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Comparison of Predicted with Actual Body Weight Selection Gains of *Coturnix coturnix japonica**

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Summary. Results of nine generations of individual selection for six-week large and small body weight of Japanese quail *(Coturnix coturnix japonica)* are reported. The objectives of this study were three-fold: 1) To estimate genetic variation of body weight of *Coturnix* quail at six weeks; 2) To predict selection gains when selecting on an individual basis for large and small body weight; and 3) To conduct a selection program for large and small females and males, respectively, with greater response in the positive direction. Generally the actual gain was predicted more accurately in the females than in the males.

Introduction

One of the purposes of quantitative genetics is the estimation of genetic, environmental and interaction variances of a population. With this information the plant and animal breeder can predict selection gains even with different selection systems.

Response to selection depends on the selection differential and the heritability of the trait in question. Differences between the computed expectation and the results actually achieved can arise because: 1) real populations are limited in number and, therefore, may show random deviations from expectations, and 2) biological factors not taken into account by the model, for example, maternal effects.

Results of selection experiments for traits with little or no relation to fitness were reported by Clayton et al. (1957) in an experiment with *Drosophila* that was designed to test the short- and long-term validity of quantitative genetic theory. Their results, as well as the results of other investigators indicate that predictions of selection response remain fairly valid as long as selection lasts only a few (twelve to twenty) generations. The agreement with prediction was best at high intensities of selection, the response at lower intensities being below expectation. Selection for large six-week body weight in Japanese quail has shown response patterns comparable to those found in chicken populations (Abplanalp, 1967).

Discussed below are results of nine generations of individual selection of *Coturnix* quail for large and small six-week body weight and the actual gains compared to the predicted gains.

Materials and Methods

The birds used in this study were obtained from a random-bred population of Japanese quail *(Coturnix coturnix japonica)* consisting of about 800 females with one male for every five females maintained at the Washington State University poultry center.

For the base generation six-week-old birds were weighed to the nearest gram and sixty random single-paired matings made. When the eggs were hatched on the 17th day the chicks were wing-banded according to mating. When they were six weeks old they were weighed to the nearest gram. The parental and progeny mean body weights were used to determine the covariances and regressions of dam-daughter, dam-son, sire-daughter and sire-son.

The control, large and small lines were formed from a total of 79 females and 90 males as follows: 20 females and 20 males were first chosen at random for the control line; from the rest of the birds the 20 largest females and 20 largest males were then designated as the large line, and 20 smallest females and 20 smallest males as the small line. Birds within each line were randomly singlepair mated in separate cages The offspring of these matings provided the first selected generation.

All subsequent selection (eight generations) was as follows: the heaviest 12 females and 12 males in the large line and the lightest 12 females and 12 males in the small line were selected for large and small body weight, respectively. A similar number of control females and males was randomly chosen from the control line. The number of progeny averaged about 42 individuals for each sex in a line except for the small

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Table 1. The means and phenotypic variances of body weight of quail from the base generation

Sex	Mean Body Weight (gm) ± S.E.*	Phenotypic Variance
Dams	132.59 ± 1.74	181.50
Sires	106.15 ± 1.05	66.07
Daughters	128.54 ± 1.05	86.56
Sons	102.09 ± 0.73	47.81

* S.E. = Standard Error

Table 2. The parent-offspring relationships of quail from the base generation

Relationship	D.F.*	Covariance	Regression Coefficient ± S.E.
Dam-daughter	38	7.26	0.04 ± 0.09
Dam-son	38	2.95	0.02 ± 0.07
Sire-daughter	42	37.60	0.56 ± 0.13
Sire-son	42	10.90	0.16 ± 0.09

* D.F. = Degrees of Freedom

females which averaged 33.4 individuals. Matings were made at random in each line with the restriction of non-mating of sibs. The theoretical (selection intensity determined from mathematical tables) and actual selection differentials were determined following selection of parents for the next generation; the weighted selection differential was adjusted according to the number of offspring weighted in each mating at six weeks of age.

After setting eggs for the seventh selected generation, all birds in the sixth generation were randomly single-pair mated within each line. There were 41, 38 and 32 matings in the large, control and small lines, respectively. The offspring of these matings were weighed to the nearest gram at six weeks and the covariances and regressions were compared to those obtained in the base generation.

