

EVALUATION OF FOUR TESTERS FOR EVALUATING MAIZE (*Zea mays* L.) LINES IN A HYBRID DEVELOPMENT PROGRAM

R. de Rissi and A.R. Hallauer

ABSTRACT

Choice of tester is important in the evaluation of maize (*Zea mays* L.) lines for potential use in hybrids. The objective of this study was to determine the relative merits of four testers for evaluating inbred lines in a hybrid development program. One hundred S₂ lines were derived from each of two brachytic (*br2*) populations under recurrent selection, and these were crossed to two genetically broad-based testers (parental and unrelated populations) and to two genetically narrow-based testers (an unrelated single cross and one inbred line). In all instances, variance component estimates of lines were greater than their respective line x tester interactions. Greater tester x line interaction did not occur with the use of narrow-based testers than with the use of broad-based testers. The parental-population testers provided more consistent discrimination among S₂ lines. The results suggested that genetically narrow-based testers, such as inbred lines and single crosses, can be effectively used to identify lines having good general combining ability (GCA). There was evidence that unrelated testers and inbred-line testers with poor GCA and good performance per se were better testers for discriminating among S₂ lines. The highly significant phenotypic correlations between testers and the percentage of coincidence of selected lines with good GCA suggested that either type of tester can be used to classify 50% of lines with good combining ability.

INTRODUCTION

The main objectives of maize (*Zea mays* L.) hybrid breeding programs are to develop new improved inbred lines and hybrids. In both instances, maize breeders have to choose the tester for evaluating new inbred lines. Choice of an appropriate

tester plays an important role in the ultimate success of a hybrid development program.

The different types of testers can be classified and compared as follows: testers that are genetically either narrow- or broad-based, testers that are either related or unrelated to the lines being evaluated, testers that have either a high or a low frequency of favorable alleles, and testers that are either high or low yielding per se. The definition of a "good tester" depends upon the objective of the breeding program. A "good tester" for inbred-line development programs is the one that correctly classifies and discriminates the relative potential of the lines in crosses. The prevailing theory on testers states that the most efficient tester is the one with a lower frequency of favorable alleles, but this rule does not apply to testers in hybrid-development programs (Hallauer and Miranda, 1988). A tester with a lower frequency of favorable alleles allows the expression, even in the presence of dominant gene effects, of the favorable alleles present in the lines under test (Rawlings and Thompson, 1962). A tester with a lower frequency of favorable alleles may not identify superior hybrids in the initial evaluation of the lines, but it will probably identify lines with good combining ability. In this situation, maize breeders may have to change the tester for one with higher combining ability. The use of two different testers requires a two-stage testing program, which is not the most desirable approach: use of a tester with a lower frequency of favorable alleles for initial testing to identify superior inbred lines and use of a second tester to identify superior crosses.

The objective of this study was to provide further information on testers by comparing the relative merits of related vs. unrelated testers and of genetically broad-based vs. genetically narrow-based testers in the evaluation of S_2 lines of two brachytic2 (*br2*) populations.

MATERIALS AND METHODS

Two brachytic maize populations (D219B00 and F209B00) undergoing interpopulation selection were used in this study. The populations D219B00 and F209B00 correspond to the "Composite Dent Brachytic" and to the "Composite Flint Brachytic", respectively. Both populations were developed at the "Escola Superior de Agricultura Luiz de Queiróz", University of São Paulo, by Dr. José Branco de Miranda Filho. Composite Dent, which was formed by intercrossing yellow and white populations from Central and South America, includes primarily "Tuxpeno" germplasm. The Composite Flint was formed by intermating flint populations from the Caribbean, Colombia, and Brazil. The brachytic-2 (*br2*) donor parent was the variety "Pirancio", developed by Dr. Paterniani and used for both populations by making one backcrosses to the recurrent parents.

The ear-to-row procedure was used to derive 100 S_2 lines from each population (F209B00 and D219B00). The lines were crossed to four testers to produce 800 testcrosses for evaluation. The testers for lines derived from population D219B00 were 1) D219B00 parental population; 2) F209B00, opposite population; 3) (FBR2-89 x FBR2-84B), unrelated single-cross; and 4) FBR2-89, unrelated inbred line. For lines derived from population F209B00 the testers were 1) F209B00, parental population; 2) D219B00, opposite population; 3) (RBR2-305 x DBR2-9), unrelated single-cross; and 4) RBR2-305, unrelated inbred line. Previous information on the lines included in the pedigree of the tester indicates that DBR2-9 and FBR2-89 have better general combining ability (GCA) and poorer performances per se than do RBR2-305 and FBR2-848.

