



Selection of inbred maize (*Zea mays* L.) progenies by topcrosses conducted in contrasting environments

C.S. Rodrigues¹, C.A.P. Pacheco², M.L. Guedes¹, R.G.V. Pinho¹ and C.R. Castro³

¹Departamento de Biologia, Universidade Federal de Lavras, Lavras, MG, Brasil

²Embrapa Tabuleiros Costeiros, Aracaju, SE, Brasil

³Departamento de Agronomia, Universidade Estadual de Maringá, Maringá, PR, Brasil

Corresponding author: C.S. Rodrigues
E-mail: cinthia-sr@hotmail.com

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ABSTRACT. The aim of this study was to identify inbred progenies of $S_{0.1}$ maize (*Zea mays* L.) plants that were efficient at a low level of technology and responsive at a high level of technology through the use of topcrosses. Two contrasting environments were created using two levels of base fertilization and topdressing, so that the levels of nitrogen, phosphorus, and potassium were applied four times higher in one environment than in the other. We used $S_{0.1}$ progenies derived from commercial hybrids in topcrosses with two testers (an elite line from the flint heterotic group and an elite line from the dent heterotic group). The progenies and three controls were evaluated in an augmented block

design in Nossa Senhora das Dores, SE, Brazil in the 2010 crop season. The average grain yield in the high-technological level was 21.44% greater than that in the low-technological level. There were no changes in progeny behavior in the two technological levels for grain yield. The testers did not differ in the average grain yield of the progenies at the two technological levels. Therefore, it is possible to select progenies derived from commercial hybrids that have an efficient response to fertilization.

Key words: Fertilization; Topcross; Grain yield

INTRODUCTION

Maize (*Zea mays* L.) is one of the most important crop species in the world, mainly because of the cultivation of hybrids and/or improved varieties that are adapted to adverse environments, which made it possible to break variety yield barriers at the beginning of the 20th century.

In 2008, Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA) began a maize breeding program in Northeast Brazil. The aim of this program is to obtain varieties, variety crosses, and conventional hybrids (double cross, three-way, and single cross) that are adapted to the main maize producing regions of the Brazilian Northeast by obtaining and combining local lines.

The success of a breeding program is as dependent on the environments chosen for testing as on the germplasm used in selection (Balestre et al., 2009). Breeding programs generally evaluate a large number of genotypes in a few environments in the initial phase, followed by an increase in the number of environments to the degree that the genotypes selected are reduced at each phase of evaluation (Rodrigues et al., 2013).

The genotype x environment interaction burdens breeding programs because they need to evaluate the materials in a series of environments that represent the region, or the soil and climatic conditions, so that the materials can achieve all of their genetic potential and the economic problems caused by their fragility can be avoided. Nevertheless, it is possible to reduce the cost of, and time spent, setting up experiments by simulating environmental variation through fertilization concentrations and other controllable factors.

One way of optimizing the selection of genotypes is to create differentiated environments with regard to technological level, which is an effective method for identifying superior materials. However, the use of different areas that are large enough for crop development is not very common, and even less so is the use of areas that differ in concentrations of nitrogen (N), phosphorus (P), and potassium (K), which represents the environmental extremes to which cultivars can be subjected.

We tested the hypothesis that a crop that is at the same time productive at a low level of technology, represented by low levels of N, P, and K, and responsive at a high level of technology, represented by high levels of N, P, and K, is the ideal genotype, because of its high performance under favorable conditions and stability under unfavorable conditions. Therefore, the goal of this study was to select inbred progenies of maize that are efficient at a low level of technology and responsive to a high level of technology by using topcrosses.

MATERIAL AND METHODS

The experiment was conducted at the Jorge Sobral Experimental Field, EMBRAPA Tabuleiros Costeiros, Nossa Senhora das Dores, Sergipe, Brazil. The area is georeferenced by the Universal Transverse Mercator coordinates 697,454 m N and 8,842,614 m E (24L) and is at 209 m above mean sea level. The soil is classified as a Latossolo Amarelo Distrocoeso típico, with a moderate A horizon, medium/clayey texture, flat topography, is moderately to well drained, and not rocky. The mean annual rainfall in the last 10 years has been 1163 mm.