The four different parent-offspring regression coefficients obtained in the base generation were employed to predict selection gains. These regressions were multiplied by the combined theoretical, actual and adjusted selection differentials to give the predicted gains. By keeping the sexes separate it was possible to calculate the dams' and sires' contributions to their daughters and sons.

With the sexes maintained separately, the predicted selection gain is given by the formulas:

$$\Delta G♀♀ = S_D \frac{\text{cov(DF)}}{\sigma^2 P(D)} + S_S \frac{\text{cov(SF)}}{\sigma^2 P(S)} \quad (1)$$

$$\Delta G♂♂ = S_D \frac{\text{cov(DM)}}{\sigma^2 P(D)} + S_S \frac{\text{cov(SM)}}{\sigma^2 P(S)} \quad (2)$$

where ΔG♀♀ and ΔG♂♂ are predicted gains in daughters and sons, respectively; S_D and S_S are selection differentials for dams and sires, respectively; cov is covariance: (DF) is dam-daughter; (DM) is dam-son; (SF) is sire-daughter; (SM) is sire-son; P(D) and P(S) are phenotypic variances of dams and sires, respectively.

Using this method, the numerator of the regression coefficient is the covariance of the future offspring and the tested material. When selecting on an individual's performance, the tested material is the individual and his (or her) future offspring are his immediate offspring. Therefore, the numerator of the regression coefficient is a covariance of relatives which, in the case of individual (or mass) selection is the parent-offspring covariance, estimating one-half of the additive and one-fourth of the additive times additive genetic variance. The denominator of the regression coefficient is the variance of the selection units, which are the individual dams and sires.

Egg production was recorded on 35, 50 and 39 females in the large, control and small lines, respectively during the ninth generation for 95 days to find out what effect, if any, selection had on this trait.

Results

The base generation parental and offspring body weight means and phenotypic variances are given in Table 1 while the parent-offspring covariances and regression coefficients are given in Table 2. The regression coefficients associated with the sires were larger than the regressions associated with the dams, indicating that maternal effects were not affecting these specific estimates. There were wide deviations of the sire-daughter (0.56 ± 0.13) and, to a lesser degree, the sire-son (0.16 ± 0.09) from the dam-daughter (0.04 ± 0.09) and the dam-son (0.02 ± 0.07) regression coefficients. The regression coefficients in Table 1 were used to predict selection gains during the nine generations of selection.

The combined selection differentials for the nine generations are presented in Table 3 by line and sex. Throughout the experiment, the three types of selection differential were used cumulatively to predict the respective selection gains.

The theoretical selection differentials were obtained by multiplying the phenotypic standard deviation times the selection intensity (Becker, 1975). One of the main assumptions of the theoretical selection differentials is that the population from which parents are selected is normal in distribution. If it is not, then the actual selection differential will differ from the theoretical selection differential.

The actual selection differential was the mean of the selected parents minus the population mean. The

Table 3. Combined selection differentials (g) for large and small body weights over nine generations by method of calculation

Method of Calculation	Large		Small	
	S_D	S_S	S_D	S_S
Theoretical	66.27	53.33	-58.18	-39.41
Actual	108.94	71.64	-74.63	-59.90
Adjusted	105.10	69.10	-59.59	-51.35

Note: S_D = Selection differential for dams.
S_S = Selection differentials for sires.

adjusted selection differentials reflected the infertility of males and lack of egg laying by females as well as the differential mortality of the offspring.

The theoretical differential was less than the actual differential, a possible indication of non-normality of the population distribution curve. There was a 3.84 gm and 2.54 gm difference between the combined actual and adjusted selection differentials for the large dams and sires, respectively. The corresponding differences for the small dams and sires were -15.04 gm and -8.55 gm, respectively. This would indicate that natural selection took the greatest toll in the small line. It is apparent, therefore, that natural selection was operating against artificial selection, especially against selection in the negative direction.