All of the testcrosses were produced by hand pollination at Germinal Research Farm in Matão, São Paulo, Brazil. Testers and S_2 lines were planted in paired rows using the broad-genetic based testers and the single-cross testers as the seed parent. For inbred line testers, S_2 lines were used as the seed parent. At least 20 plants were pollinated and at least 10 ears were harvested to produce the testcross seed.

From each population, 400 entries were produced. The 400 entries were represented by 100 S_2 lines crossed with the four testers. The 800 entries were assigned to eight sets, with each set including 25 lines crossed with four testers. Each set, therefore, included 100 testcrosses. The experimental design for each set was a split-plot with main plots arranged in a randomized complete block design with four replications. The main plots were the S_2 lines, and the sub-plots were the four testers.

The experimental unit for the main plots (lines) was a four-row plot of testcrosses for each S_2 line and the four testers. For the sub-plots (testers), the experimental unit was a single-row plot, or the testcross between the tester and the inbred line. Rows were spaced 100 cm in all sets. Within rows, plants were spaced 20 cm. Plots were overplanted and thinned in the five to eight-leaf stage, to a maximum of 25 plants per plot for the desired stand of 50,000 plants/ha.

Yield trials were conducted at three locations in Brazil during the 1984/85 agricultural year. These locations, which were situated between parallels 16 S and 23 S, were Matão, in the State of São Paulo; Ituiutaba, in the State of Minas Gerais; and Rio Verde, in the State of Goiás. The cultural practices used in the yield trials were the same for each of the three locations. All yield trials were planted and harvested by hand.

At each of the three locations, data were collected for five traits: grain yield, stand, moisture, erect plants, and visual appearance (index). Plant and ear height and days-to-flower were measured only at Matão and Ituiutaba locations. Data were collected in the following manner:

1. Grain yield: Ears from every plant in the plot were hand-harvested and shelled in a small shelling machine. Total grain yield was recorded in Kg/plot and later adjusted to Mg/ha at 15.5% moisture.

2. Moisture: Grain moisture was determined by a portable moisture tester after total plot grain-yield was recorded. From the total plot grain-yield, a 200 g sample was taken and used to determine the percentage of grain moisture.

3. Erect plants: One day before harvesting, the total number of erect plants was recorded. All plants leaning less than 30° from vertical were considered erect. Before the analyses of variance, the number of erect plants was expressed as a percentage of the observed stand.

4. Stand: At 40 to 50 days after planting, the number of plants per plot was recorded. The perfect stand was 25 plants per row.

5. Visual appearance: At milk stage, the plots were rated subjectively from 1 to 9 according to their phenotypic appearance. Lines with the best appearance were rated 1, and lines with the worst appearance were rated 9.

6. Plant height: After flowering, plant height was measured for five competitive plants per sub-plot. Plant height was measured in centimeters from the ground to the flag leaf collar. The averages of the five plants were used for the analyses of variance.

7. Ear height: Ear height of five competitive plants per sub-plot was measured in centimeters. Plants were measured from the ground to the uppermost ear-bearing node. The average ear heights of the five plants were used for the analyses of variance.

8. Days-to-flower: The number of days from planting to silk exposure for 50% of the plants in the plot was recorded.

Analyses of variance pooled over sets and combined over locations were performed for each trait. Entry and entry by location sums of squares were partitioned orthogonally for each source of lines and for each of the four testers. To make F-tests for the different sources of variation, lines and locations were assumed to be random effects, and testers were assumed to be fixed effects. Variance components and their respective error variance were estimated using the procedures of Comstock and Moll (1963). Phenotypic correlations between testcrosses were calculated for grain yield.

RESULTS

The coefficients of variation averaged over both populations were relatively high for grain yield (25.4% and 17.0% for main plots and subplots, respectively) and visual appearance (20.6% and 13.3% for main plots and subplots, respectively). For all other traits, they ranged from 2.1 (days-to-flower) to 11.3% (ear height).

