Full-Sib and Half-Sib Estimates of Genetic Variance in an Open-Pollinated Variety of Corn, Zea mays L.

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THE ability to predict the effects of alternative procedures on rate of progress and potential improvement is a key factor in choosing plant breeding methods. Reliable prediction depends on the relative magnitudes of various gene effects and of genotype and environment interactions. For quantitative characters statistical procedures are frequently used for measuring the mass action of genes. The utility of the statistics in providing basic information about the nature of the inheritance of the characters is based on the genetic expectations of the statistics for specified models.

Sprague (11) and Comstock (1) discussed some of the problems in utilizing genetic variability and in applying statistical models. Sprague pointed out that the lack of basic information on the various genetic parameters, the uncertainty of the current interpretation of some information available, and the difficulties of applying models to the real biological situation have meant that plant breeding is largely empirical. A considerable number of estimates of some of the genetic parameters for corn have been reported. The diversity of the approaches used and of the populations studied has been such that critical comparisons of the methods used and results obtained is not yet adequate for acceptable generalization.

An extensive mathematical methodology concerned with the inheritance of quantitative characters has been derived (6). Estimates of the genetic variances and their relation to selection potential and to type of gene action in open-pollinated varieties have been reported (9, 10). These authors used a model which utilizes full-sib and half-sib families as proposed by Comstock and Robinson (2, 3). Kempthorne (6, p. 426) suggested an extension of the model which would provide a series of estimates from a group of family relationships.

The purpose of the present study was to estimate from an analysis of full-sib and half-sib progenies of some of the genetic parameters descriptive of the inheritance of quantitative characters within the open-pollinated variety of corn, 'Reid Yellow Dent'. The study is the initial stage of a program in which the plan proposed by Kempthorne is to be applied to one Corn Belt open-pollinated variety of corn for the estimation of various genetic parameters. Eventually, the program should lead not only to a relatively complete genetic analysis of quantitative characters in a random-mating population but also to a critical evaluation of the techniques and models used.

MATERIALS AND METHODS

Ames, Iowa. As a result, 192 full-sib progenies of pairs of half-sib progenies were obtained and designed. At the same time each of the male plants was selfed to obtain fully pollinated ears of the male plants, which were pollinated after two days with pollen from a strain heterozygous for the dominant genetic factor for purple. Three days later these same ears were exposed to open-pollination for purple provided a genetic mechanism by which the middle and basal portions of the ear resulting from cross pollination could be separated from the remainder, resulting in a partial self-pollination. Only two pollinations were required to set a fully developed ear from which physical measurements could be obtained. The male plants were artificially dried, and yield of ear length, ear diameter, number of kernel rows, and weight per 100 kernels was determined. The self-pollinated ears retained for further use. An additional group of ears was analogous in construction to that of Sample I and was designated Sample II.

The 192 progenies of Sample I were grown in complete block designs with 4 replications at Ankeny and 1959. Plots were single rows 40 inches apart containing 13 ears separated from each plot and dried in a forced-air dryer to a grain moisture content of 18%. The grain data were for moisture content were measured in the data. Weight of 100 kernels was obtained for each plant. A few samples for moisture content were made in the data. Weight of shelled grain (yield), ear length, ear diameter, weight per 100 kernels and number of kernel rows were obtained for each plant. The average of 2 ears, both of which were included in the data were the topmost ears.

The 192 progenies of Sample II were grown at Ankeny. The procedures were the same as for Sample I except in some cases on weight per 100 kernels were obtained on 2 ears. The procedures were the same as for Sample I except in some cases the procedures were the same as for Sample I except in some cases on weight per 100 kernels were obtained on 2 ears.

Statistical methods. An analysis of variance was used to estimate the components of variance for each character. The form of the analysis of variance for 192 families for 1 year is shown in Table 1. The experiments were balanced with 5 plants per plot. Variance components from linear functions of the mean squares were:

- \( \hat{\sigma}_{w}^2 = M_i; \)
- \( \hat{\sigma}_{e}^2 = (M_i - M) / 5; \)
- \( \hat{\sigma}_{e}^2 = (M_i - M) / 40. \)

The analysis of Table 1 was extended in the following manner to obtain combined estimates of the components of variance for each character. The open-pollinated variety was considered to be a random-mating population. For each plot to 30,000 plants of the variety were grown and the populations simulating isolation. Seed stocks were a large number of randomly chosen open-pollinated parental plants used in making crosses for this study. It was considered to be non-inbred random members of the population. The assumptions were (1) regular diploid behavior, (2) no linkage or equilibrium phases, (3) no selection of individual traits, and (5) no epistasis.

For the breeding plan design used, the following assumptions are valid:

- \( \hat{\sigma}_{w} = \text{Cov}(\hat{H}, \hat{E}) \)
- \( \hat{\sigma}_{e} = \text{Cov}(\hat{H}, \hat{E}) \)
- \( \hat{\sigma}_{e} = \text{Cov}(\hat{H}, \hat{E}) \)
- \( \hat{\sigma}_{e} = \text{Cov}(\hat{H}, \hat{E}) \)
- \( \hat{\sigma}_{e} = \text{Cov}(\hat{H}, \hat{E}) \)

Table 1. Estimates of the components of variance for the 192 open-pollinated families

<table>
<thead>
<tr>
<th>Character</th>
<th>( \hat{\sigma}_{w}^2 )</th>
<th>( \hat{\sigma}_{e}^2 )</th>
<th>( \hat{\sigma}_{e}^2 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ear length</td>
<td>5.67</td>
<td>0.07</td>
<td>0.02</td>
</tr>
<tr>
<td>Ear diameter</td>
<td>5.67</td>
<td>0.07</td>
<td>0.02</td>
</tr>
<tr>
<td>Number of kernel rows</td>
<td>5.67</td>
<td>0.07</td>
<td>0.02</td>
</tr>
<tr>
<td>Weight per 100 kernels</td>
<td>5.67</td>
<td>0.07</td>
<td>0.02</td>
</tr>
</tbody>
</table>

The diversity of the approaches used and of the populations studied has been such that critical comparisons of the methods used and results obtained is not yet adequate for acceptable generalization.