Figure 1 depicts selection response in the females as deviations from the control line. At the ninth generation of selection the large females had a total gain of 38.30 gm over the control females while the small females had lost a total of -21.92 gm, resulting in a 60.22 gm difference between the mean body weights of the large and small females. The actual gain in the large female's line rate of actual gain was much faster, averaging 7.95 gm per generation. The decrease in the small females' line averaged -2.44 gm per generation for the nine generations.

In general the predicted responses slightly overestimated the actual gains with two exceptions: the actual gain was underestimated at the second generation of small females and the seventh generation of large females.

Figure 2 shows the males' response to selection, also as deviations from the control line. The large males gained a total of 31.50 gm over the control males at the ninth generation, against -19.36 gm for the small males, a 50.86 gm difference between the mean body weights of the large and small males. Until the fourth generation the large males had actually gained only 4.89 gm. From the fourth to the ninth generation the rate of gain increased, averaging 5.32 gm per generation, against an average of 3.50 gm per generation for the nine generations.

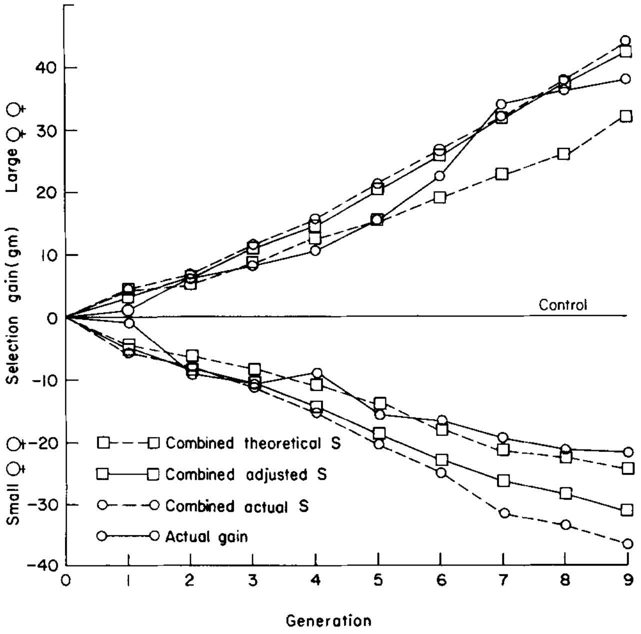

Fig. 1. Results of females selected for large and small body size expressed as deviation from control

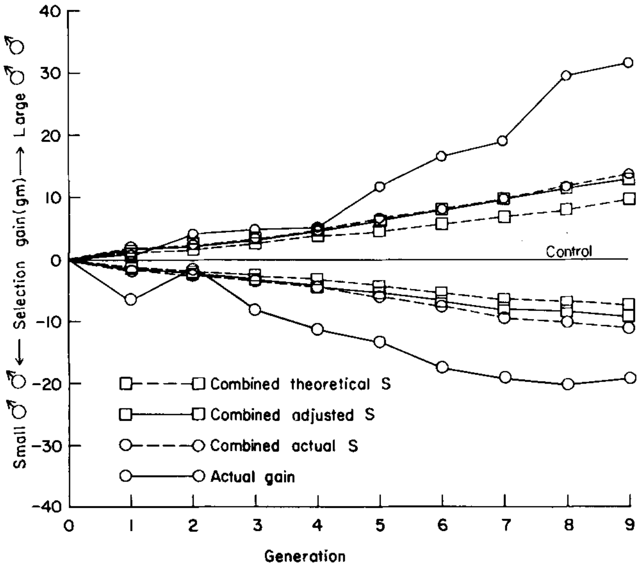

Fig. 2. Results of males selected for large and small body size expressed as deviation from control

Table 4. The parent-offspring relationships at the sixth generation of selection by line

Relationship	Large			Control			Small		
	D.F.	Cov.*	b ± S.E.**	D.F.	Cov.	b ± S.E.	D.F.	Cov.	b ± S.E.
Dam-daughter	40	-32.83	-0.23 ± 0.33	37	38.84	0.26 ± 0.28	31	9.62	0.11 ± 0.37
Dam-son	40	-18.48	-0.13 ± 0.25	37	6.43	0.04 ± 0.20	31	1.38	0.02 ± 0.18
Sire-daughter	40	30.62	0.51 ± 0.51	37	13.81	0.58 ± 0.74	31	-7.38	-0.21 ± 0.60
Sire-son	40	14.41	0.24 ± 0.38	37	8.07	0.34 ± 0.52	31	9.21	0.26 ± 0.39

