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Comparison of Two Breeding Methods in Corn. IV. Correlation of Inbred Lines (S_2 Parents) and Testcross Performance¹ /

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ABSTRACT

The experiment reported in this paper was initiated to obtain information on the relative value of inbred line selection and selection based on testcross performance. To evaluate both methods, fourth cycle inbred lines (S_2 parents) and their testcrosses were tested in one and two locations, respectively, over one year. There was a significant positive correlation between the two evaluation methods for all traits studied, except ears per plant in population B. These results suggest that visual selection among lines in one environment may be effective for the elimination of undesirable traits in hybrids, especially for stalk strength, ear height and husk score.

INTRODUCTION

With the advent of single-cross corn hybrids, breeders have become interested in increasing the yield of parental line *per se* and the hybrids developed using these inbred lines.

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COMPENDIO

El experimento reportado en este artículo fue iniciado para obtener respuesta sobre el valor relativo de selección de líneas *per se* y selección basada en los cruces de prueba. Para evaluar ambos métodos, líneas puras obtenidas del cuarto ciclo y sus respectivos híbridos fueron probados en una y dos localidades, respectivamente durante un año. Hubo una correlación significativa entre los dos métodos de evaluación para todos los tratamientos estudiados, a excepción de número de mazorcas por planta en la Población B. Esos resultados sugieren que selección visual entre líneas *per se* en un ambiente puede ser efectivo para la eliminación de características indeseables en los híbridos, especialmente para resistencia de tallo al acame, altura de mazorca y extensión de la tusa.

The first evaluation of S_1 and S_2 line selection was made by Davis (2) in which lines were selfed for two generations, then crossed with an unrelated open-pollinated variety tester. Davis found that the average yield of S_1 and S_2 lines was more reliable than that of testcrosses for selection.

Genter and Alexander (4) made comparative performance tests between S_1 lines selected on the basis of S_1 progeny yield and S_1 lines selected on the basis of testcross performance with single-cross testers. They reported more dispersed means (larger variance) and fewer environmental effects from S_1 progenies than from testcrosses. After two cycles of selection, Genter and Alexander (5) found that

inbred lines obtained from S_1 progeny population showed a yield increase of 31.4%. However, only a 17.9% yield increase was obtained using the testcross method with the parental population as the tester. The more productive S_1 lines tend to produce the more productive crosses, but the correlation between S_1 line and testcross yield decreased from 0.61% to 0.15% from the first to the second cycle of selection. Koble and Rinke (6) compared random S_1 progenies and testcrosses with related and unrelated population testers. They concluded that the S_1 selection method could replace the testcross selection method. Lonnquist and Castro (7) and Lonnquist and Lindsey (8) reported that the S_1 progeny method seems to be a more logical procedure in the preliminary selection of desirable parents than the testcross method with related and unrelated testers.

Clucas (1) evaluated 400 S_2 lines and their respective testcrosses in three environments in Iowa. He found that the mean grain yield and stand percentage of the visually selected lines were 169 kg/ha and 2.58% greater, respectively, than those of the randomly selected lines. No significant differences were observed between means of testcross progenies of visually and randomly selected lines. Correlations between S_1 lines traits and the same traits in testcrosses were 0.19, 0.59, 0.51, 0.48, and 0.29 for grain yield, grain moisture content, stalk lodging, root lodging, and vertical root-pull resistance, respectively. He concluded that selection for superior testcross performance based on S_2 performance *per se* is not practical.

MATERIALS AND METHODS

S_2 lines for the S_2 progeny method were obtained by saving only one selfed ear from each parental S_1 line. Two-hundred-seventy-eight inbred lines from populations A and B were grown in two replications at one location near Gainesville, Florida, in 1984. Row-to-row spacing was 91 cm and plant-to-plant distance in the row was 30.5 cm. About 15 plants per plot were maintained. Standard agronomic practices were used, including irrigation and insect control when needed. During the growing period stalk quality, ear height, husk score, and ears per plant were recorded for each line. Stalk quality and husk score were determined on a scale from one (best) to nine (worst). Ear height was measured from the ground to the node of attachment of the highest ear. The plots were hand harvested, and the lines were evaluated for ear quality on a scale from one to five.

In a parallel test, the same S_2 lines were evaluated for performance of their testcrosses using inbred testers. An S_3 line from population A was used as a

tester to evaluate lines from population B, and vice-versa. These testcrosses were evaluated at two locations near Gainesville, Florida, in 1984. About 25 plants were maintained per plot. A randomized complete block design (RCBD) with five replications at each location was used to evaluate testcross performance. A plot combine was used for harvest.

Correlations were calculated using entry means over two environments for the testcrosses and means from one environment for the S_2 lines. Simple correlation coefficients of the means for five traits observed were calculated to determine the relationship between S_2 parents and testcross traits.

Table 1. Simple correlation coefficients between S_2 lines and testcross performance for five traits in 1984.

Trait	Population	
	A	B
Stalk quality	0.36**	0.51**
Ear height	0.57**	0.42**
Husk score	0.58**	0.62**
Ear quality	0.20**	0.17**
Ears per plant	0.30**	0.10ns

** Significantly larger than zero at the 0.01 level (276 df)
ns = not significant

RESULTS AND DISCUSSION

Simple correlation coefficients for five traits observed in the screening tests are given in Table 1.

Inbred line and testcross performances were positively correlated for all traits studied, except ears per plant in population B. Even though the two methods were positively correlated, however, the R^2 values were small. The highest R^2 was equal to 0.38 for the correlation of husk score in S_2 lines and testcrosses in population B. The simple correlation between S_2 and testcross ear height was significantly larger for population A ($r = 0.57$) than population B ($r = 0.42$). Conversely, for stalk quality in population B, the correlation between S_2 lines and their testcrosses ($r = 0.51$) was significantly greater than that of population A ($r = 0.36$). Correlations between S_2 and testcross husk score entry means were the largest of any calculated ($r = 0.58$ and $r = 0.62$) for populations A and B, respectively. However, for ear quality, and particularly for ears per plant, correlations of performance between S_2 lines and testcrosses seemed of little value. These results, which are similar to those reported by Clucas (1), indicate that visual selection among lines in one environment may be effective for the elimination of undesirable traits in hybrids,

especially for stalk strength, ear height and husk score. However, these results are in disagreement with those of Gama *et al.* (3), who found very low correlations for plant and ear traits between S_7 lines from BSSS and their single cross hybrids. Perhaps such highly homozygous lines (S_7) are more subject to genotype by environment interaction than S_1 or S_2 lines.

The response of selection for number of ears per plant in population B was not as good as expected.

This population was noticeably poorer in appearance of S_1 and S_2 lines than population A. More visual selection among lines of good agronomic type has been carried out in population B than in population A during the inbreeding and preparation of hybrid phases. This selection may have produced a shift in gene frequencies of loci favorable for ear number in the negative direction. Another possible explanation is that inbred tester A may have carried dominant genes which masked the genotypes of B lines.

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