Genetic Variability in Two Open-Pollinated Varieties of Corn (Zea mays L.) and Their F₁ Progenies

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Although the "dominance of favorable genes" hypothesis proposed by Bruce (1) may not provide a complete explanation of heterosis, additive gene action with partial to complete dominance is adequate to explain most of the results found in the literature on corn. Robinson et al. (6) examined genetic variances among full-sib and half-sib families within two varieties and in crosses between them. Their results were consistent with the above hypothesis. The genetic variances in the varieties and their intercrosses were obtained with different samples of males and in different years. The authors recognized the hazards of comparing genetic variances made under different environmental conditions, but considered the consistency of the estimates to lend credence to their value.

As a consequence of an experiment involving a diallel cross of open-pollinated varieties reported by Lonnquist, two varieties, 'Golden Republic' and 'Barber Reid', were chosen to initiate a reciprocal recurrent selection program. In initiating such a program an experiment was designed which would not only provide a basis for the selection of plants in the first cycle but which would also yield valuable information on heterosis and the nature of gene action involved in quantitative inheritance.

The purpose of this paper is to report on the genetic variances observed among full-sib and half-sib families within varieties and in inter-variety crosses. Theoretical relationships of the kind considered by Robinson et al. (6) are also considered in this paper but without the restrictions which the nature of their experiment imposed.

MATERIALS AND METHODS

Individual plants from each of the 2 varieties were selfed and at the same time crossed to 6 female (seed) plants, 3 randomly chosen from the same variety and 3 from the other variety. A male group thus consisted of 3 half-sib intra-variety families and three half-sib inter-variety families. Four male groups with the 6 full-sib families per male were then assigned at random to each block for field testing. The block consisted of 2 replications with 24 entries (families). A total of 160 Barber Reid and 120 Golden Republic males were progeny tested in this way on both an inter- and intra-variety basis. There were a total of 40 blocks with Barber Reid males and 30 blocks with Golden Republic males. The material was grown in the Agronomy Farm, Lincoln, Nebr., in 1961 and 1962. There were a total of 3840 plots involving Barber Reid males and 2888 with Golden Republic males, or a grand total of 6728 plots.

Data were taken in both years on the 3 characters grain yield (pounds/plant), ear number per plant, and lodging score (a score of 0 to 5, with 0 scored when most of the plants were erect and 5 if virtually all were rootlodged). Two other characters, number of days from planting until approximately 50% of the plants in a plot were shedding pollen. Considerable early root topping was observed in 1962 preventing data being taken on this character in that year. Except for lodging score and analyses were of mean plot values computed on a sample taken from each plot at harvest. Individual yields, were taken on 1 random plot from both the intra-variety families and 1 plot from every 2 blocks of the inter-variety families.

The data for each type of cross in each block were analyzed separately and the results were pooled to form the analysis of variance of the form shown in Table 1 (characters ear height and days-to-flower, in which no type interactions could not be estimated).

The procedure for estimation of variance components (Design I) has been reported by Robinson (4) and simply involves equating observed mean squares to the expected expectations and solving the set of equations algebraically.

The difference between this experiment and the usual Design I experiment is that, for the Inter-varietal progenies, the males were from one variety and the females from the other. The male variance in this case is a measure of genetic differences among male genotypes but with the other variety used as the tester. It cannot be equated to ¼ σ² and does not relate to any definable population. The intra-variety portion is identical to the usual Design I, with three tester-females for each male.

Cockerham (2) presented the genetic expectations for the Design I experiment in terms of covariances among full-sibs, respectively. Then

\[ S.E. = \frac{1}{c} \sqrt{\frac{2\Sigma M_i}{(f_i + 2)}} \]

where: \( M_i = \) the i-th mean square in the function by which the component is estimated

\( f_i = \) the degrees of freedom for the i-th mean square

\( c = \) the divisor of the mean square function

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\[ \sigma^2_m = \text{Cov HS}, \quad \text{and} \quad \sigma^2_r = \text{Cov FS} - \text{Cov HS}. \]

Table 1. Form of the analysis of variance used to determine genetic variances of yield and other data and estimate the essential environmental components of variance obtained from full-sib and half-sib families of corn tested in 2 years.

| Source of variation | d.f. | m.s. | Expectations of means
<table>
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<tr>
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<tbody>
<tr>
<td>Years (Y) M/B</td>
<td>(y - 1)</td>
<td></td>
<td>( M_Y \sigma^2 + r(\sigma^2_Y + \sigma^2_B) + r(\sigma^2_Y + \sigma^2_B) )</td>
</tr>
<tr>
<td>Blocks (B)Y</td>
<td>(y - 1)</td>
<td></td>
<td>( M_B \sigma^2 + r(\sigma^2_Y + \sigma^2_B) + r(\sigma^2_Y + \sigma^2_B) )</td>
</tr>
<tr>
<td>Males (M/B)</td>
<td>(y - 1)</td>
<td></td>
<td>( M_M \sigma^2 + r(\sigma^2_Y + \sigma^2_B) + r(\sigma^2_Y + \sigma^2_B) )</td>
</tr>
<tr>
<td>Females (F)/M/B</td>
<td>(b - 1)</td>
<td></td>
<td>( M_F \sigma^2 + r(\sigma^2_Y + \sigma^2_B) + r(\sigma^2_Y + \sigma^2_B) )</td>
</tr>
<tr>
<td>Years × M/B</td>
<td>(y - 1)(y - 1)</td>
<td></td>
<td>( M_Y M_B \sigma^2 + r(\sigma^2_Y + \sigma^2_B) + r(\sigma^2_Y + \sigma^2_B) )</td>
</tr>
<tr>
<td>Years × F/M/B</td>
<td>(b - 1)(b - 1)</td>
<td></td>
<td>( M_Y F_B \sigma^2 + r(\sigma^2_Y + \sigma^2_B) + r(\sigma^2_Y + \sigma^2_B) )</td>
</tr>
<tr>
<td>Pooled Error</td>
<td>(b - 1)(y - 1)</td>
<td></td>
<td>( M_P \sigma^2 + r(\sigma^2_Y + \sigma^2_B) + r(\sigma^2_Y + \sigma^2_B) )</td>
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