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ESTIMATES OF GENETIC VARIABILITY AMONG TOPCROSSES OF TWO BRACHYTIC MAIZE (ZEA MAYS L.) POPULATIONS

Iowa State University PH.D. 1987

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Estimates of genetic variability among topcrosses of two brachytic maize (*Zea mays* L.) populations

by

Roberto de Rissi

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INTRODUCTION

The inbred-hybrid method proposed by Shull (1909) is the most widely accepted maize (Zea mays L.) breeding method. It became widely accepted with the production of double cross hybrids proposed by Jones (1918). Since then, maize breeders have continuously produced superior new hybrids. However, they have been facing two main problems. The first one refers to inbred line evaluation. There is a consensus among maize breeders that the production of inbred lines is not a barrier for developing maize hybrids. The challenge has been the evaluation and the identification of inbred lines that will produce better hybrid combinations. The second problem is how to increase the probability of developing superior inbred lines. The level of this probability is determined by the parents included in the basic population, and, therefore, the choice of the parents is one of the most important decisions in any maize breeding program.

Quantitative genetics studies indicate that to increase the probability of developing superior inbred lines it is necessary to increase the frequency of favorable alleles in the basic population. Experimental results have shown that recurrent selection is a powerful method to achieve this goal in a continuous and cyclical manner. Therefore, modern maize breeding programs may need to integrate the inbred line development program with a population improvement program for having a more efficient resource allocation. The present study was conducted to provide information on inbred-line evaluation and on

population improvement in an integrated maize breeding program.

In tropical areas, another challenge faced by maize breeders in developing improved hybrids is the excessive plant and ear height of the tropical germplasm. It has been reported that short plants are more adapted to mechanical harvest and more resistant to stalk and root lodging. These are desirable traits that should be considered in the inbred line development program.

Maize breeders can use two strategies to resolve this problem: 1) select polygenes for shorter plants in a normal population or 2) introduce a major gene such as the brachytic-2 gene in a population and select modifiers for increased plant height. The first alternative was inconvenient because of the high and significative genetic correlation between plant height and grain yield that has been reported in tropical germplasm. The second was inconvenient because of the negative indirect effect of the br2 gene on grain yield. However, it has been emphasized that recurrent selection for intermediate plant height and high grain yield could overcome the negative indirect effect on yield of the br2 gene. This study provides information on the potential use of br2 gene in maize breeding populations.

The objectives of this study were: 1) To compare the relative merits of broad vs. narrow genetic base testers and related vs. unrelated testers to classify the merit of S2 lines and to discriminate the variation among them; 2) To determine the relationship of the performance of S2 lines among the different types of testers; and 3) To estimate the additive genetic variance, heritability, and predicted

genetic gain from reciprocal recurrent selection based on the heterosis expressed in crosses.

LITERATURE REVIEW

Testers and Combining Ability

The identification of high combining ability inbred lines is one of the most important objectives in maize inbred-hybrid development programs. In the United States, from 1920 to 1930, a diallel of n(n-1)/2 combinations was the normal procedure to evaluate a set of n lines. However, the diallel method of evaluating lines is not feasible as the number of inbred lines increases.

To overcome this limitation, Davis (1927) suggested the topcross procedure as a method for identifying lines with good general combining ability. The topcross procedure was widely accepted after the report of Jenkins and Brunson (1932). They suggested that based on the performance of the topcrosses, 50% of the lines could be discarded without serious danger of losing valuable material. The remaining lines could be further evaluated in other types of hybrid combination, such as single or three-way crosses. Lindstrom (1931), Jenkins (1934), St. John (1934), Johnson and Hayes (1936), and Jugenheimer (1936) provided further support of the efficiency of the topcross procedure for discarding a large number of lines in preliminary testing for combining ability.

Sprague and Tatum (1942) introduced the concepts of general (GCA) and specific (SCA) combining ability to designate the performance of inbred lines in hybrid combinations. The term general combining ability refers to the average performance of a line in hybrid combinations,

while specific combining ability is used to indicate the performance of a specific hybrid combination, which can be relatively better or worse than would be expected on the basis of the average performance of the lines involved. The main difference between general and specific combining ability is the genetic basis of the tester. Estimates of general combining ability are obtained with use of broad-genetic base tester, and estimates of specific combining ability are determined with narrow-genetic base tester. Hallauer and Miranda Filho (1981) pointed out that such differences are essentially a matter of differences in allele frequencies. In broad-base testers, frequencies of alleles for different loci may vary from 0 to 1.0, whereas in the narrow-base testers gene frequencies may be limited to a few values, such as 0, 0.5, and 1.0.

The topcross progenies used by Davis (1927) for evaluating inbred lines were the crosses between the inbred lines and a variety (broad-base tester). However, with the concept of GCA and SCA, new approaches for inbred line evaluation and population improvement were introduced. Different types of testers were used and the term testcross was broadly used to designate a cross between an inbred line and any type of tester.

Jenkins (1935) and Sprague (1939, 1946) suggested the early testing procedure. With early testing, inbred lines are developed in a sequential process. During first stages of inbreeding, some inbred lines are discarded based on their poor performance in testcrosses and others are eliminated by later tests. Therefore, breeding efforts are concentrated in the most promising inbred lines during the inbreeding

process. This procedure provided new opportunities in plant breeding. Probably, the most important one was the opportunity to integrate inbred line development and population improvement programs more efficiently. The most questionable point, however, is concerned with the choice of the tester.

The different types of testers can be classified and compared as follows: 1) broad-genetic base versus narrow-genetic base; 2) related versus unrelated, 3) high gene frequency versus low gene frequency, and 4) high yielding versus low yielding. These different types of testers create a problem in choosing the appropriate tester for inbred line evaluation or population improvement. For inbred line evaluation, Matzinger (1953) defined a desirable tester as one that combines simplicity in use with the maximum information on the expected performance of the tested lines with other testers. Rawlings and Thompson (1962) defined a good tester as one that correctly classifies the relative performance and efficiently discriminates the lines under test. Allison and Curnow (1966) described a "best tester" as one that maximizes the expected mean yield of the synthetic variety produced by random mating the selected genotypes. Hallauer (1975) stated that in general a suitable tester should include simplicity in use, provide information that correctly classifies the relative merit of lines, and maximize genetic gain.

In either integrated or inbred-hybrid maize breeding programs, the most questionable point is the choice of a tester to evaluate combining ability. The choice of a tester is determined to a considerable extent

upon the expected use for a particular group of lines. As emphasized by Hallauer and Miranda Filho (1981), if the objective is the replacement of a line in a hybrid, specific combining ability is of prime importance and the most appropriate tester is the opposite inbred-line parent of a single cross or the opposite single-cross parent of the double cross. If a group of lines is designated as replacements for lines in existing hybrid combinations, the tester chosen will certainly differ from that selected if the lines are to be screened for average performance and the survivors tested subsequently in new combinations (Matzinger, 1953).

The critical point in choosing the tester is in the situations where testers are changed through the breeding program or new combinations are sought, which is the usual procedure in either inbred-hybrid development or integrated maize breeding programs. Most of the early studies indicate that in this situation a broad-genetic base tester would be more appropriate. Matzinger (1953) compared three types of testers. The testers included 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. Lonnquist and Rumbaugh (1958) evaluated the relative merits of a broad and narrow genetic-base tester in evaluating inbred lines of maize for subsequent use in synthetic varieties. Their results supported the use of the broad genetic-base tester for selecting lines with high general combining ability, which was followed by a test for specific combining ability among the selected group of lines based on GCA. For related line testers, Hallauer and Lopez-Perez (1979) also

found that as the heterogeneity of the testers increased, the line x tester interaction decreased. Therefore, these studies indicate that genetically broad-base testers are more efficient than genetically narrow-base testers in selecting lines that have a better performance over a range of testers.

Sprague and Federer (1951) and Rojas and Sprague (1952) reported that the tester x environment interaction decreased as the heterogeneity of the tester increased. Eberhart and Russell (1969) and Wright et al. (1971) found the same trend. These studies indicate that the narrow genetic-base testers may cause a greater bias of the genetic variance than broad genetic-base tester, unless a sufficient number of environments is sampled. However, more recently, Hallauer and Lopez-Perez (1979) conducted a comprehensive study involving an unselected sample of 50 S1 and 50 S8 lines derived from Iowa Stiff Stalk Synthetic (BSSS) and five testers. They detected no trend for higher tester x environment interaction in narrow-base testers.

Although early studies of testers indicated that narrow genetic-base testers would improve specific combining ability (SCA), but would have little value for improving general combining ability (GCA), recent reports indicate that narrow genetic-base testers can also improve GCA. Results from two recurrent selection programs in maize (Darrah et al., 1972; Horner et al., 1973) have shown that the genetic variance among testcross families was approximately twice as large for an inbred tester as for the population used as a tester. Studies conducted by Horner et al. (1973) and Russell et al. (1973) showed that the method proposed by

Hull (1945) (i.e., recurrent selection for SCA using an inbred line as a tester) resulted in improvement of the population when evaluated in crosses with other testers.

Based on the evidence from use of genetically narrow-base testers, Russell and Eberhart (1975) proposed the use of an inbred tester for reciprocal recurrent selection. The inbred lines would be derived from previous cycles of selection and used as testers for the interpopulation crosses instead of the population themselves. They also reported that inbred lines were effective in selecting genes with additive effects, and that nonadditive gene action, other than partial to complete dominance, was relatively unimportant. They emphasized that the gain from selection would be greater with use of an inbred instead of the populations themselves. However, Comstock (1979) theoretically demonstrated that the use of populations as testers in reciprocal recurrent selection are expected to be slightly superior to inbred lines as testers for changing allele frequency. He concluded that there was no reason to expect better results using the inbred tester instead of the populations as originally proposed by Comstock et al. (1949).

Recent results of Horner et al. (1976), Sprague and Eberhart (1977), Walejko and Russell (1977), and Zambezi et al. (1986) also support the use of inbred-line testers in recurrent selection programs. Hallauer and Lopez-Perez (1979) found that the tester x line interactions were greater for narrow genetic-base testers, but interaction components were smaller than testcross components of variance. They concluded that narrow-genetic base testers can be

effectively used to identify lines having good GCA. Sprague and Eberhart (1977) and Walejko and Russell (1977) suggested that the testers could be replaced by better lines as the selection program progresses without deleterious results relative to population improvement because no selection pressure can be applied at loci where the tester is fixed for the favorable allele.

It has been emphasized that the broad genetic-base testers may induce bias in the genetic effects of the lines due to sampling size. St. John (1934) reported the yields of 51 topcrosses made reciprocally. The average yield of all crosses made with a variety as seed parent was significantly greater than their reciprocals. Sprague (1939) studied the problem of sampling heterogeneous testers with respect to number of plants. He found that 10 plants would be an adequate sample for the majority of the experiments. Marquez-Sanchez and Hallauer (1970) conducted a study to determine the influence of sampling size on the estimation of genetic components of variance for Design I. They concluded that at least four females per male should be used and that six to eight females mated to at least 48 males would be preferable for estimating components of genetic variance for yield. Salazar and Lonnquist (1963) studied the problem of differences in maturity between lines and a heterogeneous tester. They found that all characters studied had higher values when the lines were pollinated using pollen from the later flowering plants of the tester. They emphasized that different dates of planting of a heterogeneous tester is an important technique to avoid the influence of the tester on the evaluation of

inbred lines.

Probably, the most discussed comparison for choosing testers for inbred line evaluation has been between testers with high and low frequency of favorable alleles. The central point of the discussion is the hypothesis of Hull (1945). He stated that the masking effects of the dominant desirable alleles render them ineffective, and that the most efficient tester would be a homozygous recessive tester at all loci. Thus, the best yielding lines in commercial use are worthless as testers. His hypothesis was based on the constant parent regression method, where the performance of the hybrids was regressed on the performance of the variable parents for a particular constant parent. The regression coefficient was largest when the gene frequency of the tester was zero. Thus, a strong positive regression would be desirable since this would provide a greater range among the lines under evaluation.

Several studies supported Hull's (1945) hypothesis. Green (1948) compared U.S. 35, a high yielding, lodging resistant, double-cross hybrid, and 'Black Yellow Dent', a low yielding, lodging susceptible, open pollinated variety, as testers in topcross evaluation of F2 plants. He found that for root and stalk lodging the low yielding tester provided greater opportunity for selection among segregants than did the high yielding parent. Russell (1961) used five testers (2 inbred lines, 2 single crosses, and 1 double cross), that were susceptible, highly resistant, and intermediate in resistant to Diplodia stalk rot. His results agreed with Hull's hypothesis that the highly resistant tester

revealed the smallest line difference while the susceptible tester revealed the greatest line difference. Astralaga (1956) had previously reported similar conclusions.

Rawlings and Thompson (1962) studied the hypothesis that the best tester for discriminating the genetic variation among inbred lines is the one with lowest frequency of favorable alleles. Assuming no epistasis, they examined the genetic variability among testers for different levels of dominance and different gene frequencies in the tester. They found that the genetic variation among testcrosses was directly proportional to the square of $[1 + (1-2r_i)a_i]$, where r_i is the gene frequency at the i^{th} locus for the tester and a_i is a measure of dominance at the i^{th} locus. Their results also showed that the genetic variance among testcross progenies was independent of tester gene frequency only when dominance is zero at all loci. Thus, with no dominance all testers discriminated among testcrosses equally relative to the genetic variation. Also, if the tester gene frequency was $r = 0.5$, the genetic variance among testcrosses was equal for all levels of dominance. However, if the tester gene frequency is $r = 0$, the genetic variation among testcrosses is always greater than any other tester for any level of dominance, except for no dominance. Therefore, the power of the tester in discriminating the genetic variation among lines in testcross evaluation increases as the tester gene frequency of favorable alleles decreases.

Rawlings and Thompson (1962) conducted a study to determine if the performance level of testers had an effect on the usefulness of the

testers for measuring general combining ability for yield. They found that the "low" testers had higher sensitivities and greater variance among their testcross progenies than those with "high" testers. They stated that in all instances the trend of the data favored the low performing tester.

Allison and Curnow (1966) examined the choice of testers for improving varieties of maize. Their conclusions support Hull's (1945) hypothesis and are in agreement with the conclusions of Rawlings and Thompson (1962). They concluded that the ideal tester should be homozygous recessive at all loci, but just any low-yielding variety would not be a good tester. The low-yield tester must have high frequencies of recessive alleles at the same loci under selection in the variety. In addition, in practice the allele frequency and the amount and direction of dominance in the tester is not known. Thus, they suggested the use of parental variety as the best choice of tester. Use of other varieties as testers may not be desirable because the other variety may have contrasting allele frequencies. They also proposed selecting for a low-yield tester within the parental variety.

Lonnquist and Lindsey (1970) crossed 348 S1 lines to a high- and low-yielding broad genetic-base tester. Based upon the topcross performance, a high- and a low-yielding group of lines were evaluated in crosses with four elite lines as testers. The difference (H-L) averaged greater for lines selected originally on the basis of the low yielding. Furthermore, lines selected as high yielding on the basis of crosses with the low tester averaged 5% greater yield in testcrosses with the

elite lines than those selected high on the basis of topcross performance with the high tester. Their data supported use of low yielding testers for inbred line evaluation.

Hallauer and Lopez-Perez (1979) evaluated 50 unselected S1 and 50 unselected S8 lines crossed with five testers that were selected for their expected differences in allele frequency for yield. Their data supported Hull's (1945) hypothesis that the most efficient tester was one having a low frequency of favorable alleles. Mendez and Galan (1982) determined the relative efficiency of low-yielding and high yielding varieties as testers for the general combining ability of inbred lines of maize. They concluded that the best GCA tester for inbred lines of maize might be a low-yielding variety.

Evidence against Hull's (1945) hypothesis, however, was presented by Keller (1949). He found that high and low combining lines were, on the average, of equal value as testers when the arithmetic mean of the estimated variance components (S^2_{LT}) was calculated.

Maize breeders are also interested in comparing related versus unrelated testers in evaluating inbred lines. Keller (1949) evaluated a group of 98 individual F2 plants of maize with a related and an unrelated single-cross tester. He found that the estimates of variability for percentage of stand, ear height, percentage of moisture, and percentage of root lodging were not equal. His data suggested that the two testers did not yield similar measures of combining ability as regards the ranking of the lines. He stated that this lack of agreement between the two testers may be attributed largely to differences in

specific combining ability. He was unable to determine which one of the two testers was the best for evaluating lines. Singh (1958) used seven related and three unrelated testers to estimate relative GCA for yield, maturity, and stalk lodging resistance of 20 S6 lines. The correlation coefficients between the average of all related and unrelated testers were high and significant for all traits. He concluded that either type of testers, as a group, was reliable to determine the relative GCA of the S6 lines.

Lonnquist (1968) evaluated 169 S1 lines as lines per se, testcrosses to an unrelated tester, and testcrosses to the parental population. The three highest- and three lowest-yielding from each of the three evaluation series were used to study their intercross behavior. Three groups were formed for each evaluation series: LL, HL, and HH. The difference between high and low lines selected on the basis of the parental population testcrosses was greater over all testers than that for the other two groups. The smallest average difference (H-L) was obtained from the unrelated tester series. These results support the conclusion of Allison and Curnow (1966) that population improvement would be best accomplished where the parental population (related) is the tester (Lonnquist, 1968).

Maize breeders are also concerned about the use of more than one tester for evaluating inbred lines regardless of whether the tester is a broad or narrow genetic-base or related or unrelated. Perhaps, the reasons for these concerns are: 1) maize breeders need better information on the general combining ability of the lines, 2) testers

are not ranking the lines in the same order, and 3) breeders desire faster rates of developing new hybrid combinations and hybrids.

Federer and Sprague (1947) evaluated the error, tester x line interaction, and line components of variance in a series of topcross experiments. They concluded that for a fixed number of plots the greatest gain in total combining ability can be expected from an increase in number of testers, followed in order by an increase in lines. The increase in number of replications is the least efficient. Singh (1958) and Keller (1949) reported similar conclusions and found that beyond the use of 8 to 10 inbred line testers the gain in average combining ability was very slight.

Use of br2 Gene in Maize Breeding

The use of dwarf varieties has been one of the most important contributions of plant breeding to agriculture. Allard (1960) pointed out that no other factor had contributed as much as the use dwarf varieties of sorghum for the final success of the grain sorghum in the USA. The dwarf characteristic has also been successfully used in other crops such as wheat and rice. In maize, however, dwarf varieties have not produced the same results as in other crops. The main reason for this disappointment was the lower yield of the dwarf varieties compared to their normal counterparts. In addition, the plant and ear height of the hybrids in the temperate regions were not a serious problem. Campbell (1965) also reported that the use of the same plant density and cultural practices used for normal maize, the low number of backcrosses

used to convert the normal lines to dwarf, and the absence of selection for modifiers are some of the causes that contributed to the failure of the dwarf hybrids in the USA.

In tropical areas, however, maize breeders are concerned with the excessive plant and ear height of the tropical materials. De Castro (1983) reported the plant and ear height of five Brazilian populations and their brachytic counterparts. The ear height of the normal populations ranged from 143 to 170 cm, while the brachytic versions ranged from 85 to 98 cm. Tropical maize breeders are studying alternative breeding strategies to reduce the excessive plant and ear height of maize in these areas. The use of br2 gene is one of them.

The br2 gene is located in the long arm of chromosome 1, and its main effect is the reduction of plant and ear height (Kempton, 1920; Leng, 1957; Anderson and Chow, 1963; and Paterniani, 1973). It also affects other parts of the plant such as stalk diameter, leaf width, days-to-flower, etc. Kempton (1920), Anderson and Chow (1963), and Leite (1973) reported an increase in the stalk diameter. Anderson and Chow (1963) noted an increase in the number of kernels per row, leaf width, and days-to-flower and a reduction in the leaf length.

The br2 gene also affects important agronomic traits such as grain yield and root and stalk lodging. Leng (1957) pointed out that good yields and good stalk quality were not an incompatible objective in brachytic maize breeding programs. One of the most important advantages of the brachytic maize was the superior stalk quality (reduced root and stalk lodging). Leng (1957), Anderson and Chow (1963), Campbell (1965),

Paterniani (1973), Galvao (1974), Khehra et al. (1975), Solonenko and Chalyr (1975), Sokolov et al. (1976), and De Castro (1985) reported that the brachytic versions were more resistant to root and stalk lodging than the respective normal counterparts.

Leng (1957) reported that the brachytic versions produced 8% to 20% less yield than the normal counterparts. Similar results were reported by Anderson and Chow (1963), Campbell (1965), Bullow (1971), and Solonenko and Chalyr (1975). However, they also reported that some brachytic hybrids were not significantly different from the normal counterparts and some of them had similar yields. This may indicate that the genetic background can have an important role on the effect of the br2 gene on yield. Thus, if the br2 gene is introduced in an appropriate plant genetic background, it may be possible to develop higher yielding brachytic varieties.

Another alternative breeding strategy is to adapt the plant genetic background to br2 gene. To accomplish this objective, Paterniani (1973, 1974) proposed the use of the br2 gene through population improvement. With this procedure, the negative effect of the br2 gene on grain yield could be overcome by selecting modifier genes through recurrent selection. Rissi and Paterniani (1981) reported narrow-sense heritability coefficients on plant basis of 14% and 29% for grain yield of two brachytic populations. These data indicate that selection should be efficient in improving grain yield in brachytic populations. They also found a significant positive additive genetic correlation between grain yield and plant and ear height. Therefore, it was expected that

selection for plant and ear height modifiers (intermediate plant height) will give an additional increase in grain yield. Their findings supported the assumption that recurrent selection can overcome the negative effects of the br2 gene on yield.

MATERIAL AND METHODS

Populations

Two brachytic maize populations, D219B00 and F209B00, were used in the study. The D219B00 population corresponds to the 'Composite Dent Brachytic' and the F209B00 population corresponds to the 'Composite Flint Brachytic'. Both populations were developed by Dr. Jose Branco de Miranda Filho at University of Sao Paulo. To develop these populations, he used the backcross procedure followed by phenotypic recurrent selection for agronomic traits. The recurrent parents were the normal 'Dent' and 'Flint Composites', and the donor parent was the brachytic (br2br2) variety 'Piranao'. Dent Composite includes primarily 'Tuxpeno' germplasm, and it was formed by intercrossing yellow and white populations from Central and South America. The Flint Composite was formed mainly by intermating populations from Central America, Colombia, and Brazil. The Piranao variety (br2br2) was developed by Dr. Paterniani at University of Sao Paulo, Brazil and also has Tuxpeno germplasm.

In 1971 the Dent and Flint Composites were crossed with the brachytic variety Piranao. In 1972 the F1 plants were backcrossed (BC1) to the Dent and Flint Composites. The BC1 plants were selfed in 1973. In 1974 the BC1F2 normal plants were eliminated and only the homozygous plants for br2 gene were allowed to intermate. In 1975 and 1976 two cycles of recurrent phenotypic selection for intermediate plant and ear height and other agronomic traits were performed before flowering. From

1978 to 1980, three additional cycles of phenotypic recurrent selection were conducted at "Sementes Germinal."

Testcrosses

One hundred S2 lines were derived from each population using the ear-to-row procedure. In 1981 the S0 populations were planted, and about 1000 plants in each population were self-pollinated to produce S1 lines. In 1982, a random sample of 200 S1 lines was planted in the nursery for this study. The other S1 lines were used for the inbred line development program. Three plants within each S1 line were pollinated, but only one ear from each S1 line was saved to advance the line for next generation. In 1983, the 200 S2 lines were crossed with four testers to produce testcrosses for evaluation. However, only 100 S2 lines produced enough seeds for testing. The testers used included: 1) a parental population, 2) an opposite population, 3) an unrelated single-cross, and 4) an unrelated inbred line.

For the lines derived from population D219B00, the testers were: 1) D219B00 (parental population); 2) F209B00 (opposite population); 3) (FBR2-89 x FBR2-848), a single cross, and 4) FBR2-89 (inbred line). The FBR2-89 and FBR2-848 inbred lines were derived from population F209B00.

For the lines derived from population F209B00, the testers were: 1) F209B00 (parental population); 2) D219B00 (opposite population); 3) (RBR2-305 x DBR2-9), a single cross, and 4) RBR2-305 (inbred line). The RBR2-305 inbred line was derived from a pedigree selection program and

the DBR2-9 was derived from D219B00 population.

All of the testcrosses were produced by hand pollination at Germinal Research Farm in Matao, Sao Paulo, Brazil. The testers and the S2 lines were planted in paired rows using the broad-genetic base testers and the single cross testers as the seed parent. For the inbred line testers, the S2 lines were used as seed parent. At least 20 plants were pollinated and at least 10 ears were harvested to produce the testcross seeds.

Yield Trials

From each population 400 entries were produced. The 400 entries were represented by 100 S_2 lines crossed with four types of testers. The 800 entries were divided in 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 the main plots arranged in a complete randomized block design with four replications. The main plots were S2 lines and the sub-plots were the four testers.

The experimental unit for the main plots (lines) was a 4-row-plot of testcrosses between the S2 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 the plants were spaced 20 cm. The plots were overplanted and thinned in the 5- to 8-leaf stage to a maximum of 25 plants per plot to have a desired stand of 50,000 plants/ha.

The yield trials were conducted at three locations in Brazil during the 1984/85 agricultural year. The three locations were Matao, located in the State of Sao Paulo, Ituiutaba, located in the State of Minas Gerais, and Rio Verde, located in the State of Goias. They are located between parallel 16 S and 23 S. The cultural practices used in the yield trials were the same for the three locations. All yield trials were planted and harvested by hand.

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

Grain yield (YIELD) Ears from every plant in the plot were hand harvested and shelled in a small shelling machine. The total grain yield was recorded in Kg/plot and later adjusted to Mg/ha at 15.5% moisture.

Moisture (MOIST) Grain moisture was determined by a portable moisture tester just after the total plot grain yield was recorded. From the total grain yield of the plot, a sample of about 200g was taken and used to determine the grain moisture percentage.

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

Stand (STAND) At 40 to 50 days after planting the number of plants per plot was recorded. Stand was expressed as it was taken. The perfect stand was 25 plants per row.

Visual appearance (INDEX) At milk stage, the plots were rated from 1 to 9 according to their phenotypic appearance. These data were of a subjective nature and dependent on the breeder. Lines with a excellent appearance were rated 1 and the lines with a very poor appearance were rated 9.

Plant height (PH) After flowering, plant height was measured on five competitive plants per sub-plot. Plant height was measured in centimeters from the ground to the flag leaf collar. The average of the five plants was used for analyses of variance.

Ear height (EH) Ear height also was measured in centimeters on five competitive plants per sub-plot. The plants were measured from the ground to the uppermost ear-bearing node. The average of the five plants was used for analyses of variance.

Days-to-flower (FLOW) The number of days from planting to silk exposure of 50% of the plants in the plot were recorded.

Statistical Procedures

Analyses of variance

The analyses of variance for a single set in each location were performed according to the following model:

$$Y_{klm} = u + R_k + L_l + (RL)_{kl} + T_m + (LT)_{lm} + e_{klm} ,$$

where

Y_{klm}: observed value for the l^{th} line crossed to m^{th} tester in the k^{th} replication;

k: number of replications, k = 1,2,3,4;

l: number of lines, l = 1,2,...,25;

m : number of testers, m = 1,2,3,4;

u : overall mean;

R_k : effect of the k^{th} replication, k = 1,2,3,4;

L_l : effect of the l^{th} line, l = 1,2,...,25;

$(RL)_{lk}$: effect of the interaction between the l^{th} line and the k^{th} replication, which is an estimate of error a;

T_m : effect of the m^{th} tester;

$(LT)_{lm}$: effect of the interaction between the l^{th} S_2 line and the m^{th} tester; and

e_{ijk} : error b.

The analyses of variance were performed according to the linear model. The form of analyses of variance and the expected mean squares are shown in Table 1.

For one location, the eight sets were pooled and the analyses of variance as well as the expected mean squares are presented in Table 2. The analyses of variance pooled over sets at each location were performed according to the following model:

$$Y_{jkl_m} = u + S_j + (R/S)_{jk} + (L/S)_{jl} + (RL/S)_{jkl} + (T/S)_{jm} + (LT/S)_{jlm} + e_{jklm},$$

where

Table 1. Analysis of variance and the expected mean squares for one set of a split-plot experiment conducted in a single location with 25 S2 lines as the main plots and four testers as the sub-plots

Source of variation	df	Mean squares	Expected mean squares[a]
Replications (R)	3	M_6	$\sigma^2_b + t\sigma^2_a + tl\sigma^2_r$
Lines (L)	24	M_5	$\sigma^2_b + t\sigma^2_a + rt\sigma^2_l$
Error (a)	72	M_4	$\sigma^2_b + t\sigma^2_a$
Tester (T)	3	M_3	$\sigma^2_b + r\sigma^2_{lt} + rlK^2_t$
L x T	72	M_2	$\sigma^2_b + r\sigma^2_{lt}$
Error (b)	225	M_1	σ^2_b

[a]r, l, and t represent the number of replications, S2 lines, and testers, respectively. In this experiment r = 4, l = 25, and t = 4.

Table 2. Pooled analysis of variance of eight sets of a split-plot experiment conducted in a single location with 25 S2 lines as the main plots and four testers as the sub-plots

Source of variation	df	Mean squares	Expected mean squares[a]
Sets (S)	7	M_7	$\sigma^2_b + tl\sigma^2_r + rtl\sigma^2_s$
Replications /S	24	M_6	$\sigma^2_b + t\sigma^2_a + tl\sigma^2_{r/s}$
Lines /S	192	M_5	$\sigma^2_b + t\sigma^2_a + rt\sigma^2_{l/s}$
Pooled error(a)	576	M_4	$\sigma^2_b + t\sigma^2_a$
Tester /S	24	M_3	$\sigma^2_b + r\sigma^2_{lt/s} + rlK^2_{t/s}$
L x T /S	576	M_2	$\sigma^2_b + r\sigma^2_{lt/s}$
Pooled error(b)	1800	M_1	σ^2_b

[a] r, l, and t represent the number of replications, S2 lines, and testers, respectively. In this experiment r = 4, l = 25, and t = 4.

j : number of sets, $j = 1,2,\ldots,8$;

k : number of replications, $k = 1,2,3,4$;

l : number of lines, $l = 1,2,\ldots,25$;

m : number of testers, $m = 1,2,3,4$;

u : overall mean;

Y_{jklm} : observed value for the l^{th} line crossed to m^{th} tester in the k^{th} replication and j^{th} set;

S_j : effect of the j^{th} set, $j = 1,2,\ldots,8$;

$(R/S)_{jk}$: effect of the k^{th} replication within the i^{th} set;

$(L/S)_{jl}$: effect of the l^{th} line within the i^{th} set;

$(RL/S)_{jkl}$: effect of the interaction between the l^{th} line and the k^{th} replication within the j^{th} set, which is the error a;

$(T/S)j_m$: effect of the m^{th} tester within the j^{th} set;

$(LT/S)_{jlm}$: effect of the interaction between the l^{th} S_2 line and the m^{th} tester within the j^{th} set;

e_{jklm} : error b.

