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

<table>
<thead>
<tr>
<th>Sex</th>
<th>Mean Body Weight (gm) ± S.E.</th>
<th>Phenotypic Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dams</td>
<td>132.59 ± 1.74</td>
<td>181.50</td>
</tr>
<tr>
<td>Sires</td>
<td>106.15 ± 1.05</td>
<td>66.07</td>
</tr>
<tr>
<td>Daughters</td>
<td>128.54 ± 1.05</td>
<td>86.56</td>
</tr>
<tr>
<td>Sons</td>
<td>102.09 ± 0.73</td>
<td>47.81</td>
</tr>
</tbody>
</table>

* S.E. = Standard Error

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

<table>
<thead>
<tr>
<th>Relationship</th>
<th>D.F.</th>
<th>Covariance</th>
<th>Regression Coefficient ± S.E.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dam-daughter</td>
<td>38</td>
<td>7.26</td>
<td>0.04 ± 0.09</td>
</tr>
<tr>
<td>Dam-son</td>
<td>38</td>
<td>2.95</td>
<td>0.02 ± 0.07</td>
</tr>
<tr>
<td>Sire-daughter</td>
<td>42</td>
<td>37.60</td>
<td>0.13 ± 0.09</td>
</tr>
<tr>
<td>Sire-son</td>
<td>42</td>
<td>10.90</td>
<td>0.16 ± 0.09</td>
</tr>
</tbody>
</table>

* 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:

\[
\Delta G_{DD} = S_D \frac{\text{cov}(DF)}{\sigma^2_D} + S_S \frac{\text{cov}(SF)}{\sigma^2_S}
\]

\[
\Delta G_{DS} = S_D \frac{\text{cov}(DM)}{\sigma^2_D} + S_S \frac{\text{cov}(SM)}{\sigma^2_S}
\]

where \(\Delta G_{DD}\) and \(\Delta G_{DS}\) are predicted gains in daughters and sons, respectively; \(S_D\) and \(S_S\) are selection differentials for dams and sires, respectively; \(\text{cov}\) is covariance: \((DF)\) is dam-daughter; \((DM)\) is dam-son; \((SF)\) is sire-daughter; \((SM)\) is sire-son; \(\sigma^2_D\) and \(\sigma^2_S\) are phenotypic variances of dams and sires, respectively.

Using this method, the numerator 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