Hybrid Expression of Mutations Affecting Quantitative Characters in Inbred Lines of Zea mays L.

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The current production of corn, Zea mays L., in the United States is based primarily upon the use of hybrids. Inbred lines are used in the production of these hybrids because of the known and repeatable characteristics of these lines. The methods of maintaining inbred lines varies among breeders, but, generally, some form of selfing or sibbing is used. Mutations affecting quantitative and qualitative characters do occur while maintaining inbred lines, but probably only the easily recognizable mutations are observed. Mutations having small effects on quantitative characters are more difficult to recognize unless replicated measurements are taken.

Sprague et al. (3) used 11 doubled monoploid lines of corn to study the rate of mutation affecting quantitatively inherited characters. An estimated rate of 4.5 mutations per attribute per 100 gametes tested, with possible pleiotropism considered, suggested a mutation rate much higher than the commonly accepted figure, $1 \times 10^{-5}$. The suggestion was made that monoploidy may have been a causal factor for this high mutation rate. These original doubled monoploid parents and one or more of their divergent sublines were crossed with the inbred testers, WF9 and B14, to determine if yield changes had occurred in hybrid combination. The number of significant differences observed was no greater than expected on the basis of sampling.

Russell et al. (4) studied six long-time inbred lines of corn to estimate mutation rates for comparison with the doubled monoploids. These inbred lines had been maintained on an ear-to-row basis under continuous selfing and selection before the initiation of the study. The number of quantitative mutations varied among the inbreds, but an over-all rate of 2.8 mutations per attribute per 100 gametes tested was calculated.

The objective of the study reported here was to test sublines of two inbreds to determine the extent to which changes of expression among sublines of an inbred could be detected in hybrid combinations with unrelated testers. The inbreds selected were two lines reported by Russell et al. (4) to have shown at least one change for every character measured. This would serve as a verification of the changes found in the inbred lines, although some of the mutations may not be expressed in hybrids because of the masking effects of the testers.

MATERIALS AND METHODS

The two inbred lines selected for this investigation were Os420 and M14, which had shown at least one change for each character in the inbred study (4). Each inbred family consisted of 31 sublines representing 5 successive generations. The dichotomous scheme for development of these lines has been described by Russell et al. (4).

Inbred lines, B14 and B46, were used as unrelated testers. Each inbred tester was crossed to each subline of Os420 and M14. When the sublines were utilized as females, a minimum of 5 plants per cross was used, and a minimum of 3 plants was crossed when the testers were used as females. The inbreds used as testers were only one year removed from ear-to-row maintenance, and it is believed that adequate sampling was accomplished.

Testcrosses of M14 and Os420 sublines were grown in 2 different experiments on the Iowa State University Agronomy Field in 1962. A split-plot field design was used for each experiment, with the split being on testers. Ten replications of each experiment were planted, and each entry was represented by a single-plot row of 10 plants. A purple marker hybrid was planted in the alleyways between ranges to provide competition to the end plants of the rows. Also, spaces in the row because of nonviable seed or loss of plants in the seedling stage were platted to the purple marker hybrid to provide equal competition for all plants.

The characters were the same as those used in the inbred study (4), and the methods of measurement were similar with the exception of ear diameter and ear length. The ears from one plot were placed together for one measurement rather than taking individual ear measurements. Leaf width, plant height, ear diameter, and ear length were measured in centimeters; 100-kernel weight and grain yields were measured in grams.

An analysis of variance was calculated on the plot means for each character. t-tests were performed on all analyses by using error "b" as an estimate of $\sigma^2$, to test sublines and sublines X testers interactions. A set of orthogonal comparisons was utilized to determine subline differences within generations. If the interaction was significant at the 5% level, the sublines were partitioned on an individual tester basis, retaining error "b" or the combined analysis as the best estimate of $\sigma^2$. The significant sublines X testers interactions were not partitioned orthogonally because the causes of this type of interaction could be determined from the separate tester comparisons, and the tests of significance would be of little value in the interpretation of the results.

Five generations of sublines are represented in this study. The set of orthogonal comparisons was developed to allow the partitioning of subline testcrosses within each generation, except generation one, but not parent-progeny comparisons. Since this set of orthogonal comparisons differed from the analysis used by Russell et al. (4), the recalculation of the inbred data also was necessary.

At the 5% level, many significant comparisons could arise due to chance. Two criteria were necessary before a significant comparison was called a biological change in the hybrid: (1) the hybrid and the inbred sublines for the same comparisons were significant at the 5% level, (2) the means, plotted on dichotomous diagrams for the testcrosses and inbred, showed corresponding changes in the same sublines.

EXPERIMENTAL RESULTS

Significant differences between testers were detected for most attributes, but the interest was not in tester effects. The main interest was in differences among testcrosses of the sublines and tester X subline interactions.

The $F$ tests of the subplot mean squares, sublines, indicated 7 of the 9 attributes in each study had significantly greater than random variation. Russell et al. (4) when studying the same sublines as inbreds for the same characters, obtained significant differences among sublines for all nine characters.

Characters which showed significance among sublines for M14 were date silked, leaf width, plant height, tassel branch number, kernel row number, ear: length, and 100 kernel weight. Significant interactions were detected in three plant characters, date silked, leaf width, and plant height. All characters of Os420 sublines were significant except for date silked and grain yield. Interactions were significant for date silked, grain yield, leaf width, plant height, and tassel branch number.

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