selection experiments provide the framework for the study of the inheritance of complex traits and allow the evaluation of theoretical predictions by testing observations against expectations (Martinez *et al*. (2000)). The basis for development of a selection strategy is the variation and covariation within and among populations (Saatci *et al.* (2006)), so estimation of genetic parameters provide an opportunity to develop the desired characteristics as well as evaluation of breeding programs (Minvielle *et al.* (2000); Schuler *et al.* (1998)). Estimation of genetic parameters for a number of traits in Japanese quail was reported by several studies (Toelle *et al.* (1991); Minvielle *et al.* (2000); Vali *et al.* (2005); Saatci *et al.* (2006); Mielenz *et al.* (2006)). Anatomical responses to selection under varying diets (Ricklefs and Marks (1985)), the relationships between egg weight, hatch weight, and growth rates (Marks (1975)), and survival rates (Aggrey (2002)) have all been documented.

The objective of the present study was to investigate the effect of short-term selection for increased 4wk BW of Japanese quail and estimation of genetic parameters for carcass traits and egg weight.

Materials and methods

Animal and traits. 234 birds were randomly selected from the base population (consisting of 500 birds) and divided randomly in two lines: a control line (C) plus a line selected (S) for 4 wk BW. Chickens had access to artificially lighted housing for 24 hours per day, and a standard commercial feed containing 26 % CP and 2900 Kcal Kg/ ME. Food and water were available ad libitum. The data were analyzed by an animal model to predict the breeding values of birds by ASREML software (Gilmour et al., 2000). The superior birds (78 females and 39 males) were selected as the parents of the next generation. At 4 wk of age (early 29 d of age) after 2 h without food, approximately 80 birds of each line were slaughtered, then each carcass without feet was weighed (empty carcass weight). Carcass percent was calculated as the ratio of empty body weight relative to 4 wk BW. Breast and leg were separated and residual calculated as back.

Statistical Analysis. Comparison of means was done by SAS (SAS Institute 2000) software 9.2 and the following generalized linear model:

$$Y_{ijklm} = \mu + L_i + H_j + S_k + G_l + e_{ijklm}$$

Where: Y_{ijklm} was an individual observation for the trait Y, μ was the overall mean, L_i was the fixed effect of i$^{\text{th}}$ line, H_j was the j$^{\text{th}}$ hatch fixed effect, S_k was the k$^{\text{th}}$ sex fixed effect, G_l was the l$^{\text{th}}$ generation fixed effect and e_{ijklm} was residual random effect.

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Genetic analyses were carried out with the records of 1579 (from 151 males and 288 females) fully pedigreed quail. Initial models included the additive direct genetic effect, a maternal permanent environment effect, an additive maternal genetic effect, and a covariance between direct and maternal genetic effects. The significance of components was determined using a likelihood ratio test (P = 0.05) comparing models with and without the component. Permanent environmental variance was only significant for BW.

Results and discussion

Selection response and realized heritability for 4wk BW is presented in Table 1. Genetic improvement was 9.6, 8.8 and 8.2 g for generations 2, 3 and 4 respectively. Selection for 4 wk BW improved indirectly FCR 0.18 units over the selection period. The quails from the second hatch generally were heavier (P<0.01) but not different for other traits. There were a significant difference for all traits considered (except percentages for breast, leg and back) between the two lines (P<0.001). Sex was a source of difference between and within lines as females showed higher weights than males (P<0.001). Heritability and correlations between traits were estimated in bivariate analyses and the results are shown in Table 2. Inbreeding caused a decline for all traits (exception leg and back percent) but was only significant for 4 wk BW and carcass weight (P<0.05).

Table 1: Selection response for 4 wk BW, differential and realized heritability

Generation	Population mean		Selected mean	Selection differential	Response		Corrected response
	Selected	Control			Selected	Control	
0	164	164					
1	167.5	164.5	182	14.5			
2	180.4	167.8	196.7	16.3	12.9	3.3	9.6
3	193.2	171.8	210	17.2	12.8	4	8.8
4	200.5	170.9			7.3	-0.9	8.2
				Sum=48			Sum=26.6
			Realized heritability=26.6/48=0.55				

Table 2: Heritability (h^2) (on diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations of body weight and carcass weights.