* Cov. = Covariance

** b ± S.E. = Regression coefficient ± standard error.

The selection response in the small males was rather erratic. Initially the small males registered the greatest response of -6.67 gm, against 0.54 gm for the large males. In the second generation the actual response was -1.30 gm, with the total response -19.36 gm in the ninth generation. The unexpected actual gain in the second generation was the only one that came close to the predicted gain. The average actual response per generation was -2.15 gm. Generally the predicted selection gains were less than the actual gains except for the first generation of the large males and the second generation of the small males.

As to why the actual selection gains in the males were underestimated by the predicted gains is difficult to explain. This pattern of response might be attributed to sex-linked effects influencing six-week body weight in males although ordinarily one would not expect sex linkage to have such an important effect.

A greater asymmetry of selection response was observed in the females. As already mentioned, the predicted response to selection depends on the regression coefficient and the selection differential. Differentials differed between the positive and the negative directions (Table 3) with the former being larger than the latter.

An expanded population of all birds before selection provided the parent-offspring covariances and regression coefficients after six generations of selection as given in Table 4 by sex and line. Once again the sire-daughter and sire-son regression coefficients (except small sire-daughter) were considerably larger than the dam-daughter and dam-son regression coefficients. The dam-daughter and dam-son regressions were negative in the large line but positive and relatively small in the control and small lines.

The mean egg numbers in generation 9 and confidence intervals (95%) are given in Table 5. Egg production in the control females was intermediate between that in the large and small females, but was not significantly different from either one. There was a significant difference at the 5% level between the large and small females, with the mean egg production of the small females exceeding that of the large females by 18.0 eggs. This finding indicates that the correlated response, i.e. egg production, was negative for both the small and large body weight females.

Discussion

Collins and Abplanalp (1968) found evidence for the involvement of sexlinked genes and maternal effects in their study of changes in body and organ weights of Japanese quail selected for six-week body weight. They also observed that reproductive organs, especially in females, responded to selection for total body size.

Wilson et al. (1961) have reported that fully developed ovaries and shell glands in *Coturnix* quail account for about 25% of the total female body size. Therefore selection of females, of the type practiced in the present study, is likely to favor those with early sexual development (large females) and those with late sexual development (small females). In males selection would act primarily on carcass weight. Variability of six-week body weight is, therefore, in-

Table 5. Egg production over a 95-day period after nine generations of selection

	Large	Control	Small
Number of females	35	50	39
Mean ± S.E.	64.7 ± 4.6	78.2 ± 3.0	82.7 ± 2.2

fluenced by these factors. In a selection experiment for increased six-week body size of Japanese quail Collins et al. (1970) found that the selection response was considerably less than that published for other avian species. Low genetic correlation of body size of males and females was considered to be responsible for the relative impediment of selection response.

Sefton and Siegel (1974) obtained high heritabilities for males at six of age (51 to 72 %) and variable estimates for females (-21 to 148 %). This variability was attributed so sexual maturity. Some females were laying eggs and others were just approaching egg production.

Chahil and Johnson (1974) found heritabilities of 0.44 ± 0.31 and 0.24 ± 0.22 from daughter-dam and son-dam regressions, respectively.

In mammals, reports by Wilson et al. (1971) of their long term selection for body weight in mice showed that individual regressions of male and female offspring 60-day weight on sire 60-day weight were approximately equal, thus indicating that sex-linked genes were not a major factor determining 60-day body weight in the population of mice studied. In another study involving *Tribolium castanoum*, Wilson et al. (1966) found that regressions of pupa weight on dam pupa weight generally did not exceed those of offspring on sire, indicating that maternal effects were not an important influence on the trait studied.

The method for predicting selection gains used in this paper where the sexes were analyzed separately provides a more detailed analysis of selection gains than when the sexes are averaged, as is usually the case. However, separating the regressions subjects them to high sampling errors so that some of them are in disagreement with the observed response.

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