The analyses of variance pooled over sets, combined over locations, and the expected mean squares are presented in Table 3. The analyses of variance pooled over sets and combined over locations were performed according to the following model:

$$Y_{ijk^{l}m} = u + E_i + S_j + (ES)_{ij} + (R/SE)_{ijk} + (L/S/E)_{ijl} + (LE/S)_{ijl} + (RL/S/E)_{ijkl} + (T/S/E)_{ijm} + (TE/S)_{ijm} + (TL/S/E)_{ijlm} + (TLE/S)_{ijlm} + e_{ijklm} ,$$

where

Table 3. Analysis of variance pooled over sets and combined over three locations for a split-plot experiment with 25 S2 lines as the main plots and four testers as the sub-plots

Sources of variation[a]	df	MS	Expected mean squares[b]
Locations (E)	2		$\sigma^2_{bL} + lt\sigma^2_{R/SE} + rlt\sigma^2_{SE} + srlt\sigma^2_{E}$
Sets (S)	7		$\sigma^2_{bL} + lt\sigma^2_{R/SE} + rlt\sigma^2_{SE} + erlt\sigma^2_{S}$
E x S	14		$o^2_{bL} + lt\sigma^2_{R/SE} + rlt\sigma^2_{SE}$
Reps/S x E	72		$\sigma^2_{bL} + lt\sigma^2_{R/SE}$
Lines/S (L)	192	ML_{80}	$\sigma^2_{bL} + t\sigma^2_{aL} + rt\sigma^2_{LE/S} + ret\sigma^2_{L/S}$
D-Lines/S (D)	96	MD_{80}	$\sigma^2_{bD} + t\sigma^2_{aD} + rt\sigma^2_{DE/S} + ret\sigma^2_{D/S}$
F-Lines/S (F)	96	MF_{80}	$\sigma^2_{bF} + t\sigma^2_{aF} + rt\sigma^2_{FE/S} + ret\sigma^2_{F/S}$
Lines x E/S	384	ML_{70}	$\sigma^2_{bL} + t\sigma^2_{aL} + rt\sigma^2_{LE/S}$
D-Lines x E/S	192	MD_{70}	$\sigma^2_{bD} + t\sigma^2_{aD} + rt\sigma^2_{DE/S}$
F-Lines x E/S	192	MF_{70}	$\sigma^2_{bF} + t\sigma^2_{aF} + rt\sigma^2_{FE/S}$
Error a	1728	ML_{60}	$\sigma^2_{bL} + t\sigma^2_{aL}$
Error a D-Lines	864	MD_{60}	$\sigma^2_{bD} + t\sigma^2_{aD}$
Error a F-Lines	864	MF_{60}	$\sigma^2_{bF} + t\sigma^2_{aF}$
Tester/S	24	ML_{50}	$\sigma^2_{bL} + r\sigma^2_{TLE/S} + re\sigma^2_{TL/S} + rl\sigma^2_{TE/S} + relK^2_{T/S}$
Tester/D-Sets	12	MD_{50}	$\sigma^2_{bD} + r\sigma^2_{TDE/S} + re\sigma^2_{TD/S} + rl\sigma^2_{TE/DS} + relK^2_{T/DS}$
BBT vs NBT	4	MD_{51}	$\sigma^2_{bD1} + r\sigma^2_{TDE/S} + re\sigma^2_{TD/S} + rl\sigma^2_{TE/DS} + relK^2$(BBT vs NBT)/DS
Broad-base (BBT)	4	MD_{52}	$\sigma^2_{bD2} + r\sigma^2_{TDE/S} + re\sigma^2_{TD/S} + rl\sigma^2_{TE/DS} + relK^2$(NRT vs RET)/DS
Narrow-base (NBT)	4	MD_{53}	$\sigma^2_{bD3} + r\sigma^2_{TDE/S} + re\sigma^2_{TD/S} + rl\sigma^2_{TE/DS} + relK^2$(SCT vs ILT)/DS
Tester/F-Sets	12	MF_{50}	$\sigma^2_{bF} + r\sigma^2_{TFE/S} + re\sigma^2_{TF/S} + rl\sigma^2_{TE/FS} + relK^2_{T/FS}$
BBT vs NBT	4	MF_{51}	$\sigma^2_{bF1} + r\sigma^2_{TFE/S} + re\sigma^2_{TF/S} + rl\sigma^2_{TE/FS} + relK^2$(BBT vs NBT)/FS
Broad-base	4	MF_{52}	$\sigma^2_{bF2} + r\sigma^2_{TFE/S} + re\sigma^2_{TF/S} + rl\sigma^2_{TE/FS} + relK^2$(NRT vs RET)/FS
Narrow-base	4	MF_{53}	$\sigma^2_{bF3} + r\sigma^2_{TFE/S} + re\sigma^2_{TF/S} + rl\sigma^2_{TE/FS} + relK^2$(SCT vs ILT)/FS
Tester x E/S	48	ML_{40}	$\sigma^2_{bL} + r\sigma^2_{TLE/S} + rl\sigma^2_{TE/S}$
Tester x E/D-Sets	24	MD_{40}	$\sigma^2_{bD} + r\sigma^2_{TDE/S} + rl\sigma^2_{TE/DS}$
BBT vs NBT	8	MD_{41}	$\sigma^2_{bD1} + r\sigma^2_{TDE/S} + rl\sigma^2$(BBT vs NBT)E/DS
Broad-base	8	MD_{42}	$\sigma^2_{bD2} + r\sigma^2_{TDE/S} + rl\sigma^2$(NRT vs RET)E/DS
Narrow-base	8	MD_{43}	$\sigma^2_{bD3} + r\sigma^2_{TDE/S} + rl\sigma^2$(SCT vs ILT)E/DS
Tester x E/F-Sets	24	MF_{40}	$\sigma^2_{bF} + r\sigma^2_{TFE/S} + rl\sigma^2_{TE/FS}$
BBT vs NBT	8	MF_{41}	$\sigma^2_{bF1} + r\sigma^2_{TFE/S} + rl\sigma^2$(BBT vs NBT)E/FS

Broad-base	8	MF_{42}	$\delta^2_{bF2} + r\delta^2_{TFE/S} + rl\delta^2(NRT\ vs\ RET)E/FS$
Narrow-base	8	MF_{43}	$\delta^2_{bF3} + r\delta^2_{TFE/S} + rl\delta^2(SCT\ vs\ ILT)E/FS$
Tester x Lines/S	576	ML_{30}	$\sigma^2_{bL} + r\sigma^2_{TLE/S} + re\sigma^2_{TL/S}$
Tester x D-Lines/S	288	MD_{30}	$\delta^2_{bD} + r\delta^2_{TDE/S} + re\delta^2_{TD/S}$
BBT vs NBT	96	MD_{31}	$\delta^2_{bD1} + r\delta^2_{TDE/S} + re\delta^2(BBT\ vs\ NBT)D/S$
Broad-base	96	MD_{32}	$\delta^2_{bD2} + r\delta^2_{TDE/S} + re\delta^2(NRT\ vs\ RET)D/S$
Narrow-base	96	ML_{33}	$\delta^2_{bD3} + r\delta^2_{TDE/S} + re\delta^2(SCT\ vs\ ILT)D/S$
Tester x F-Lines/S	288	MF_{30}	$\sigma^2_{bF} + r\sigma^2_{TFE/S} + re\sigma^2_{TF/S}$
BBT vs NBT	96	MF_{31}	$\delta^2_{bF1} + r\delta^2_{TFE/S} + re\delta^2(BBT\ vs\ NBT)F/S$
Broad-base	96	MF_{32}	$\delta^2_{bF2} + r\delta^2_{TFE/S} + re\delta^2(NRT\ vs\ RET)F/S$
Narrow-base	96	MF_{33}	$\delta^2_{bF3} + r\delta^2_{TFE/S} + re\delta^2(SCT\ vs\ ILT)F/S$
Tester x Lines x E/S	1152	ML_{20}	$\delta^2_{bL} + r\delta^2_{TLE/S}$
Tester x D x E/S	576	MD_{20}	$\delta^2_{bD} + r\delta^2_{TDE/S}$
BBT vs NBT	192	MD_{21}	$\delta^2_{bD1} + r\delta^2(BBT\ vs\ NBT)DE/S$
Broad-base	192	MD_{22}	$\delta^2_{bD2} + r\sigma^2(NRT\ vs\ RET)DE/S$
Narrow-base	192	MD_{23}	$\delta^2_{bD3} + r\delta^2(SCT\ vs\ ILT)DE/S$
Tester x F x E/S	576	MF_{20}	$\delta^2_{bF} + r\delta^2_{TFE/S}$
BBT vs NBT	192	MF_{21}	$\sigma^2_{bF1} + r\sigma^2(BBT\ vs\ NBT)FE/S$
Broad-base	192	MF_{22}	$\sigma^2_{bF2} + r\sigma^2(NRT\ vs\ RET)FE/S$
Narrow-base	192	MF_{23}	$\sigma^2_{bF3} + r\delta^2(SCT\ vs\ ILT)FE/S$
Error b	5400	ML_{10}	δ^2_{bL}
Error b/D-Lines	2700	MD_{10}	σ^2_{bD}
BBT vs NBT	900	MD_{11}	σ^2_{bD1}
Broad-base	900	MD_{12}	σ^2_{bD2}
Narrow-base	900	MD_{13}	δ^2_{bD3}
Error b/F-Lines	2700	MF_{10}	δ^2_{bF}
BBT vs NBT	900	MF_{11}	δ^2_{bF1}
Broad-base	900	MF_{12}	δ^2_{bF2}
Narrow-base	900	MF_{13}	δ^2_{bF2}

[a]D and F indicate lines from D219B00 and F209B00 populations, respectively. BBT indicates broad-base testers, NBT indicates narrow-base testers.

[b]r, l, t, e, and s represent the number of replications, S2 lines, testers, locations, and sets, respectively. In this experiment, r = 4, l = 25, t = 4, e = 3, and s = 8.

Y_{ijklm} : observed value for the l^{th} line crossed to m^{th} tester in the k^{th} replication, j^{th} set, and i^{th} location;

i : number of locations, $i = 1,2,3$;

j : number of sets, $j = 1,2,\ldots,8$;

k : number of replications, $k = 1,2,3,4$;

l : number of lines, $l = 1,2,\ldots,25$;

m : number of testers, $m = 1,2,3,4$;

u : overall mean;

E_i : effect of the i^{th} location, $i = 1,2,3$;

S_j : effect of the j^{th} set, $j = 1,2,\ldots,8$;

$(ES)_{ij}$: effect of the interaction between the i^{th} location and the j^{th} set;

$(R/SE)_{ijk}$: effect of the k^{th} replication in the ij^{th} location-set combination;

$(L/S/E)_{ijl}$: effect of the l^{th} line within the i^{th} set in the i^{th} location;

$(LE/S)_{ijl}$: effect of the interaction between the l^{th} line and the i^{th} location within the j^{th} set;

$(RL/S/E)_{ijkl}$: effect of the interaction between the l^{th} line and the k^{th} replication within the j^{th} set and the i^{th} location, which is the error a;

$(T/S/E)_{ijm}$: effect of the m^{th} tester within the j^{th} set and the i^{th} location;

$(TE/S)_{ijm}$: effect of the interaction between the m^{th} tester and the i^{th} location within the j^{th} set;

$(TL/S/E)_{ijlm}$: effect of the interaction between the l^{th} line and the m^{th} tester within the j^{th} set and the i^{th} location;

$(TLE/S)_{ijlm}$: effect of the interaction of the m^{th} tester, l^{th} line and the i^{th} location within the j^{th} set; and

e_{ijklm} : pooled error b.

Analyses of variance were performed as randomized complete block design for each individual type of progeny. The analysis of variance pooled over sets and combined over locations was performed according to the following model and is shown in Table 4.

$$Y_{ijkl} = u + E_i + S_j + (ES)_{ij} + (R/SE)_{ijk} + (L/S/E)_{ijl} + (LE/S)_{ijl} + e_{ijkl} ,$$

where

Y_{ijkl} : observed value for the l^{th} testcross in the k^{th} replication, j^{th} set, and i^{th} location;

i : number of locations, $i = 1,2,3$;

j : number of sets, $j = 1,2,\ldots,8$;

k : number of replications, $k = 1,2,3,4$;

l : number of lines, $l = 1,2,\ldots,25$;

u : overall mean;

E_i : effect of the i^{th} location, $i = 1,2,3$;

S_j : effect of the j^{th} set, $j = 1,2,\ldots,8$;

Table 4. Analysis of variance pooled over sets and combined over locations for individual testcrosses arranged as a randomized complete block design

Sources of variation	df	Mean squares	Expected mean squares[a]
Locations (E)	2		
Set (S)	7		
S x E	14		
Rep/S x E	72		
Testcross (TC)/S	192	MS_3TL_m	$\sigma^2_{TL_m} + r\sigma^2_{TL_mE/S} + re\sigma^2_{TL_m/S}$
Dent-TC/S	96	MS_3T_{Dm}	$\sigma^2_{TDm} + r\sigma^2_{TD_mE/S} + re\sigma^2_{TDm/S}$
Flint-TC/S	96	MS_3T_{Fm}	$\sigma^2_{TF_m} + r\sigma^2_{TF_mE/S} + re\sigma^2_{TF_m/S}$
Testcross x E/S	384	MS_2TL_m	$\sigma^2_{TL_m} + r\sigma^2_{TL_mE/S}$
Dent-TC x E/S	192	MS_2T_{Dm}	$\sigma^2_{TD_m} + r\sigma^2_{TD_mE/S}$
Flint-TC x E/S	192	MS_2T_{Fm}	$\sigma^2_{TF_m} + r\sigma^2_{TF_mE/S}$
Pooled error	1728	MS_1TL_m	$\sigma^2_{TL_m}$
Dent-TC error	864	MS_1T_{Dm}	$\sigma^2_{TD_m}$
Flint-TC error	864	MS_1T_{Fm}	$\sigma^2_{TF_m}$

[a] r and e represent the number of replications and locations, respectively. In this experiment:

r = 4

e = 3 for YIELD, EREPL, STAND, MOIST, and INDEX

e = 2 for PH, EH and FLOW

T_{Dm} correspond to testcrosses from population D219B00 made with tester m; m = n = 1,2,3,4;

T_{Fm} correspond to testcrosses from population F209B00 made with tester m; m = n = 1,2,3,4;

m = n testers, 1,2,3,4 with:

1 = parental population

2 = opposite population

3 = unrelated single-cross

4 = unrelated inbred line.

$(ES)_{ij}$: effect of the interaction between the i^{th} location and the j^{th} set;

$(R/SE)_{ijk}$: effect of the k^{th} replication in the ij^{th} location-set combination;

$(L/S/E)_{ijl}$: effect of the l^{th} line within the i^{th} set in the i^{th} location;

$(LE/S)_{ijl}$: effect of the interaction between the l^{th} line and the i^{th} location within the j^{th} set;

e_{ijkl} : effect of the interaction between the l^{th} line and the k^{th} replication within the j^{th} set and the i^{th} location, which is the experimental error;

In the analyses of variance, F-tests were performed with their proper degrees of freedom to test if the effects were different from zero. Direct F-tests were available for all sources of variation except for testers. The quasi F-ratio (Steel and Torrie, 1980) was used to test its significance. For the analyses of variance pooled over sets and combined over locations (Table 3), the quasi F-ratio used to determine the significance of testers was:

$$F' = \frac{ML_{50} + ML_{20}}{ML_{30} + ML_{40}}$$

with approximate numerator and denominator degrees of freedom:

$$\text{numerator df} = \frac{(ML_{50} + ML_{20})^2}{\frac{(ML_{50})^2}{dfML_{50}} + \frac{(ML_{20})^2}{dfML_{20}}}$$

$$\text{and denominator df} = \frac{(ML_{30} + ML_{40})^2}{\frac{(ML_{30})^2}{dfML_{30}} + \frac{(ML_{40})^2}{dfML_{40}}}$$

where: ML_{20}, ML_{30}, ML_{40}, and ML_{50} are the mean squares from the analyses of variance pooled over sets and combined over locations (Table 3). The symbols: $dfML_{20}$, $dfML_{30}$, $dfML_{40}$, and $dfML_{50}$ represent the degrees of freedom associated with the respective mean squares.

Analyses of covariance

The analysis of covariance for a trait X in the performance of the S2 lines with one tester and with the other testers was performed. The analysis of covariance pooled over sets and combined over locations is presented in Table 5.

An analysis of covariance between traits X and Y for the testcrosses with tester 1 (parental population) was performed. The analysis of covariance pooled over sets and combined over locations is presented in Table 6.

Statistical Genetic Procedures

Variance components

Estimates of variance components for S2 lines, line x tester, and tester x location interaction were obtained from the analyses of variance pooled over sets and combined over locations (Table 3). The formulas used to estimate the variance components and their respective variances were computed using the formulas of Comstock and Moll (1963). The formulas are presented for the variance components of both

Table 5. Analysis of covariance for grain yield pooled over sets and combined over locations between the performance of S2 lines with one tester and the other testers arranged as randomized complete block design

Sources of variation[a]	df	Mean products	Expected cross products[b]
Locations (E)	2		
Set (S)	7		
S x E	14		
Rep/S x E	72		
Testcross (TC)/S	192	M_3TL_m M_3TL_n	$\sigma_{TL_mT_n} + r\sigma_{GETL_mTL_n/S} + re\sigma_{GTL_mTL_n/S}$
Dent-TC/S	96	$M3TD_m$ M_3TD_n	$\sigma_{TD_mTD_n} + r\sigma_{GETD_mTD_n/S} + re\sigma_{GTD_mD_n/S}$
Flint-TC/S	96	M_3TF_m M_3TF_n	$\sigma_{TF_mTF_n} + r\sigma_{GETF_mTF_n/S} + re\sigma_{GTF_mF_n/S}$
TC x Location(E)/S	384	M_2TL_m M_2TL_n	$\sigma_{T_mT_n} + r\sigma_{GET_mT_n/S}$
Dent-TC x E/S	192	M_2TD_m M_2TD_n	$\sigma_{TD_mTD_n} + r\sigma_{GETD_mTD_n/S}$
Flint-TC x E/S	192	M_2TF_m M_2TF_n	$\sigma_{TF_mTF_n} + r\sigma_{GETF_mTF_n/S}$
Pooled error	1728	M_1TL_m M_1TL_n	$\sigma_{TL_mTL_n}$
Dent-TC error	864	M_1TD_m M_1TD_n	$\sigma_{TD_mTD_n}$
Flint-TC error	864	M_1TF_m M_1TF_n	$\sigma_{TF_mTF_n}$

[a]Dent-TC and Flint-TC represent the testcrosses from D219B00 and F209B00 populations, respectively.

[b]r and e: represent the number of replications and locations, respectively. T_{Dm}, T_{Dn} and TFm, TFn: represent the testcrosses from D219B00 and F209B00 populations made with tester m and n, respectively; m = n = testers 1,2,3, or 4; 1: parental population; 2: opposite population; 3: unrelated single cross; and 4: unrelated inbred line.

Table 6. Analysis of covariance pooled over sets and combined over locations between traits X and Y performed on testcrosses with tester 1 (parental population) arranged as randomized complete block design

Sources of variation[a]	df	Mean products		Expected cross products[b]
Locations (E)	2			
Set (S)	7			
S x E	14			
Rep/S x E	72			
Testcross (TC)/S	192	M_3T_x	M_3T_y	$\sigma_{T_{Lx}T_{Ly}} + r\sigma_{GE^{T}x^{T}y/S} + re\sigma_{G^{T}x^{T}y/S}$
Dent-TC/S	96	M_3T_{Dx}	M_3T_{Dy}	$\sigma_{T_{Dx}T_{Dy}} + r\sigma_{GE^{T}Dx^{T}Dy/S} + re\sigma_{G^{T}Dx^{T}Dy/S}$
Flint-TC/S	96	M_3T_{Fx}	M_3T_{Fy}	$\sigma_{T_{Fx}T_{Fy}} + r\sigma_{GE^{T^{F}}x^{T^{F}}y/S} + re\sigma_{G^{T}Fx^{T}Fy/S}$
TC x Location (E)/S	384	M_2T_x	M_2T_y	$\sigma_{T_xT_y} + r\sigma_{GE^{T}x^{T}y/S}$
Dent-TC x E/S	192	M_2T_{Dx}	M_2T_{Dy}	$\sigma_{T_{Dx}T_{Dy}} + r\sigma_{GE^{T}Dx^{T}Dy/S}$
Flint-TC x E/S	192	M_2T_{Fx}	M_2T_{Fy}	$\sigma_{T_{Fx}T_{Fy}} + r\sigma_{GE^{T}Fx^{T}Fy/S}$
Pooled error	1728	M_1T_x	M_1T_y	$\sigma_{T_xT_y}$
Dent-TC error	864	M_1T_{Dx}	M_1T_{Dy}	$\sigma_{T_{Dx}T_{Dy}}$
Flint-TC error	864	M_1T_{Fx}	M_1T_{Fy}	$\sigma_{T_{Fx}T_{Fy}}$

[a]Dent-TC and Flint-TC represent the testcrosses from D219B00 and F209B00 populations, respectively.

[b]r and e: represent the number of replications and locations, respectively. T_D and T_F: represent the testcrosses made with tester 1 (own population) of D219B00 and F209B00 populations, respectively. x : trait x; and y : trait y.

populations (subscript "L"). For D219B00 and F209B00 populations, the subscript "L" must be replaced by "D" and "F", respectively.

1. Variance among half-sibs of S_2 lines:

$$\delta^2_{L/s} = \frac{ML_{80} - ML_{70}}{ret}$$

$$V(\delta^2_{L/s}) = \frac{2}{(ret)^2}\left[\frac{(ML_{80})^2}{df_{(ML80)}+2} + \frac{(ML_{70})^2}{df_{(ML80)}+2}\right]$$

2. Tester x line interaction:

$$\delta^2_{TL/S} = \frac{ML_{30} - ML_{20}}{re}$$

$$V(\delta^2_{TL/S}) = \frac{2}{(re)^2}\left[\frac{(ML_{30})^2}{df_{(ML30)}+2} + \frac{(ML_{20})^2}{df_{(ML20)}+2}\right]$$

3. Tester x location interaction:

$$\delta^2_{TE/S} = \frac{ML_{40} - ML_{20}}{rl}$$

$$V(\delta^2_{TE/S}) = \frac{2}{(rl)^2}\left[\frac{(ML_{40})^2}{df_{(ML40)}+2} + \frac{(ML_{20})^2}{df_{(ML20)}+2}\right]$$

Components of variance were also estimated from the expected mean squares of the analyses of variance performed for each individual tester. The variances of these components were calculated using formulas presented by Comstock and Moll (1963). The formulas presented are for the variance components of both populations (subscript "L"). For D219B00 and F209B00 populations, the subscript "L" must be replaced by "D" and "F", respectively. These components and their variances were estimated from the Table 4 as follows:

1. Variance among testcrosses

$$\delta^2_{TL_m} = \frac{MS_3TL_m - MS_2TL_m}{re}$$

$$V(\delta^2_{TL_m}) = \frac{2}{(re)_2}\left[\frac{(MS_3TL_m)^2}{df(MS_3TL_m)+ 2} + \frac{(MS_2TL_m)^2}{df(MS_2TL_m)+ 2}\right]$$

2. Testcross x location interaction

$$\delta^2_{TL_mE} = \frac{MS2TL_m - MS1TL_m}{r};$$

$$V(\delta^2_{TL_mE}) = \frac{2}{(r)_2}\left[\frac{(MS_2TL_m)^2}{df(MS_2TL_m)+ 2} + \frac{(MS_1TL_m)^2}{df(MS_1TL_m)+ 2}\right]$$

Genetic and phenotypic parameters

Additive genetic variance, heritability coefficients on progeny mean basis, and genetic and phenotypic correlations between traits X and Y were calculated for both populations. For grain yield, expected genetic gain on the heterosis of the interpopulation hybrid between the two populations using reciprocal recurrent selection was also estimated. In addition, the phenotypic correlation coefficients between all possible pair of testers were estimated. These parameters were estimated as follows:

Additive genetic variances As shown before, the variance among testcrosses was calculated from the analyses of variance pooled over sets and combined over locations for each type of testcross (Table 4). When the parental population was used as a tester (tester 1), the variance among testcrosses correspond to the variance among

intrapopulation half-sib progenies (σ^2_G). This variance can be shown to be equivalent to (1+F)/4 of the additive genetic variance (σ^2_A), where F is the inbreeding coefficient of the parents. Therefore, the additive genetic variance (σ^2_A) for each population can be estimated as:

$$\sigma^2_A = \frac{4\ \sigma^2_G}{1 + F}$$

In this study, the inbreeding coefficient for parents (S_2 lines) was 3/4. Thus, the additive genetic variance (σ^2_A) and its variance [$V(\sigma^2_A)$] was estimated by the formula:

$$\sigma^2_A = 16/7\sigma^2_G$$

$$V(\sigma^2_A) = (16/7)^2\ V(\sigma^2_G);$$

where:

σ^2_G : genetic variance among testcrosses of S2 lines.

Heritability coefficients The coefficients of heritability were calculated on progeny mean basis from the analyses of variance pooled over sets and combined over locations for each individual type of testcross (Table 4). For each type of testcross, the heritability was calculated as follows:

$$h^2_D = \frac{\sigma^2_{TD_m/S}}{\frac{MS_3TD_m}{re}} \qquad V(h^2_D) = \frac{V(\sigma^2_{TD_m/S})}{\frac{MS_3TD_m}{re}}$$

$$h^2_F = \frac{\sigma^2_{TF_m/S}}{\frac{MS_3TF_m}{re}} \qquad V(h^2_F) = \frac{V(\sigma^2_{TF_m/S})}{\frac{MS_3TF_m}{re}}$$

where:

h^2_D and h^2_F : represent the heritability coefficients for D219B00 and F209B00 populations, respectively;

$V(h^2_D)$ and $V(h^2_F)$: represent the variance of the heritability coefficients for D219B00 and F209B00 populations, respectively;

$\sigma^2_{TD_m/S}$ and $\sigma^2_{TF_m/S}$: represent the genetic variance among testcrosses made with tester m for D219B00 and F209B00 populations, respectively;

MS_3TD_m and MS_3TF_m : represent the mean squares of testcrossess for D219B00 and F209B00 populations, respectively; and

r and e : represent the number of replications and locations, respectively.

Genetic and phenotypic correlations between traits Genetic and phenotypic correlations between grain yield, plant height, ear height, percentage of erect plants, and days-to-flower were calculated for intra- and interpopulation half-sib progenies. Variance and covariance components were obtained from the analyses of variance and covariance pooled over sets and combined over locations shown in Tables 4 and 6, respectively. The formulas presented are for the correlation coefficients considering both populations (subscript "L"). For D219B00

and F209B00 populations, the subscript "L" must be replaced by "D" and "F", respectively. The general formulas used to estimate these correlations were:

$$r_{phTL_xTL_y} = \frac{M_3TL_x \; M_3TL_y}{(MS_3TL_x \; MS_3TL_y)^{1/2}} \text{ ; and}$$

$$r_{GTL_xTL_y} = \frac{\sigma_{GTL_mTL_n/S}}{(\sigma^2_{TL_x/S} \; \sigma^2_{TL_y/S})^{1/2}};$$

where

$r_{phTL_xTL_y}$: phenotypic correlation between traits X and Y for each testcross; and

$r_{GTL_xTL_y}$: genotypic correlation between traits X and Y for each testcross.

Phenotypic correlations between testcrosses made with different testers Phenotypic correlations between testcrosses made with different testers were calculated for grain yield. Variance and covariance components were obtained from the analyses of variance and covariance pooled over sets and combined over locations shown in Tables 4 and 5, respectively. The general formulas used to estimate these correlations were:

$$r_{phTD_mTD_n} = \frac{M_3TD_m \; M_3TD_n}{(MS_3TD_m \; MS_3TD_n)^{1/2}} \text{ ; and}$$

$$r_{ph^{TF}m^{TF}n} = \frac{M_3TF_m \; M_3TF_n}{(MS_3TF_m \; MS_3TF_n)^{1/2}} \; ;$$

where

$r_{ph^{TD}m^{TD}n}$: phenotypic correlation between testcrosses made with tester m and testcross made with tester n for D219B00 population; and

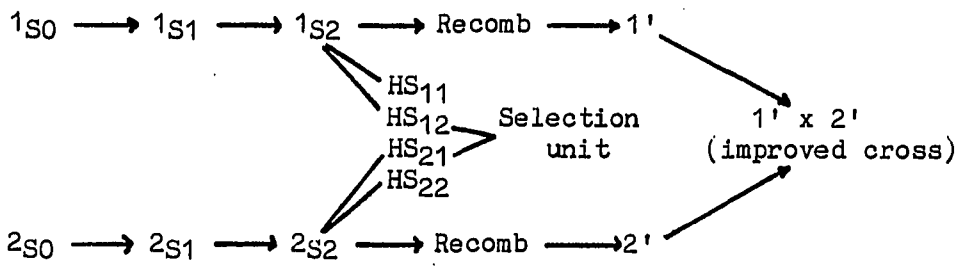
$r_{ph^{TF}m^{TF}n}$: phenotypic correlation between testcrosses made with tester m and testcross made with tester n for F209B00 population.

Expected genetic gain on heterosis The gain on heterosis of the population cross was calculated for reciprocal recurrent selection based on testcrosses of S2 lines. In this selection method, S2 lines are developed from each population. The S2 lines are crossed to the opposite population to produce the testcrosses for evaluation. The best testcrosses are selected and remnant seeds of the S2 lines are recombined to form the two improved populations.

Miranda Filho (1982) presented a method to estimate the heterosis of a population cross when noninbred parents are used to produce the testcrosses. The method used in the present study is an extension of his method, and it was developed considering the inbreeding level of the testcross parents.

The method requires two types of progenies for each population, intra- and interpopulation half-sibs. The S2 lines derived from a

population "1" are crossed to the parental population ("1") to produce the intrapopulation half-sibs and to the opposite population "2" to produce the interpopulation half-sibs. Similarly, the lines derived from population "2" are crossed to the populations "2" and "1".



The heterosis between 1' x 2' (improved cross) is estimated as follow:

$$g_h = g_{12} - \frac{1}{2}(g_{11} + g_{22}),$$

where:

g_h : heterosis of the improved cross;

g_{12} : expected genetic gain for the testcrosses between populations 1 and 2 ;

g_{11} : expected genetic gain for population 1 ;

g_{22} : expected genetic gain for population 2.

The components of variance were obtained from Table 7 as follows:

$$\sigma^2_{G_{11}} = \frac{P_{11} - I_{11}}{re} \quad ; \qquad \sigma^2_{G_{22}} = \frac{P_{22} - I_{22}}{re} \quad ;$$

Table 7. Analysis of variance pooled over sets and combined over locations for intra- and interpopulation progenies arranged as randomized complete block design

Sources[a] of variation	df	D219B00 1 as tester[b]		F209B00 as tester[b]	
		MS	Expected mean squares[c]	MS	Expected mean squares[c]
Locations (E)	2				
Set (S)	7				
S x E	14				
Rep/S x E	72				
Progenies(P)/S[b]	192				
D-P/S	96	P_{11}	$\sigma^2 + r\sigma^2_{GE_{11}/S} + re\sigma^2_{G_{11}/S}$	P_{12}	$\sigma^2 + r\sigma^2_{GE_{12}/S} + re\sigma^2_{G_{12}/S}$
F-P/S	96	P_{21}	$\sigma^2 + r\sigma^2_{GE_{21}/S} + re\sigma^2_{G_{21}/S}$	P_{22}	$\sigma^2 + r\sigma^2_{GE_{22}/S} + re\sigma^2_{G_{22}/S}$
P x E/S	384				
D-P x E/S	192	I_{11}	$\sigma^2 + r\sigma^2_{GE_{11}/S}$	I_{12}	$\sigma^2 + r\sigma^2_{GE_{12}/S}$
F-P x E/S	192	I_{21}	$\sigma^2 + r\sigma^2_{GE_{21}/S}$	I_{22}	$\sigma^2 + r\sigma^2_{GE_{22}/S}$
Pooled error	1728				
D-P error	864	E_{11}	σ^2	E_{12}	σ^2
F-P error	864	E_{21}	σ^2	E_{22}	σ^2

[a]D-P and F-P represent the lines from D219B00 and F209B00 populations, respectively.