Mean squares for lines, testers, their interactions with locations, and line x tester interactions were highly significant ($P \leq 0.01$) for all traits, except for stand (analyses not shown). The partition of the mean squares into D219B00 and F209B00 populations was highly significant for lines for all traits, indicating the presence of genetic variability within populations. Tester effects were highly significant for all traits except for those of grain moisture, visual appearance, and ear height in the F209B00 population. Tester x line interaction was not significant for days-to-flower in the F219B00 populations, indicating that testers classified lines differently for the other traits.

Partitioning testers into either broad-genetic based (BBT) or narrow-genetic based (NBT) allowed three orthogonal comparisons: BBT vs. NBT, within BBT, and within NBT. In all instances, the greater contribution for the tester x line interaction was the (BBT vs. NBT) x line interaction, indicating that the broad- and narrow-genetic based testers classified lines differently.

The means, minimum and maximum values, range of variation, and genetic coefficients of variation for each type of testcross and population are shown in Table I. Narrow-genetic based testers tended to have testcrosses with higher grain yields than did broad-genetic based testers. The significantly higher grain-yield means of the testcrosses with FBR2-89, tester number 4 for the D219B00 population, than of the testcrosses with (FBR2-89 x FBR2-848), tester 3 for the source population, provides further evidence that FBR2-89 has a higher GCA than FBR2-848 does. Similarly, the higher grain-yield mean for testcrosses with tester 3 for the F209B00 population (RBR2-305 x DBR2-9) than the testcrosses with tester 4 (RBR2-305) indicates that DBR2-9 has a higher GCA than RBR2-305 does.

The genetic coefficients of variation for plant and ear height were greater with narrow-genetic based testers than for broad-genetic based testers. Although no clear trend was detected for other traits, there was a tendency for higher genetic coefficients of variation when the inbred line RBR2-305 was included in the tester pedigree. RBR2-305 was developed out of an F_2 population having no relation to the two populations under recurrent selection.

The frequency distributions for grain yields of the four types of testcrosses are shown in Figures 1 and 2 for populations D219B00 and F209B00, respectively. For population D219B00, the single-cross tester (tester 3) performed similarly to the parental population tester (tester 1). For population F209B00, there was a clearer separation between the broad-genetic based and the narrow-genetic based testers. Broad-genetic based testers had lower means and ranges of variation than narrow-genetic based testers did.

Table I - Means, minimum and maximum values, range of variation, and the genetic coefficient of variation (CVg) for five traits of testcrosses made with four testers within two populations.

Traits	Population	Tester ^a	Mean	Minimum	Maximum	Range	CVg%
Yield (Mg/ha)	D219B00	1	4.42	3.00	5.73	2.73	9.25
		2	4.70	3.55	5.73	2.18	7.09
		3	4.40	3.34	5.65	2.31	7.87
		4	5.35	4.12	6.24	2.12	5.68
	F209B00	1	4.44	3.15	5.49	2.34	9.42
		2	4.61	3.29	5.77	2.48	8.75
		3	5.19	2.50	6.15	3.65	10.71
		4	4.93	2.01	6.16	4.15	11.38
Ear plants (%)	D219B00	1	89.0	74.3	95.7	21.4	2.20
		2	89.5	78.3	97.1	18.8	2.39
		3	87.5	72.6	96.4	23.8	2.90
		4	91.5	70.3	98.0	19.7	2.23
	F209B00	1	91.3	78.1	97.7	19.6	2.65
		2	91.4	79.4	98.3	18.9	1.47
		3	92.9	68.2	98.0	29.8	3.48
		4	90.4	64.0	96.7	32.7	4.85
Plant height (cm)	D219B00	1	175	152	200	48	4.19
		2	177	160	205	45	3.73
		3	171	147	193	46	4.21
		4	177	157	201	44	4.70
	F209B00	1	176	156	201	45	4.03
		2	176	155	201	46	4.05
		3	177	158	199	41	4.41
		4	173	153	194	41	4.39
Ear height (cm)	D219B00	1	88	71	104	33	6.32
		2	91	77	106	29	6.09
		3	86	71	105	34	6.66
		4	92	76	110	34	6.70

Continued

Table I - Continued.