Trait	4wk Body Weight	Carcass Weight	Breast Weight	Leg Weight	Back Weight
4wk Body Weight (g)	0.26±0.05	0.95±0.07	0.90±0.12	0.85±0.15	0.90±0.12
Carcass Weight (g)	0.86±0.02	0.22±0.07	0.88±0.1	0.90±0.1	0.89±0.16
Breast Weight(g)	0.73±0.06	0.43±0.05	0.32±0.03	0.73±0.1	0.70±0.07
Leg Weight(g)	0.69±0.03	0.71±0.08	0.37±0.7	0.14±0.03	0.66±0.1
Back Weight(g)	0.57±0.04	0.71±0.03	0.29±0.1	0.3±0.08	0.15±0.04

Results from this study showed that there is a genetic variation to respond to selection (Table 1). Total genetic improvement over the selection period was 26.6 g. This agrees with early responses from Nestor and Bacon (1982) reporting 7 generations of selection for 4 wk BW producing 6, 10, 11, 11, 19, 20 and 26 g BW increase per generation, respectively. Baylan *et al.* (2009) reported genetic improvement in 2nd generation of 15.1, 21.9 and 17.8 g in males, females and mixed sex, respectively. Syed Hussien *et al.* (1995) reported an increase of 44% (79 g) and 41.2% (73 g) in gain of 5 wk BW of males and females, respectively after 10 consecutive generations of selection this trait. It is clear that different responses to selection in these experiments depended on selection intensity and genetic variance in the population.

There is a wide range (109 -200 g) of 4 wk BW and carcass weights in the literature (Vali *et al.* (2005); Turkmut *at al.* (1999); Baylan *et al.* (2009); Shokoohmand *et al.* (2007); Minvielle *et al.* (2000)). These differences can be a feature of population genetic structure, diet and environmental conditions.

Mean of FCR for S and C lines in the first generation was 2.62 and 2.59 and in last generation, 2.44 and 2.57, respectively. Buyse *et al.* (1999) stated selection for low FCR result in indirect selection for leanness. Knizetova (1996) concluded live weight at 4 wk of age affected the relative growth rate and feed efficiency (weight gain/feed). Generally there is a favorable correlation between growth and FCR (Buyse *et al.* (1999); Leclercq *et al.* (1989)).

A wide range of heritability estimates for body weights has been reported in the literature. By analysis of pedigree data it was found to be 0.26 in the current study with a small standard error (0.05).

Falconer (1960) reported that heritability for a particular trait can take different values according to the population, the environmental condition surrounding the animal and the calculation method. Prado-Gonzalea *et al.* (2003) reported differences in heritability may be due to method of estimation, population genetic structure, environmental effects and sampling error from small data set or sample size.

Vali *et al.* (2005) reported the values 0.27, 0.26 and 0.28 of heritability for carcass weight, breast weight and leg weight, respectively. Although these values partially differ from those found in this study the genetic and phenotypic correlations agree with their estimates.

The results of the current study indicated that direct selection for 4 wk BW can be used as selection criteria to improve carcass related traits, but age at sexual maturity will increase indirectly.

In this study birds were selected on estimated breeding values (exception generation 1) but the heritability was estimated on pedigree data is less than realized heritability (0.55 from Table 2). The same situation have been reported by Collins et al. (1968) for two genetic groups of Japanese quail selected body weight in which values were 0.18 and 0.38 by progeny-sire regression and 0.34 and 0.68 as realized heritability. The mean of reliability for males and females in generation 4 were 0.313 and 0.314, respectively. This equals a correlation between true and estimated breeding values of 0.56, in agreement with the realized heritability. The assumption of phenotypic selection for estimation of realized heritability is not fulfilled in this study, and the estimate obtained rather reflects the realized accuracy of selection.

Conclusion

The results of the current study indicated that direct selection for 4 wk BW can be used as selection criteria to improve carcass related traits, but age at sexual maturity will increase indirectly.

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