The genitors were chosen based on the results of regional trials of maize cultivars in the Northeast region, and the results of the Early, Normal, and Very Early National Trials of the Middle West area of Brazil (Ensaio Nacionais Precoce Normal e Superprecoce do Centro Oeste). Commercial single hybrids with good adaptability, stability, and superior performance in the main production regions of Brazil were identified. Based on these evaluations, 17 commercial hybrids were selected and were used as parents.

Inbred progenies were obtained from self-pollination of the parents. Initially, the S_0 generations were obtained by the self-pollination of five plants and the selection of the two best ears within each parent. For the following self-pollination cycle for each parent, a bulk collection of seeds from the two best S_0 ears was conducted, which were sown in plots of eight 5-m-long rows with 70 cm between rows and 20 cm between plants, in order to obtain 25 plants per row after thinning. At the time of flowering, 100 to 120 competitive, vigorous, healthy plants, with a good ear set, were self-pollinated within each plot. Around 30 days after flowering, a phenotypic selection was made for leaf and stalk health, the pollination bags were removed from discarded plants, and at least 70 to 80 plants were selected. At harvest, a phenotypic selection was made of the stalks and ears for health, type of ear, and ear row alignment. Around 40 $S_{0.1}$ ears were selected on average.

Two elite lines were obtained from the single hybrid 'BRS 1040', and were designated as L1 (flint heterotic group) and L2 (dent heterotic group). A total of 673 $S_{0.1}$ inbred progenies were sown (female rows) in two detasseled lots, isolated in time. We used 3-m-long rows with 70 cm between them and 20 cm between plants, in order to obtain 15 plants per row after thinning. In each topcross, a male row, sown with seeds from one of the tester lines, was inserted for every two female rows. This yielded Topcross 1, from crossing with line L1, and Topcross 2, from crossing with line L2.

Detasseling was begun at the pre-flowering stage in the female rows, to obtain crosses with the respective testers. The isolated lots were harvested, and progenies with a high occurrence of leaf and stalk diseases, ear health problems, or those that produced fewer than 650 seeds were discarded. This last criterion was adopted with a view toward selection for the production ability of $S_{0.1}$ seeds, and to ensure that the quantity of seeds was sufficient for setting up at least six preliminary trials with two replications of 25 seeds per row.

The ears selected within each inbred progeny were shelled and the seeds were homogenized before counting for setting up the trials, and the remaining seeds were kept in cold, dry storage for reevaluation in the following crop season.

The two topcrosses were evaluated in the 2010 crop year in the high- and low-technology environments. An area of around 5 ha was chosen, which was divided in half longitudinally for the creation of two contrasting environments, a high-technology strip and a low-technology strip. Soil chemical analysis was conducted using subsamples taken from the four quadrants of the total area.

Soil in the high-technology strip was amended with 800 kg/ha dolomitic limestone and received 180.00 kg/ha N, 149.80 kg/ha P₂O₅, and 85.60 kg/ha K₂O, whereas the low-technology strip did not receive limestone and received 45.00 kg/ha N, 37.8 kg/ha P₂O₅, and 21.60 kg/ha K₂O. Fertilizer was applied in the form of 535 and 135 kg/ha, respectively, of 8-28-16+Zn at sowing and the remaining N in topdressing in the form of urea at 21 days after emergence. Other crop treatments, such as weed and pest control, were identical for the two environmental conditions.

Because of the large number of treatments, only one replication per environment was used in an augmented block design (Federer, 1956). The plots consisted of 6-m-long rows containing 21 plants. The topcrosses were arranged in blocks of 49 treatments, three of which were the controls 'AG 7088', 'BRS 1040', and '2B707'. In Topcross 1 (with the Tester 1 line), 477 topcrosses were evaluated, and in Topcross 2 (with the Tester 2 line), 476 topcrosses were evaluated.