[b]D219B00 and F209B00 populations were populations 1 and 2 respectively.

[c]r and e represent the number of replications and locations, respectively.

$$\sigma^2_{G_{21}} = \frac{P_{21} - I_{21}}{re} \quad ; \text{ and } \quad \sigma^2_{G12} = \frac{P_{12} - I_{12}}{re} ,$$

where:

$\sigma^2_{G_{11}}$ and $\sigma^2_{G_{22}}$: variance among intrapopulation half-sib progenies for populations D219B00 and F209B00, respectively;

$\sigma^2_{G_{21}}$ and $\sigma^2_{G_{12}}$: variance among interpopulation half-sib progenies for populations F209B00 and D219B00, respectively.

The components of covariance were obtained from Table 8 as follows:

$$\sigma_{P_{11}P_{12}} = \frac{MP_{11}MP_{12} - MI_{11}MI_{12}}{re} \quad ; \text{ and}$$

$$\sigma_{P_{21}P_{22}} = \frac{MP_{21}MP_{22} - MI_{21}MI_{22}}{re} ,$$

where:

$\sigma_{P_{11}P_{12}}$: genetic covariance between intra- and interpopulation half-sib progenies for population 1; and

$\sigma_{P_{21}P_{22}}$: genetic covariance between intra- and interpopulation half-sib progenies for population 2.

Assuming no epistasis and gene frequency equal to 1/2 for both populations, the components of variance and covariance have the following genetic interpretation:

Table 8. Analysis of covariance pooled over sets and combined over locations for intra- and interpopulation progenies arranged as a randomized complete block design

Sources of variation[a]	df	Mean squares	Expected cross products[b]
Locations (E)	2		
Set (S)	7		
S x E	14		
Rep/S x E	72		
Progenies(Prog)/S	192		
Dent-Prog/S	96	MP_{11} MP_{12}	$\sigma_{E_{11}E_{12}} + r\sigma_{I_{11}I_{12}} + re\sigma_{P_{11}P_{12}}$
Flint-Prog/S	96	MP_{21} MP_{22}	$\sigma_{E_{21}E_{22}} + r\sigma_{I_{21}I_{22}} + re\sigma_{P_{21}P_{22}}$
Prog x E/S	384		
Dent-Prog x E/S	192	MI_{11} MI_{12}	$\sigma_{E_{11}E_{12}} + r\sigma_{I_{11}I_{12}}$
Flint-Prog x E/S	192	MI_{21} MI_{22}	$\sigma_{E_{21}E_{22}} + r\sigma_{I_{21}I_{22}}$
Pooled error	1728		
Dent-Prog error	864	ME_{11} ME_{12}	$\sigma_{E_{11}E_{12}}$
Flint-Prog error	864	ME_{21} ME_{22}	$\sigma_{E_{21}E_{22}}$

[a]Dent and Flint represent the D219B00 and F209B00 populations, respectively.

[b]r and e represent the number of replications and locations, respectively.

$$\sigma^2_{G_{11}} = (1 + F)/4\ \sigma^2_{A_{11}} ;$$

$$\sigma^2_{G_{22}} = (1 + F)/4\ \sigma^2_{A_{22}} ;$$

$$\sigma^2_{G_{12}} = (1 + F)/8\ \sigma^2_{A_{12}} ;$$

$$\sigma^2_{G_{21}} = (1 + F)/8\ \sigma^2_{A_{21}} ;$$

$$\sigma_{P_{11}P_{12}} = (1 + F)/8\ \sigma_{A_1A_2} ; \text{ and}$$

$$\sigma_{P_{21}P_{22}} = (1 + F)/8\ \sigma_{A_2A_1} ,$$

where:

$\sigma^2_{A_{11}}$ and $\sigma^2_{A_{22}}$: additive genetic variance among intrapopulation half-sib progenies for populations 1 and 2, respectively;

$\sigma^2_{A_{12}}$ and $\sigma^2_{A_{21}}$: additive genetic variance among interpopulation half-sib progenies between population 1 (S2 lines) and 2 (tester), and between populations 2 (S2 lines) and 1 (tester), respectively;

$\sigma_{A_1A_2}$ and $\sigma_{A_2A_1}$: additive genetic covariance among intra- and interpopulational half-sib progenies of populations 1 (S2 lines) and 2 (tester), and among population 2 (S2 lines) and 1 (tester), respectively;

The expected genetic gains per cycle for intra- and interpopulation selections were calculated using the components of variance and covariance from Tables 7 and 8. Interpopulation testcrosses (S2 lines crossed with the opposite population) were the unit of evaluation, and S2 lines were the unit of recombination. The formulas used to calculate the expected genetic gain were:

$$g_{11} = ck \frac{\sigma_{P_{11}P_{12}}}{(P_{12}/re)^{1/2}}$$

$$g_{22} = ck \frac{\sigma_{P_{21}P_{22}}}{(P_{21}/re)^{1/2}}$$

$$g_{12} = \frac{ck}{2} \left(\frac{\delta^2_{P_{12}}}{(P_{12}/re)^{1/2}} + \frac{\delta^2_{P_{21}}}{(P_{21}/re)^{1/2}} \right)$$

where:

g_{11} : expected genetic gain for population 1;

g_{22} : expected genetic gain for population 2;

g_{12} : expected genetic gain for the testcrosses between populations 1 and 2;

c : Parental control. In this situation, c = 2;

k : Standardized selection intensity;

r and e : Number of replications and locations, respectively;

$\delta P_{11}P_{12}$ and $\delta P_{21}P_{22}$: 7/16 of the additive genetic covariances between intra- and interpopulation testcrosses of populations 1 and 2 and vice versa, respectively;

$\delta^2 P_{12}$ and $\delta^2 P_{21}$: 7/16 of the additive genetic variance among

interpopulation testcrosses of populations 1 and 2, and 2 and 1, respectively;

P12 and P21 : Mean squares of interpopulation testcrosses between populations 1 and 2, and 2 and 1, respectively.

RESULTS AND DISCUSSION

The analyses of variance pooled over sets, means and coefficients of variation (CVs) for each individual location are presented in the Appendix, Tables A1 to A5. The means for grain yield ranged from 4.33 Mg/ha (Ituiutaba) to 5.44 Mg/ha (Matao). The CVs for main plots were 17.8%, 19.5%, and 36.8% for Matao, Ituiutaba, and Rio Verde, respectively. For the sub plots the values were 15.0% (Matao), 14.1% (Ituiutaba), and 21.3% (Rio Verde). The highest CVs were from Rio Verde where the experimental area was very heterogeneous for soil fertility.

The analyses of variance pooled over sets and combined over locations for eight traits are shown in Tables 9 and 10. The coefficients of variation averaged over both populations were relatively high for yield and index. For yield, the CV was 25.4% for the main plots and 17.0% for the subplots, while for index they were 20.6% for the main plots and 13.3% for the subplots. For the other traits they ranged from 2.1% (days-to-flower) to 11.3% (ear height), which are relatively small.

Mean squares for lines, testers, their interactions with locations, and line x tester interactions in the combined analyses were significantly ($P \leq 0.01$) different from zero for all traits, except for stand. The nonsignificant main and interaction effects for stand indicate that the entries within each experiment had very uniform stands. Stand was used only to express percentage of erect plants. It was not used to adjust yield because of small differences in stand among

Table 9. Analysis of variance pooled over sets and combined over locations of a split-plot experiment planted at three locations in Brazil during the 1984/85 agricultural year

Sources of variation[b]	df	Mean squares[a]				
		YIELD (Mg/ha)	EREPL (%)	MOIST (%)	STAND	INDEX
Locations (E)	2	1140.6255**	34397.72**	75385.26**	234.81*	56.30ns
Sets (S)	7	6.1762ns	3793.81ns	958.80ns	70.84ns	22.09ns
E x S	14	18.1048**	2153.58**	514.05**	61.29**	64.95**
Reps/S x E	72	3.2557**	223.90**	52.38**	10.90**	8.38**
Lines/S (L)	192	8.8935**	394.56**	18.69**	6.37ns	7.05**
D-Lines/S	96	7.2971**	310.38**	18.40**	7.87ns	4.81**
F-Lines/S	96	10.4900**	478.75**	18.98**	4.88ns	9.28**
Lines x E/S	384	2.0563**	133.84**	6.56**	5.16ns	3.38**
D-Lines x E/S	192	2.1107**	145.10**	6.23**	6.40ns	2.89**
F-Lines x E/S	192	2.0018**	122.58**	6.90**	3.92ns	3.87**
Error a	1728	1.4687**	83.90**	2.49**	5.21**	1.59**
Error a D-Lines	864	1.5173**	88.88**	2.39**	6.45**	1.51**
Error a F-Lines	864	1.4201**	78.92**	2.60**	3.97**	1.66**
Tester/S	24	46.7720**	651.99**	53.60**	6.16ns	20.05**
Tester/D-Lines	12	59.8007**	929.21**	96.30**	4.95ns	29.42**
BBT vs NBT	4	29.6826ns	153.85ns	267.81**	7.67ns	2.58ns
Broad-base (BBT)	4	12.4111*	65.83ns	4.47ns	1.77ns	1.44ns
Narrow-base (NBT)	4	137.3083**	2567.97**	16.61**	5.40ns	84.25**
Tester/F-Lines	12	33.7434**	374.76**	10.90ns	7.37ns	10.68ns
BBT vs NBT	4	83.3901**	102.14ns	25.46ns	10.62ns	28.29ns
Broad-base	4	4.7415*	53.01ns	3.66ns	3.95ns	2.11ns
Narrow-base	4	13.0986ns	969.14**	3.56ns	7.53ns	1.63ns

[a]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; STAND: plants available at harvest; and INDEX: eye appearance, rated from 1 (excellent) to 9 (poor).

[b]D indicates lines from the dent population (D219B00), F indicates lines from the flint population (F209B00), BBT indicates broad-base testers, NBT indicates narrow-base testers. The broad-base testers were the parental and opposite populations, and the narrow-base testers were a single cross and an inbred line.

*$p \leq .05$.

**$p \leq .01$.

Table 9. (continued)

Sources of variation[b]	df	Mean squares[a] YIELD (Mg/ha)	EREPL (%)	MOIST (%)	STAND	INDEX
Tester x E/S	48	3.8997**	161.98**	9.95**	4.67ns	4.87**
Tester x E/D-Sets	24	5.1431**	260.08**	11.13**	5.11ns	3.12**
BBT vs NBT	8	10.6765**	270.25*	29.14**	5.23ns	2.80**
Broad-base	8	2.2194*	98.68ns	2.75**	4.56ns	0.96ns
Narrow-base	8	2.5335**	411.30**	1.51ns	5.53ns	5.61**
Tester x E/F-Sets	24	2.6563**	63.89ns	8.77**	4.23ns	6.61**
BBT vs NBT	8	3.0187**	45.01ns	17.64**	4.47ns	10.61**
Broad-base	8	0.6658ns	46.54ns	1.44ns	5.45ns	0.71ns
Narrow-base	8	4.2843**	100.10ns	7.22**	2.75ns	8.51**
Tester x Lines/S	576	1.3865**	100.82**	1.87**	3.78ns	1.08**
Tester x D-Lines/S	288	1.0997*	102.48*	1.87**	4.36ns	0.82**
(BBT vs NBT)	96	1.4178**	106.75ns	2.42**	4.75ns	0.85ns
(Broad-base)	96	0.9214ns	92.05ns	1.52*	3.52ns	0.90ns
(Narrow-base)	96	0.9599ns	108.63**	1.68**	4.81ns	0.71ns
Tester x F-Lines/S	288	1.6734**	99.16**	1.86**	3.20ns	1.34**
(BBT vs NBT)	96	3.0251**	136.94**	2.18**	3.46ns	2.19**
(Broad-base)	96	1.0186**	82.17ns	1.96ns	3.63ns	0.80ns
(Narrow-base)	96	0.9764*	78.38ns	1.45ns	2.52ns	1.01ns
Tester x Line x E/S	1152	0.7608**	75.02**	1.21ns	3.94ns	0.83**
Tester x D x E/S	576	0.8658**	81.55ns	1.05ns	4.15ns	0.79**
(BBT vs NBT)	192	0.8406ns	104.34**	1.10ns	4.51ns	0.83ns
Broad-base	192	0.9275*	69.45ns	1.02ns	3.84ns	0.69ns
Narrow-base	192	0.8293ns	70.86ns	1.05ns	4.11ns	0.87**
Tester x F x E/S	576	0.6559*	68.49**	1.37ns	3.73*	0.87**
(BBT vs NBT)	192	0.6965ns	64.02ns	1.50ns	3.66ns	1.04**
Broad-base	192	0.5767ns	69.14*	1.47ns	4.35ns	0.72ns
Narrow-base	192	0.6945*	72.32**	1.13*	3.18*	0.85ns
Error b	5400	0.6570	67.58	1.13	3.90	0.70
Error b/D-Lines	2700	0.7274	78.46	1.00	4.44	0.65
(BBT vs NBT)	900	0.7540	77.01	1.04	4.48	0.70
Broad base	900	0.7301	81.03	1.05	4.53	0.59
Narrow base	900	0.6982	77.34	0.91	4.32	0.67
Error b/F-Lines	2700	0.5866	56.71	1.25	3.35	0.74
(BBT vs NBT)	900	0.5918	56.52	1.28	3.49	0.78
Broad base	900	0.6032	57.80	1.56	3.95	0.66
Narrow base	900	0.5647	55.80	0.92	2.60	0.79

Table 9. (continued)

Sources of variation[b]	df	Mean squares[a]				
		YIELD (Mg/ha)	EREPL (%)	MOIST (%)	STAND	INDEX
Mean		4.76	90.5	20.5	24.3	6.3
Mean D-Lines		4.72	89.4	19.9	24.1	6.3
Mean F-Lines		4.81	91.5	21.2	24.5	6.3
CVa (%)[c]		25.4	10.1	7.7	9.4	20.0
CVa D-Lines		26.1	10.5	7.8	10.5	19.5
CVa F-Lines		24.8	9.7	7.6	8.1	20.6
CVb (%)[c]		17.0	9.1	5.2	8.1	13.3
CVb D-Lines		18.1	9.9	5.0	8.7	12.8
CVb F-Lines		15.9	8.2	5.3	7.5	13.8

[c]CVa is coefficient of variation for whole plots and CVb is coefficient of variation for subplots.

Table 10. Analysis of variance pooled over sets and combined over locations of a split-plot experiment planted at three locations in Brazil during the 1984/85 agricultural year

Sources of variation[b]	df	Mean squares[a]		
		PH (cm)	EH (cm)	FLOW
Locations (E)	1	8249.18ns	44526.28ns	8681.58**
Sets (S)	7	5408.22ns	3036.36ns	168.71ns
E x S	7	6536.64**	4398.01**	272.15**
Reps/S x E	48	523.18**	399.69**	15.80**
Lines/S (L)	192	1841.37**	1159.35**	26.82**
D-Lines/S	96	1848.95**	1063.71**	24.86**
F-Lines/S	96	1833.80**	1254.98**	28.79**
Lines x E/S	192	257.50**	161.90**	7.65**
D-Lines x E/S	96	265.46**	154.60**	7.08**
F-Lines x E/S	96	249.53**	169.20**	8.22**
Error a	1152	145.75**	100.68**	4.82**
Error a D-Lines	576	131.08**	82.04**	4.33**
Error a F-Lines	576	160.41**	119.32**	5.31**
Tester/S	24	1351.28**	823.58**	157.27**
Tester/D-Lines	12	1880.54**	1550.72**	194.27**
BBT vs NBT	4	1209.62**	199.47ns	569.59**
Broad-base	4	461.27**	827.01**	9.29ns
Narrow-base	4	3970.74**	3625.67**	3.92ns
Tester/F-Lines	12	822.02**	96.45ns	120.27**
BBT vs NBT	4	195.92ns	150.54ns	349.71**
Broad-base	4	55.05ns	105.09ns	4.50ns
Narrow-base	4	2215.09**	33.72ns	6.59ns

[a]PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]D indicates lines from the dent population (D219B00), F indicates lines from the flint population (F209B00), BBT indicates broad-base testers, NBT indicates narrow-base testers. The broad-base testers were the parental and opposite populations, and the narrow-base testers were a single cross and an inbred line.

* $p \leq .05$.

** $p \leq .01$.

Table 10. (continued)

Sources of variation[b]	df	Mean squares[a] PH (cm)	EH (cm)	FLOW
Tester x E/S	24	220.77**	128.80**	6.44**
Tester x E/D-Sets	12	206.00**	163.08**	7.20**
BBT vs NBT	4	174.23*	88.05ns	18.16**
Broad-base	4	45.13ns	18.39ns	1.62ns
Narrow-base	4	398.64**	382.80**	1.82ns
Tester x E/F-Sets	12	235.53**	94.52ns	5.68*
BBT vs NBT	4	333.24**	127.32**	13.84**
Broad-base	4	96.13ns	73.98ns	0.89ns
Narrow-base	4	277.23**	82.28ns	2.31ns
Tester x Lines/S	576	114.06**	94.53**	3.51**
Tester x D-Lines/S	288	113.32**	98.16**	3.81**
(BBT vs NBT) x D/S	96	117.78**	83.98**	3.95*
Broad-base x D/S	96	127.08*	113.84*	3.32*
Narrow-base x D/S	96	95.10**	96.65**	4.17**
Tester x F-Lines/S	288	114.79**	90.90**	3.21ns
(BBT vs NBT) x F/S	96	135.45**	103.38**	4.49**
Broad-base x F/S	96	126.14**	97.59*	2.95ns
Narrow-base x F/S	96	82.79*	71.74*	2.20ns
Tester x Lines x E/S	576	58.08ns	51.70ns	2.51ns
Tester x D x E/S	288	59.12ns	50.26ns	2.29ns
(BBT vs NBT) x D x E/S	96	52.90ns	46.12ns	2.59ns
Broad-base x D x E/S	96	89.23ns	70.05ns	2.32ns
Narrow-base x D x E/S	96	35.24ns	34.61ns	1.95ns
Tester x F x E/S	288	57.04ns	53.15ns	2.73**
(BBT vs NBT) x F x E/S	96	50.97ns	46.53ns	2.32ns
Broad-base x F x E/S	96	68.66ns	65.35*	3.18**
Narrow-base x F x E/S	96	51.47ns	47.55ns	2.71ns
Error b	3600	56.93	49.09	2.30
Error b/D-Lines	1800	58.27	49.10	2.43
Error b/(BBT vs NBT)	600	59.16	47.66	2.61
Error b/(Broad base)	600	72.73	57.63	2.51
Error b/(Narrow base)	600	42.92	42.02	2.15
Error b/F-Lines	1800	55.58	49.09	2.17
Error b/(BBT vs NBT)	600	56.34	49.72	2.11
Error b/(Broad base)	600	60.58	50.77	2.26
Error b/(Narrow base)	600	49.84	46.77	2.13
Mean		175.1	89.0	71.2
Mean D-Lines		174.8	88.8	71.2
Mean F-Lines		175.4	89.2	71.2

Table 10. (continued)

Sources of variation[b]	df	Mean squares[a] PH (cm)	EH (cm)	FLOW
CVa (%)[c]		6.9	11.3	3.1
CVa D-Lines		6.5	10.2	2.9
CVa F-Lines		7.2	12.2	3.2
CVb (%)[c]		4.3	7.9	2.1
CVb D-Lines		4.4	7.9	2.2
CVb F-Lines		4.2	7.9	2.1

[c]CVa is coefficient of variation for whole plots and CVb is coefficient of variation for subplots.

entries. The partition of the mean squares for lines and lines x locations into D219B00 and F209B00 populations showed that they also were highly significant ($P \leq 0.01$), indicating the presence of genetic variability and an inconsistent performance of the lines across locations within these two populations for all traits.

The mean squares for testers were highly significant for D219B00 population for all traits, but they were not significant for moisture, index, and ear height in the F209B00 population. Mean squares for tester x location interaction were significant for both populations except for percentage of erect plants and ear height in the F209B00 population. Tester x line interactions were significant ($P \leq 0.05$) for yield and percentage of erect plants in the D219B00 population and nonsignificant for days-to-flower in the F219B00 population. For the other traits they were highly significant for both populations.

The testers were divided in broad-genetic base tester (BBT) and narrow-genetic base tester (NBT). This partition permitted three orthogonal comparisons: 1) BBT vs. NBT, 2) within BBT, and 3) within NBT. Narrow-base testers, followed by broad vs. narrow and broad-genetic base testers, had the greatest contribution to tester effects in the D219B00 population for all traits, except for moisture and days-to-flower. For population F209B00, the trend was broad vs. narrow, narrow, and broad-genetic base testers, except for percentage of erect plants and plant height. Broad-base testers were significantly different for plant and ear height ($P \leq 0.01$) in the D219B00 population and yield in both populations ($P \leq 0.05$). The mean squares for the narrow-genetic

base testers were highly significant for all traits, except for days-to-flower in the D219B00 population. For the F209B00 population, however, the narrow-genetic base testers were significantly different ($P \leq 0.01$) only for yield and plant height.

The BBT x location interaction was significant only for yield ($P \leq 0.05$) and moisture ($P \leq 0.01$) in the D219B00 population. The NBT x location interaction was significant for all traits, except for percentage of erect plants and ear height in the F209B00 population and for days-to-flower in both populations. This indicates that broad-base testers were more stable across locations than were narrow-base testers.

For the F209B00 population, the (BBT vs NBT) x line interaction mean squares were significant for all traits and had the greatest contribution for the line x tester interaction for all traits. The broad base x tester and narrow base x tester interaction mean squares were significant for yield and plant and ear height. For the D219B00 population, the (BBT vs NBT) x line interaction mean squares were significant for all traits, except for percentage of erect plants and index. The broad-base tester x line interaction mean squares were significant ($P \leq 0.05$) for moisture, days-to-flower, and plant and ear height. The narrow-base tester x line interaction was significant for all traits except for yield and index.

The means of the 800 topcrosses over replications and locations are presented in the Appendix in Table A8. The means, minimum and maximum values, range of variation, and the genetic variation coefficient (CVg) for five traits, each tester, and population are shown in Table 11.

Table 11. 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

Trait[a]	Pop	Tester[b]	Mean	Min	Max	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
EREPL (%)	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	78.3	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
PH (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

[a]YIELD: grain yield; EREPL: percentage of erect plants; PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]Testers 1 and 2 are genetically broad-base testers and testers 3 and 4 are genetically narrow-base testers.

Table 11. (continued)

Trait[a]	Pop	Tester[b]	Mean	Min	Max	Range	CVg %
EH (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
	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
FLOW	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

Comparisons of these means can be performed by the F-tests from Tables 10 and 11. Testers 1 (parental population) and 2 (opposite population) were broad-genetic base testers, while testers 3 (single cross) and 4 (inbred line) were narrow-genetic base testers. For both populations the means of testcrosses with tester 2 were higher than the means of testcrosses with tester 1 for all traits, except for plant height in the population F209B00, and days-to-flower in both populations, where the values were equal. However, the means were significantly different for plant and ear height ($P \leq 0.01$) in the D219B00 population and for yield in both populations ($P \leq 0.05$). These results indicate that the two types of testcrosses have some similarities and little heterosis should be expected between the two populations. Heterosis for grain yield on mid parents was 0.225 Mg/ha or 5%.

The LSD.05 values for comparing the means of both populations were 0.14 Mg/ha for grain yield, 1.39% for percentage of erect plants, 1.49cm for plant height, 1.40cm for ear height, and 0.31 for days-to-flower. Except for ear height, no significant differences were found for the other traits, indicating that the two populations had similar performance. This similar performance maybe due to the number of backcrosses (BC1), and the use of the same donor parent during the conversion program of the normal populations to brachytic.

The means of D219B00 lines with tester 3 were significantly ($P \leq 0.01$) lower than the means of the lines with tester 4 for all traits, except for days-to-flower, which was not significant. Tester 3 for D219B00 population was a single cross (FBR2-89 x FBR2-848) and

tester 4 an inbred line (FBR2-89). Both testers had the one inbred line FBR2-89 in common. The FBR2-89 and FBR2-848 lines were previously selected for general combining ability (GCA) based on topcrosses with D219B00 population. There were indications that for yield the GCA of FBR2-89 line was higher than FBR2-848. The significantly lower mean of the testcrosses with the single cross (FBR2-89 x FBR2-848) tester provides further evidence on the relative combining ability of two lines. Considering that the two testers were evaluated with the same set of 100 S2 lines, the average performance of the testers over the lines is a measure of the GCA of these two testers. Therefore, the inbred line FBR2-89 had higher general combining than did the single cross (FBR2-89 x FBR2-848).

For F209B00 population, the means of the lines with tester 3 were higher than the means with tester 4 for all traits, except for ear height where the values were equal. The differences, however, were significant only for percentage of erect plants and plant height. Tester 3 was a single cross formed by the RBR2-305 and DBR2-9 lines; tester 4 was the inbred line RBR2-305. The DBR2-9 line was previously selected by its high yielding ability in topcross with the F209B00 population. Line RBR2-305 was derived from a pedigree selection program and selected for its high performance per se. Although the grain yield mean of the lines with tester 3 (RBR2-305 x DBR2-9) was not significantly higher than the mean of the lines with tester 4 (RBR2-305), there was a tendency for higher means of the lines with tester 3 than with tester 4. This may indicate that the DBR2-9 line has

higher GCA than line RBR2-305.

The coefficients of genetic variation for plant and ear height had the tendency to be higher with narrow-genetic base testers (testers 3 and 4) than for broad-genetic base testers. For the other traits, no clear trend was detected. However, there was a strong tendency for higher CVg when the inbred line RBR2-305 was included in the pedigree of the testers.

The frequency distributions for grain yield of the four types of testcrosses are shown in Figs. 1 and 2 for the D219B00 and F209B00 populations, respectively. For the D219B00 population, tester 3 (single cross) had a tendency to have a performance very similar to the parental population. The mean and maximum values were similar, but the single cross had higher minimum values and, consequently, a lower range. Comparing the broad-genetic base testers, testers 1 and 2, tester 2 had a frequency distribution similar to tester 1 (parental population) with a tendency to have higher mean values in the D219B00 population. The narrow-genetic base testers had a different overall performance. In population D219B00 the inbred line tester had greater mean values and smaller range of variation. Considering that the difference between these two testers 3 and 4 was the line FBR2-848, and that they were crossed to the same gene array, this suggests FBR2-848 line has lower GCA than line FBR2-89. For the F209B00 population there is a clearer separation between broad-genetic base testers and narrow-genetic base testers. Broad-base testers had lower means and ranges of variation than did narrow-genetic base testers. Both testers had similar means,

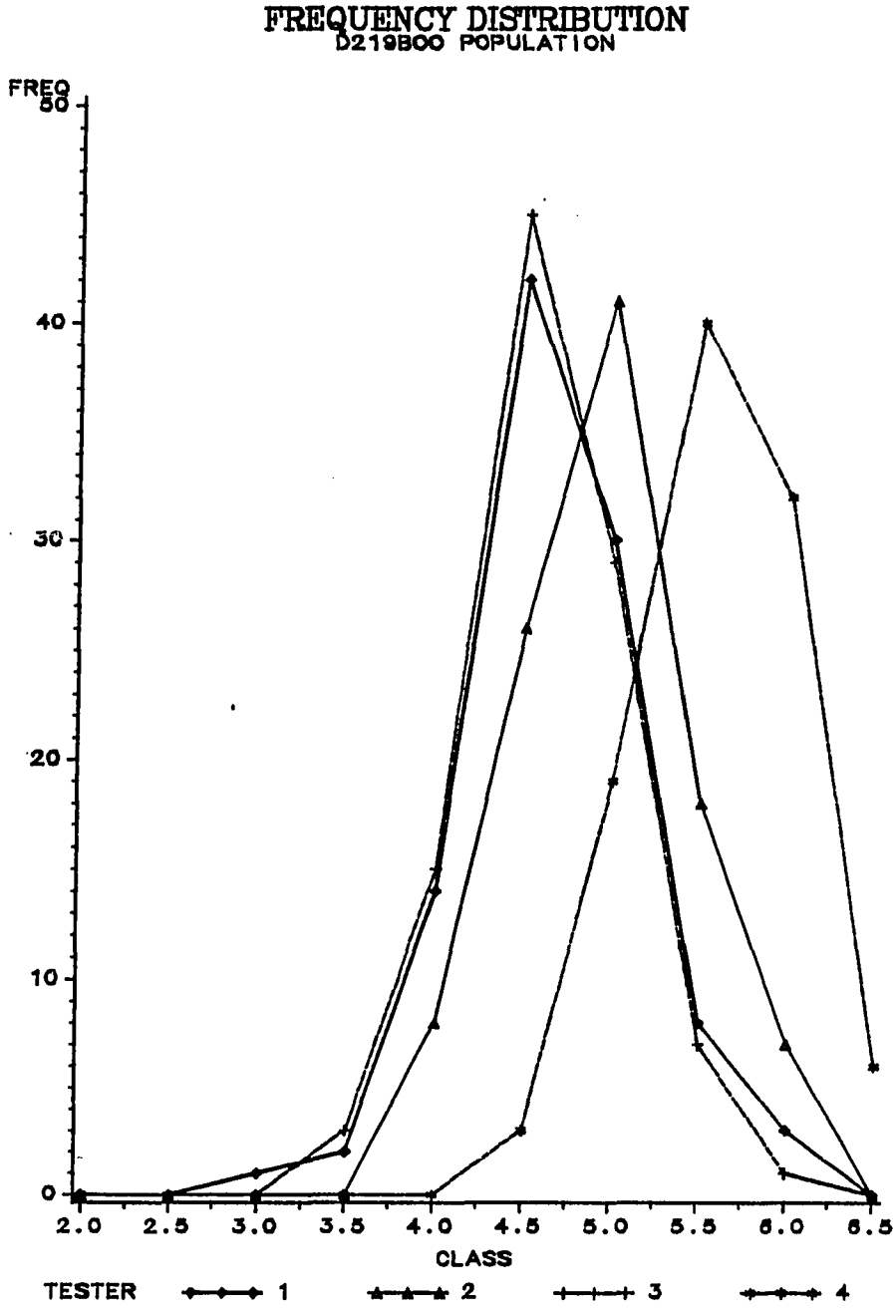


Fig. 1. Frequency distribution of yield of four types of testcrosses produced by crossing S2 lines derived from D219B00 population with the parental population (tester 1), opposite population (tester 2), unrelated single cross (tester 3), and unrelated inbred line (tester 4)

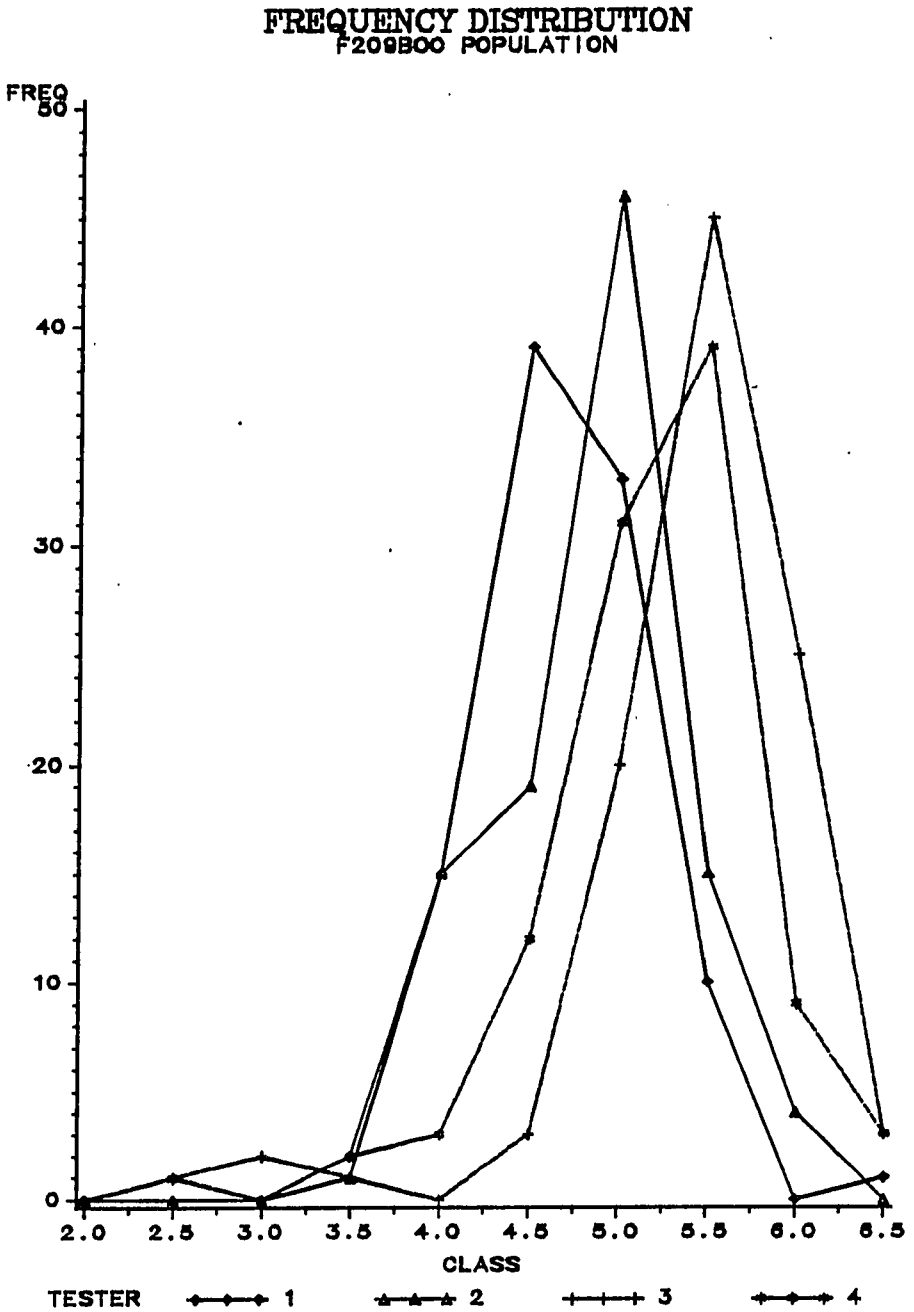


Fig. 2. Frequency distribution of yield of four types of testcrosses produced by crossing S2 lines derived from F209800 population with the parental population (tester 1), opposite population (tester 2), unrelated single cross (tester 3), and unrelated inbred line (tester 4)

but the range of variation was lower for the single cross. Although no significant difference was detected between the combining ability of the two narrow-base testers, the single-cross tester (RBR2-305 x DBR2-9) had better combining ability than did the inbred-line tester DBR2-9. Previous information indicates that the RBR2-305 inbred line has lower combining ability and better performance per se than DBR2-9. Therefore, in both populations, lines with lower GCA had greater range of variation and CVg. The F209B00 lines crossed with tester 3 (RBR2-305 x DBR2-9) had a slightly higher mean than the same lines crossed with tester 4 (RBR2-305) and had a tendency to have a larger number of testcrosses above the mean of the inbred line tester (RBR2-305). Therefore, DBR2-9 inbred line could transmit its higher combining ability to the testcrosses even when it is in combination with RBR2-305 line. This suggests that the higher GCA of DBR2-9 line was due to the presence of favorable alleles at loci not present in RBR2-305.