Traits	Population	Tester ^a	Mean	Minimum	Maximum	Range	CVg%
	F209B00	1	90	73	114	41	6.24
		2	89	73	112	39	7.12
		3	89	76	114	38	6.84
		4	89	73	107	34	7.18
Days to silk (no.)	D219B00	1	72	69	75	6	1.11
		2	72	69	75	6	1.19
		3	70	68	73	5	1.05
		4	71	68	74	6	1.32
	F209B00	1	72	69	75	6	1.33
		2	72	68	75	7	1.10
		3	71	69	74	5	1.21
		4	70	69	75	6	0.98

^a Testers 1 and 2 are genetically broad-based testers and testers 3 and 4 are genetically narrow-based testers.

Estimates of the genetic components of variance for lines, tester x line interactions, and tester x location interactions of the analyses of variance pooled over sets and combined over locations are presented in Table II. In all instances, estimates of the genetic components of variance of the S₂ lines were greater than those of the tester x line interaction, suggesting consistent performance of the lines over testers. The variance component among lines for the F209B00 population was approximately twice the component among lines for the D219B00 population. Because both populations were broad-based populations, the difference in variability among lines between the F209B00 and D219B00 was not expected. F209B00 and D219B00 were formed by intermating a large number of varieties with no intentional selection among S₂ lines for yield. In addition, no differential criterion of selection between the two populations was used during the development of the S₂ lines. It seems that this large difference in the line components of variance between the two populations can be attributed to the different testers.

Except for the percentages of erect plants and grain moisture, visual appearance, ear height, and days-to-flower in the D219B00 population, the (broad vs. narrow) x line interaction made the greatest contribution to the total tester x line