Plots were sown in each environment with a plot seeder, with 50 cm between rows and 28.5 cm between plants, resulting in a population of 70,000 plants/ha. The traits evaluated were plant height (PH), ear height (EH), stand (ST), number of broken or lodged plants (BLP), number of ears (NE), percent of diseased ears (%DE), and ear weight (EW).

Initially, the data from the topcrosses were subjected to individual analyses of variance (ANOVAs) at each technological level and for each trait separately, using an augmented complete block model (Federer, 1956) that was based on the following model:

$$Y_{ij} = m + g_i + b_j + e_{ij} \quad (\text{Equation 1})$$

where Y_{ij} is the observation of treatment i within block j , m is the overall mean of the experiment, g_i is the random effect of the common treatment and of the regular treatments i , b_j is the random effect of block j , and e_{ij} is the experimental error associated with the common treatment y_{ij} .

Subsequently, a combined ANOVA was conducted for each trait separately based on the fitted means, taking into consideration the two topcrosses in the two levels of technology:

$$Y_{iks} = m + t_i + a_k + ta_{ik} + e_{iks} \quad (\text{Equation 2})$$

where Y_{iks} is the observation in reference to treatment i within environment k in tester s , m is the overall mean of the experiment, t_i is the random effect of treatment i , a_k is the fixed effect of the environment k , ta_{ik} is the random effect of the interaction between treatment i and environment k , and e_{iks} is the random effect of the mean experimental error of the individual analyses in each environment k in the two topcrosses.

In the combined analysis, the sums of squares of the treatments were broken down into topcrosses, controls, and their contrasts, and interactions between these and the technology levels. In addition, the sums of squares of the topcrosses were broken down for each of the testers and the contrasts between them.

The fitted means of the common treatments of Topcrosses 1 and 2, with the exception of the controls, of each individual analysis were organized in order to only conduct diallel analysis for PH, EH, and EW. The analysis was performed according to method 4 of model I

from Griffing (1956), which was adapted for partial diallels in multiple environments (Ferreira et al., 1993). This method is used when a set of hybrids is available without their reciprocals. The statistical model was as follows:

$$Y_{rsl} = m + a_l + g_r + g'_s + s_{rs} + (ag)_{rl} + (ag')_{sl} + (as)_{rsl} + e_{rsl} \quad (\text{Equation 3})$$

where Y_{rsl} is the mean value observed in the hybrid combination between the r th tester with the s th line at technological level l ; a_l is the effect of technological level l ($l = 1, 2$); g_r is the effect of the overall combining ability of the r th tester ($r = 1, 2$); g'_s is the effect of the overall combining ability of the s th progeny ($s = 1, 2, 3, \dots, 394$); s_{rs} is the effect of the specific combining ability (SCA) between the tester r and the progeny s ; $(ag)_{rl}$ is the effect of the interaction between the overall combining ability of the r th tester and the effect of the technological level; $(ag')_{sl}$ is the effect of the interaction between the overall combining ability of the s th progeny and the effect of the technological level; $(as)_{rsl}$ is the effect of the interaction between the SCA between the testers r and the progenies s and the effect of the technological level; and e_{rsl} is the mean experimental error considering the mean sum of squares of the residues, fitted to the number of observations.

Differentiation between the efficient and responsive progenies in the technology levels was performed using the method of Fageria and Kluthcouski (1980), which consists of classifying genotypes into four classes that result from the combination of two factors according to their efficiency in the use of nutrients at low availability and their ability to respond to high nutrient availability, and were designated as efficient responsive, non-efficient responsive, non-efficient non-responsive, and efficient non-responsive.