The estimates of genetic components for lines, tester x line, and tester x location interactions of the analyses of variance pooled over sets and combined over locations are presented in Tables 12 and 13. In all instances, the estimates of the genetic components of variance of the S2 lines were greater than the tester x line interaction, suggesting consistent performance of the lines over testers. The variance component among lines for F209B00 population was approximately twice the component among lines for D219B00 population. This result was unexpected because both populations were broad-base populations; both were formed by recombining a large number of varieties with no

Table 12. Estimates of variance components and standard errors for four traits of S2 lines and tester x line and tester x location interactions evaluated at three locations in Brazil

Sources of variation[b]	Traits[a]			
	YIELD (Mg/ha)	EREPL %	MOIST %	INDEX
D219B00 lines (D-lines)	0.1080 ± 0.0222	3.44 ± 0.97	0.25 ± 0.06	0.04 ± 0.02
F209B00 lines (F-lines)	0.1768 ± 0.0315	7.42 ± 1.45	0.25 ± 0.06	0.11 ± 0.03
Testers x Lines	0.0521 ± 0.0104	2.15 ± 0.79	0.05 ± 0.01	0.02 ± 0.01
Testers x D-lines	0.0195 ± 0.0087	1.74 ± 0.81	0.07 ± 0.01	0.00 ± 0.01
(BBT vs NBT) x D-lines	0.0481 ± 0.0183	0.20 ± 1.55	0.11 ± 0.03	0.00 ± 0.01
Broad base x D-lines	-0.0005 ± 0.0135	1.88 ± 1.24	0.04 ± 0.02	0.02 ± 0.01
Narrow base x D-lines	0.0109 ± 0.0134	3.15 ± 1.43	0.05 ± 0.02	-0.01 ± 0.01
Testers x F-lines	0.0848 ± 0.0120	2.56 ± 0.76	0.04 ± 0.01	0.04 ± 0.01
(BBT vs NBT) x F-lines	0.1941 ± 0.0365	6.08 ± 1.72	0.06 ± 0.03	0.10 ± 0.03
Broad base x F-lines	0.0368 ± 0.0131	1.09 ± 1.14	0.04 ± 0.03	0.01 ± 0.01
Narrow base x F-lines	0.0235 ± 0.0130	0.50 ± 1.12	0.03 ± 0.02	0.01 ± 0.01
Tester x location	0.0314 ± 0.0078	0.87 ± 0.33	0.09 ± 0.02	0.04 ± 0.01
Tester x location/D-lines	0.0428 ± 0.0143	1.79 ± 0.72	0.10 ± 0.03	0.02 ± 0.01
(BBT vs NBT) x L/D-lines	0.0984 ± 0.0478	1.66 ± 1.21	0.28 ± 0.13	0.02 ± 0.01
Broad base x L/D-lines	0.0129 ± 0.0100	0.29 ± 0.45	0.02 ± 0.01	0.00 ± 0.00
Narrow base x L/D-lines	0.0170 ± 0.0114	3.40 ± 1.84	0.00 ± 0.01	0.05 ± 0.03
Tester x location/F-lines	0.0200 ± 0.0074	-0.05 ± 0.18	0.07 ± 0.02	0.06 ± 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
Broad base x L/F-lines	0.0009 ± 0.0030	-0.23 ± 0.22	0.00 ± 0.01	0.00 ± 0.00
Narrow base x L/F-lines	0.0359 ± 0.0192	0.28 ± 0.45	0.06 ± 0.03	0.08 ± 0.04

[a]BBT indicates broad-base testers, NBT indicates narrow-base testers. The broad-base testers were the parental and opposite populations, and the narrow-base testers were a single cross and an inbred line.

[b]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; and INDEX: eye appearance, rated from 1 (excellent) to 9 (poor).

Table 13. Estimates of variance components and standard errors for three traits of S2 lines and tester x line and tester x location interactions evaluated at three locations in Brazil

Sources of variation[b]	Traits[a]		
	PH (cm)	EH (cm)	FLOW
D219B00 lines	49.48 ± 8.30	28.41 ± 4.77	0.56 ± 0.11
F209B00 lines	49.51 ± 8.22	33.93 ± 5.63	0.64 ± 0.13
Testers x Lines	7.00 ± 1.26	5.35 ± 1.05	0.13 ± 0.04
Testers x D-lines	6.77 ± 1.25	5.99 ± 1.08	0.19 ± 0.04
(BBT vs NBT) x D-lines	8.11 ± 2.21	4.73 ± 1.61	0.17 ± 0.08
Broad-base x D-lines	4.73 ± 2.54	5.47 ± 2.22	0.12 ± 0.07
Narrow-base x D-lines	7.48 ± 1.76	7.75 ± 1.78	0.28 ± 0.08
Testers x F-lines	7.22 ± 1.26	4.72 ± 1.02	0.06 ± 0.04
(BBT vs NBT) x F-lines	10.56 ± 2.50	7.11 ± 1.94	0.27 ± 0.09
Broad-base x F-lines	7.18 ± 2.42	4.03 ± 1.93	-0.03 ± 0.07
Narrow-base x F-lines	3.91 ± 1.62	3.02 ± 1.42	-0.06 ± 0.05
Tester x locations	1.63 ± 0.61	0.77 ± 0.36	0.04 ± 0.02
Testers x locations/D-lines	1.47 ± 0.78	1.13 ± 0.62	0.05 ± 0.03
(BBT vs NBT) x L/D-lines	1.21 ± 1.01	0.42 ± 0.51	0.16 ± 0.10
Broad base x L/D-lines	-0.44 ± 0.29	-0.52 ± 0.15	-0.01 ± 0.01
Narrow base x L/D-lines	3.63 ± 2.30	3.63 ± 2.21	0.00 ± 0.01
Testers x locations/F-lines	1.78 ± 0.89	0.41 ± 0.36	0.03 ± 0.02
(BBT vs NBT) x L/F-lines	2.82 ± 1.93	0.81 ± 0.74	0.12 ± 0.08
Broad base x L/F-lines	0.27 ± 0.56	0.27 ± 0.44	-0.02 ± 0.01
Narrow base x L/F-lines	2.26 ± 1.60	2.26 ± 0.48	0.00 ± 0.01

[a]PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]D indicates lines from the dent population (D219B00), F indicates lines from the flint population (F209B00), BBT indicates broad-base testers, NBT indicates narrow-base testers. The broad-base testers were the parental and opposite populations, and the narrow-base testers were a single cross and an inbred line.

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 the this large difference in the line components of variance between the two populations can be attributed to the effects of the different testers.

Except for percentage of erect plants, grain moisture, index, ear height, and days-to-flower in the D219B00 population, the (broad vs narrow) x line interaction had the greatest contribution for the total tester x line interaction in both populations. No trend for higher tester x line interaction for narrow-genetic base testers in comparison with broad-genetic base testers was found for any trait. In the D219B00 population, the narrow-genetic base testers had consistently higher line x tester interaction than broad-genetic base testers for all traits except for index. On the other hand, the narrow-genetic base testers used to evaluate the F209B00 lines had less tester x line interaction than broad-genetic base testers for all traits, except for index.

The higher narrow-base tester x line interaction than broad-base tester interaction in the D219B00 population was not associated with presence of narrow-base testers having high frequency of favorable allele, because one of the two inbred lines involved in the narrow-base testers had high frequency of favorable alleles (FBR2-89), and the other low frequency of favorable alleles (FBR2-848). Therefore, no further conclusions can be taken. The lower narrow-base tester x line interaction than broad-base tester x line interaction in the F219B00 population was most probably associated with the presence of the

unrelated inbred-line tester RBR2-305 derived from outside of the populations used for reciprocal recurrent selection. This result supports the use of an unrelated inbred-line tester for identyfing lines having good GCA inbred lines.

Matzinger (1953) compared three types of testers. The testers included 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. For related line testers, Hallauer and Lopez-Perez (1979) also found that as the heterogeneity of the testers increased, the line x tester interaction decreased. However, they found that testcrosses involving B73 and Mo17 (the only tester not of BSSS origin) were the only group that had a nonsignificant interaction with testers at the S8 level. Their results showed that this group had almost half the tester x line interaction compared with the broad-base tester x line interaction.

Although the two populations used in this study (D219B00 and F209B00) were chosen for a reciprocal recurrent selection program, it was shown previously that they have more similarities than differences. Thus, the lines derived from these populations and used as testers for lines derived from the opposite populations should be more related than unrelated. RBR2-305 line was the only unrelated line that did not originate from the populations used for reciprocal recurrent selection. For unrelated testers the line x tester interaction was lower for the narrow-genetic base tester than for the broad-genetic base testers. These results agree with previous results of Hallauer and Lopez-Perez

(1979). However, for related line testers, the component of variance of line x tester interaction was greater in narrow-genetic base testers than in broad-genetic base testers. For related testers, therefore, these results also agree with previous results reported by Matzinger (1953) and Hallauer and Lopez-Perez (1979).

In all instances the broad-genetic base tester had lower tester x locations interaction than did narrow-genetic base testers, indicating that, on the average, broad-base testers were more stable across locations than narrow-base testers. These results agree with the results of Sprague and Federer (1951), Rojas and Sprague (1952), Eberhart and Russell (1969), and Wright et al. (1971). They reported that the tester x environment interaction decreased as the heterogeneity of the tester increased. However, Hallauer and Lopez-Perez (1980), conducting a comprehensive study involving an unselected sample of 50 S1 and 50 S8 lines derived from Iowa Stiff Stalk Synthetic (BSSS) and five testers, detected no trend for broad genetic-base testers vs narrow genetic-base testers for interactions with environment.

Analyses for each individual type of testcrosses are presented in Tables 14 to 21. The mean squares for testcrosses were significant for all traits in both populations, except for stand in both populations, percentage of erect plants in the F209B00 population, and index in the D219B00 population. Testcross x locations interaction was not significant for ear height in tester 1 and percentage of erect plants in tester 4. For D219B00 testcrosses, the testcross x locations interaction was not significant for percentage of erect plants, plant

Table 14. Analysis of variance pooled over sets and combined over locations for testcrosses made with the related population as tester (tester 1) arranged as randomized complete block design

Source of variation[b]	df	Mean squares[a]				
		YIELD (Mg/ha)	EREPL %	MOIST %	STAND no.	INDEX
Locations (E)	2	209.8746	10752.95	21278.01	110.75	15.47
Set (S)	7	1.7024	928.72	155.05	10.65	5.94
S x E	14	4.5683	621.02	139.79	16.76	13.14
Rep/S x E	72	1.7033	88.88	14.43	6.56	2.28
Lines/Set[a]	192	3.0770**	149.08**	7.12**	4.04ns	2.00**
D-Lines/S	96	3.1942**	139.60**	6.56**	4.51ns	1.87*
F-Lines/S	96	2.9598**	158.55**	7.68**	3.57ns	2.14**
Lines x E/S	384	1.0222*	91.07**	2.98**	3.71ns	1.21**
D-Lines x E/S	192	1.1856*	93.76ns	2.10**	3.79ns	1.31**
F-Lines x E/S	192	0.8588ns	88.37**	3.86**	3.63ns	1.11**
Pooled error	1728	0.8560	72.60	1.85	4.33	0.87
D-Lines error	864	0.9841	80.01	1.51	4.84	0.88
F-Lines error	864	0.7278	65.20	2.20	3.82	0.85
Mean		4.44	90.2	20.8	24.3	6.4
Mean D-Lines		4.42	89.1	20.4	24.2	6.3
Mean F-Lines		4.46	91.3	21.3	24.4	6.5
CV (%)		20.8	9.4	6.5	8.6	14.5
CV D-Lines		22.4	10.0	6.0	9.1	14.8
CV F-Lines		19.1	8.8	7.0	8.0	14.3

[a]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; STAND: plants available at harvest; and INDEX: eye appearance, rated from 1 (excellent) to 9 (poor).

[b]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

*$p \leq .05$.

**$p \leq .01$.

Table 15. Analysis of variance pooled over sets and combined over locations for testcrosses made with the related population tester (tester 1) arranged as randomized complete block design

Source of variation[b]	df	Mean squares[a]		
		PH cm	EH cm	FLOW no.
Locations (E)	1	533.61	12859.56	2211.35
Set (S)	7	1255.13	1023.73	65.99
S x E	7	1129.17	958.38	83.21
Rep/S x E	48	195.03	133.04	6.36
Lines/Set[a]	192	531.09**	329.18**	10.30**
D-Lines/S	96	539.27**	316.97**	8.84**
F-Lines/S	96	522.91**	341.39**	11.77**
Lines x E/S	192	114.64*	79.04ns	4.09**
D-Lines x E/S	96	108.94ns	69.43ns	3.72*
F-Lines x E/S	96	120.33*	88.65ns	4.45**
Pooled error	1152	90.49	70.87	2.93
D-Lines error	576	88.11	66.53	2.83
F-Lines error	576	92.87	75.21	3.04
Mean		175.5	88.9	72.0
Mean D-Lines		174.9	87.8	72.2
Mean F-Lines		176.0	90.0	71.8
CV (%)		5.4	9.5	2.4
CV D-Lines		5.4	9.3	2.3
CV F-Lines		5.5	9.6	2.4

[a]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

[b]PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

* $p \leq .05$.

** $p \leq .01$.

Table 16. Analysis of variance pooled over sets and combined over locations for testcrosses made with the unrelated population as tester (tester 2) arranged as randomized complete block design

Source of variation[b]	df	Mean squares[a]				
		YIELD (Mg/ha)	EREPL %	MOIST %	STAND no.	INDEX
Locations (E)	2	253.2814	9564.68	19996.34	72.40	9.13
Set (S)	7	1.6414	905.40	212.53	19.46	4.94
S x E	14	3.0549	611.46	138.94	19.37	11.42
Rep/S x E	72	1.0613	111.67	13.30	5.96	2.64
Lines/Set[a]	192	2.8329**	128.64**	5.78**	5.77ns	1.68ns
D-Lines/S	96	2.6015**	146.00**	5.89**	6.43ns	1.47ns
F-Lines	96	3.0643**	111.27ns	5.67**	5.11ns	1.90ns
Lines x E/S	384	1.1888**	90.29**	2.28**	4.84ns	1.41**
D-Lines x E/S	192	1.2704**	90.95ns	2.51**	5.13ns	1.22**
F-Lines x E/S	192	1.1073*	89.63**	2.06**	4.54ns	1.59**
Pooled error	1728	0.9050	74.36	1.38	5.10	0.84
D-Lines error	864	0.9230	84.45	1.37	5.63	0.75
F-Lines error	864	0.8870	64.28	1.39	4.57	0.94
Mean		4.66	90.5	20.8	24.2	6.3
Mean D-Lines		4.70	89.5	20.3	24.1	6.3
Mean F-Lines		4.63	91.4	21.4	24.4	6.4
CV (%)		20.4	9.5	5.6	9.3	14.5
CV D-Lines		20.4	10.3	5.8	9.9	13.8
CV F-Lines		20.4	8.8	5.5	8.8	15.2

[a]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; STAND: plants available at harvest; and INDEX: eye appearance, rated from 1 (excellent) to 9 (poor).

[b]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

*$p \leq .05$.

**$p \leq .01$.

Table 17. Analysis of variance pooled over sets and combined over locations for testcrosses made with the unrelated population tester (tester 2) arranged as randomized complete block design

Source of variation[b]	df	Mean squares[a]		
		PH cm	EH cm	FLOW no.
Locations (E)	1	1004.89	14089.69	2097.64
Set (S)	7	1645.77	789.41	40.02
S x E	7	1754.75	1086.01	64.13
Rep/S x E	48	221.34	167.16	5.81
Lines/Set[a]	192	517.73**	376.83**	9.19**
D-Lines/S	96	505.05**	338.92**	9.25**
F-Lines/S	96	530.41**	414.74**	9.13**
Lines x E/S	192	140.44**	93.18**	3.77*
D-Lines x E/S	96	155.66**	94.36**	3.40ns
F-Lines x E/S	96	125.22**	92.01*	4.15*
Pooled error	1152	92.82	66.80	3.07
D-Lines error	576	99.92	66.97	3.05
F-Lines error	576	85.71	66.62	3.08
Mean		176.4	89.8	71.9
Mean D-Lines		177.1	90.6	72.0
Mean F-Lines		175.8	89.0	71.9
CV (%)		5.5	9.1	2.4
CV D-Lines		5.6	9.0	2.4
CV F-Lines		5.3	9.2	2.4

[a]PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

* $p \leq .05$.

** $p \leq .01$.

Table 18. Analysis of variance pooled over sets and combined over locations for testcrosses made with one unrelated single-cross hybrid tester (tester 3) arranged as randomized complete block design

Source of variation[b]	df	Mean squares[a]				
		YIELD (Mg/ha)	EREPL %	MOIST %	STAND no.	INDEX
Locations (E)	2	299.7332	9021.35	17620.92	64.16	11.65
Set (S)	7	57.3899	3360.65	369.26	30.54	29.41
S x E	14	6.2203	969.21	121.22	12.06	24.54
Rep/S x E	72	1.6024	78.65	14.53	4.31	2.74
Lines/Set[a]	192	3.5266**	199.40**	5.23**	3.70ns	2.95**
D-Lines/S	96	2.3662**	209.46**	4.98**	4.92ns	1.58ns
F-Lines/S	96	4.6871**	189.34**	5.48**	2.49ns	4.32**
Lines x E/S	384	0.9549**	98.25**	2.27**	4.04ns	1.52**
D-Lines x E/S	192	0.9261ns	132.37**	2.30**	4.71ns	1.21**
F-Lines x E/S	192	0.9838*	64.14**	2.23**	3.37ns	1.84**
Pooled error	1728	0.7955	69.89	1.32	3.53	0.89
D-Lines error	864	0.7841	90.08	1.32	4.47	0.84
F-Lines error	864	0.8069	49.69	1.33	2.58	0.93
Mean		4.80	90.2	20.2	24.4	6.4
Mean D-Lines		4.40	87.5	19.2	24.2	6.7
Mean F-Lines		5.20	92.9	21.1	24.7	6.2
CV (%)		18.6	9.3	5.7	7.7	14.7
CV D-Lines		20.1	10.8	6.0	8.7	13.7
CV F-Lines		17.3	7.6	5.5	6.5	15.7

[a]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; STAND: plants available at harvest; and INDEX: eye appearance, rated from 1 (excellent) to 9 (poor).

[b]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

*$p \leq .05$.

**$p \leq .01$.

Table 19. Analysis of variance pooled over sets and combined over locations for testcrosses made with one unrelated single tester (tester 3) arranged as randomized complete block design

Source of variation[b]	df	Mean squares[a]		
		PH cm	EH cm	FLOW no.
Locations (E)	1	4576.52	6520.56	2308.80
Set (S)	7	3627.10	1512.47	61.20
S x E	7	1535.50	1033.05	71.44
Rep/S x E	48	170.29	130.40	6.95
Lines/Set[a]	192	552.26**	353.59**	9.08**
D-Lines/S	96	516.85**	334.65**	8.63**
F-Lines/S	96	587.66**	372.53**	9.53**
Lines x E/S	192	100.81**	75.56**	3.94**
D-Lines x E/S	96	103.32**	75.02**	4.24**
F-Lines x E/S	96	98.31ns	76.10ns	3.64ns
Pooled error	1152	69.60	57.77	2.95
D-Lines error	576	60.67	50.11	3.00
F-Lines error	576	78.53	65.43	2.90
Mean		173.9	87.2	70.5
Mean D-Lines		170.5	85.4	70.4
Mean F-Lines		177.3	88.9	70.7
CV (%)		4.8	8.7	2.4
CV D-Lines		4.6	8.3	2.5
CV F-Lines		5.0	9.1	2.4

[a]PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

* $p \leq .05$.

** $p \leq .01$.

Table 20. Analysis of variance pooled over sets and combined over locations for testcrosses made with one unrelated inbred line as tester (tester 4) arranged as randomized complete block design

Source of variation[b]	df	Mean squares[a]				
		YIELD (Mg/ha)	EREPL %	MOIST %	STAND no.	INDEX
Locations (E)	2	401.2723	5908.21	16673.33	18.54	46.65
Set (S)	7	15.7660	685.78	275.15	24.19	11.44
S x E	14	14.2694	385.89	122.03	24.66	28.73
Rep/S x E	72	1.1695	111.45	13.77	4.98	3.94
Lines/Set[a]	192	3.6166**	219.91**	6.16**	4.21ns	3.65**
D-Lines/S	96	2.4343**	122.75**	6.59**	5.09ns	2.36**
F-Lines/S	96	4.7990**	317.08**	5.73**	3.32ns	4.93**
Lines x E/S	384	1.1728**	79.29ns	2.67**	4.40ns	1.73**
D-Lines x E/S	192	1.3261**	72.67ns	2.48**	5.23ns	1.53**
F-Lines x E/S	192	1.0195**	85.92ns	2.85**	3.56ns	1.94**
Pooled error	1728	0.8703	71.30	1.31	3.97	1.04
D-Lines error	864	0.9764	70.88	1.20	4.94	0.95
F-Lines error	864	0.7642	71.73	1.41	3.01	1.13
Mean		5.15	91.0	20.3	24.3	6.0
Mean D-Lines		5.35	91.6	19.6	24.1	5.9
Mean F-Lines		4.94	90.4	21.0	24.5	6.1
CV (%)		18.1	9.3	5.6	8.2	17.0
CV D-LINE		18.5	9.2	5.6	9.2	16.4
CV F-Lines		17.7	9.4	5.6	7.1	17.5

[a]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; STAND: plants available at harvest; and INDEX: eye appearance, rated from 1 (excellent) to 9 (poor).

[b]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

*$p \leq .05$.

**$p \leq .01$.

Table 21. Analysis of variance pooled over sets and combined over locations for testcrosses made with one unrelated inbred tester (tester 4) arranged as randomized complete block design

Source of variation[b]	df	Mean squares[a]		
		PH cm	EH cm	FLOW no.
Locations (E)	1	3504.64	11919.18	2067.98
Set (S)	7	2705.46	1287.27	41.51
S x E	7	2678.36	1638.93	74.86
Rep/S x E	48	143.14	121.92	7.42
Lines/Set[a]	192	582.47**	383.34**	8.79**
D-Lines/S	96	627.74**	367.64**	9.57**
F-Lines/S	96	537.20**	399.03**	8.00**
Lines x E/S	192	75.85*	69.22**	3.39**
D-Lines x E/S	96	74.91*	66.56**	2.60ns
F-Lines x E/S	96	76.79ns	71.88ns	4.18**
Pooled error	1152	62.13	52.29	2.60
D-Lines error	576	54.34	45.51	2.45
F-Lines error	576	69.91	59.06	2.75
Mean		174.7	90.2	70.4
Mean D-Lines		176.7	91.3	70.5
Mean F-Lines		172.7	89.0	70.4
CV (%)		4.5	8.0	2.3
CV D-LINE		4.2	7.4	2.2
CV F-Lines		4.8	8.6	2.4

[a]PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

* $p \leq .05$.

** $p \leq .01$.

and ear height in tester 1, percentage of erect plants and days-to-flower in tester 2, yield in tester 3, and days-to-flower and erect plants in tester 4.

For F209B00 testcrosses, the testcross x location interaction was not significant for yield and plant height with tester 1, plant and ear height with testers 3 and 4, days-to-flower with tester 3, and percentage of erect plants in tester 4. These results indicate that the stands were uniform for all testers.

The estimates of the genetic and genotype x location interaction components of variance for each individual type of testcross are presented in Tables 22 and 23. In the F209B00 population, the narrow-genetic base testers had greater genetic components of variance than broad-genetic base testers for all traits, except for grain moisture and days-to-flower. For grain moisture, broad-genetic base testers had higher genetic variation and for days-to-flower there was no clear trend. The parental population tester had a greater genetic variance components than the opposite population tester for all traits, except for plant and ear height. For yield, the genetic variances were similar. Inbred-line tester had higher genetic variation than the single cross for yield, percentage of erect plants, index, and ear height. For yield, percentage of erect plants, and index the genetic variation among testcrosses for narrow-genetic base testers was approximately twice the genetic variation of the broad-base testers.

For population D219B00, narrow-genetic base testers had greater genetic variance component only for percentage of erect plants and ear

Table 22. Estimates of genotypic variance ($o2_G$), genotype x location interaction, and their standard errors for testcrosses of S2 lines with population testers evaluated at three locations in Brazil

Variance component	Testcrosses		Traits[a]			
	Population	Tester[b]	YIELD (Mg/ha)	EREPL %	MOIST %	INDEX
6^2_G	D219B00	1	0.1674 ± 0.0393	3.82 ± 1.84	0.37 ± 0.08	0.05 ± 0.02
	F209B00	1	0.1751 ± 0.0360	5.85 ± 2.03	0.32 ± 0.10	0.09 ± 0.03
	D219B00	2	0.1109 ± 0.0328	4.59 ± 1.90	0.28 ± 0.07	0.02 ± 0.02
	F209B00	2	0.1631 ± 0.0377	1.80 ± 1.53	0.30 ± 0.07	0.03 ± 0.03
	D219B00	3	0.1200 ± 0.0292	6.42 ± 2.73	0.22 ± 0.06	0.03 ± 0.02
	F209B00	3	0.3086 ± 0.0564	10.43 ± 2.32	0.27 ± 0.07	0.21 ± 0.05
	D219B00	4	0.0923 ± 0.0311	4.17 ± 1.59	0.34 ± 0.08	0.07 ± 0.03
	F209B00	4	0.3150 ± 0.0578	19.26 ± 3.84	0.24 ± 0.07	0.25 ± 0.06
6^2_{GE}	D219B00	1	0.0504 ± 0.0323	3.44 ± 2.57	0.15 ± 0.06	0.11 ± 0.03
	F209B00	1	0.0328 ± 0.0235	5.79 ± 2.38	0.41 ± 0.10	0.06 ± 0.03
	D219B00	2	0.0868 ± 0.0341	1.63 ± 2.52	0.28 ± 0.07	0.12 ± 0.03
	F209B00	2	0.0551 ± 0.0301	6.34 ± 2.40	0.17 ± 0.05	0.16 ± 0.04
	D219B00	3	0.0355 ± 0.0253	10.57 ± 3.53	0.25 ± 0.06	0.09 ± 0.03
	F209B00	3	0.0442 ± 0.0268	3.61 ± 1.73	0.23 ± 0.06	0.23 ± 0.05
	D219B00	4	0.0874 ± 0.0356	0.45 ± 2.03	0.32 ± 0.06	0.14 ± 0.04
	F209B00	4	0.0638 ± 0.0275	3.55 ± 2.34	0.36 ± 0.07	0.20 ± 0.05

[a]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; and INDEX: eye appearance, rated from 1 (excellent) to 9 (poor).

[b]Tester 1: parental population, tester 2: opposite population; tester 3: unrelated single cross, tester 4: unrelated inbred line.

Table 23. Estimates of genotypic variance (δ^2_G), genotype x location interaction, and their standard errors for three traits of testcrosses of S2 lines evaluated at three locations in Brazil

Variance component	Testcrosses		Traits[a]		
	Population	Tester[b]	PH (cm)	EH (cm)	FLOW (no)
δ^2_G	D219B00	1	53.79 ± 9.73	30.94 ± 5.73	0.64 ± 0.16
	F209B00	1	50.32 ± 9.46	31.59 ± 6.20	0.91 ± 0.22
	D219B00	2	43.67 ± 9.23	30.57 ± 6.17	0.73 ± 0.17
	F209B00	2	50.65 ± 9.60	40.34 ± 7.50	0.62 ± 0.17
	D219B00	3	51.69 ± 9.32	32.45 ± 6.05	0.55 ± 0.16
	F209B00	3	61.17 ± 10.57	37.05 ± 6.72	0.74 ± 0.18
	D219B00	4	69.10 ± 11.25	37.63 ± 6.62	0.87 ± 0.17
	F209B00	4	57.55 ± 9.64	40.89 ± 7.18	0.48 ± 0.15
δ^2_{GE}	D219B00	1	5.21 ± 2.96	0.72 ± 1.94	0.22 ± 0.10
	F209B00	1	6.86 ± 3.25	3.36 ± 2.42	0.35 ± 0.12
	D219B00	2	13.94 ± 4.13	6.85 ± 2.53	0.09 ± 0.09
	F209B00	2	9.88 ± 3.34	6.35 ± 2.47	0.27 ± 0.11
	D219B00	3	10.66 ± 2.72	6.23 ± 2.00	0.31 ± 0.11
	F209B00	3	4.94 ± 2.67	2.67 ± 2.09	0.18 ± 0.10
	D219B00	4	5.14 ± 2.01	5.26 ± 1.78	0.04 ± 0.07
	F209B00	4	1.72 ± 2.12	3.20 ± 1.96	0.36 ± 0.11

[a]PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]Tester 1: parental population; Tester 2: opposite population; Tester 3: unrelated single cross; Tester 4: unrelated inbred line.

height. For the other traits, there was no clear trend. The parental population had greater genetic variance component than the opposite population for all traits, except for percentage of erect plants and days-to-flower. The inbred line also had higher genetic variance component than the single cross for all traits, except for yield and percentage of erect plants.