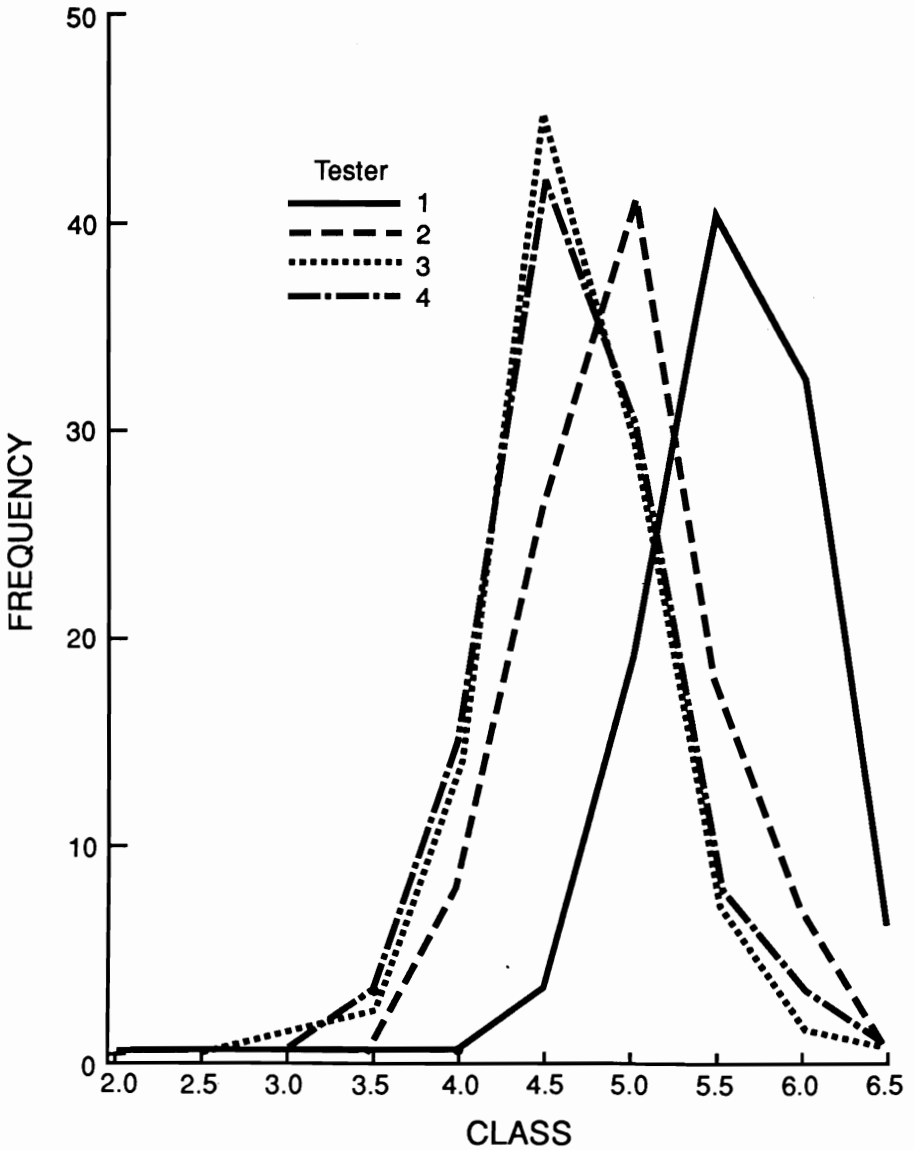


Figure 1 - Frequency distributions of grain yield for four types of testcrosses produced by crossing 100 S₂ lines derived from the D219B00 population. Tester 1 is the D219B00 parental population, tester 2 is the F209B00 population, tester 3 is the unrelated single cross (FBR2-89 x FBR2-848), and tester 4 is the unrelated inbred line (FBR2-89).

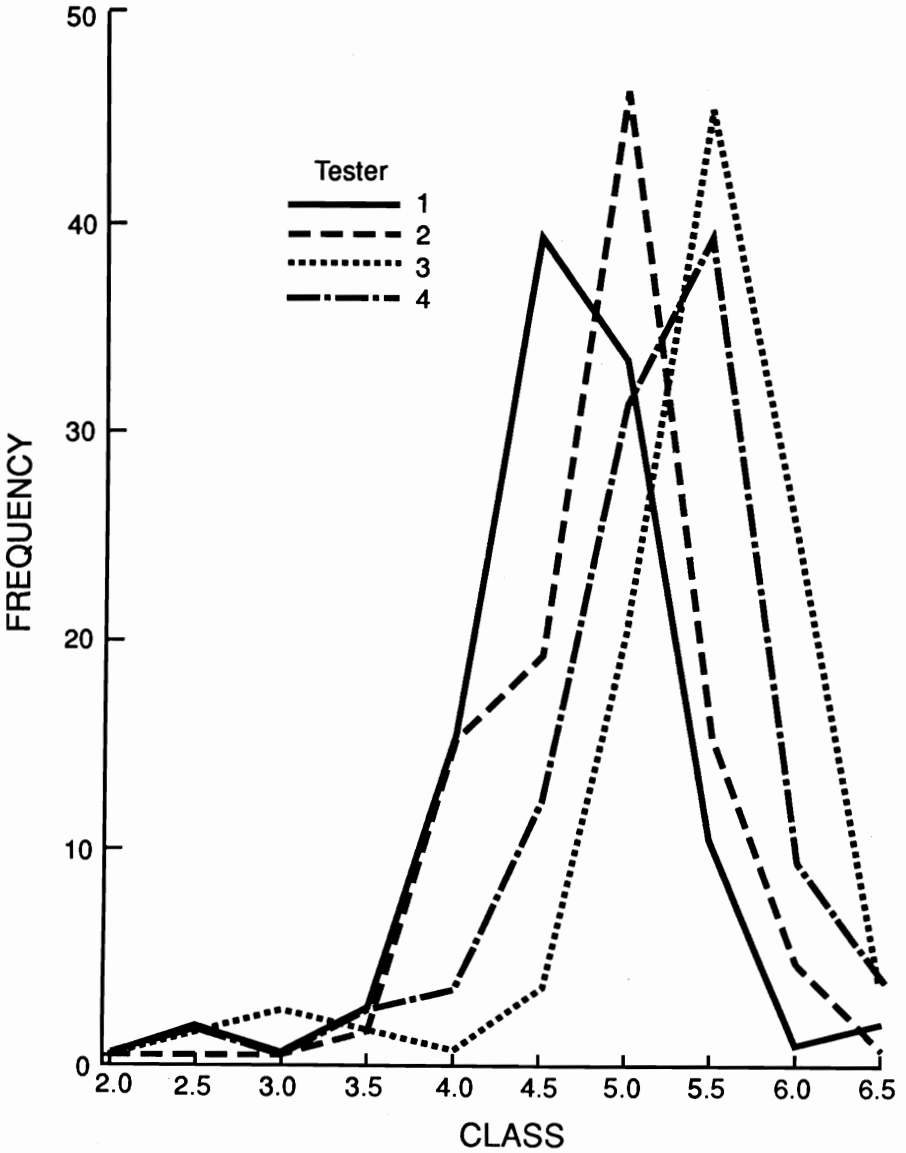


Figure 2 - Frequency distributions of grain yield for four types of testcrosses produced by crossing 100 S₂ lines derived from the F209B00 population. Tester 1 is the F209B00 parental population, tester 2 is the F219B00 population, tester 3 is the unrelated single cross (RBR2-305 x DBR2-9) and tester 4 is the unrelated line (RBR2-305).