Efficiency in the use of nutrients corresponds to the mean grain yield at a low level of fertilization (YLL). The ability to respond to a high nutrient availability was defined by the alpha parameter and estimated by the following equation:

$$\alpha = (YHL - YLL) / DEN \quad (\text{Equation 4})$$

where YHL is the yield at a high level of technology, YLL is the yield at a low level of technology, and DEN is the difference between the nutrient application rates (kg/ha). To be classified as efficient, a cultivar needed to have a YLL value that was above the mean YLL value. The criterion to be classified as responsive was to have an α value that was above the mean α value.

RESULTS AND DISCUSSION

The experimental precision, as evaluated by the coefficient of variation (CV), was considered high for the traits PH and ST, because the CVs were less than 10%. For the traits EH, NE, and EW, the CV was less than 20%, which indicates medium experimental precision (Table 1).

However, for the traits BLP and %DE, the CV was greater than 30%, indicating low experimental precision according to the classification of Pimentel-Gomes (1990). These high CVs can be explained by the fact that these characteristics had a binomial distribution and commonly have high CV estimates (Silva, 1984; Hallauer and Miranda Filho, 1988).

Table 1. Results of a combined analysis of variance for plant height (PH), ear height (EH), stand (ST), broken or lodged plants (BLP), number of ears (NE), percentage of diseased ears (%DE), and ear weight (EW).

SV	d.f.	Mean square						
		PH	EH	ST	BLP	NE	%DE	EW
Technological level (TL)	1	7.6948**	24,245.2**	2.6669 ^{ns}	937.69**	150.160**	2641.36**	878,741,962**
Treatments	955	0.0335**	176.5**	8.1614**	22.94**	10.708**	77.78**	4,140,296**
Progenies	952	0.0336**	177.0**	8.1802**	22.91**	10.734**	77.99**	4,146,777**
Topcross 1 (TC 1)	476	0.0348**	175**	9.403**	27.79**	12.11**	36775**	5,016,652**
Topcross 2 (TC 2)	475	0.02876**	178.4**	4.897**	16.09**	7.2757**	72.36**	2,985,507**
TC 1 vs TC 2	1	1.7073 ^{ns}	454 ^{ns}	985.72 ^{ns}	937.8 ^{ns}	1000.2 ^{ns}	3100**	141,690,091 ^{ns}
Controls	2	0.008573 ^{ns}	41.154 ^{ns}	2.58614 ^{ns}	39.619**	3.5571 ^{ns}	8.0538 ^{ns}	227,178 ^{ns}
Controls vs Progenies	1	0.007854 ^{ns}	2.693 ^{ns}	1.3277 ^{ns}	14.262 ^{ns}	0.5859 ^{ns}	12.924 ^{ns}	5,796,560 ^{ns}
Treatment x TL	955	0.0166 ^{ns}	101.0 ^{ns}	3.5338 ^{ns}	8.95 ^{ns}	4.7144 ^{ns}	51.12 ^{ns}	2,165,294 ^{ns}
Progeny x TL	952	0.0167 ^{ns}	101.2 ^{ns}	3.5443 ^{ns}	8.97 ^{ns}	4.728 ^{ns}	51.26 ^{ns}	2,168,872 ^{ns}
TC 1 x TL	476	0.0151 ^{ns}	92.5 ^{ns}	3.797 ^{ns}	11.53 ^{ns}	4.57 ^{ns}	57.69 ^{ns}	2,217,720 ^{ns}
TC 2 x TL	475	0.01806**	110.4**	3.003 ^{ns}	6.40 ^{ns}	4.1228 ^{ns}	44.90 ^{ns}	1,494,090 ^{ns}
(TC 1 vs TC 2) x TL	1	0.0998**	5 ^{ns}	139.94**	14.2 ^{ns}	368.7**	13 ^{ns}	299,438,924**
Controls x TL	2	0.000165 ^{ns}	4.119 ^{ns}	0.29291 ^{ns}	1.701 ^{ns}	0.2766 ^{ns}	5.5910 ^{ns}	387,854 ^{ns}
(Progenies vs Controls) x TL	1	0.010669 ^{ns}	59.761 ^{ns}	0.1142 ^{ns}	1.398 ^{ns}	0.2467 ^{ns}	4.8179 ^{ns}	2,313,243 ^{ns}
Residue	80	0.01337	76.85515	3.29682	9.74008	5.228968	47.60547	1,824,101
Mean low TL	-	1.75	80.77	19.74	4.47	18.75	1.42	8,236.00
Mean high TL	-	1.88	88.31	19.68	5.93	19.34	9.88	10,002.01
CV (%)		6.35	10.37	9.2	60.0	12.0	122	15.3
Yield		Low TL	High TL	Mean				
Topcross 1		7,446.4	9,590.23	8,518.3				
Topcross 2		8,784.4	9,342.8	9,063.6				
Controls		8,477.2	11,072.9	9,775.1				