For yield, the genetic variance components among lines using the parental populations as testers were similar in both populations. These components estimate 7/16 of the total additive genetic variance present in the two populations. No bias due to the difference in gene frequency of the tester and the lines under evaluation is present if the populations were adequately sampled. For the other testers, the estimate of the genetic variance may have bias because the other testers are unrelated. Therefore, the estimates of the genetic variance provided by the parental population tester is the most adequate estimate of the additive genetic variance in both populations. For F209B00 population, the genetic variance component among testcrosses using the opposite population as tester was similar to the component of variance using the parental population. However, for D219B00 population this component was lower with the opposite population than with the parental population. On the assumption of partial to complete dominance, this may indicate that the F209B00 population has higher frequency of favorable alleles that are masking the gene effects of the D219B00 population.

Genetic components of variance for yield in narrow-genetic base

testers were twice the genetic components of variance for broad-genetic base testers in the F209B00 population. These results agree with those reported by Darrah et al. (1972), Horner et al. (1973), Russell et al. (1973), and Russell and Eberhart (1975). The greater genetic variance components for narrow-genetic base testers in the F209B00 population were associated with the presence of the unrelated line RBR2-305 in the testers. The genetic variation exhibited by tester 4 (RBR2-305 line) and by the single-cross tester 3 (RBR2-305 x DBR2-9) were similar. This suggests the presence of common recessive alleles in the DBR2-9 and RBR2-305 lines. However, the single cross (RBR2-305 x DBR2-9) is a high-yielding tester (data not shown, but this was the main reason for choosing this single cross as one of the testers), indicating that this single cross has a high frequency of favorable alleles or complementary alleles from the two lines. This information suggests that high-yielding testers per-se can be used as efficiently as low-yielding testers to discriminate the genetic variance among testcrosses. This suggests that either the frequency of favorable alleles were low in both testers relative to the population of S2 lines or that gene effects were primarily in the partial to complete dominance range.

The single cross (B73 x Mo17) is one of the highest-yielding hybrids in the United States. Hallauer and Lopez-Perez (1979) found that the genetic component of variance among S8 line testcrosses with Mo17 was almost twice those among testcrosses with broad-genetic base testers. For the testcrosses with B73, however, the genetic components of variance were lower than for broad-genetic base testers, probably

because the high frequency of favorable alleles in B73, (B73 x Mo17) has high frequency of favorable alleles or the two lines complement each one at most of the important loci for yield. If the genetic component of variance among testcrosses is the average between the genetic component of each individual line, then gene effects are primarily in the partial to complete dominance range. However, a significantly higher genetic component of the single cross relative to the average of the two individual lines may indicate the presence of overdominant loci controlling yield.

For grain yield, the genetic variation among testcrosses with the FBR2-89 inbred-line tester was lower than the genetic variation among testcrosses with the parental population. FBR2-89 was the line with highest GCA indicating the presence of high frequency of favorable alleles. The low genetic variation among these testcrosses can be explained by the presence of favorable alleles in the FBR2-89 line, which masked the gene effects of the D219B00 population.

The phenotypic correlations between testers are presented in Table 24. The correlations were highly significant in all instances and had useful magnitudes. High correlation coefficients were obtained between testers 1 and 2 (broad-genetic base testers) and between testers 3 and 4 (narrow-genetic base testers). These high and significant correlation coefficients suggest that selection for either GCA or SCA based on only one tester, can be as effective as selection based on more than one tester. The correlations between the broad and narrow-genetic base

Table 24. Phenotypic correlations between the mean yield of one testcross and the mean yield of the other testcrosses

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**

r = 0.20 for P.05 and r = 0.26 for P.01

[a]Tester 1: parental population; Tester 2: opposite population; Tester 3: unrelated single cross; Tester 4: unrelated inbred line.

** $p \leq .01$.

testers were sufficiently high to indicate that either narrow or broad-genetic base tester was reliable for estimating GCA of the lines.

Table 25 shows the percentage of coincidence of selected lines when selection is practiced for GCA based on grain yield of topcrosses with the parental population. It was calculated assuming truncation selection for grain yield. As expected, the values increased as the selection intensity decreased. The values ranged from 20% (5% selection intensity) to 72% (40% selection intensity). With 40% selection intensity there was at least 62% of coincidence for any tester. These results support the conclusions of Jenkins and Brunson (1932) that, based on the performance of topcrosses, 50% of the lines could be discarded without serious danger of losing valuable material. In addition, any type of tester, broad base, narrow base, related, or unrelated tester, can be used to discard 50% of the lines without serious danger of losing valuable material.

For both populations the percentages of coincidence were similar for the opposite population and for the single-cross testers. For the inbred-line testers, however, the 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 derived. The inbred line used to test the lines derived from D219B00 population was derived from the opposite population F209B00, and it was the line with highest GCA when evaluated with D210B00 population. These results indicate that an unrelated inbred line is more reliable for ranking the lines for GCA than one line with high GCA derived from the opposite population.

Table 25. Percentage of common lines when lines are selected for general combining ability based on testcrosses made with the parental population

Selection intensity (%)	Testers					
	Opposite pop.		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

The heritability estimates on a progeny mean basis are presented in Table 26. For the F219B00 population, there was a tendency for narrow-genetic base testers to have higher heritability coefficients than broad base testers. For the D219B00 population, there was no clear trend. For grain, yield the lowest heritability estimate (0.46) was with the FBR2-89 tester, which had the highest GCA with D219B00 population. The highest heritability coefficient was with the RBR2-305 tester, which was the only unrelated line. The best heritability estimates that are not confounded with gene frequencies of unrelated testers are the estimates obtained by crossing S2 lines with their respective parental populations. These estimates are based on covariance of half-sibs, and the variance among half-sibs is 7/16 δ^2A. The estimates of heritability with the parental population as tester tend to be greater than those with use of opposite population as tester for D219B00 (Table 26).

The single-cross (RBR2-305 x DBR2-9) tester also showed high heritability coefficients. The phenotypic variation among progeny means was greater for the single-cross tester (RBR2-305 x DBR2-9) and for the inbred-line tester (RBR2-305) than those for broad-genetic base testers. This indicates that the two lines had important common loci for yield in the recessive form, which allowed a better discrimination of the genetic variability among F209B00 lines.

Early studies on testers indicated that narrow genetic-base testers would improve SCA, but would have little value for improving GCA. Recent results suggest that narrow genetic-base testers can also improve GCA (Darrah et al., 1972; Horner et al., 1973; Russell et al., 1973;

Table 26. Heritability estimates on progeny mean basis and their standard errors for seven traits

Trait[a]	Tester[b]	Population	
		D219B00	F219B00
YIELD	1	0.63 ± 0.15	0.71 ± 0.15
	2	0.51 ± 0.15	0.64 ± 0.15
	3	0.61 ± 0.15	0.79 ± 0.14
	4	0.46 ± 0.15	0.79 ± 0.14
EREPL	1	0.33 ± 0.16	0.44 ± 0.15
	2	0.38 ± 0.16	0.19 ± 0.16
	3	0.37 ± 0.16	0.66 ± 0.15
	4	0.41 ± 0.15	0.73 ± 0.15
MOIST	1	0.68 ± 0.15	0.50 ± 0.15
	2	0.57 ± 0.15	0.64 ± 0.15
	3	0.54 ± 0.15	0.59 ± 0.15
	4	0.62 ± 0.15	0.50 ± 0.15
INDEX	1	0.30 ± 0.16	0.48 ± 0.15
	2	0.17 ± 0.17	0.16 ± 0.17
	3	0.23 ± 0.16	0.57 ± 0.15
	4	0.35 ± 0.16	0.61 ± 0.15
PH	1	0.80 ± 0.14	0.77 ± 0.14
	2	0.69 ± 0.15	0.76 ± 0.14
	3	0.80 ± 0.14	0.83 ± 0.14
	4	0.88 ± 0.14	0.86 ± 0.14

[a]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; INDEX: eye appearance, rated from 1 (excellent) to 9 (poor); PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]Testers 1 and 2 are genetically broad-base testers and testers 3 and 4 are genetically narrow-base testers.

Table 26. (continued)

Trait[a]	Tester[b]	Population	
		D219B00	F219B00
EH	1	0.78 ± 0.14	0.74 ± 0.15
	2	0.72 ± 0.15	0.78 ± 0.14
	3	0.78 ± 0.14	0.80 ± 0.14
	4	0.82 ± 0.14	0.82 ± 0.14
FLOW	1	0.58 ± 0.15	0.62 ± 0.15
	2	0.63 ± 0.15	0.55 ± 0.15
	3	0.51 ± 0.15	0.62 ± 0.15
	4	0.73 ± 0.15	0.48 ± 0.15

Russell and Eberhart, 1975; Horner et al., 1976; Sprague and Eberhart, 1977; Walejko and Russell, 1977; and Zambezi et al., 1986). Hallauer and Lopez-Perez (1979) reported that the tester x line interactions were greater for narrow-base testers, but interaction components were smaller than testcross components of variance. They concluded that narrow genetic base testers can be effectively used to identify lines having good GCA.

The results found in this study indicate that inbred lines can be effective to improve GCA or to identify lines having good GCA. However, the identification of lines with high GCA would be better if an appropriate inbred-line tester is used for evaluating the inbred lines. The genetic components of variance for yield in narrow-genetic base testers were twice those of the genetic components of variance for broad-genetic base testers when the unrelated inbred-line RBR2-305 was present in the tester (narrow-base testers for lines derived from F209B00 population). However, the genetic components of variance for narrow-genetic base testers were lower than those for broad-genetic base testers for lines derived from D219B00 population. The greater genetic variance components for narrow-genetic base testers used to evaluate the lines derived from F209B00 population were associated with the presence of the unrelated line RBR2-305 in the testers. The lowest genetic component of variance among testcrosses in D219B00 population was associated with the presense of the line having good GCA (FBR2-89) in the tester.

The correlations between the broad- and narrow-base testers were

sufficiently high to indicate that either narrow- or broad-genetic base tester was reliable for estimating GCA. The percentage of coincidence for the inbred line testers was consistently higher for RBR2-305 tester. On the other hand, the FBR2-89 tester derived from the opposite population (F209B00) and with the high GCA when evaluated with D210B00 population, had the lowest percentage of coincidence. The lowest heritability was obtained when the line with highest GCA was used as tester (FBR2-89). The highest heritability coefficient was with the RBR2-305 tester, which was the only unrelated line.

These results indicate that some inbred-line testers were more efficient than others to discriminate the S2 lines for GCA. The GCA and the degree of relationship of the line used as tester with the lines under evaluation have an important role in choosing inbred lines as testers. The unrelated inbred line RBR2-305 was better for ranking the lines for GCA than the broad-base testers. However, the FBR2-89 with high GCA derived from the opposite population was poorer than broad-base testers. Therefore, there was evidence that an unrelated line or a line with low GCA was the most efficient tester for improving or identifying lines having good GCA. The unrelated lines have more practical advantages because they do not have to be a poor line per se.

Russell and Eberhart (1975) proposed the use of an inbred tester for reciprocal recurrent selection. The inbred lines would be derived from previous cycles of selection and used as testers for the interpopulation crosses instead of the population themselves. They also reported that inbred lines were effective in selecting genes with

additive effects, and that nonadditive gene action, other than partial to complete dominance, was relatively unimportant. They emphasized that the gain from selection would be greater with use of an inbred instead of the populations themselves. However, Comstock (1979) theoretically demonstrated that the use of populations as testers in reciprocal recurrent selection was expected to be slightly superior to inbred lines as testers for changing allele frequency. He concluded that there was no reason to expect better results using the inbred tester instead of the populations as originally proposed by Comstock et al. (1949).

The differences in response, on average, would favor the use of parental populations as testers. The use of inbred tester would depend on the frequency of the alleles, which would depend on the choice of inbred lines used as testers. If a high GCA inbred line derived from the opposite population is used as tester, the genetic gain from selection tends to be lower than the use of the populations as testers. On the other hand, if an unrelated line is used as tester, the genetic gain from selection tends to be higher for inbred line testers than for the populations as testers. Therefore, the use of inbred lines in reciprocal recurrent selection depends on the GCA of the line used as tester.

Sprague and Eberhart (1977) and Walejko and Russell (1977) suggested that the testers could be replaced by better lines as the selection program progresses without deleterious results relative to population improvement because no selection pressure can be applied at loci where the tester is fixed for the favorable allele. If the lines

are replaced by lines derived from the opposite population having higher GCA than the replaced one, it may be possible that the new tester does not discriminate the genetic variation among lines as well as the old tester. Therefore, small genetic gain from selection may be expected.

Hull (1945) stated that a tester with low frequency of favorable alleles is the most appropriate tester. He emphasized that the masking effects of the dominant alleles render the testers ineffective, and that the most efficient tester would be a homozygous recessive tester at all loci. Thus, the best yielding lines in commercial use are worthless as testers. Theoretical and empirical studies tend to support to Hull's (1945) hypothesis (Green, 1948; Russell, 1961; Astralaga, 1956; Rawlings and Thompson, 1962; Allison and Curnow, 1966; Lonnquist and Lindsey (1970); Hallauer and Lopez-Perez, 1979; and Mendez and Galan, 1982). My results also suggest that testers with low frequency of favorable alleles are the most appropriate testers.

The phenotypic and genotypic correlations among the four traits using the parental and the opposite population as testers are given in Table 27. For the parental population tester, the correlations correspond to the intrapopulation additive genetic correlation and for the opposite population tester the genetic correlation correspond to the additive genetic correlation between intra- and interpopulation progenies. Most of the correlations were too small. The magnitudes of the phenotypic and genotypic correlations between yield and plant and ear height and between yield and days-to-flower and plant and ear height were high enough to be useful in maize breeding programs. For yield and

Table 27. Phenotypic and genotypic correlations among five traits for testcrosses made with tester 1 (F209B00) and tester 2 (D219B00)

Traits[a]		YIELD		EREPL		PH		EH		FLOW E	
	Pop\Tester	D219B00	F209B00	D219B00	F209B00	D219B00	F209B00	D219B00	F209B00	D219B00	F209B00
YIELD	D219B00			0.12[b]	0.13	0.38	0.26	0.41	0.29	-0.28	-0.17
	F209B00			0.22	0.12	0.28	0.37	0.22	0.29	-0.42	-0.38
EREPL	D219B00	0.10	0.06			0.02	0.04	0.09	-0.09	0.14	0.05
	F209B00	0.43	0.11			0.14	0.22	0.20	0.12	-0.12	0.13
PH	D219B00	0.58	0.40	0.10	0.32			0.78	0.77	0.10	0.16
	F209B00	0.37	0.57	0.16	0.35			0.82	0.84	0.03	-0.03
EH	D219B00	0.68	0.44	0.24	-0.01	0.78	0.76			0.07	0.17
	F209B00	0.30	0.43	0.55	0.19	0.86	0.86			0.09	0.08
FLOW	D219B00	-0.42	-0.23	0.30	0.12	0.25	0.28	0.15	0.29		
	F209B00	-0.57	-0.65	-0.29	0.43	0.20	0.03	0.27	0.16		

r = 0.20 for P.05 and r = 0.26 for P.01

[a]YIELD: grain yield; EREPL: percentage of erect plants; PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]The r values above the diagonal are the phenotypic correlations. The r values below the diagonal are the genotypic correlations.

plant and ear height, the correlations were significant and positive. For yield and days-to-flower the correlations were significant and negative. These results indicate that selection for improving yield can indirectly increase plant and ear height and reduce days-to-flower.

Genetic correlations between yield and plant height or ear height, and days-to-flower, and plant and ear height have been reported. A positive association between yield and either ear height or plant height was observed by Green (1955), Horner et al. (1973), Gardner (1969), Hallauer and Sears (1969), Vera and Crane (1970), Darrah et al. (1972), and Rissi and Paterniani (1981). Selection for yield has caused correlated responses in plant and ear height and maturity, indicating the presence of genetic correlation between these traits. Positive association between plant and ear height were reported by Acosta and Crane (1972), and Rissi and Paterniani (1981).

A negative association between days-to-flower and yield was reported by Troyer (1976). He selected the earliest 2% of plants to flower in 18 F2 populations. In one group of eight populations, the effect of selection was 340 Kg/ha yield increase, 0.6% grain moisture decrease, and 0.6 less days-to-flower. For the second group (10 F2 populations), selected in the same manner, the selection effect per cycle averaged 250 Kg/ha yield increase, 1% grain moisture decrease, 1.2 less days-to-flower.

The positive genetic and phenotypic correlations between yield and plant or ear height indicate that selection for modifier genes for increased plant and ear height in brachytic populations will help to

overcome the negative effect of the br2 gene on yield. In addition, the negative correlation between yield and days-to-flower indicates that selection for earliness could can also cause a yield increase.

Mean squares for the analyses of variance for testcrosses made with tester 1 (parental population) and tester 2 (opposite population) and the mean cross products between the two testers are shown in Table 28. Progeny mean squares were significant for both populations, indicating presence of additive genetic variance in both populations. Tables 29 and 30 show the variance and covariance components among testcrosses, testcrosses x location interaction, and pooled error. These variance and covariance components were used to estimate the additive genetic variance among intra- and interpopulation testcrosses (half sibs) and the additive genetic covariance between these two types of progenies are presented in Table 31. The additive genetic variances and covariance were calculated by considering the relationship:

$$\sigma^2_A = 4\ \sigma^2_g/(1+F)$$

where:

σ^2_A : additive genetic variance,

σ^2_g : genetic component of variance, and

F : inbreeding coefficient of the lines.

For S2 lines, this relationship becomes: $\sigma^2_A = (16/7)\ \sigma^2_g$.

The values of the additive genetic variances were similar for both populations. However, the value of the additive genetic variance among interpopulation testcrosses for D219B00 population was lower than the value for F209B00 population. This may indicate that F209B00 population

Table 28. Mean squares for the analysis of variance for testcrosses made with tester 1 and 2 and the mean cross products (M.C.P.) between tester 1 and 2 for grain yield

Sources of variation[b]	df	Mean squares[a]		M.C.P
		Tester 1	Tester 2	T1 x T2
Locations (E)	2			
Set (S)	7			
S x E	14			
Rep/S x E	72			
Lines/Set[a]	192	3.0770**	2.8329**	1.9849**
D-Lines/S	96	3.1942**	2.6015**	1.9764**
F-Lines/S	96	2.9598**	3.0643**	1.9934**
Lines x E/S	384	1.0222*	1.1888**	0.3534**
D-Lines x E/S	192	1.1856*	1.2704**	0.3005**
F-Lines x E/S	192	0.8588ns	1.1073*	0.4064**
Pooled error	1728	0.8560	0.9050	0.2119
D-Lines error	864	0.9841	0.9230	0.2257
F-Lines error	864	0.7278	0.8870	0.1981
Total	2399			

[a]Tester 1: parental population; Tester 2: opposite population.

[b]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

* $p \leq .05$.

** $p \leq .01$.

Table 29. Estimates of the variance components for grain yield of intra- and interpopulation half-sib progenies

Testcross		Variance	Estimates
Population	Tester	Component	
F209B00	F209B00	$\sigma^2_{P_{11}}$	0.1751 ± 0.0360
	D219B00	$\sigma^2_{P_{12}}$	0.1631 ± 0.0377
D219B00	D219B00	$\sigma^2_{P_{22}}$	0.1674 ± 0.0393
	F209B00	$\sigma^2_{P_{21}}$	0.1109 ± 0.0328
F209B00	F209B00	$\sigma^2_{PL_{11}}$	0.0328 ± 0.0235
	D219B00	$\sigma^2_{PL_{12}}$	0.0551 ± 0.0301
D219B00	D219B00	$\sigma^2_{PL_{22}}$	0.0504 ± 0.0323
	F209B00	$\sigma^2_{PL_{21}}$	0.0868 ± 0.0341
F209B00	F209B00	$\sigma^2_{E_{11}}$	0.7278 ± 0.0000
	D219B00	$\sigma^2_{E_{12}}$	0.8870 ± 0.0000
D219B00	D219B00	$\sigma^2_{E_{22}}$	0.9841 ± 0.0000
	F209B00	$\sigma^2_{E_{21}}$	0.9230 ± 0.0000

Table 30. Estimates of the covariance components between intra- and interpopulation half-sib progenies for grain yield

Intrapopulation half-sibs	Interpopulation half-sibs	Covariance component	Estimate
F209B00 x F209B00	F209B00 x D219B00	$\sigma_{P_{11}P_{12}}$	0.1323
D219B00 x D219B00	D219B00 x F209B00	$\sigma_{P_{22}P_{21}}$	0.1397
F209B00 x F209B00	F209B00 x D219B00	$\sigma_{PL_{11}PL_{12}}$	0.0521
D219B00 x D219B00	D219B00 x F209B00	$\sigma_{PL_{22}PL_{21}}$	0.0187
F209B00 x F209B00	F209B00 x D219B00	$\sigma_{E_{11}E_{12}}$	0.1981
D219B00 x D219B00	D219B00 x F209B00	$\sigma_{E_{22}E_{21}}$	0.2257

Table 31. Estimates of additive genetic variances for intra- and interpopulation testcrosses (half sibs) and additive genetic covariance between these two types of progenies

F209B00		D219B00	
Parameters	Estimates	Parameters	Estimates
σ^2_{A11}	0.4002	σ^2_{A22}	0.3826
σ^2_{A12}	0.3728	σ^2_{A21}	0.2535
σ_{A1A2}	0.3024	σ_{A2A1}	0.3193

has higher frequency of favorable alleles than D219B00 population. On this assumption, dominant alleles from F209B00 population masked the effects of recessive alleles in the D219B00 population causing a reduction in the additive genetic variance among interpopulational testcrosses of D219B00 population.

Ramalho (1978) reported an average estimate of 0.32 for the additive genetic variance for 30 Brazilian populations. Rissi and Paterniani (1981) estimated the additive genetic variance for two brachytic populations. They reported an estimate of 0.34 for Piranao-A and 0.62 for Piranao-B. The estimates of additive genetic variance for D219B00 and F209B00 populations were 0.38 and 0.40, respectively. These values are within the range reported for other populations with a tendency to be higher than the average estimate reported for normal maize. Relatively large genetic gains are expected in both populations.

Expected progress from selection is shown in Table 32. The expected genetic gains from selection were calculated for reciprocal recurrent selection based on testcrosses of S2 lines and recombination of remnant S2 seeds, using the covariance between intra- and interpopulational testcrosses, as outlined by Miranda Filho (1982). Genetic gain was based on two seasons per year, only one season for testing and two generations of intermating.

The estimated genetic gains were relatively high and the two populations did not show much genetic divergence. The heterosis over midparent was only 5%. The predicted gain on heterosis did not have any tendency for heterosis increasing with one cycle of reciprocal recurrent

Table 32. Expected genetic gain in F209B00 and D219B00 populations, D219B00 x F219B00 population cross, and heterosis for reciprocal recurrent selection based on S2 testcrosses

Selection intensity	Population	Original population mean	Expected gain[a]	
			Cycle (Mg/ha)	Year[b] %
5%	F209B00	4.44	1.079	6.1
	D219B00	4.42	1.237	7.0
	F209B00 x D219B00	4.66	1.157	6.2
	Heterosis	0.23	-0.002	-0.2
10%	F209B00	4.44	0.918	5.2
	D219B00	4.42	1.053	5.9
	F209B00 x D219B00	4.66	0.984	5.3
	Heterosis	0.23	-0.001	-0.1
15%	F209B00	4.44	0.813	4.6
	D219B00	4.42	0.933	5.3
	F209B00 x D219B00	4.66	0.872	4.7
	Heterosis	0.23	-0.001	-0.1
20%	F209B00	4.44	0.733	4.1
	D219B00	4.42	0.840	4.7
	F209B00 x D219B00	4.66	0.785	4.2
	Heterosis	0.23	-0.001	-0.1

[a]Gain from selection for reciprocal recurrent selection was based on testcrosses of S2 lines and recombination of S2 families.

[b]Expected gain from selection per year was calculated considering 4 years per cycle.

selection. The expected gain on populations per se account for most the gain by reciprocal recurrent selection.

Miranda Filho and Paterniani (1983) estimated the gain in heterosis by reciprocal recurrent selection for Piramex and Cateto Brazilian populations. They found an expected increase in the heterosis of 0.041 ton/ha, or 0.8% in relation to the original population cross mean. However, Hallauer and Miranda Filho (1981) reported that 50% of the studies with reciprocal recurrent selection showed a decrease in intervarietal heterosis. They pointed out that the apparent failure of reciprocal recurrent selection to increase heterosis may be attributable to differences in magnitude of effects of genes controlling yield.

The results of this study indicate that reciprocal recurrent selection will not significantly increase the heterosis between the D219B00 and F209B00 populations. The gain in population mean cross was accounted by the improvement in the populations per se. The lack of increase in heterosis for D219B00 and F209B00 was probably due to the relatedness of the two populations.

SUMMARY AND CONCLUSIONS

In integrated population-hybrid improvement programs, breeders are interested in finding the appropriate tester for testing combining ability of inbred lines and for improving the basic populations. This study was conducted to provide further information on these two aspects of a maize breeding program.

From each one of the D219B00 and F209B00 populations, 100 S2 lines were derived. The S2 lines were crossed to the parental population, the opposite population, a single cross, and an inbred line, producing a total of 800 testcrosses. For D219B00 S2 derived lines, (FBR2-89 x FBR2-848) was the single-cross tester and FBR2-89 was the inbred line tester. Both inbred lines were derived from the opposite population F209B00. For F209B00 S2 derived lines, (RBR2-305 x DBR2-9) was the single-cross tester and RBR2-305 was the inbred line tester. RBR2-305 was derived from pedigree selection using different germplams of the two broad-base populations. DBR2-9 was derived from the opposite population, F209B00.

The 800 testcrosses were divided into eight sets. Each set included 100 testcrosses; 25 lines crossed to four testers. The sets were evaluated in three locations of Brazil in a split-plot design with four replications. The main plots were lines and the sub plots were testers. Five traits were measured in all three locations: yield, stand, moisture, percentage of erect plants, and index. Plant and ear height, and days-to-flower were measured only at two locations.

The analyses of variance were performed as a split plot design for all testcrosses and as a randomized complete block design for each individual type of testcross. The coefficients of variation averaged over both populations were relatively high for yield and index. For yield, the CV% was 25.4% for the main plots and 17.0% for the subplots, while for index they were 20.6% and 13.3%, respectively. For the other traits, they ranged from 2.1% (days-to-flower) to 11.3% (ear height), which are relatively small.

Mean squares for lines, testers, their interactions with locations, and line x tester interaction were significantly different from zero for all traits, except for stand. For both populations, the means of testcrosses with the opposite population tester were higher than the means of testcrosses with the parental population tester for most traits. However, the means were significantly different only for plant and ear height in the D219B00 population and yield for both populations. These results indicate that the two populations did not have big genetic differences. The heterosis for grain yield on mid parents were 0.225 Mg/ha or 5%. Except for ear height, no significant differences were found between the two populations for all other traits, indicating that they had similar performance. This similar performance may be due to the number of backcrosses (BC1) and the use of the same donor parent during the conversion program of the normal populations to brachytic. (FBR2-89 x FBR2-848) tester had significantly lower means than the FBR2-89 tester for all traits, except for days-to-flower. This result indicates that FBR2-89 line had higher general combining ability (GCA)

than FBR2-848. (RBR2-305 x DBR2-9) tester was significant different from RBR2-305 tester only for percentage of erect plants and plant height.

Mean squares for tester x location interaction were significant for both populations except for percentage of erect plants and ear height in the F209B00 population. Broad-base testers had significant tester x location interaction only for yield and moisture in the D219B00 population. Narrow-genetic base testers had significant tester x location interaction for all traits, except for percentage of erect plants and ear height in the F209B00 population and for days-to-flower in both populations.

Tester x Lines interactions were significant for all traits, except for days-to-flower in the F219B00 population. For yield, the (BBT vs NBT) had the greatest contribution for the line x tester interaction and no significant tester x line interaction was detected in narrow or broad-base testers in the D219B00 population.

The coefficients of genetic variation (CVg) were higher when the unrelated inbred line RBR2-305 participated in the pedigree of the testers. Lines with lower combining ability had greater range of variation and CVg. In all instances the estimates of the genetic components of variance of the S2 lines were much greater than the tester x line interaction, suggesting good consistency of the performance of the lines over testers. The variance component among lines for F209B00 population was approximately twice the component among lines for D219B00 population. This result was unexpected because both populations are

broad-base populations formed by recombining a large number of varieties, and no intentional selection for yield was practiced during the development of the S2 lines. In addition, no differential criterion of selection between the two populations was used during the development of the S2 lines. The difference between the two populations was attributable to effect of the different testers.

The (broad vs narrow) x line interaction accounted for most of the inconsistency of the lines over testers. No trend for higher tester x line interaction in narrow-genetic base testers than broad-genetic base testers was found in any trait. For unrelated testers the line x tester interaction was lower for the narrow-genetic base tester than for the broad-genetic base testers. For related testers, however, the component of variance of line x tester interaction was greater in narrow-genetic base testers than in broad-genetic base testers. In all instances, the broad-genetic base tester had lower tester x locations interaction than narrow-genetic base testers, indicating that, on the average, broad-base testers were more stable across locations than narrow-base testers

Analyses for each individual type of testcrosses in the F209B00 population showed that the narrow-genetic base testers had higher genetic component of variance than broad-genetic base testers for all traits, except for grain moisture and days-to-flower. The parental population tester had greater genetic variance component than did the opposite population tester for almost all traits. For yield, the genetic variances were similar. For yield, percentage of erect plants, and index, the genetic variation among testcrosses for narrow-genetic

base testers were approximately twice as big as the genetic variation of the broad-base testers. The greater genetic variance components for narrow-genetic base testers was associated with the presence of the unrelated line RBR2-305 in the testers, which was the only line derived from outside of the populations used for reciprocal recurrent selection.

The components of variance for population D219B00 show that broad genetic base testers had greater genetic variance component for almost all traits. The parental population had greater genetic variance component than the opposite population for all traits, except for percentage of erect plants and days-to-flower.

The genetic component variance among F209B00 line testcrosses with the opposite population (D219B00) as tester was similar to the component of variance using the parental population as tester. However, for D219B00 line testcrosses with the opposite population (F209B00) as tester, the genetic component was lower than with the parental population. On the assumption of partial to complete dominance, this may indicate that the F209B00 population has higher frequency of favorable alleles that are masking the gene effects of D219B00 population.

The genetic variation among D219B00 line testcrosses with the FBR2-89 line as tester was much lower than the genetic variation among testcrosses with the parental population for yield. The line FBR2-89 had the highest GCA, indicating the presence of high frequency of favorable alleles. The low genetic variation among these testcrosses can be explained by the presence of favorable alleles in the FBR2-89

line, which masked the gene effects of the recessive alleles in the D219B00 population.

