SERUM ALBUMIN POLYMORPHISM IN QUAIL AND CHICKEN-QUAIL HYBRIDS

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SERUM albumin polymorphism has been reported in such animals as pigs (KRISTJANSSON 1963), horses (STORMONT and SUZUKI 1963), cattle (ASHTON 1964; ASHTON and LAMPKIN 1965), chickens (MCINDOE 1962) and turkeys (QUINTEROS, STEVENS, STORMONT and ASMUNDSON 1964). BECKMAN, CONTERIO and MAINARDI (1963) examined the serum protein patterns of avian species hybrids and found that in eight out of 11 interspecific crosses there was a difference between the parental species with respect to the major fast moving protein. In the hybrids, both parental protein components were present.

At this laboratory, similar differences of serum protein fractions have been observed in Japanese quail and in chicken-quail hybrids. SMITHIES (1955) has shown that the major protein component of human serum in starch gel electrophoresis is albumin. The corresponding major component in chickens was reported to be albumin by its solubility characteristics (MCINDOE 1962). By analogy the major protein component in other species has been designated as albumin (KRISTJANSSON 1963; STORMONT and SUZUKI 1963; QUINTEROS et al., 1964). Thus, from migration rate and quantitative considerations the corresponding major protein fractions in quail serum have also been designated as albumin.

This report describes the phenotypic differences observed in Japanese quail and in chicken-quail hybrids and attributes the differences to a genetically variable locus determining albumin fractions in quail.

MATERIALS AND METHODS

Females from three lines of Japanese quail (Coturnix coturnix japonica) are artificially inseminated with semen from chicken (Gallus domesticus) and those females showing the highest fertility are selected each generation to reproduce the quail lines. These three selected lines (909, 910 and 916) show higher fertility and produce more hybrids when mated with chickens than do the unselected control lines of quail (905, 903 and 916 respectively) from which they originated.

Separate blood samples drawn from the chickens, the quail and their hybrids were mixed with citrated saline (2% sodium citrate + 0.5 percent NaCl) in the ratio of 1 ml citrate to 2 ml of blood.

Horizontal starch gel electrophoresis was carried out using the method described by FEENEY, ABPLANALP, CLARY, EDWARDS and CLARK (1963). The gel buffer (pH 8.6) contained 0.076 M Tris, 0.005 M citric acid, and 2.0 M urea; the electrode buffer (pH 8.6), 0.3 M boric acid and 0.06 M NaOH. However, the procedure in the present study differed in that electrophoresis was
carried out at room temperature at 150 volts, 15 ma for the first half hour, at which time the sample filter papers were removed and the voltage set at 350. The runs were stopped when the borate boundary had migrated 10.5 cm from the point of insertion. Gels were stained in a solution of one percent Buffalo Black in water, methanol and acetic acid at a ratio of 50:50:10.

RESULTS AND DISCUSSION

Three albumin phenotypes Q, Q, and Q, Q, were observed in quail of both sexes as shown in Figure 1. Each of the phenotypes Q, Q, and Q, Q, is characterized by a single dark staining zone with Q, Q, migrating at a faster rate than Q, Q, and Q, Q, faster to Q, Q, and Q, Q, respectively. The phenotype Q, Q, has two zones, the slower of which corresponds to Q, Q, and the faster to Q, Q, and Q, Q. These observations suggest that the three phenotypes are controlled by a pair of codominant autosomal alleles, herein designated as Alb, and Alb.

Data on parents and offspring from pair matings of quail are presented in Table 1. Since this study was carried out in retrospect, no Q, Q, × Q, Q, matings
TABLE 1

Results of various crosses involving serum albumin alleles AlbQ1 and AlbQ2 in Japanese quail

<table>
<thead>
<tr>
<th>Mating type</th>
<th>No. of mated pairs</th>
<th>Offspring genotype</th>
<th>P of $\chi^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q1,Q1 x Q1,Q1</td>
<td>14</td>
<td>AlbQ1AlbQ1, AlbQ1AlbQ2, AlbQ1AlbQ2</td>
<td>...</td>
</tr>
<tr>
<td>Q1,Q1 x Q1,Q2</td>
<td>6</td>
<td>49</td>
<td>0</td>
</tr>
<tr>
<td>Q1,Q1 x Q1,Q2</td>
<td>6</td>
<td>21</td>
<td>24</td>
</tr>
<tr>
<td>Q1,Q2 x Q1,Q2</td>
<td>3</td>
<td>0</td>
<td>26</td>
</tr>
<tr>
<td>Q1,Q2 x Q1,Q2</td>
<td>4</td>
<td>8</td>
<td>15</td>
</tr>
</tbody>
</table>

TABLE 2

Gene frequency of AlbQ1 and AlbQ2 in three Japanese quail populations

<table>
<thead>
<tr>
<th>Line</th>
<th>Line of origin</th>
<th>Genotype frequency</th>
<th>Gene frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>909</td>
<td>905</td>
<td>17 / 57 / 18</td>
<td>.49 / .51</td>
</tr>
<tr>
<td>910</td>
<td>903</td>
<td>21 / 22</td>
<td>.74 / .26</td>
</tr>
<tr>
<td>916</td>
<td>908</td>
<td>40 / ...</td>
<td>1.00 / .00</td>
</tr>
</tbody>
</table>

were available among those made to reproduce the lines, but observed matings are consistent with the hypothesis of two codominant alleles at one autosomal locus.

The above results were obtained from pooled data of the three lines 909, 910 and 916. Genotype frequencies of separate lines are given in Table 2. The Q2 allele is predominant in line 909 which originated from control line 905. The presence of the Q2 allele in line 910 has been traced in retrospect to two 909 birds introduced into line 910. One such mating occurred in generation 4 and one in generation 7. Up to this time no Q1Q2 x Q1Q2 matings have been made in line 910 which explains the lack of Q2Q2 individuals. Line 916 apparently lacks the Q2 gene.

The phenotypes observed in chicken-quail hybrids are shown in Figure 2. To attain greater separation of zones for illustrative purposes the borate buffer front in this gel was allowed to migrate 12.5 cm rather than the standard 10.5 cm for all other gels. The chicken male parent possesses a serum albumin fraction (C,C1) which migrates faster than either of the two quail serum albumins described. Figure 2 shows the results of a cross of a chicken (C,C1) with a heterozygous female quail Q1,Q2. One hybrid has the genotype Alb67, Alb61, while the other has Alb61, Alb62. This result agrees with the genetic hypothesis concerning the Alb locus in that the hybrid receives one allele (C1) from the chicken and either allele Q1 or Q2 from the quail.

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SUMMARY

By means of starch gel electrophoresis three serum albumin phenotypes designated \(Q_1Q_1\), \(Q_1Q_2\) and \(Q_2Q_2\) have been demonstrated in quail. From family data it is concluded that these are controlled by two codominant autosomal alleles \(Alb^q\) and \(Alb^r\). Allele \(Q_1\) was present in all quail populations studied while allele \(Q_2\) originated from one control line. All chickens studied showed only one serum albumin phenotype \((C,C)\) which migrated at a faster rate than did either quail phenotype. Hybrids derived from crossing chicken and quail always show two serum albumin zones, one acquired from the chicken and one from the quail. Thus, hybrids were found to be of either genotype \(Alb^q; Alb^r\), or \(Alb^q; Alb^r\).

LITERATURE CITED