Table II - Estimates of variance components and standard errors for seven traits of S₂ lines and tester x line and tester x location interactions evaluated at three locations in Brazil.

Sources of variation	Traits						
	Yield	Erect plants	Moisture	Visual appearance ^c	Plant height	Ear height	Days to Silk
	Mg ha ⁻¹	-----%	-----	1 - 9 ^c	----- cm	-----	no.
D219B00 lines (D-lines) ^a	0.1080 ± 0.0222	3.44 ± 0.97	0.25 ± 0.06	0.04 ± 0.02	49.48 ± 8.30	28.41 ± 4.77	0.56 ± 0.11
F209B00 lines (F-lines)	0.1768 ± 0.0315	7.42 ± 1.45	0.25 ± 0.06	0.11 ± 0.03	49.51 ± 8.22	33.93 ± 5.63	0.64 ± 0.13
Testers x Lines	0.0521 ± 0.0104	2.15 ± 0.79	0.05 ± 0.01	0.02 ± 0.01	7.00 ± 1.29	5.35 ± 1.05	0.13 ± 0.04
Testers x D-lines	0.0195 ± 0.0087	1.74 ± 0.81	0.07 ± 0.01	0.00 ± 0.01	6.77 ± 1.25	5.99 ± 1.08	0.19 ± 0.04
(BBT vs. NBT) x D-lines ^b	0.0481 ± 0.0183	0.20 ± 1.55	0.11 ± 0.03	0.00 ± 0.01	8.11 ± 2.21	4.73 ± 1.61	0.17 ± 0.08
Broad base x D-lines	-0.0005 ± 0.0135	1.88 ± 1.24	0.04 ± 0.02	0.02 ± 0.01	4.73 ± 2.54	5.47 ± 2.22	0.12 ± 0.07
Narrow base x D-lines	0.0109 ± 0.0134	3.15 ± 1.43	0.05 ± 0.02	-0.01 ± 0.01	7.48 ± 1.76	7.75 ± 1.78	0.28 ± 0.08
Testers x F-lines	0.0848 ± 0.0120	2.56 ± 0.76	0.04 ± 0.01	0.04 ± 0.01	7.22 ± 1.26	4.72 ± 1.02	0.06 ± 0.04
(BBT vs. NBT) x F-lines	0.1941 ± 0.0365	6.08 ± 1.72	0.06 ± 0.03	0.10 ± 0.03	10.56 ± 2.50	7.11 ± 1.94	0.27 ± 0.09
Broad base x F-lines	0.0368 ± 0.0131	1.09 ± 1.14	0.04 ± 0.03	0.01 ± 0.01	7.18 ± 2.42	4.03 ± 1.93	-0.03 ± 0.07
Narrow base x F-lines	0.0235 ± 0.0130	0.50 ± 1.12	0.03 ± 0.02	0.01 ± 0.01	3.91 ± 1.62	3.02 ± 1.42	-0.06 ± 0.05

Continued

Table II - Continued.