The phenotypic correlations between testers were highly significant in all instances and had useful magnitudes. The greatest correlations were between parental and opposite populations and between single-cross and inbred-line testers. These results suggest that selection for general combining ability (GCA) or specific combining ability (SCA) with only one tester can be as effective as selection based on more than one tester. The correlation coefficients between the parental or opposite population and between single-cross or inbred-line testers were sufficiently high to indicate that either narrow- or broad-genetic base tester is reliable for estimating GCA of S2 lines.

The percentage of coincidence of selected lines for GCA based on topcross with the parental population as tester ranged from 20% to 72%. With 40% selection intensity there was at least 62% of coincidence for any tester. Therefore, any type of tester can be used to discard 50% of the lines without serious danger of losing valuable material. For inbred line testers, the values were consistently higher for the unrelated line RBR2-305, which was the only line derived from out of the populations used for reciprocal recurrent selection. On the other hand, the highest inbred-line tester for GCA (FBR2-89) had the poorest coincidence values. These results indicate that an unrelated inbred line may be more adequate for ranking the lines for GCA than a line with high general combining ability derived from the opposite population.

For yield, the lower heritability coefficient was obtained with

FBR2-89 line tester and the highest one with the RBR2-305 line tester. Consistently high heritability coefficients were obtained with the parental population tester, suggesting that inbred lines were not necessarily better testers than broad-genetic base testers or vice versa. The GCA of the line and the degree of relationship with the lines under evaluation have an important role in choosing inbred lines as testers. If there is insufficient information on the inbred line, the parental population seems to be the most appropriate tester.

The results of this study provide evidence that testers with low frequency of favorable alleles are more appropriate than testers with high frequency of favorable alleles. The results also indicate that inbred lines can be used to improve GCA or to identify lines having good GCA. Hòwever, the identification of lines with high GCA can be better if an appropriate inbred line tester is used for evaluating the inbred lines.

The phenotypic and genotypic correlations between Yield and plant and ear height, yield and days-to-flower and plant and ear height were significant and relatively high. The correlations between yield and plant and ear height, plant and ear height were positive. Between yield and days-to-flower, the correlations were negative. These results indicate that selection for improving yield can indirectly increases plant and ear height and reduce maturity. The positive genetic and phenotypic correlations between yield and plant or ear height indicate that selection for modifier genes for higher plant and ear height in brachytic populations will help to overcome the negative effects of the

br2 gene on yield. In addition, the negative correlation between yield and days-to-flower indicate that selection for earliness can also improve yield. The values of the additive genetic variances were similar for both populations. The estimates of additive genetic variance for D219B00 and F209B00 populations were 0.38 and 0.40, respectively. These values are within the range reported for other populations with a tendency to be higher than the average estimate reported for normal maize. Relatively large genetic gains are expected in both populations. The expected genetic gains from selection were calculated for reciprocal recurrent selection based on testcrosses of S2 lines and recombination of remnant S2 seeds, using the covariance between intra- and interpopulational testcrosses.

The estimated genetic gains were relatively high and the two populations did not show great genetic divergence. The heterosis over mid-parent was only 5%. The predicted gain on heterosis did not have any tendency for heterosis increasing with one cycle of reciprocal recurrent selection. The expected gain on population per se accounted for most of the gain through reciprocal recurrent selection. The results of this study indicate that reciprocal recurrent selection will not increase the heterosis between the D219B00 and F209B00 populations.

LITERATURE CITED

Acosta, A. F., and P. L. Crane. 1972. Further selection for lower ear height in maize. Crop Sci. 12: 165-167.

Allard, R. W. 1960. Principles of plant breeding. John Wiley and Sons, Inc., New York.

Allison, J. C. S., and R. N. Curnow. 1966. On the choice of tester parent for the breeding of synthetic varieties of maize (Zea mays L.). Crop Sci. 6: 541-544.

Anderson, J. C. and P. N. Chow. 1963. Phenotypes and grain yield associated with brachytic-2 gene in single cross hybrids of dent corn. Crop Sci. 3: 111-113.

Astralaga, R. 1956. Comparisons of four types of testers for evaluating the resistance of inbred lines of corn to Diplodia stalk rot. Unpublished M.S. thesis. Library, Iowa State University, Ames, Iowa.

Bullow, J. F. W. V. 1971. Efeito do gene braquitico-2 em populacoes analogas e em hibrido de milho (Zea mays, L.). Pesq. Agrop. Bras., Brasilia. 6: 155-161.

Campbell, C. M. 1965. New dwarfs & modifiers. Proc. Annu. Hybrid Corn. Ind. Res. Conf. 20: 22-29.

Comstock, R. E. 1979. Inbred lines versus the populations as testers in reciprocal recurrent selection. Crop Sci. 19: 881-886.

Comstock, R. E., and R. H. Moll. 1963. Genotype-environment interaction. p. 164-194. In H. F. Robinson (ed.) Statistical genetics and plant breeding. NAS-NRS, Publ. 1982.

Comstock, R. E.; H. F. Robinson; and P. H. Harvey. 1949. A breeding procedure designed to make use of both general and specific combining ability. Agron. J. 41: 360-367.

Darrah, L. L., S. A. Eberhart, and L. H. Penny. 1972. A maize breeding method study in Kenya. Crop Sci. 12: 605-608

Davis, R. L. 1927. Report of the plant breeder. Puerto Rico Agric. Exp. Stn. Rept. 1927: 14-15.

De Castro, E. M. 1983. Competicao entre populacoes de milho normais e braquiticas. Tese de doutoramento. Piracicaba. ESALQ/USP.

Eberhart, S. A., and W. A. Russell. 1969. Yield and stability for a 10-line diallel of single-cross and double-cross maize hybrids. Crop Sci. 9: 357-361.

Federer, W. T., and G. F. Sprague. 1947. A comparison of variance components in corn yield trials: I. Error, tester x line, and line components in topcross experiments. J. Am. Soc. Agron. 39: 453-463.

Galvao, J. D. 1974. Comportamento do milho Piranao (braquitico-2) e de milhos de porte normal em diferentes niveis de nitrogenio e populacoes de plantas. Unpublished Ph.D. Dissertation. Library, ESALQ/USP Piracicaba.

Gardner, C. O. 1969. The role of mass selection and mutagenic treatment in modern corn breeding. Corn and Sorghum Res. Conf. 24: 15-21.

Green, J. M. 1948. Relative value of two testers for estimating topcross performance in segregating maize progenies. J. Am. Soc. Agron. 40: 45-57.

Green, V. E., Jr. 1955. Asociacion de altura de planta y cosecha em maiz tropical. Turrialba 1: 55-58.

Hallauer, A. R., and J. H. Sears. 1969. Mass selection for yield in two varieties of maize. Crop Sci. 9: 47-50.

Hallauer, A. R. 1975. Relation of gene action and type of tester in maize breeding procedures. Corn and Sorghum Res. Conf. 30: 150-165.

Hallauer, A. R., and E. Lopez-Perez. 1979. Comparisons among testers for evaluating lines of corn. Proc. Annu. Hybrid Corn. Ind. Res. Conf. 34: 57-75.

Hallauer, A. R., and J. B. Miranda Filho. 1981. Quantitative genetics in maize breeding. Iowa State University Press, Ames, Iowa.

Horner, E. S.; H. W. Lundy; M. C. Lutrick; and W. A. Chapman. 1973. Comparisons of three methods of recurrent selection in maize. Crop Sci. 13: 485-489.

Horner, E. S.; M. C. Lutrick; W. A. Chapman; and F. G. Martin. 1976. Effect of recurrent selection for combining ability with a single-cross tester in maize. Crop Sci. 16: 5-8.

Hull, H. F. 1945. Recurrent selection for specific combining ability in corn. J. Am. Soc. Agron. 37: 134-145.

Jenkins, M. T. 1934. Methods of estimating the performance of double crosses in corn. J. Am. Soc. Agron. 26: 199-204.

Jenkins, M. T. 1935. The effect of inbreeding and selection within inbred lines of maize upon the hybrids made after successive generations of selfing. Iowa State Coll. J. Sci. 6: 429-450.

Jenkins, M. T., and A. M. Brunson. 1932. Methods of testing inbred lines of maize in crossbred combinations. J. Am. Soc. Agron. 24: 523-530.

Johnson, I. J., and H. K. Hayes. 1936. The combining ability of inbred lines of Golden Bantam sweet corn. J. Am. Soc. Agron. 28: 246-252.

Jones, D. F. 1918. The effects of inbreeding upon development. Connecticut Agric. Exp. Stn. Bull. 207: 1-100.

Jugenheimer, R. W. 1936. A comparison of certain inbred lines of maize in top, three-way and double crosses. Unpublished M.S. thesis. Library, Iowa State University, Ames, Iowa.

Keller, K. R. 1949. A comparison involving the number of, and relationship between, testers in evaluating inbred lines of maize. Agron. J. 41: 323-331.

Kempton, J. H. 1920. Heritable characters in maize. III- brachytic culms. The Journal of Heredity 11: 111-115.

Khehra, A. S.; V. V. Malhotra; V. K. Saxena; and B. S. Dhillon. 1975. Role of brachytic-2 in genetic improvement of maize. Egyptian Journal of Genetics and Cytology 4: 430-432.

Leng, E. R. 1957. Genetic production of short stalked hybrids. Proc. Annu. Hybrid Corn. Ind. Res. Conf. 12: 80-86.

Leite, D. R. 1975. Comportamento do Milho (Zea mays, L.) braquitico-2 em diferentes densidades de Plantio. Tese de mestrado. ESALQ/USP. Piracicaba.

Lindstrom, E. W. 1931. Prepotency of inbred lines on commercial varieties of maize. J. Am. Soc. Agron. 23: 652-661.

Lonnquist, J. H. 1968. Further evidence on testcross versus line performance in maize. Crop Sci. 8: 50-53.

Lonnquist, J. H., and M. F. Lindsey. 1970. Tester performance level for the evaluation of lines for hybrid performance. Crop Sci. 10: 602-604.

Lonnquist, J. H., and M. D. Rumbaugh. 1958. Relative importance of test sequence for general and specific combining ability in corn breeding. Agron. J. 541-544.

Marquez-Sanchez, F., and A. R. Hallauer. 1970. Influence of sample size on the estimation of genetic variances in a synthetic variety of maize. Crop Sci. 10: 357-361.

Matzinger, D. F. 1953. Comparison of three types of testers for the evaluation of inbred lines of corn. Agron. J. 45: 493-495.

Mendez, R. C. A., and J. D. Molina Galan. 1982. High and low yielding testers for general combining ability in inbred maize lines. Agrociencia 47: 117-130.

Miranda Filho, J. B. 1982. Mating schemes to predict gain on heterosis in reciprocal recurrent selection. Brazil. J. Genetics 5: 745-760.

Miranda Filho, J. B., and E. Paterniani. 1983. Intra- and Interpopulation genetic parameter estimates and implications in selection. Brazil. J. Genetics 6: 15-27.

Paterniani, E. 1973. Origem e comportamento do milho Piranao. Relatorio cientifico do departamento e instituto de genetica, ESALQ/USP, Piracicaba. 7: 148-161.

Paterniani, E. 1974. Selecao entre e dentro de familias de meios irmaos no milho Piranao. Relatorio cientifico do departamento e instituto de genetica, ESALQ/USP, Piracicaba. 8: 174-179.

Ramalho, M. A. P., 1978. Eficiencia de alguns processos de selecao intra populacional no milho baseados em familias nao endogamas. Tese de doutoramento. Piracicaba, ESALQ/USP.

Rawlings, J. C., and D. L. Thompson. 1962. Performance level as criterion for the choice of maize testers. Crop Sci. 2: 217-220.

Rissi, R., and E. Paterniani. 1981. Estimates of genetic parameters in two sub-populations of the variety of maize (Zea mays, L.) Piranao. Brazil. J. Genetics 4: 579-592.

Rojas, B. A., and G. F. Sprague. 1952. A comparison of variance components in corn yield trials: III. General and specific combining ability and their interactions with locations and years. Agron. J. 44: 462-467.

Russell, W. A. 1961. A comparison of five types of testers in evaluating the relationships of stalk rot resistance in corn inbred lines and stalk rot resistance in hybrid combinations. Crop Sci. 1: 393-397.

Russell, W. A., and S. A. Eberhart. 1975. Hybrid performance of selected maize lines from reciprocal recurrent and testcross selection programs. Crop Sci. 15: 1-4.

Russell, W. A.; S. A. Eberhart; and Urbano A. Vega. 1973. Recurrent selection for specific combining ability for yield in two maize populations. Crop Sci. 13: 257-261.

Salazar, B. A., and J. H. Lonnquist. 1963. Tester sampling bias in the topcrossing of inbred lines of corn. Crop Sci. 3: 317-318.

Shull, G. H. 1909. A pure line method of corn breeding. Am. Breed. Assoc. Rept. 5: 51-59.

Singh, R. D. 1958. Evaluation of second cycle inbreds of maize by different types of related and unrelated testers. Indian J. Gen. Plant Breed. 18: 199-205.

Sokolov, B. P.; P.P. Domashnev; and L. I. Pavlenko. 1976. Results of work on the production of short maize forms. Plant Breeding Abstracts 46(4): 277.

Solonenko, T. A., and T. S. Chalyr. 1975. A study of dwarf maize hybrids. Plant Breeding Abstracts 45(5): 279.

Sprague, G. F. 1939. An estimation of the number of topcrossed plants required for adequate representation of a corn variety. J. Am. Soc. Agron. 38: 108-117.

Sprague, G. F. 1946. Early testing of inbred lines of corn. J. Am. Soc. Agron. 38: 108-117.

Sprague, G. F., and S. A. Eberhart. 1977. Corn breeding. p. 305-354. In G. F. Sprague (ed.) Corn and corn improvement. Am. Soc. Agron., Madison, Wisconsin.

Sprague, G. F., and W. T. Federer. 1951. A comparison of variance components in corn yield trials. II. Error, year x variety, location x variety and variety components. Agron. J. 43: 535-541.

Sprague, G. F., and L. A. Tatum. 1942. General and specific combining ability in single crosses of corn. J. Am. Soc. Agron. 34: 923-932.

Steel, R. G. D., and J. H. Torrie. 1980. Principles and procedures of statistics: a biometrical approach. 2nd ed. McGraw-Hill, Inc., New York.

St. John, R. R. 1934. A comparison of reciprocal topcrosses in corn. J. Am. Soc. Agron. 26: 721-724.

Troyer, A. F. 1976. Selection for early flowering in corn: Seven late synthetics. Crop Sci. 16: 767-772.

Vera, G. A., and P. L. Crane. 1970. Effects of selection for lower ear height in synthetic populations of maize. Crop Sci. 10: 286-288.

Walejko, R. N., and W. A. Russell. 1977. Evaluation of recurrent selection for specific combining ability in two open pollinated maize cultivars. Crop Sci. 17: 647-651.

Wright, J. A.; A. R. Hallauer; L. H. Penny; and S. A. Eberhart. 1971. Estimating genetic variance in maize by use of single ear and three-way crosses among unselected inbred lines. Crop Sci. 11: 690-695.

Zambezi, B. T.; E. S. Horner; and F. G. Martin. 1986. Inbred lines as testers for general combining ability in maize. Crop Sci. 26: 908-910.

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APPENDIX

Table A1. Pooled analysis of variance of eight sets of a split-plot experiment conducted in Matao, SP, Brazil with 25 S2 lines as the main plots and four testers as the sub-plots

Sources of variation[a]	df	Mean squares[b]			
		YIELD	EREPL	MOIST	STAND
Sets (S)	7	27.1669**	5160.20**	1768.98**	46.56**
Replications/S	24	3.0505**	394.86**	126.13**	7.71**
Lines/S	192	5.1362**	303.59**	4.55**	4.36ns
D219B00 lines (D-lines)	96	3.6850**	350.28**	5.26**	4.88ns
F209B00 lines (F-Lines)	96	6.5875**	256.90**	3.84**	3.84ns
Pooled error (a)	576	0.9386**	117.20**	2.12**	3.81**
Error (a) D-lines	288	0.9132ns	135.70ns	2.25**	4.08*
Error (a) F-lines	288	0.8597**	98.71**	1.98**	3.55*
Testers (T)/S	24	23.3727**	578.25**	7.48**	3.63ns
Tester/D-lines	12	34.7779**	859.88**	12.33**	4.80ns
(Narrow vs Broad)	4	31.4921**	102.31ns	34.54**	7.06ns
Broad base	4	8.7052**	74.94ns	0.55ns	1.82ns
Narrow base	4	64.1362**	2402.38**	1.91**	5.53ns
Tester/F-lines	12	11.9674**	296.62**	2.63**	2.46ns
(Narrow vs Broad)	4	31.9915**	84.15ns	5.25**	1.38ns
Broad base	4	1.6725*	45.22ns	2.24**	0.93ns
Narrow base	4	2.2383**	760.50**	0.41ns	5.08ns
(Lines x Testers)/S	576	1.0200**	111.95**	0.59ns	2.95ns
Tester x D-lines	288	1.0675*	137.66*	0.60ns	2.94ns
(Narrow vs Broad)	96	1.1428**	156.37*	0.63ns	2.86ns
Broad base	96	1.0630**	122.43ns	0.74ns	2.48ns
Narrow base	96	0.9966*	134.18ns	0.41ns	3.49ns
Tester x F-lines	288	0.9724**	86.24**	0.59ns	2.96ns
(Narrow vs Broad)	96	1.5493**	91.78**	0.63ns	3.02ns
Broad base	96	0.7178ns	86.52ns	0.52ns	3.00ns
Narrow base	96	0.6502ns	80.42ns	0.60ns	2.87ns

[a]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

[b]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; and STAND: plants available at harvest.

*$p \leq .05$.

**$p \leq .01$.

Table A1. (continued)

Sources of variation[a]	df	Mean squares[b]			
		YIELD	EREPL	MOIST	STAND
Error b	1800	0.6710	91.85	0.55	3.19
Error b/D-lines	900	0.7673	116.49	0.58	3.40
Error b (Narrow vs Broad)	300	0.8377	110.10	0.61	3.52
Error b Broad base	300	0.7092	120.31	0.65	3.29
Error b Narrow base	300	0.7549	119.05	0.49	3.40
Error b/F-lines	900	0.5747	67.22	0.52	2.97
Error b (Narrow vs Broad)	300	0.5754	65.60	0.59	3.35
Error b Broad base	300	0.6338	70.15	0.48	3.33
Error b Narrow base	300	0.5151	65.90	0.48	2.24
Mean		5.44	89.2	18.9	24.6
Mean D-lines		5.44	86.7	17.3	24.4
Mean F-lines		5.45	91.8	20.4	24.7
CVa		17.8	12.1	7.7	7.9
CVa D-lines		17.6	13.4	8.7	8.3
CVa F-lines		17.0	10.8	6.9	7.6
CVb		15.0	10.7	3.9	7.3
CVb D-lines		16.1	12.4	4.4	7.6
CVb F-lines		13.9	8.9	3.5	7.0

Table A2. Pooled analysis of variance of eight sets of a split-plot experiment conducted in Matao, SP, Brazil with 25 S2 lines as the main plots and four testers as the sub-plots

Sources of variation[a]	df	Mean squares[b]			
		INDEX	PH	EH	FLOW
Sets (S)	7	89.16**	2727.40**	2260.86**	243.01**
Replications/S	24	15.87**	329.81**	250.18**	8.73**
Lines/S	192	5.89**	722.91**	519.84**	10.90**
D219B00 lines (D-lines)	96	3.41**	652.80**	438.33**	11.58**
F209B00 lines (F-Lines)	96	8.38**	793.01**	601.34**	10.22**
Pooled error (a)	576	1.62**	81.24**	60.97**	3.80**
Error (a) D-lines	288	1.38**	87.83**	61.81**	3.96**
Error (a) F-lines	288	1.86**	74.65**	60.13**	3.65**
Testers (T)/S	24	16.57**	371.65**	249.67**	87.53**
Tester/D-lines	12	17.92**	498.87**	428.63**	127.61**
(Narrow vs Broad)	4	6.54**	317.15**	67.55ns	372.05**
Broad base	4	0.93ns	196.92*	362.74**	9.02**
Narrow base	4	46.30**	982.54**	855.61**	1.78ns
Tester/F-lines	12	15.22**	244.42**	70.70*	47.45**
(Narrow vs Broad)	4	41.02**	99.25ns	21.32ns	131.53**
Broad base	4	0.30ns	14.39ns	104.50*	4.23ns
Narrow base	4	4.35**	619.63**	86.28*	6.59*
(Lines x Testers)/S	576	1.04**	60.00**	58.81**	2.84*
Tester x D-lines	288	0.79ns	58.95**	59.22**	3.13ns
(Narrow vs Broad)	96	0.79ns	55.93*	49.33**	3.05ns
Broad base	96	0.80*	59.91*	73.66**	3.14ns
Narrow base	96	0.79ns	61.02**	54.68**	3.20ns
Tester x F-lines	288	1.29**	61.04**	58.40**	2.55*
(Narrow vs Broad)	96	2.08**	69.91**	65.06**	3.26**
Broad base	96	0.87*	59.01*	55.15**	2.70ns
Narrow base	96	0.91ns	54.21**	55.01**	1.70ns

[a]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

[b]INDEX: eye appearance, rated from 1 (excellent) to 9 (poor). PH: plant height; EH: ear height; and FLOW: number of days from planting to silking

*$p \leq .05$.

**$p \leq .01$.

Table A2. (continued)

Sources of variation[a]	df	Mean squares[b]			
		INDEX	PH	EH	FLOW
Error b	1800	0.74	38.42	35.16	2.50
Error b/D-lines	900	0.71	38.58	35.59	2.83
Error b (Narrow vs Broad)	300	0.80	40.89	32.99	3.10
Error b Broad base	300	0.61	43.36	43.38	2.89
Error b Narrow base	300	0.72	31.48	30.41	2.50
Error b/F-lines	900	0.78	38.26	34.73	2.17
Error b (Narrow vs Broad)	300	0.84	39.35	37.64	2.14
Error b Broad base	300	0.61	41.58	35.83	2.30
Error b Narrow base	300	0.88	33.83	30.71	2.08
Mean		6.3	176.3	86.4	72.4
Mean D-lines		6.6	174.2	84.4	72.6
Mean F-lines		5.9	178.4	88.4	72.2
CVa		20.4	5.1	9.0	2.7
CVa D-lines		17.9	5.4	9.3	2.7
CVa F-lines		23.0	4.8	8.8	2.6
CVb		13.8	3.5	6.9	2.2
CVb D-lines		12.8	3.6	7.1	2.3
CVb F-lines		14.9	3.5	6.7	2.0

Table A3. Pooled analysis of variance of eight sets of a split-plot experiment conducted in Ituiutaba, MG, Brazil with 25 S2 lines as the main plots and four testers as the sub-plots

Sources of variation[a]	df	Mean squares[b]			
		YIELD	EREPL	MOIST	STAND
Sets (S)	7	10.8957**	2122.62**	62.44**	127.48**
Replications/S	24	2.9409**	154.83**	12.01**	6.52**
Lines/S	192	2.6218**	231.16**	6.13**	4.25**
D219B00 lines (D-lines)	96	2.2061**	181.86**	6.38**	5.29**
F209B00 lines (F-Lines)	96	3.0374**	280.46**	5.87**	3.22ns
Pooled error (a)	576	0.7142**	87.83**	0.92**	3.08ns
Error (a) D-lines	288	0.5469**	88.56**	0.93**	3.42ns
Error (a) F-lines	288	0.8815**	87.09**	0.90**	2.74ns
Testers (T)/S	24	12.4379**	273.74**	11.09**	3.91ns
Tester/D-lines	12	9.6773**	469.26**	18.88**	5.07ns
(Narrow vs Broad)	4	0.9180ns	559.96**	50.24**	4.72ns
Broad base	4	0.5766ns	163.39ns	0.44ns	5.05ns
Narrow base	4	27.5373**	684.42**	5.96**	5.44ns
Tester/F-lines	12	15.1985**	78.23ns	3.30**	2.76ns
(Narrow vs Broad)	4	42.8713**	28.52ns	1.77ns	2.65ns
Broad base	4	1.4377**	38.02ns	3.77**	2.87ns
Narrow base	4	1.2865*	168.15*	4.37**	2.76ns
(Lines x Testers)/S	576	0.6133**	84.40**	0.79**	3.02ns
Tester x D-lines	288	0.5008**	80.99ns	0.81**	3.13ns
(Narrow vs Broad)	96	0.5348*	105.61ns	1.05**	3.71ns
Broad base	96	0.5224ns	72.48ns	0.82**	2.25ns
Narrow base	96	0.4453**	64.88ns	0.55*	3.43ns
Tester x F-lines	288	0.7257**	87.81**	0.78**	2.91ns
(Narrow vs Broad)	96	1.0265**	95.09**	0.84**	3.14ns
Broad base	96	0.5137**	82.23ns	0.86**	2.49ns
Narrow base	96	0.6367**	86.10*	0.64*	3.11ns

[a]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

[b]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; and STAND: plants available at harvest.

*$p \leq .05$.

**$p \leq .01$.

Table A3. (continued)

Sources of variation[a]	df	Mean squares[b]			
		YIELD	EREPL	MOIST	STAND
Error b	1800	0.3727	67.54	0.49	2.85
Error b/D-lines	900	0.3775	71.19	0.46	3.22
Error b (Narrow vs Broad)	300	0.3811	74.05	0.48	3.13
Error b Broad base	300	0.4478	77.22	0.50	3.02
Error b Narrow base	300	0.3035	62.29	0.39	3.53
Error b/F-lines	900	0.3680	63.89	0.51	2.48
Error b (Narrow vs Broad)	300	0.3492	62.66	0.51	2.72
Error b Broad base	300	0.3269	64.94	0.58	2.54
Error b Narrow base	300	0.4278	64.08	0.45	2.20
Mean		4.33	88.0	16.7	24.3
Mean D-lines		4.23	86.5	16.8	24.1
Mean F-lines		4.43	89.4	16.6	24.6
CVa		19.5	8.9	5.7	7.2
CVa D-lines		17.5	10.9	5.8	7.7
CVa F-lines		21.2	10.4	5.7	6.7
CVb		14.1	9.3	4.2	6.9
CVb D-lines		14.5	9.7	4.0	7.4
CVb F-lines		13.7	8.9	4.3	6.4

Table A4. Pooled analysis of variance of eight sets of a split-plot experiment conducted in Ituiutaba, MG, Brazil with 25 S2 lines as the main plots and four testers as the sub-plots

Sources of variation[a]	df	Mean squares[b]			
		INDEX	PH	EH	FLOW
Sets (S)	7	37.87**	9217.46**	5173.51**	197.86**
Replications/S	24	6.70**	716.56**	549.21**	22.87**
Lines/S	192	3.03**	1375.97**	82.66**	23.57**
D219B00 lines (D-lines)	96	1.98**	1461.60**	779.98**	20.36**
F209B00 lines (F-Lines)	96	4.08**	1290.33**	822.84**	26.78**
Pooled error (a)	576	1.16**	210.25**	140.39**	5.83**
Error (a) D-lines	288	1.14**	174.33**	102.27**	4.70**
Error (a) F-lines	288	1.17**	246.17**	178.50**	6.97**
Testers (T)/S	24	4.15**	1200.40**	702.72**	76.17**
Tester/D-lines	12	2.62**	1587.67**	1285.17**	73.85**
(Narrow vs Broad)	4	0.56ns	1066.69**	219.97**	215.71**
Broad base	4	0.09*	309.47**	482.66**	1.90ns
Narrow base	4	7.21**	3386.84**	3152.86**	3.96ns
Tester/F-lines	12	5.69**	813.13**	120.27**	78.50**
(Narrow vs Broad)	4	8.15**	429.91**	256.54**	232.02**
Broad base	4	1.10ns	136.78ns	74.56ns	1.16ns
Narrow base	4	7.81**	1872.69**	29.72ns	2.31ns
(Lines x Testers)/S	576	0.71**	112.14**	87.42**	3.18**
Tester x D-lines	288	0.65*	113.49**	89.19**	2.97**
(Narrow vs Broad)	96	0.75*	114.75**	80.77*	3.49**
Broad base	96	0.63ns	156.40**	110.23**	2.50ns
Narrow base	96	0.58ns	69.32ns	76.58*	2.92**
Tester x F-lines	288	0.77**	110.78**	85.65**	3.39**
(Narrow vs Broad)	96	1.20**	116.52**	84.86*	3.54**
Broad base	96	0.39ns	135.78**	107.79**	3.42**
Narrow base	96	0.72*	80.05ns	64.29ns	3.21*

[a]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

[b]INDEX: eye appearance, rated from 1 (excellent) to 9 (poor). PH: plant height; EH: ear height; and FLOW: number of days from planting to silking.

*$p \leq .05$.

**$p \leq .01$.

Table A4. (continued)

Sources of variation[a]	df	Mean squares[b]			
		INDEX	PH	EH	FLOW
Error b	1800	0.50	75.44	63.03	2.09
Error b/D-lines	900	0.53	77.96	62.61	2.02
Error b (Narrow vs Broad)	300	0.56	77.44	62.33	2.13
Error b Broad base	300	0.52	102.09	71.88	2.13
Error b Narrow base	300	0.51	54.35	53.62	1.79
Error b/F-lines	900	0.47	72.91	63.45	2.16
Error b (Narrow vs Broad)	300	0.43	73.33	61.80	2.09
Error b Broad base	300	0.47	79.57	65.70	2.23
Error b Narrow base	300	0.50	65.84	62.84	2.17
Mean		6.2	174.0	91.7	70.1
Mean D-lines		6.0	175.4	93.2	69.9
Mean F-lines		6.3	172.5	90.1	70.2
CVa		17.4	8.3	12.9	3.4
CVa D-lines		17.7	7.5	10.9	3.1
CVa F-lines		17.1	9.1	14.8	3.8
CVb		11.4	5.0	8.7	2.1
CVb D-lines		12.1	5.0	8.5	2.0
CVb F-lines		10.8	4.9	8.8	2.1

Table A5. Pooled analysis of variance of eight sets of a split-plot experiment conducted in Rio Verde, GO, Brazil with 25 S2 lines as the main plots and four testers a the sub-plots

Sources of variation[a]	df	Mean squares[b]				
		YIELD	EREPL	MOIST	STAND	INDEX
Sets (S)	7	4.3232ns	818.14**	155.48**	19.37ns	24.96**
Replications/S	24	3.7757ns	122.02**	19.01**	18.48**	2.58ns
Lines/S	192	5.2481**	127.49**	21.13**	8.08ns	4.87**
D-lines	96	5.6274**	68.42**	19.21**	10.51ns	5.20**
F-Lines	96	4.8687**	186.55**	23.06**	5.65ns	4.54**
Pooled error (a)	576	2.7534**	46.67ns	4.44**	8.74**	1.98**
Error (a) D-lines	288	2.9876**	42.39ns	3.98**	11.86**	2.01**
Error (a) F-lines	288	2.5192**	50.95**	4.90**	5.62*	1.95**
Testers (T)/S	24	18.7609**	123.96**	54.92**	7.94ns	9.06**
Tester/D-lines	12	25.6318**	120.23**	87.35**	5.29ns	15.13**
(Narrow vs Broad)	4	18.6255**	32.08ns	241.33**	6.35ns	1.08ns
Broad base	4	7.5680**	24.85ns	8.97**	4.03ns	2.34**
Narrow base	4	50.7017**	303.76**	11.76**	5.49ns	41.96**
Tester/F-lines	12	11.8900**	127.68**	22.49**	10.60*	2.99**
(Narrow vs Broad)	4	14.5646**	79.49ns	53.72**	15.54**	0.33ns
Broad base	4	2.9629**	62.86ns	0.55ns	11.06ns	2.14ns
Narrow base	4	18.1424**	240.70**	13.21**	5.20ns	6.49**
(Lines x Testers)/S	576	1.2750**	54.51**	2.91**	5.69ns	0.99*
Tester x D-lines	288	1.2630*	46.92ns	2.58**	6.59ns	0.96**
(Narrow vs Broad)	96	1.4214*	53.45ns	2.94**	7.20ns	0.96ns
Broad base	96	1.1910ns	36.04ns	2.00ns	6.46ns	0.84*
Narrow base	96	1.1765ns	51.28ns	2.81**	6.10ns	1.08*
Tester x F-lines	288	1.2870**	62.10**	3.23*	4.79ns	1.02ns
(Narrow vs Broad)	96	1.8422**	78.11**	3.72*	4.62ns	1.00ns
Broad base	96	0.9404ns	51.68*	3.52ns	6.83ns	0.98ns
Narrow base	96	1.0785*	56.50**	2.46*	2.90ns	1.08ns

[a]D and F indicate lines derived from D219B00 and F209B00 populations, respectively.

