Types of Gene Action in Yield Heterosis in Maize

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THE relative importance of the role of overdominance and the accumulation of favorable dominant genes at numerous loci as possible explanations of heterosis has been a major topic of discussion among plant and animal breeders and geneticists for many years. Most of the discussions have revolved around theoretical considerations. Few data that could be used for a critical evaluation of the importance of the postulated types of gene action have been accumulated.

Robinson et al. (4) and Gardner et al. (2) obtained estimates of the degree of dominance for yield genes in the overdominance range in F2 populations derived from single crosses among inbred lines. In both reports (2, 4) the authors recognized and discussed the possibility that such estimates of overdominance could be obtained as the result of repulsion phase linkages even though none of the genes involved had more than partial dominance. Gardner and Lonququist (3) obtained an estimate of the degree of dominance in the overdominance range for genes affecting yield in a study with the F2 generation of a cross between two lines. However, when the F2 generation of the same cross was used, an estimate in the partial dominance range was obtained. These results tended to substantiate the possibility that linkage may have been responsible for earlier estimates in the overdominance range in studies involving the F2 generation from single crosses of inbred lines. Robinson et al. (5) studied the relative magnitudes of estimates of additive genetic variance and dominance variance for yield obtained from three open-pollinated varieties. The estimates of additive genetic variance were considerably in excess of the estimates of dominance variance. The authors concluded that either all genes involved were partially to completely dominant or there was a mixture of genes some of which were partially dominant and the others were in the overdominance range.

Sprague and Miller (6) proposed a method for obtaining information on the relative importance of dominance and overdominance in yield heterosis. The proposed method employs the procedure of recurrent selection for specific combining ability outlined by Hull (1). A recurrent selection program is conducted with two populations, A and B, with the same homozygous inbred line being used as tester for both populations. Insofar as selection relative to this tester is effective in changing gene frequencies in the two populations, the two populations would be expected to become more alike genetically. Information on the relative importance of dominance and overdominance in yield heterosis is obtainable from a comparison of the cross between the two original populations with crosses between the derived populations from comparable cycles of selection. Since the two populations undergoing selection are assumed to become more alike genetically as selection progresses, the inter-crosses, $A_1 \times B_1$, $A_2 \times B_2$, $A_3 \times B_3$, etc., should exhibit a decreasing degree of heterozygosity. If overdominance is of major importance, these crosses should exhibit a decreasing yield trend. However, if selection has resulted primarily in the accumulation of favorable dominant or partially dominant genes at numerous loci, the population crosses should exhibit an increasing yield trend.

Two selection programs of the type proposed by Sprague and Miller (6) are being conducted in Iowa with maize. Progress from one of these programs was reported by Sprague and Russell (7) and Sprague et al. (8). A combination of partial and complete dominance provided the best explanation of the yield trends obtained. Data obtained at the conclusion of two cycles of recurrent selection in the second program are the subject of the present report.

MATERIALS AND METHODS

Two heterogeneous and heterogeneous populations of maize were used as source material for a recurrent selection program. One of the populations was a highly variable open-pollinated strain designated as Alph. The other base population consisted of the F2 generation of the cross WF9 x B7. The homozygous inbred line B14 was used as tester parent of the test crosses in each cycle of selection in both selection sources.

Individual plants from the original populations, herein designated Alph C0 and (WF9 x B7) C0, were self-pollinated and also crossed to the tester. Both sets of test crosses were grown at the same location in 1950. The Alph and (WF9 x B7) C0 experiments contained 79 and 53 test crosses, respectively. S1 progenies of the 10 selections from Alph C0 having the highest test-cross yields were intercrossed in all possible combinations in 1951. These 45 crosses grown in 1953 in individual rows constituted a new derived population for a second cycle of selection for high yield. This new derived population was designated Alph C1 High. In addition, a composite sample consisting of equal numbers of kernels from each of the 45 intercrosses was planted; the plants were interpollinated at random; and a bulk sample of the sync 1 generation seed was put into cold storage for future reference and experimentation. S1 progenies of the 10 selections from Alph C0 having the lowest test-cross yields in the 1950 testcross yield trials were intercrossed in all possible combinations to provide a new derived population for a second cycle of selection for low yield. This population was designated Alph C1 Low. In like manner new derived populations were developed from the WF9 x B7 selection source and were designated (WF9 x B7) C2 High and (WF9 x B7) C2 Low. The sync 1 generation of each of these populations was produced and put into storage for later use.

Test crosses of individual plants from each of the 4 C1 populations were grown in separate yield trials at 2 locations in 1951. The Alph C1 High, Alph C1 Low, (WF9 x B7) C2 High, and (WF9 x B7) C2 Low experiments contained 97, 91, 78, and 57 test crosses, respectively. Data obtained from these trials were used as the basis for choosing a group of selections from each of the 2 high-yield populations whose test crosses were highest in yield and a group of selections from each of the 2 low-yield populations whose test crosses were lowest in yield. Only six selections were included in the group chosen from each of the high-yield populations and the group chosen from each of the low-yield populations. The S1 progenies of these four sets of selections were used to produce new derived populations designated Alph C0 High, Alph C0 Low, (WF9 x B7) C1 High, and (WF9 x B7) C1 Low. The sync 1 generation of each of the C0 populations was produced in the same manner as described for the C1 populations.

An estimate of the expected genetic advance was obtained from the test cross trials of each population in each cycle of selection. The estimate was calculated as follows:

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