Sources of variation	Traits						
	Yield	Erect plants	Moisture	Visual appearance ^c	Plant height	Ear height	Days to Silk
	Mg ha ⁻¹	----- % -----	-----	1 - 9 ^c	----- cm -----	-----	no.
Tester x location	0.0314 ± 0.0078	0.87 ± 0.33	0.09 ± 0.02	0.04 ± 0.01	1.63 ± 0.61	0.77 ± 0.36	0.04 ± 0.02
Tester x location/D-lines	0.0428 ± 0.0143	1.79 ± 0.72	0.10 ± 0.03	0.02 ± 0.01	1.47 ± 0.78	1.13 ± 0.62	0.05 ± 0.03
(BBT vs. NBT) x L/D-lines	0.0984 ± 0.0478	1.66 ± 1.21	0.28 ± 0.13	0.02 ± 0.01	1.21 ± 1.01	0.42 ± 0.51	0.16 ± 0.10
Broad base x L/D-lines	0.0129 ± 0.0100	0.29 ± 0.45	0.02 ± 0.01	0.00 ± 0.00	-0.44 ± 0.29	-0.52 ± 0.15	-0.01 ± 0.01
Narrow base x L/D-lines	0.0170 ± 0.0114	3.40 ± 1.84	0.00 ± 0.01	0.05 ± 0.03	3.63 ± 2.30	3.63 ± 2.21	0.00 ± 0.01
Tester x location/F-lines	0.0200 ± 0.0074	-0.05 ± 0.18	0.07 ± 0.02	0.06 ± 0.02	1.78 ± 0.89	0.41 ± 0.36	0.03 ± 0.02
(BBT vs. NBT) x L/F-lines	0.0232 ± 0.0135	-0.19 ± 0.21	0.16 ± 0.08	0.10 ± 0.05	2.82 ± 1.93	0.81 ± 0.74	0.12 ± 0.08
Broad base x L/F-lines	0.0009 ± 0.0030	-0.23 ± 0.22	0.00 ± 0.01	0.00 ± 0.00	0.27 ± 0.56	0.27 ± 0.44	-0.02 ± 0.01
Narrow base x F/F-lines	0.0359 ± 0.0192	0.28 ± 0.45	0.06 ± 0.03	0.08 ± 0.04	2.26 ± 1.60	2.26 ± 0.48	0.00 ± 0.01

^a D indicates lines derived from dent population (D219B00), and F indicates lines derived from flint population (F209B00).

^b BBT indicates broad-genetic based testers, NBT indicates narrow-genetic based testers. The broad-genetic based testers were the parental and opposite populations, and the narrow-genetic based testers were a single cross and an inbred line.

^c Plots rated at milk stage with 1 having best appearance and 9 having worst appearance.

interaction in both populations. No trend for higher tester x line interaction for narrow-genetic based testers in comparison with broad-genetic based testers was found for any trait. In the D219B00 population, the narrow-genetic based testers had consistently greater line x tester interactions than the broad-genetic based testers did, for all traits except visual appearance. The narrow-genetic based testers used to evaluate the F209B00 lines, however, had less tester x line interactions than the broad-genetic based testers did for all traits except visual appearance.

The larger narrow-genetic based tester x line interaction in the D219B00 populations was not associated with the presence of narrow-genetic based testers having higher frequencies of favorable alleles. One of the two inbred lines involved in the narrow-genetic based testers had a higher frequency of favorable alleles (FBR2-89), whereas the other had a lower frequency of favorable alleles (FBR2-848). The lower narrow-genetic based tester x line interactions in the F219B00 population were probably associated with the presence of the unrelated inbred-line tester RBR2-305 derived from sources other than the populations used for reciprocal recurrent selection. This result supports the use of an unrelated inbred-line tester for identifying lines with good GCA.

Matzinger (1953) compared three types of testers: two double crosses, four single crosses, and eight inbred lines. He concluded that the tester x line interaction decreased with the heterogeneity or heterozygosity of the testers. Hallauer and Lopez-Perez (1979) also found that as the heterogeneity of related line testers increased, the line x tester interaction decreased. They found, however, that testcrosses involving B73 and Mo17 (the only tester not related to the lines tested) were the only groups having nonsignificant interactions with testers at the S_g level. Their results showed that the B73 and Mo17 testcross interactions were about 50% smaller than the broad-genetic based tester x line interaction.

Although the two populations used in this study (D219B00 and F209B00) were chosen for a reciprocal recurrent selection program, it had been shown previously that they exhibited more similarities than differences. Thus, the lines derived from these populations and used as testers for lines derived from the opposite populations should be related to the same extent. RBR2-305 was the only unrelated line not originating from the populations used for reciprocal recurrent selection. For unrelated testers, the line x tester interaction was less for the narrow-genetic based tester than for the broad-genetic based testers. These results agree with those reported by Hallauer and Lopez-Perez (1979). For related line testers, however, the component of variance of the line x tester interaction was greater in narrow-genetic based testers than in broad-genetic based testers. For related testers, therefore, these results agree with the results reported by Matzinger (1953) and by Hallauer and Lopez-Perez (1979).