[b]YIELD: grain yield; EREPL: percentage of erect plants; MOIST: moisture of grain at harvest; and STAND: plants available at harvest.

*$p \leq .05$.

**$p \leq .01$.

Table A5. (continued)

Sources of variation[a]	df	Mean squares[b]				
		YIELD	EREPL	MOIST	STAND	INDEX
Error b	1800	0.9272	43.36	2.34	5.64	0.85
Error b/D-lines	900	1.0375	47.71	1.96	6.71	0.72
(Narrow vs Broad)	300	1.0431	46.88	2.02	6.81	0.74
Broad base	300	1.0333	45.57	2.00	7.27	0.63
Narrow base	300	1.0360	50.70	1.86	6.04	0.79
Error b/F-lines	900	0.8169	39.00	2.73	4.58	0.99
(Narrow vs Broad)	300	0.8509	41.30	2.72	4.39	1.07
Broad base	300	0.8489	38.30	3.62	5.98	0.90
Narrow base	300	0.7511	37.42	1.85	3.37	0.99
Mean		4.51	94.2	26.0	24.0	6.4
Mean D-lines		4.49	95.0	25.5	23.9	6.3
Mean F-lines		4.54	93.3	26.5	24.2	6.6
CVa		36.8	7.3	8.1	12.3	21.9
CVa D-lines		38.5	6.9	7.8	14.4	22.5
CVa F-lines		35.0	7.6	8.4	9.8	21.3
CVb		21.3	7.0	5.9	9.9	14.4
CVb D-lines		22.7	7.3	5.5	10.8	13.5
CVb F-lines		19.9	6.7	6.2	8.9	15.2

Table A6. Analysis of covariance pooled over sets and combined over locations testcrosses made with the parental population as tester (tester 1) arranged as randomized complete block design

Sources of variation[b]	df	YIELD[a] + EREPL	df	YIELD + PH	YIELD + EH	YIELD + FLOW	EREPL + PH	EREPL + EH	EREPL + FLOW	PH + EH	PH + FLOW	EH + FLOW
Locations (E)	2		1									
Set (S)	7		7									
S x E	14		7									
Rep/S x E	72		48									
Lines/Set[a]	192	2.61	192	15.17	11.18	-1.87	34.38	23.68	5.23	337.35	2.25	4.42
D-Lines/S	96	2.63	96	15.62	13.01	-1.49	5.46	19.91	5.02	321.63	6.59	3.85
F-Lines/S	96	2.59	96	14.72	9.35	-2.25	63.30	27.44	5.44	353.07	-2.09	4.98
Lines x E/S	384	1.46	192	1.44	0.94	-0.29	4.94	3.16	-0.59	73.43	-4.40	-1.65
D-Lines x E/S	192	1.69	96	1.59	0.66	-0.40	-6.03	-0.78	1.31	66.63	-5.25	-1.46
F-Lines x E/S	192	1.23	96	1.30	1.21	-0.18	15.92	7.10	-2.50	80.24	-3.56	-1.85
Pooled error	1728	0.98	1152	2.27	1.77	-0.47	11.01	5.76	0.32	59.22	-3.54	-3.15
D-Lines error	864	0.75	576	2.04	1.61	-0.45	11.14	6.75	1.30	57.97	-2.62	-2.29
F-Lines error	864	1.20	576	2.50	1.93	-0.49	10.89	4.77	-0.65	60.48	-4.46	-4.02
Total	2399		1599									

[a]YIELD: grain yield; EREPL: percentage of erect plants; PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]D and F indicate lines from D219B00 and F209B00 populations, respectively.

Table A7. Analysis of covariance pooled over sets and combined over locations for testcrosses made with the opposite population as tester (tester 2) arranged as randomized complete block design

Sources of variation[b]	df	YIELD[a] + EREPL	df	YIELD + PH	YIELD + EH	YIELD + FLOW	EREPL + PH	EREPL + EH	EREPL + FLOW	PH + EH	PH + FLOW	EH + FLOW
Locations (E)	2		1									
Set (S)	7		7									
S x E	14		7									
Rep/S x E	72		48									
Lines/Set[a]	192	3.31	192	10.37	8.31	-1.54	22.28	10.97	-0.98	352.68	6.73	7.43
D-Lines/S	96	2.47	96	9.58	8.69	-0.85	11.05	-20.27	1.73	319.62	11.25	9.50
F-Lines/S	96	4.14	96	11.16	7.94	-2.24	33.51	42.21	-3.69	385.75	2.21	5.35
Lines x E/S	384	1.64	192	2.62	2.00	-0.55	-2.08	-7.26	-0.61	86.72	-3.92	-3.58
D-Lines x E/S	192	1.94	96	2.61	2.26	-0.31	-25.11	-18.88	-0.02	97.66	-1.29	-1.59
F-Lines x E/S	192	1.35	96	2.63	1.74	-0.78	20.96	4.36	-1.20	75.78	-6.56	-5.57
Pooled error	1728	1.32	1152	2.39	1.83	-0.49	6.19	5.28	-0.57	58.24	-3.54	-3.47
D-Lines error	864	1.67	576	1.98	1.34	-0.46	8.89	6.28	-0.73	58.80	-3.08	-2.66
F-Lines error	864	0.97	576	2.80	2.32	-0.51	3.49	4.28	-0.41	57.68	-3.99	-4.28
Total	2399		1599									

[a]YIELD: grain yield; EREPL: percentage of erect plants; PH: plant height; EH: ear height; FLOW: number of days from planting to silking.

[b]D and F indicate lines from D219B00 and F209B00 populations, respectively.

Table A8. Means of eight traits obtained from 800 testcrosses evaluated in three locations of Brazil during the 1984/85 agricultural year

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
84	1	8401	4.29	22.0	24	96.2	6	170	79	72
84	1	8402	4.81	21.7	23	91.8	7	177	99	70
84	1	8403	4.78	20.0	25	84.7	6	182	85	70
84	1	8404	5.15	20.7	25	94.7	6	178	88	70
84	1	8405	4.89	21.4	25	90.8	6	170	83	72
84	1	8406	4.79	20.9	25	95.5	6	190	98	73
84	1	8407	4.14	20.4	24	90.6	7	169	89	72
84	1	8408	5.25	20.8	24	95.7	6	174	90	71
84	1	8409	4.71	23.1	25	89.9	6	184	95	73
84	1	8410	3.70	21.1	23	84.7	7	197	98	73
84	1	8411	3.66	20.1	24	88.2	7	164	85	70
84	1	8412	4.77	20.8	25	93.1	6	172	89	72
84	1	8413	4.95	20.3	25	92.7	6	182	93	70
84	1	8414	4.60	20.9	23	93.9	6	170	79	71
84	1	8415	4.53	20.9	25	90.0	6	173	86	72
84	1	8416	3.76	20.8	24	94.6	6	173	86	73
84	1	8417	5.20	21.6	25	91.4	6	193	102	72
84	1	8418	4.21	21.5	25	90.4	6	160	77	73
84	1	8419	4.62	20.9	23	87.8	6	179	87	71
84	1	8420	3.60	21.1	24	91.7	6	173	87	73
84	1	8421	4.37	20.9	25	88.2	7	171	88	71
84	1	8422	4.45	22.2	25	92.5	6	168	89	73
84	1	8423	4.01	22.0	24	89.9	6	167	82	73
84	1	8424	4.40	21.8	24	89.3	6	190	96	72
84	1	8425	4.99	21.4	25	87.3	7	170	82	71
85	1	8501	4.07	20.3	24	83.6	6	174	82	73
85	1	8502	4.10	20.9	23	87.9	7	160	71	72
85	1	8503	4.48	19.7	24	89.9	7	175	88	74
85	1	8504	4.47	20.9	25	84.9	6	179	87	74

[a]Set 80 through 83 correspond to F209B00 population; Set 84 through 87 correspond to D219B00 population.

[b]Testers: 1) parental population, 2) opposite population, 3) unrelated single cross, and 4) unrelated inbred line.

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
85	1	8505	3.96	21.3	23	86.2	6	178	90	73
85	1	8506	4.22	19.9	23	91.2	7	169	81	72
85	1	8507	4.19	20.1	24	90.0	7	181	93	74
85	1	8508	4.31	21.6	24	87.5	7	167	84	73
85	1	8509	4.82	21.0	25	92.3	6	177	98	72
85	1	8510	3.94	21.0	24	87.7	7	163	85	73
85	1	8511	4.89	20.1	25	89.5	6	178	93	72
85	1	8512	4.51	19.3	24	88.5	7	181	86	72
85	1	8513	4.10	20.4	23	87.6	6	172	90	74
85	1	8514	4.76	19.7	25	74.3	7	179	93	71
85	1	8515	4.27	19.8	24	90.5	7	177	90	72
85	1	8516	4.30	20.5	25	87.7	7	169	79	71
85	1	8517	5.16	21.1	24	84.9	6	170	88	72
85	1	8518	4.19	19.7	25	83.0	7	169	85	72
85	1	8519	5.73	22.1	25	88.0	6	184	94	73
85	1	8520	4.58	20.0	24	86.2	7	164	80	70
85	1	8521	4.18	20.7	24	88.7	7	165	84	72
85	1	8522	4.43	19.2	25	89.0	7	171	81	73
85	1	8523	3.75	21.3	23	89.8	6	176	84	75
85	1	8524	4.14	20.7	25	88.1	7	169	84	71
85	1	8525	4.48	20.4	25	93.3	6	175	83	73
86	1	8601	3.56	19.0	24	87.0	6	177	88	73
86	1	8602	4.87	19.5	24	89.5	6	171	84	73
86	1	8603	3.85	20.3	24	89.1	6	171	80	72
86	1	8604	4.04	21.5	24	86.7	6	180	93	73
86	1	8605	4.88	21.1	24	94.1	6	188	97	73
86	1	8606	4.76	19.8	24	93.6	6	183	94	73
86	1	8607	5.64	20.2	24	90.9	6	173	87	72
86	1	8608	4.06	18.5	24	83.2	7	177	86	72
86	1	8609	3.55	20.3	23	87.5	6	165	83	73
86	1	8610	4.69	19.7	25	86.5	7	182	88	72
86	1	8611	4.21	20.2	24	91.7	6	178	86	73
86	1	8612	4.90	20.6	24	87.3	6	175	90	72
86	1	8613	4.91	19.3	24	87.9	6	165	84	70
86	1	8614	5.02	19.3	23	88.9	6	183	91	73
86	1	8615	4.10	19.5	25	85.5	7	152	77	71
86	1	8616	4.29	19.8	25	87.6	6	164	85	73
86	1	8617	4.51	20.2	25	81.8	6	177	90	73
86	1	8618	4.34	19.8	25	84.7	7	174	86	72
86	1	8619	4.17	19.1	23	87.1	7	179	88	71
86	1	8620	4.10	19.4	25	90.3	7	177	91	70
86	1	8621	4.48	21.3	25	87.8	6	180	96	74

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
86	1	8622	4.89	19.0	23	93.3	6	176	93	72
86	1	8623	4.24	19.4	24	86.7	7	172	87	73
86	1	8624	4.89	18.4	25	77.5	7	166	79	69
86	1	8625	4.80	19.7	24	88.2	6	175	90	72
87	1	8701	4.26	19.9	25	90.0	7	173	85	72
87	1	8702	4.89	20.5	24	90.8	6	177	98	73
87	1	8703	3.81	21.5	23	90.0	6	173	94	73
87	1	8704	4.48	19.0	24	90.6	6	178	93	72
87	1	8705	4.25	21.1	25	89.0	7	189	90	71
87	1	8706	5.02	20.0	25	84.9	6	186	99	73
87	1	8707	4.15	19.8	24	94.1	7	172	82	73
87	1	8708	4.04	19.8	24	94.4	7	164	89	72
87	1	8709	3.67	20.3	23	90.8	6	176	89	73
87	1	8710	3.56	20.6	25	87.8	7	166	80	72
87	1	8711	4.57	21.2	24	93.5	7	174	86	73
87	1	8712	5.35	19.4	24	87.4	6	200	96	72
87	1	8713	4.85	20.3	24	90.5	6	184	97	73
87	1	8714	4.46	20.7	24	95.6	6	177	90	72
87	1	8715	3.99	19.4	24	87.4	7	166	77	72
87	1	8716	3.50	19.5	25	92.0	6	174	82	73
87	1	8717	3.43	20.3	24	87.5	7	161	74	75
87	1	8718	4.46	21.4	25	88.9	6	180	90	73
87	1	8719	4.46	19.1	24	89.9	7	174	86	71
87	1	8720	5.03	20.6	24	90.4	6	177	94	72
87	1	8721	4.77	19.4	24	94.0	7	176	97	72
87	1	8722	4.23	20.4	24	85.4	6	179	89	72
87	1	8723	5.65	21.0	25	90.9	6	197	104	73
87	1	8724	4.05	19.6	24	84.4	6	180	93	72
87	1	8725	3.00	19.7	24	86.7	7	169	79	75
84	2	8401	5.20	22.7	24	92.4	6	178	80	73
84	2	8402	5.06	22.0	24	90.5	6	176	93	71
84	2	8403	4.50	19.6	25	84.2	7	177	87	70
84	2	8404	5.04	20.7	25	97.1	6	174	85	71
84	2	8405	5.08	20.1	25	89.7	6	175	91	71
84	2	8406	4.71	22.0	25	96.3	6	182	91	73
84	2	8407	4.14	20.5	22	86.7	6	173	89	71
84	2	8408	5.58	20.2	25	94.3	6	172	93	71
84	2	8409	5.39	22.3	25	89.3	6	186	99	72
84	2	8410	4.72	21.0	24	92.9	6	194	97	72
84	2	8411	4.31	20.1	23	95.2	6	169	90	70
84	2	8412	5.10	21.4	25	93.3	6	170	90	71

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
84	2	8413	5.69	20.8	25	87.4	6	186	102	71
84	2	8414	4.91	20.9	22	94.9	7	177	86	72
84	2	8415	4.44	21.2	24	95.5	6	179	95	72
84	2	8416	4.01	21.4	25	94.2	6	185	95	73
84	2	8417	5.73	20.8	24	93.4	6	205	106	71
84	2	8418	3.95	22.0	25	90.5	6	161	80	73
84	2	8419	4.84	21.2	24	94.0	6	182	94	72
84	2	8420	4.14	21.5	25	92.0	6	177	93	72
84	2	8421	4.51	21.0	25	89.5	7	177	89	72
84	2	8422	4.30	21.7	25	90.4	7	173	87	73
84	2	8423	3.84	21.5	25	83.0	6	177	95	73
84	2	8424	4.23	21.1	24	91.1	6	182	94	72
84	2	8425	4.90	21.5	25	92.8	7	163	80	72
85	2	8501	5.19	20.3	24	87.5	6	179	94	73
85	2	8502	4.99	20.8	25	87.5	6	168	80	72
85	2	8503	5.01	19.0	24	84.2	7	178	94	72
85	2	8504	4.68	20.0	24	91.5	6	191	99	74
85	2	8505	4.31	20.5	24	84.6	6	180	87	72
85	2	8506	4.64	19.9	23	90.9	7	175	89	70
85	2	8507	3.97	19.3	24	85.6	7	175	91	73
85	2	8508	4.52	21.1	25	92.6	7	169	85	73
85	2	8509	5.63	20.5	25	92.3	6	180	100	73
85	2	8510	4.31	20.0	23	86.1	7	160	77	71
85	2	8511	4.83	19.5	24	88.4	7	175	94	74
85	2	8512	4.69	19.5	24	87.9	6	189	90	73
85	2	8513	4.90	20.1	24	87.5	6	177	97	73
85	2	8514	5.02	19.5	24	78.3	7	186	105	71
85	2	8515	4.75	20.7	23	92.5	6	180	91	70
85	2	8516	4.72	20.3	24	86.3	7	174	83	72
85	2	8517	5.20	20.8	24	88.6	6	165	84	72
85	2	8518	4.48	19.2	24	81.0	7	169	91	73
85	2	8519	5.54	21.9	22	88.9	7	184	94	71
85	2	8520	5.18	19.7	25	88.7	6	163	81	71
85	2	8521	4.34	19.8	24	86.7	7	166	85	71
85	2	8522	4.76	20.0	25	87.8	6	178	92	73
85	2	8523	4.15	20.7	23	92.3	6	170	77	73
85	2	8524	4.88	20.2	25	91.5	7	166	79	70
85	2	8525	4.95	21.0	24	92.6	6	176	85	73
86	2	8601	4.04	19.6	24	93.7	6	175	86	71
86	2	8602	4.96	19.6	24	88.1	6	170	80	72
86	2	8603	4.35	20.2	23	89.3	7	176	91	71
86	2	8604	3.98	21.2	24	88.9	6	189	101	74

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
86	2	8605	5.13	19.9	24	95.3	6	182	98	73
86	2	8606	5.27	19.8	24	82.1	6	186	99	72
86	2	8607	5.34	19.7	23	87.7	6	181	89	71
86	2	8608	4.75	17.9	25	82.0	7	174	91	70
86	2	8609	3.55	19.7	23	85.7	7	163	82	73
86	2	8610	4.46	19.4	25	89.8	6	186	94	72
86	2	8611	4.35	20.4	25	82.5	6	177	93	73
86	2	8612	4.66	20.6	24	84.9	6	170	85	72
86	2	8613	4.52	18.7	24	86.7	6	162	85	70
86	2	8614	4.81	19.6	24	88.2	6	185	95	72
86	2	8615	4.55	19.1	24	88.0	6	165	90	72
86	2	8616	4.35	19.9	22	83.8	6	169	86	72
86	2	8617	5.42	19.6	24	87.0	6	174	93	73
86	2	8618	4.65	19.3	25	85.5	6	173	89	72
86	2	8619	4.33	19.4	23	82.1	7	179	94	72
86	2	8620	4.80	20.3	25	91.1	7	181	96	71
86	2	8621	5.07	21.0	25	89.1	5	176	90	71
86	2	8622	5.16	19.7	24	94.0	5	178	99	71
86	2	8623	4.33	19.7	24	89.0	6	178	95	73
86	2	8624	4.90	18.1	24	87.1	7	169	84	69
86	2	8625	4.94	19.8	24	87.2	6	185	99	73
87	2	8701	4.92	19.9	24	92.6	6	170	85	72
87	2	8702	4.12	20.4	24	92.4	6	189	99	74
87	2	8703	4.15	20.3	24	93.2	7	165	83	73
87	2	8704	4.76	19.2	23	92.9	6	186	98	72
87	2	8705	4.92	20.4	25	89.9	7	184	82	71
87	2	8706	5.52	19.7	24	90.1	6	183	101	73
87	2	8707	4.65	19.5	25	94.3	6	172	85	73
87	2	8708	4.70	19.7	23	89.3	6	170	89	73
87	2	8709	4.51	20.0	23	94.2	6	176	91	72
87	2	8710	4.70	20.5	25	94.6	6	180	88	72
87	2	8711	4.58	20.6	24	89.7	6	174	88	72
87	2	8712	5.58	20.3	25	94.2	6	197	100	72
87	2	8713	4.84	19.4	24	87.4	6	183	99	72
87	2	8714	4.47	20.8	25	89.0	6	186	99	72
87	2	8715	3.94	19.6	23	87.8	7	173	82	71
87	2	8716	3.92	19.9	25	96.6	6	180	88	73
87	2	8717	4.61	19.7	25	89.4	6	177	84	73
87	2	8718	4.43	21.7	25	91.5	6	174	94	75
87	2	8719	4.64	18.9	24	90.8	7	176	93	70
87	2	8720	5.14	20.3	23	87.1	6	176	89	72
87	2	8721	4.43	19.3	23	86.9	6	183	97	72

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
87	2	8722	4.31	20.1	24	84.1	6	179	90	71
87	2	8723	4.97	20.7	24	89.0	6	188	94	72
87	2	8724	4.86	19.5	24	94.9	6	186	99	72
87	2	8725	3.83	20.3	24	91.2	7	177	84	72
84	3	8401	4.32	20.5	23	91.3	6	163	72	71
84	3	8402	5.23	20.8	25	95.3	7	176	97	70
84	3	8403	4.80	18.8	25	83.4	6	174	85	69
84	3	8404	4.48	19.8	24	93.4	6	170	82	70
84	3	8405	5.43	19.2	24	96.4	6	174	78	71
84	3	8406	4.30	20.1	25	90.5	7	181	92	71
84	3	8407	4.32	19.6	23	91.4	6	163	87	70
84	3	8408	5.13	19.6	24	93.9	6	176	92	70
84	3	8409	4.97	21.4	24	95.8	6	174	87	71
84	3	8410	4.76	20.1	23	86.0	7	190	96	71
84	3	8411	4.34	19.2	25	91.6	7	168	86	70
84	3	8412	5.01	20.3	24	93.5	6	170	89	71
84	3	8413	5.07	19.2	24	91.4	7	183	98	69
84	3	8414	4.48	19.8	25	90.1	7	165	80	71
84	3	8415	4.76	19.2	25	94.7	6	169	83	70
84	3	8416	4.05	19.7	25	87.5	7	171	85	71
84	3	8417	5.65	19.6	25	95.8	6	193	105	72
84	3	8418	3.61	20.3	25	85.9	7	147	71	72
84	3	8419	4.54	20.3	25	91.4	7	173	89	71
84	3	8420	3.59	20.0	25	92.1	7	171	81	71
84	3	8421	4.37	20.5	25	88.3	7	171	82	70
84	3	8422	4.03	21.1	23	92.1	7	164	83	71
84	3	8423	3.68	20.9	25	90.2	7	172	86	72
84	3	8424	4.04	19.9	25	86.3	7	178	91	71
84	3	8425	3.83	19.9	24	83.8	7	150	73	69
85	3	8501	4.39	18.4	24	84.1	7	168	83	71
85	3	8502	4.22	19.5	23	87.8	7	160	71	70
85	3	8503	4.77	18.8	24	87.5	7	178	87	71
85	3	8504	4.48	19.1	25	86.6	7	178	86	73
85	3	8505	3.99	19.5	24	89.0	7	173	84	71
85	3	8506	4.46	19.0	24	86.3	7	163	80	69
85	3	8507	4.70	18.0	25	85.6	7	173	92	71
85	3	8508	4.20	20.2	24	88.7	7	164	82	73
85	3	8509	4.46	18.8	25	93.3	7	175	93	71
85	3	8510	4.69	19.4	25	87.4	7	162	82	70
85	3	8511	4.34	18.7	25	86.3	7	167	86	70.
85	3	8512	4.39	18.2	25	80.2	7	183	92	69
85	3	8513	4.92	18.9	24	91.8	7	170	87	71

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
85	3	8514	3.88	18.5	24	80.4	8	176	91	70
85	3	8515	4.96	18.6	25	88.8	7	176	86	69
85	3	8516	4.82	18.7	25	85.5	7	162	75	69
85	3	8517	4.19	20.7	23	87.9	6	161	81	71
85	3	8518	3.58	18.6	24	75.0	8	159	83	71
85	3	8519	4.99	21.0	25	88.2	7	178	90	70
85	3	8520	4.22	19.1	25	86.7	7	164	77	70
85	3	8521	4.22	19.1	24	86.6	7	165	83	71
85	3	8522	4.11	19.4	25	83.4	8	165	82	71
85	3	8523	3.96	19.7	25	90.2	7	174	83	72
85	3	8524	4.26	18.6	24	91.2	7	158	78	70
85	3	8525	4.35	18.5	24	77.8	7	162	76	71
86	3	8601	4.29	18.8	24	87.3	6	171	83	71
86	3	8602	4.80	18.1	23	87.9	7	170	86	69
86	3	8603	4.26	18.9	24	90.4	7	167	82	69
86	3	8604	4.76	20.1	25	85.6	7	179	96	69
86	3	8605	4.66	19.7	24	86.5	7	173	90	71
86	3	8606	4.80	18.6	24	83.9	6	182	94	72
86	3	8607	5.20	19.0	25	80.6	6	172	87	69
86	3	8608	3.85	18.2	24	83.4	7	174	83	69
86	3	8609	3.94	18.7	24	85.2	7	163	82	71
86	3	8610	4.57	18.6	24	91.0	7	177	90	69
86	3	8611	3.91	20.0	24	88.3	6	172	84	71
86	3	8612	4.69	19.6	24	75.7	6	162	73	69
86	3	8613	4.07	18.0	22	86.2	7	164	83	69
86	3	8614	3.91	18.6	23	80.9	7	175	90	69
86	3	8615	3.87	19.3	24	90.9	7	158	79	70
86	3	8616	4.54	18.4	25	72.6	6	164	83	69
86	3	8617	4.44	18.3	23	85.6	7	165	84	70
86	3	8618	4.29	18.7	24	81.1	7	169	86	68
86	3	8619	4.58	17.6	24	83.4	7	171	86	70
86	3	8620	4.30	18.7	24	89.4	7	170	85	69
86	3	8621	4.25	20.0	25	89.7	6	166	85	71
86	3	8622	4.31	18.4	24	88.4	6	171	93	68
86	3	8623	4.13	18.5	25	84.5	6	169	89	72
86	3	8624	4.62	17.9	25	83.9	7	162	77	68
86	3	8625	4.70	18.0	24	85.2	6	177	92	70
87	3	8701	4.34	19.1	24	93.3	7	166	82	69
87	3	8702	4.23	19.5	24	92.1	6	176	93	71
87	3	8703	3.84	20.3	23	89.7	7	159	80	72
87	3	8704	4.56	18.6	24	93.5	7	177	92	71
87	3	8705	4.72	19.7	25	90.0	7	183	87	70

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
87	3	8706	4.67	19.0	23	79.4	6	185	99	70
87	3	8707	4.29	19.3	25	92.4	7	165	78	70
87	3	8708	4.49	19.3	25	92.7	7	161	84	71
87	3	8709	4.02	19.6	25	85.6	7	166	81	72
87	3	8710	4.37	19.0	24	83.4	7	168	81	69
87	3	8711	4.60	18.9	25	90.7	6	175	84	70
87	3	8712	4.87	18.9	25	90.0	7	191	97	70
87	3	8713	4.91	19.0	24	87.9	6	177	88	73
87	3	8714	4.37	19.4	24	91.9	7	173	88	71
87	3	8715	4.41	18.7	25	85.7	7	167	84	70
87	3	8716	3.44	19.1	25	92.0	7	177	87	73
87	3	8717	3.34	19.2	23	88.3	7	162	73	73
87	3	8718	4.38	19.8	25	83.0	6	171	91	72
87	3	8719	4.22	18.9	25	87.8	7	167	84	70
87	3	8720	4.84	19.2	25	88.6	6	169	82	71
87	3	8721	3.92	18.5	23	81.7	7	174	93	71
87	3	8722	4.13	18.9	24	80.3	7	175	89	70
87	3	8723	5.19	18.4	25	84.7	7	186	98	70
87	3	8724	4.42	18.4	24	84.8	6	175	89	72
87	3	8725	3.43	18.8	24	85.9	7	165	79	71
84	4	8401	5.32	21.6	24	94.7	5	173	80	71
84	4	8402	5.20	20.7	24	91.6	6	175	96	71
84	4	8403	5.18	19.2	24	87.5	7	175	90	70
84	4	8404	5.46	20.4	23	97.7	5	178	89	70
84	4	8405	5.75	20.1	24	96.4	5	181	91	72
84	4	8406	5.84	20.2	24	92.3	6	193	102	69
84	4	8407	5.33	19.7	24	94.8	6	167	86	70
84	4	8408	6.11	19.8	25	98.0	6	179	93	69
84	4	8409	5.78	20.7	25	94.7	5	188	100	72
84	4	8410	5.24	21.0	23	97.6	6	194	104	71
84	4	8411	4.89	19.0	24	89.1	7	166	88	69
84	4	8412	4.99	21.0	23	89.8	5	170	86	70
84	4	8413	5.83	19.8	24	95.2	6	193	110	69
84	4	8414	5.00	20.4	23	85.6	7	176	89	70
84	4	8415	5.82	20.6	24	93.8	6	181	92	71
84	4	8416	4.40	20.3	23	98.0	6	173	87	72
84	4	8417	6.20	18.9	25	94.9	6	197	106	70
84	4	8418	4.12	21.4	23	90.8	6	157	77	72
84	4	8419	5.65	21.0	24	97.1	6	187	103	72
84	4	8420	4.66	20.4	24	94.3	6	185	100	71
84	4	8421	5.69	20.2	24	94.7	6	183	92	71
84	4	8422	4.66	21.8	24	95.7	6	166	86	71

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
84	4	8423	5.09	21.7	24	92.3	6	180	96	72
84	4	8424	5.55	20.7	24	96.9	6	190	106	72
84	4	8425	4.68	20.0	24	92.3	6	159	82	71
85	4	8501	5.30	18.9	24	89.3	5	181	91	70
85	4	8502	5.50	19.3	24	93.5	6	164	76	70
85	4	8503	5.66	19.1	25	89.0	6	188	99	72
85	4	8504	5.63	19.2	24	89.3	6	181	87	74
85	4	8505	5.06	20.0	23	96.7	6	175	91	70
85	4	8506	4.56	19.1	25	88.2	7	158	77	70
85	4	8507	5.52	18.4	25	87.3	6	181	92	71
85	4	8508	5.45	21.4	24	92.4	6	165	90	72
85	4	8509	5.34	18.6	24	94.8	6	173	98	70
85	4	8510	4.75	20.6	23	92.8	7	167	86	72
85	4	8511	5.61	18.3	26	94.2	6	177	96	70
85	4	8512	5.88	18.7	24	90.9	6	187	95	70
85	4	8513	5.98	19.4	24	90.3	6	179	92	72
85	4	8514	5.85	18.7	25	78.3	7	181	98	70
85	4	8515	5.30	19.0	23	94.3	6	180	90	70
85	4	8516	6.24	18.6	26	93.9	6	170	83	70
85	4	8517	5.77	20.0	24	90.9	6	165	86	71
85	4	8518	4.53	19.0	25	88.5	7	164	87	70
85	4	8519	5.99	21.6	25	92.5	7	185	97	70
85	4	8520	5.26	18.8	25	90.5	7	167	80	69
85	4	8521	5.32	18.8	24	87.5	7	163	89	70
85	4	8522	5.37	18.9	24	93.4	7	173	85	72
85	4	8523	5.40	19.9	24	94.6	6	181	91	73
85	4	8524	5.11	18.8	23	90.4	7	162	83	69
85	4	8525	5.00	19.4	25	86.3	6	167	78	72
86	4	8601	5.80	19.0	23	95.6	5	177	93	69
86	4	8602	6.12	18.1	24	90.6	6	171	83	69
86	4	8603	5.03	19.2	25	88.7	6	176	91	69
86	4	8604	5.16	20.9	24	86.8	6	187	100	70
86	4	8605	6.00	19.7	23	96.1	6	182	96	71
86	4	8606	5.91	18.8	23	92.6	5	191	101	71
86	4	8607	6.04	18.8	24	91.9	5	182	96	72
86	4	8608	5.04	17.4	24	90.7	6	178	89	70
86	4	8609	4.55	19.4	24	88.1	6	162	80	71
86	4	8610	5.49	18.6	24	90.3	6	181	90	69
86	4	8611	5.23	19.3	25	91.3	6	183	97	72
86	4	8612	5.65	20.4	24	90.6	5	172	88	69
86	4	8613	5.51	18.5	25	86.9	6	166	86	69
86	4	8614	4.91	19.4	23	91.0	6	182	97	70

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
86	4	8615	5.23	19.3	24	89.9	6	174	95	71
86	4	8616	5.25	18.4	23	82.8	6	167	89	71
86	4	8617	6.21	20.5	24	89.4	5	180	95	73
86	4	8618	5.59	19.0	25	90.2	6	171	92	68
86	4	8619	5.04	18.7	24	91.3	6	173	91	70
86	4	8620	4.75	18.9	25	92.4	7	183	95	69
86	4	8621	5.15	20.1	23	94.6	5	172	91	69
86	4	8622	5.59	18.9	25	89.4	6	179	93	69
86	4	8623	5.67	18.5	24	89.0	5	174	91	72
86	4	8624	5.97	18.1	25	89.1	6	177	92	68
86	4	8625	5.42	18.8	23	83.9	6	178	96	70
87	4	8701	5.71	19.6	24	91.1	5	173	86	70
87	4	8702	5.49	20.0	24	91.7	6	187	102	73
87	4	8703	5.02	19.8	23	90.4	6	169	89	70
87	4	8704	4.97	20.4	25	91.6	6	173	85	73
87	4	8705	5.92	19.3	25	96.9	6	201	103	70
87	4	8706	5.31	20.0	25	89.3	6	179	97	71
87	4	8707	5.46	19.6	24	89.2	6	172	88	70
87	4	8708	5.20	19.4	25	89.0	7	164	93	69
87	4	8709	4.78	19.7	24	91.1	6	179	91	70
87	4	8710	5.14	19.3	25	91.0	7	177	84	69
87	4	8711	5.14	19.3	24	92.0	6	177	90	72
87	4	8712	5.26	19.8	25	90.2	6	191	98	70
87	4	8713	5.77	19.7	25	92.0	6	189	99	70
87	4	8714	5.19	19.7	25	94.2	6	180	88	70
87	4	8715	5.11	18.8	24	94.2	7	170	83	70
87	4	8716	4.99	19.2	25	94.6	6	179	93	71
87	4	8717	4.66	19.0	23	95.3	7	166	78	72
87	4	8718	4.97	20.4	25	90.3	6	173	90	73
87	4	8719	5.44	19.1	24	93.6	6	173	93	70
87	4	8720	5.74	19.4	24	93.8	5	179	91	70
87	4	8721	5.54	18.6	25	92.1	6	183	97	71
87	4	8722	4.95	19.3	24	86.2	6	186	97	70
87	4	8723	5.64	19.3	24	90.0	6	190	97	71
87	4	8724	5.20	18.4	24	91.3	6	177	93	71
87	4	8725	4.38	18.9	24	87.6	7	169	85	71
80	1	8001	6.03	20.6	25	93.5	6	181	93	69
80	1	8002	4.78	18.8	25	80.7	7	171	87	70
80	1	8003	4.60	20.4	24	86.1	7	166	80	70
80	1	8004	4.43	20.6	24	96.4	6	184	95	73
80	1	8005	4.76	19.4	25	93.1	7	171	88	71
80	1	8006	4.10	19.8	24	97.5	6	184	96	73

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
80	1	8007	3.91	20.5	24	87.6	7	171	88	72
80	1	8008	4.59	20.8	25	92.3	7	169	96	71
80	1	8009	4.39	20.2	25	83.8	7	164	87	71
80	1	8010	4.25	21.2	25	93.1	7	163	84	74
80	1	8011	4.62	20.6	24	85.0	7	171	91	71
80	1	8012	5.23	21.7	25	95.6	6	176	94	70
80	1	8013	4.43	20.4	24	84.0	7	172	92	71
80	1	8014	4.64	19.0	25	95.0	6	171	88	71
80	1	8015	4.21	20.9	25	89.8	6	166	85	71
80	1	8016	3.88	21.1	25	95.0	7	175	93	75
80	1	8017	4.70	20.7	25	88.8	7	156	79	70
80	1	8018	5.47	20.3	24	91.0	6	193	95	70
80	1	8019	3.55	20.5	25	84.4	7	181	92	72
80	1	8020	4.45	19.6	23	86.7	6	163	76	71
80	1	8021	4.30	20.5	24	91.6	6	182	96	71
80	1	8022	4.86	21.3	25	90.7	7	173	90	71
80	1	8023	3.66	21.2	24	85.4	7	156	76	74
80	1	8024	3.80	19.3	24	91.6	8	165	73	69
80	1	8025	5.36	20.5	25	91.0	7	183	96	69
81	1	8101	4.14	20.9	25	94.4	6	178	88	74
81	1	8102	4.51	20.3	24	93.6	6	185	96	70
81	1	8103	4.45	20.9	23	92.6	6	160	77	71
81	1	8104	4.85	21.0	25	92.5	7	171	83	71
81	1	8105	4.58	20.7	24	87.1	7	167	85	71
81	1	8106	4.57	20.8	25	97.7	6	173	89	71
81	1	8107	4.51	24.8	25	93.3	6	172	93	72
81	1	8108	4.44	20.8	25	91.5	7	168	83	71
81	1	8109	4.25	21.5	24	90.5	7	163	82	72
81	1	8110	3.81	20.2	24	92.1	7	170	84	71
81	1	8111	4.34	20.9	24	94.3	7	180	89	73
81	1	8112	4.44	21.8	25	94.0	6	181	92	73
81	1	8113	5.00	21.1	25	88.7	7	173	88	73
81	1	8114	4.54	20.9	24	92.8	6	179	93	70
81	1	8115	4.37	20.3	23	91.9	6	168	79	73
81	1	8116	3.99	21.3	25	89.2	7	171	87	74
81	1	8117	4.88	22.0	25	91.7	6	188	97	71
81	1	8118	4.25	21.7	25	93.7	7	172	85	72
81	1	8119	3.99	21.6	24	86.7	7	171	82	73
81	1	8120	4.35	21.1	25	91.8	7	173	85	71
81	1	8121	5.43	21.3	25	93.9	6	184	89	71
81	1	8122	5.19	22.9	24	96.3	5	174	88	73
81	1	8123	4.23	21.2	25	95.7	7	174	90	70

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
81	1	8124	5.37	20.6	25	96.5	7	182	92	70
81	1	8125	4.27	21.9	24	90.7	6	184	91	73
82	1	8201	3.54	21.4	24	88.9	6	172	90	73
82	1	8202	4.04	22.1	24	95.1	6	182	90	72
82	1	8203	5.24	22.5	25	95.7	6	184	95	73
82	1	8204	4.56	21.2	24	83.8	6	185	100	72
82	1	8205	4.36	22.5	24	93.3	6	175	90	73
82	1	8206	4.97	20.5	24	88.8	6	185	99	70
82	1	8207	4.33	21.5	25	89.3	6	171	85	71
82	1	8208	4.53	21.3	25	92.7	7	169	87	71
82	1	8209	4.05	21.1	24	95.8	7	182	95	72
82	1	8210	4.08	23.4	25	94.9	6	183	99	73
82	1	8211	4.18	21.5	25	95.5	6	174	85	71
82	1	8212	4.72	21.9	25	93.0	7	184	90	71
82	1	8213	5.30	21.1	25	94.0	6	184	93	72
82	1	8214	5.24	21.8	25	87.3	6	186	101	71
82	1	8215	4.10	20.9	24	92.6	7	173	88	71
82	1	8216	3.86	21.5	25	92.3	7	171	86	73
82	1	8217	4.82	21.9	25	87.6	6	184	102	72
82	1	8218	4.26	23.1	25	93.8	6	162	79	72
82	1	8219	3.96	21.6	23	92.7	7	169	85	72
82	1	8220	4.47	21.3	25	90.8	7	165	81	71
82	1	8221	4.27	20.5	23	93.0	6	181	99	73
82	1	8222	4.70	20.4	24	90.3	6	176	97	69
82	1	8223	4.55	22.0	25	93.8	6	184	97	71
82	1	8224	4.61	20.3	24	86.0	6	189	98	71
82	1	8225	4.28	21.2	25	91.2	7	175	91	71
83	1	8301	4.43	21.6	25	91.2	6	175	87	72
83	1	8302	4.66	20.6	24	91.8	7	185	86	72
83	1	8303	5.49	21.1	25	93.9	6	196	104	72
83	1	8304	4.80	22.5	25	93.2	6	180	96	72
83	1	8305	4.72	22.6	24	88.7	6	171	86	72
83	1	8306	3.81	20.9	24	90.1	7	165	87	72
83	1	8307	4.98	21.3	25	89.3	6	177	90	73
83	1	8308	3.50	21.8	25	89.5	7	189	99	75
83	1	8309	4.35	21.9	24	91.1	6	185	96	73
83	1	8310	3.86	21.0	24	94.8	6	180	92	73
83	1	8311	4.32	21.9	24	91.0	6	183	90	73
83	1	8312	4.46	20.8	25	84.5	7	160	77	72
83	1	8313	4.18	23.1	25	91.1	7	175	97	73
83	1	8314	3.82	22.6	25	94.5	6	182	97	74
83	1	8315	4.11	20.7	25	90.1	6	180	94	73

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
83	1	8316	4.10	22.2	24	93.1	6	180	92	73
83	1	8317	4.11	22.7	24	88.6	6	180	98	75
83	1	8318	3.15	22.0	24	93.7	7	170	84	75
83	1	8319	4.60	21.4	24	93.3	7	176	91	71
83	1	8320	4.11	22.6	23	78.1	7	183	99	73
83	1	8321	4.97	22.4	25	92.7	6	186	88	70
83	1	8322	3.99	22.4	24	90.1	6	175	90	74
83	1	8323	4.94	21.9	24	95.3	6	201	114	73
83	1	8324	4.62	21.2	25	87.5	7	181	89	72
83	1	8325	4.92	21.6	25	96.0	6	176	92	73
80	2	8001	5.98	19.9	25	91.2	6	176	83	69
80	2	8002	4.73	20.0	25	84.6	7	170	82	72
80	2	8003	4.80	20.4	25	83.1	7	162	79	70
80	2	8004	4.51	20.9	25	90.9	6	179	97	72
80	2	8005	4.61	20.0	25	94.1	7	175	91	72
80	2	8006	3.84	19.8	25	93.1	7	179	96	73
80	2	8007	4.65	21.5	25	90.4	7	168	87	72
80	2	8008	4.35	20.6	25	90.0	7	175	97	71
80	2	8009	4.88	19.9	25	94.0	7	166	84	72
80	2	8010	4.39	21.3	25	88.5	7	161	86	72
80	2	8011	4.91	20.7	25	88.9	6	166	84	70
80	2	8012	5.13	21.8	25	92.7	6	165	92	71
80	2	8013	5.01	19.6	24	92.6	7	173	97	71
80	2	8014	4.91	19.9	25	93.7	6	170	86	70
80	2	8015	4.47	21.2	25	94.0	7	168	82	71
80	2	8016	4.84	21.2	25	96.6	6	173	96	74
80	2	8017	4.86	20.6	25	90.8	7	155	77	71
80	2	8018	4.91	19.9	24	86.6	7	186	90	70
80	2	8019	3.97	21.2	24	87.0	7	167	86	72
80	2	8020	5.77	20.0	25	90.5	5	166	78	70
80	2	8021	4.35	20.3	24	95.7	6	192	97	71
80	2	8022	4.98	21.1	25	90.0	7	174	94	73
80	2	8023	3.75	21.0	24	89.2	7	162	78	72
80	2	8024	4.25	19.9	24	93.1	7	166	74	70
80	2	8025	4.90	20.5	26	92.2	6	178	95	69
81	2	8101	4.06	21.1	23	95.0	6	181	91	73
81	2	8102	4.81	20.4	25	92.4	6	179	94	71
81	2	8103	4.71	21.6	24	91.1	6	162	75	72
81	2	8104	4.99	20.7	26	90.2	7	166	84	71
81	2	8105	4.71	21.6	25	89.9	7	164	73	72
81	2	8106	4.74	21.3	23	96.0	6	177	88	72
81	2	8107	4.83	22.7	23	94.0	7	184	95	73

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
81	2	8108	4.93	21.5	24	93.5	6	171	84	71
81	2	8109	4.89	21.5	25	94.7	7	171	87	71
81	2	8110	4.18	20.3	25	90.0	7	173	83	71
81	2	8111	4.03	21.5	24	93.6	7	174	91	73
81	2	8112	3.83	21.5	23	91.0	6	173	82	74
81	2	8113	4.90	21.4	25	93.4	7	179	89	72
81	2	8114	4.85	22.0	25	95.8	6	179	91	70
81	2	8115	4.74	20.4	25	94.2	7	182	92	72
81	2	8116	4.57	21.5	25	92.1	6	173	86	74
81	2	8117	4.58	22.3	24	93.0	6	180	94	72
81	2	8118	4.34	21.6	24	93.3	7	172	82	72
81	2	8119	3.29	21.5	25	85.6	7	169	78	73
81	2	8120	4.84	21.8	25	93.0	6	179	88	72
81	2	8121	5.08	22.3	24	90.8	6	176	85	71
81	2	8122	5.08	22.7	24	93.9	6	174	83	73
81	2	8123	4.23	20.6	24	90.1	6	175	83	71
81	2	8124	4.73	21.8	24	92.2	6	181	93	72
81	2	8125	4.77	21.7	25	95.1	6	173	89	72
82	2	8201	3.99	20.6	24	86.4	6	165	84	72
82	2	8203	5.54	22.9	25	91.9	6	183	91	73
82	2	8204	5.29	22.5	25	79.4	6	185	93	72
82	2	8205	4.49	22.7	24	92.2	7	175	92	72
82	2	8206	5.18	21.2	24	92.7	6	183	96	72
82	2	8207	4.47	22.1	24	92.8	7	179	91	71
82	2	8208	4.19	22.6	25	92.0	7	172	84	71
82	2	8209	4.67	20.6	24	90.9	7	179	95	73
82	2	8210	3.89	23.3	24	93.3	6	186	96	72
82	2	8211	4.62	21.2	25	91.9	5	175	87	71
82	2	8212	5.48	21.7	25	95.9	7	185	91	70
82	2	8213	5.19	21.1	25	93.7	6	185	90	72
82	2	8214	4.87	21.8	25	91.4	6	180	95	72
82	2	8215	3.83	21.1	23	93.1	7	168	84	72
82	2	8216	3.97	21.6	24	88.6	7	176	90	72
82	2	8217	4.89	22.3	25	92.7	6	182	100	72
82	2	8218	4.44	22.5	24	89.9	6	161	76	73
82	2	8219	4.54	20.7	23	88.1	6	184	96	72
82	2	8220	4.51	21.6	24	86.4	7	170	83	71
82	2	8221	4.46	20.7	23	89.6	7	180	93	72
82	2	8222	5.07	20.8	25	93.3	6	174	94	68
82	2	8223	5.24	22.2	25	93.9	6	177	94	70
82	2	8224	4.58	20.7	25	92.2	6	187	97	72
82	2	8225	4.70	22.1	24	91.5	6	179	93	72

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
83	2	8301	4.65	21.5	24	91.6	6	173	87	72
83	2	8302	5.66	21.0	25	91.6	7	185	92	71
83	2	8303	5.39	21.4	24	89.6	7	199	112	73
83	2	8304	4.41	21.4	25	91.9	7	174	84	73
83	2	8305	4.94	22.7	23	92.1	6	171	86	72
83	2	8306	4.93	21.9	26	95.7	6	171	96	73
83	2	8307	5.09	22.1	24	90.6	6	181	88	72
83	2	8308	3.73	21.1	23	83.5	7	185	98	74
83	2	8309	4.38	21.8	24	87.9	6	188	98	73
83	2	8310	5.15	21.9	25	98.3	7	192	98	72
83	2	8311	4.77	22.9	24	90.8	6	180	84	73
83	2	8312	4.34	21.4	25	88.9	7	156	76	73
83	2	8313	3.79	23.4	25	91.3	7	173	89	73
83	2	8314	4.18	22.3	25	89.5	6	190	97	74
83	2	8315	4.54	20.4	25	90.8	7	176	96	72
83	2	8316	3.64	21.9	25	85.1	7	169	77	74
83	2	8317	3.78	22.1	25	92.5	6	173	90	75
83	2	8318	3.81	21.5	23	92.8	7	169	85	73
83	2	8319	4.58	21.4	25	91.0	7	170	81	71
83	2	8320	5.17	22.3	24	88.6	7	197	105	72
83	2	8321	5.03	22.4	25	95.2	6	186	91	72
83	2	8322	4.00	22.4	24	92.5	7	176	84	74
83	2	8323	4.87	22.3	23	94.5	6	201	112	73
83	2	8324	4.68	22.2	24	91.3	7	172	81	73
83	2	8325	4.84	21.8	25	89.3	6	177	94	72
80	3	8001	6.26	20.5	25	94.3	6	184	91	69
80	3	8002	5.52	19.3	25	91.2	7	166	78	70
80	3	8003	5.57	20.8	25	92.4	6	164	76	69
80	3	8004	5.78	20.2	26	94.5	5	186	94	70
80	3	8005	5.61	19.4	24	95.2	6	176	86	70
80	3	8006	5.31	19.6	25	90.1	6	189	101	72
80	3	8007	4.97	20.5	25	92.1	6	169	87	71
80	3	8008	5.21	20.4	25	89.5	7	173	90	70
80	3	8009	5.17	20.2	25	94.4	7	168	82	71
80	3	8010	4.67	21.0	25	92.8	6	167	81	72
80	3	8011	5.96	20.6	25	93.1	6	178	93	70
80	3	8012	5.67	21.9	25	94.2	6	172	89	69
80	3	8013	5.76	19.7	25	93.4	7	172	94	70
80	3	8014	5.74	19.7	25	94.1	5	180	89	69
80	3	8015	4.27	21.1	25	91.4	6	167	79	72
80	3	8016	5.42	22.0	24	97.7	6	174	88	71
80	3	8017	5.18	20.6	25	92.6	6	161	77	70

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
80	3	8018	6.15	19.9	25	94.5	6	198	95	69
80	3	8019	2.50	20.6	24	68.2	8	158	76	73
80	3	8020	5.99	19.8	25	91.8	5	169	81	70
80	3	8021	5.57	20.4	26	91.2	5	189	98	69
80	3	8022	5.21	20.5	25	95.4	6	180	93	71
80	3	8023	4.87	20.8	25	90.2	6	165	77	70
80	3	8024	5.26	19.4	25	95.7	7	174	78	69
80	3	8025	5.77	20.0	25	94.5	6	185	94	69
81	3	8101	5.36	21.1	25	97.0	6	178	89	72
81	3	8102	5.45	20.7	25	96.4	5	185	95	71
81	3	8103	4.98	22.1	25	92.3	6	162	77	71
81	3	8104	5.82	20.4	24	93.3	6	176	86	70
81	3	8105	5.46	21.0	24	93.5	6	170	82	70
81	3	8106	5.12	20.9	24	97.4	6	172	86	70
81	3	8107	5.19	21.3	24	93.4	6	181	98	72
81	3	8108	5.39	21.0	25	93.4	6	175	81	71
81	3	8109	5.29	22.2	25	92.8	6	167	84	71
81	3	8110	4.99	20.3	25	92.2	7	164	82	70
81	3	8111	4.89	21.0	25	94.1	6	180	89	72
81	3	8112	5.49	22.1	25	95.7	6	182	87	73
81	3	8113	5.42	21.1	25	95.8	7	184	90	71
81	3	8114	5.42	21.5	25	88.4	6	182	96	70
81	3	8115	5.48	20.3	25	93.9	6	171	84	72
81	3	8116	5.08	20.5	24	94.3	7	173	87	71
81	3	8117	4.86	22.2	24	92.6	6	173	87	71
81	3	8118	5.25	20.5	25	93.0	6	169	81	71
81	3	8119	2.75	20.6	25	83.5	8	177	87	73
81	3	8120	5.30	20.7	25	97.2	6	178	87	70
81	3	8121	5.82	21.7	25	91.0	6	183	86	70
81	3	8122	5.78	22.5	25	94.6	5	173	84	71
81	3	8123	4.79	20.9	24	96.9	7	173	91	69
81	3	8124	5.46	20.8	25	93.7	6	175	87	69
81	3	8125	5.72	21.5	25	94.6	6	176	83	71
82	3	8201	5.17	20.8	25	94.7	6	172	87	70
82	3	8202	5.36	22.2	24	94.9	6	187	95	70
82	3	8203	6.10	22.0	25	96.6	6	191	101	72
82	3	8204	5.80	21.6	24	91.7	6	188	96	70
82	3	8205	5.56	21.9	25	92.2	6	176	95	70
82	3	8206	5.95	20.7	25	94.3	6	186	101	69
82	3	8207	5.19	21.6	25	89.1	6	179	94	71
82	3	8208	5.30	21.7	25	95.1	7	175	86	69
82	3	8209	4.84	20.7	24	98.0	7	177	91	72

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
82	3	8210	4.04	23.0	25	93.6	6	185	94	72
82	3	8211	4.83	21.3	25	95.0	6	171	82	69
82	3	8212	5.06	21.5	24	94.6	7	187	90	70
82	3	8213	5.59	21.3	24	94.5	6	182	90	71
82	3	8214	5.65	21.1	25	93.6	5	189	98	70
82	3	8215	4.83	20.8	25	94.6	7	170	85	71
82	3	8216	5.37	20.6	25	95.7	6	173	85	70
82	3	8217	3.35	21.4	24	85.3	8	182	100	71
82	3	8218	4.99	22.4	25	95.0	6	160	80	70
82	3	8219	5.25	21.4	25	93.5	6	182	92	70
82	3	8220	5.64	20.6	25	86.7	6	165	82	70
82	3	8221	4.84	20.7	25	91.3	6	182	94	72
82	3	8222	5.90	20.7	25	92.1	6	174	93	69
82	3	8223	5.55	22.4	24	97.3	6	185	95	70
82	3	8224	5.19	19.8	25	93.9	6	189	98	70
82	3	8225	5.06	21.3	25	94.3	6	178	95	70
83	3	8301	5.17	21.3	25	95.6	5	178	85	71
83	3	8302	5.21	21.1	24	96.2	7	180	84	70
83	3	8303	5.27	21.6	24	96.2	6	199	114	71
83	3	8304	5.68	21.8	25	93.6	6	174	87	72
83	3	8305	4.55	21.7	23	91.3	6	171	84	71
83	3	8306	5.16	21.1	25	93.7	6	173	92	71
83	3	8307	5.47	20.6	24	92.5	6	190	95	72
83	3	8308	5.30	21.3	24	89.7	7	195	102	73
83	3	8309	4.54	22.1	23	89.7	6	179	92	72
83	3	8310	5.10	21.0	25	93.0	6	188	94	72
83	3	8311	5.30	22.0	24	92.8	6	177	81	71
83	3	8312	4.87	21.6	25	92.1	7	164	79	71
83	3	8313	4.90	22.4	25	95.0	6	177	93	73
83	3	8314	5.14	21.9	25	92.7	6	183	96	72
83	3	8315	5.10	19.7	24	91.0	6	188	99	70
83	3	8316	4.37	21.3	24	93.8	7	180	87	73
83	3	8317	4.79	22.5	25	95.7	6	171	90	74
83	3	8318	5.26	21.0	25	90.1	6	167	79	72
83	3	8319	5.31	21.4	24	92.3	6	178	86	70
83	3	8320	2.90	21.7	24	75.2	8	186	99	73
83	3	8321	5.56	22.3	24	93.4	6	194	96	70
83	3	8322	4.97	21.9	24	92.2	7	177	92	71
83	3	8323	5.22	22.0	24	96.0	6	196	98	71
83	3	8324	4.68	21.9	25	91.0	6	171	81	71
83	3	8325	5.42	21.1	25	90.7	6	171	86	71
80	4	8001	6.14	20.0	26	90.3	5	178	89	69

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
80	4	8002	5.28	19.1	24	87.1	6	163	78	69
80	4	8003	4.56	19.9	24	88.0	6	161	79	69
80	4	8004	5.64	19.8	25	96.1	5	182	97	70
80	4	8005	5.23	19.7	25	93.9	6	172	89	70
80	4	8006	5.02	19.6	25	92.5	6	179	95	71
80	4	8007	4.56	19.7	25	89.5	7	164	86	70
80	4	8008	4.80	20.6	25	91.2	6	168	94	69
80	4	8009	4.84	20.1	25	95.8	6	160	78	71
80	4	8010	4.35	21.1	25	87.5	7	161	80	72
80	4	8011	5.42	20.8	25	92.6	6	173	92	70
80	4	8012	5.37	20.7	24	93.2	6	168	95	70
80	4	8013	5.14	20.4	25	88.6	7	166	95	69
80	4	8014	5.27	18.8	25	92.4	6	174	90	70
80	4	8015	4.64	21.1	24	92.5	6	174	87	72
80	4	8016	4.94	20.7	24	91.9	6	161	86	71
80	4	8017	4.50	20.7	25	83.3	6	154	75	70
80	4	8018	4.62	19.6	25	76.8	6	181	84	69
80	4	8019	3.14	19.8	25	64.0	8	153	78	71
80	4	8020	5.46	19.8	25	83.1	5	163	80	69
80	4	8021	5.13	20.2	25	92.5	6	184	99	69
80	4	8022	5.02	20.1	25	87.5	6	166	84	70
80	4	8023	3.88	20.2	25	80.3	7	158	79	70
80	4	8024	4.51	19.2	25	94.5	7	165	74	69
80	4	8025	5.08	20.2	25	92.3	6	176	93	69
81	4	8101	4.55	22.0	25	93.0	5	176	92	72
81	4	8102	4.84	19.9	25	92.7	6	181	99	70
81	4	8103	4.56	22.0	24	89.3	7	158	78	71
81	4	8104	5.60	20.8	25	90.6	6	170	92	70
81	4	8105	5.14	20.3	25	86.1	7	160	79	71
81	4	8106	5.14	20.2	24	93.7	6	168	87	70
81	4	8107	4.90	21.5	24	92.1	6	178	95	70
81	4	8108	5.28	20.4	25	90.3	6	168	82	70
81	4	8109	4.93	21.7	25	95.7	6	163	79	71
81	4	8110	4.20	20.2	24	93.0	7	162	79	71
81	4	8111	4.55	20.9	25	94.6	6	173	92	71
81	4	8112	5.08	21.5	25	95.3	6	179	88	72
81	4	8113	5.37	21.7	25	94.7	6	172	87	72
81	4	8114	5.15	21.3	25	93.1	5	175	100	69
81	4	8116	4.87	21.7	24	92.5	7	169	86	72
81	4	8117	4.59	21.5	24	92.2	6	174	89	71
81	4	8118	5.12	21.0	25	92.7	6	172	83	70
81	4	8119	2.01	20.9	24	77.1	9	162	80	75

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
81	4	8120	4.39	21.3	25	89.0	6	177	94	71
81	4	8121	5.80	20.8	24	87.7	6	177	89	70
81	4	8122	6.16	22.7	24	94.8	5	167	83	71
81	4	8123	5.18	20.0	25	92.4	6	166	84	69
81	4	8124	5.60	20.7	25	94.7	6	183	92	70
81	4	8125	4.82	21.2	24	89.4	6	178	86	71
82	4	8201	5.26	21.3	25	91.4	6	171	91	70
82	4	8202	5.13	22.0	24	95.2	6	186	96	70
82	4	8203	6.02	22.1	24	93.0	5	187	101	70
82	4	8204	5.13	21.4	24	81.6	7	185	96	69
82	4	8205	4.97	22.4	25	88.5	6	179	99	71
82	4	8206	5.70	21.2	25	91.5	6	184	100	69
82	4	8207	4.42	21.3	25	87.5	6	174	92	70
82	4	8208	4.14	21.5	23	92.5	6	160	80	70
82	4	8209	4.89	20.6	24	90.1	7	174	88	71
82	4	8210	4.44	22.8	25	95.3	5	182	100	72
82	4	8211	5.14	21.1	24	91.6	6	171	88	70
82	4	8212	5.43	21.7	24	96.7	6	186	95	69
82	4	8213	5.41	20.7	24	94.7	5	175	87	69
82	4	8214	5.39	21.2	25	91.0	5	181	93	69
82	4	8215	3.87	21.9	25	86.9	7	164	84	71
82	4	8216	4.92	20.9	25	89.5	6	166	85	70
82	4	8217	3.84	21.8	25	84.0	8	180	101	70
82	4	8218	4.46	22.8	25	95.4	6	153	73	71
82	4	8219	5.35	21.2	24	95.1	5	173	91	70
82	4	8220	4.89	20.8	24	92.1	6	165	82	69
82	4	8221	4.07	20.6	24	94.9	7	174	94	71
82	4	8222	5.17	20.1	23	91.1	6	170	91	69
82	4	8223	5.27	21.7	25	94.0	6	181	95	70
82	4	8224	5.25	20.0	25	91.2	5	180	88	69
82	4	8225	5.18	21.6	24	93.3	5	177	95	69
83	4	8301	4.92	21.4	24	89.5	5	177	87	71
83	4	8302	5.46	20.7	24	91.1	7	174	85	71
83	4	8303	5.97	21.1	25	94.8	6	188	107	70
83	4	8304	5.97	22.1	25	92.1	6	177	97	71
83	4	8305	4.93	21.3	24	90.3	6	166	79	71
83	4	8306	4.69	21.3	24	89.3	7	169	95	70
83	4	8307	5.55	20.8	26	88.3	6	177	88	70
83	4	8308	4.28	21.1	25	83.9	6	190	99	72
83	4	8309	4.47	20.6	24	89.5	6	179	96	72
83	4	8310	5.09	21.2	25	92.7	6	176	88	71
83	4	8311	5.59	21.7	24	87.7	6	176	82	71

Table A8. (continued)

SET[a]	TESTER[b]	INBRED	YIELD Mg/ha	MOIST %	STAND	EREPL %	INDEX	PH cm	EH cm	FLOW
83	4	8312	4.90	21.9	25	90.3	7	159	79	70
83	4	8313	4.76	23.3	25	93.6	6	172	93	72
83	4	8314	5.00	21.4	25	90.7	6	185	98	72
83	4	8315	5.19	19.4	24	88.4	6	182	99	70
83	4	8316	4.34	21.4	25	91.8	6	176	91	71
83	4	8317	4.60	22.7	25	89.6	6	169	89	74
83	4	8318	4.94	20.8	24	94.7	6	174	92	72
83	4	8319	4.90	21.4	25	93.8	6	169	85	70
83	4	8320	3.14	22.2	23	67.6	8	183	101	72
83	4	8321	5.39	21.8	23	93.2	6	191	92	70
83	4	8322	4.86	21.6	24	90.2	6	168	89	71
83	4	8323	5.14	21.8	25	93.1	6	194	102	71
83	4	8324	5.45	21.5	25	92.2	6	171	81	70
83	4	8325	5.45	21.0	24	91.0	6	176	92	72