Phenotypic correlations between testers are presented in Table III. Correlations were highly significant in all instances and had useful predictive value. Significant correlations also were obtained between testers 1 and 2 (broad-genetic based testers) and between testers 3 and 4 (narrow-genetic based testers). These significant correlation coefficients suggest that, for either GCA or SCA, selection based on only one tester can be as effective as selection based on more than one tester. Correlations between the broad- and narrow-genetic based testers were sufficiently large to indicate that either a narrow- or a broad-genetic based tester would be reliable for estimating the GCA of S_2 lines.

Table III - Phenotypic correlations of grain yield between four testers for two maize populations for grain yield.

Testers ^a	Populations	
	D219B00	F209B00
T1 vs. T2	0.69**	0.66**
T1 vs. T3	0.57**	0.44**
T1 vs. T4	0.55**	0.54**
T2 vs. T3	0.58**	0.43**
T2 vs. T4	0.53**	0.56**
T3 vs. T4	0.60**	0.79**

** $P \leq 0.01$, where $r = 0.20$ for $P < 0.005$ and $r = 0.26$ for $P < 0.01$.

^a Tester 1: parental population; T2: opposite population; Tester 3: unrelated cross; Tester 4: unrelated line.

Table IV illustrates the percentages of coincidence of selected lines when selection is practiced for GCA based on grain yield of topcrosses with the parental population. Percentages were calculated by assuming truncation selection for grain yield. As expected, percentages increased as selection intensity decreased. Values ranged from 20% (5% selection intensity) to 72% (40% selection intensity). At 40% selection intensity, there was at least 62% coincidence with any tester. These results support the conclusions of Jenkins and Brunson (1932) that, based on the performance of topcrosses, 50% of lines could be discarded without serious danger of losing valuable material. In addition, any type of tester (broad-genetic based, narrow-genetic based, related or unrelated) can be used to discard 50% of lines without serious danger of losing valuable material.

Table IV - Percentage of common lines selected for general combining ability based on testcrosses made with the parental population.

Selection intensity (%)	Testers					
	Opposite population		Single cross		Inbred line	
	D219B00	F209B00	D219B00	F209B00	D219B00	F209B00
5	40	20	40	40	20	40
10	60	40	50	30	40	50
15	53	53	46	46	26	46
20	55	55	45	45	30	60
30	63	66	56	53	50	66
40	72	70	62	65	65	70

With both populations, percentages of coincidence for the opposite population were similar to those of the single-cross testers. For inbred-line testers, however, values were consistently higher for the F209B00 population. The inbred line used to test the F209B00 lines was RBR2-305, which was the only unrelated tester included. The inbred line used to test lines derived from the D219B00 population was derived from the opposite population F209B00 and was the line with the highest GCA when evaluated with the D210B00 population. These results indicate that an unrelated inbred line is more reliable for ranking lines for GCA than a line with a high GCA derived from the opposite population.

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RESUMO

A escolha de provadores é importante na avaliação de linhagens de milho (*Zea mays* L.) para uso potencial em híbridos. O objetivo deste estudo foi determinar o mérito relativo de quatro provadores para avaliação de linhagens endocruzadas em um programa de desenvolvimento de híbridos. Uma centena de linhagens S_2 foram derivadas de cada duas populações "brachytic" (br2) sob seleção periódica e foram

cruzadas com dois provadores de base larga (populações parentais e não relacionadas) e com dois provadores de base estreita (um cruzamento simples e um endocruzado). Em todos os exemplares, as estimativas dos componentes de variância das linhagens foram maiores do que suas respectivas interações entre linhagem x provador. Maiores interações entre provador x linhagem não ocorreram mais com o uso de provadores de base estreita do que com os de base larga. Os provadores das populações parentais forneceram discriminação mais consistente entre as linhagens S₂. Os resultados sugeriram que, geneticamente, os provadores de base estreita, tanto os endocruzados como o de linhagens simples, podem ser usados efetivamente para identificar linhagens que têm boa habilidade geral de combinação (GCA). Haviam evidências de que provadores não relacionados e provadores endocruzados pobres em GCA e bom desempenho per se, eram melhores provadores para discriminação de linhagens S₂. As correlações fenotípicas altamente significativas entre os provadores e a porcentagem de coincidência de linhagens selecionadas com bom GCA sugerem que qualquer tipo de provador pode ser usado para classificar 50% das linhagens com boa capacidade de combinação.

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