^{ns}Not significant; **significant at 5% by F-test; CV, coefficient of variation; SV, source of variation; d.f., degrees of freedom.

Technological level had a significant F-test value ($P \leq 0.05$) for all of the traits studied, except ST, indicating that the technological levels had no influence on the number of plants that were maintained in the field up to the time of harvest. Significant differences were found in all of the variables between the treatments, indicating the existence of genetic variability among them.

Treatment was broken down into the progenies (Topcross 1, Topcross 2, and contrast between the topcrosses), controls, and contrast between the controls and the progenies. The progenies significantly differed in all of the traits examined, i.e., there were no similarities among the progenies. When analyzing each group separately, significant differences were observed within Topcrosses 1 and 2. The contrast between Topcrosses 1 and 2 was only significant for %DE; the other variables were not significantly different, indicating that the testers did not differ in relation to these characteristics. The testers used were two elite lines with contrasting loci and were part of the commercial hybrid 'BRS 1040' of the EMBRAPA plant breeding program; these lines should have had a large number of loci with fixed favorable alleles ($P = 1$). According to Vencovsky (1987), the greater the frequency of favorable alleles in the tester, the lower the discrimination of the progenies. However, the use of testers with a high frequency of favorable alleles allows the identification of the best crosses, i.e., those with the greatest SCA with these testers. In this situation, the testers should be the best elite lines of the program and of distinct heterotic groups, e.g., the two parental lines of a good commercial hybrid (Hallauer and Carena, 2009). Therefore, new lines that are identified in superior crosses could directly become parents of commercial hybrids.

There were no significant differences between the mean values of the controls and the progenies for any of the characteristics evaluated. In general, the performance of the

progenies was similar to that of the controls. It should be noted that this is desirable in a breeding program, because the ideal situation is that the genotypes evaluated exhibit a greater or equal performance to the genotypes that are already on the market. Although there were no significant differences in this contrast, it was observed that some progenies had mean yields that were greater than the yields of the controls, and these progenies should be selected.

There were no significant interactions between the treatments and technological levels for any of the variables analyzed, indicating that the treatments exhibited similar performances in the different technological levels (Table 1). This result is important, because it makes it possible to select progenies that are responsive to environmental improvement. Although the plants exhibited similar performances in both technological levels, it is necessary to know the performance in the two levels of technology, because selection should be made based on the mean values of the low- and high-technological levels.

The mean yield was 9119 kg/ha, with the topcrosses producing, on average, 8791 kg/ha and the controls producing 9775 kg/ha (Table 1). In the low-technological level environment, Topcross 2 obtained the highest mean value with 8784.4 kg/ha. In the high-technological level environment, the controls exceeded the mean values of the topcrosses, and produced around 11,073 kg/ha. The high-technological level produced a yield that was 21.4% greater than that of the low-technological level. This was expected, because maize responds very well to an increase in fertilization. In the high-technology environment, the application rate of N, P, and K was four times greater than that in the low-technology experiment (Table 1).

A combined diallel analysis was only performed for PH, EH, and EW (Table 2). Significant differences were observed ($P \leq 0.05$) between the technological levels and between the topcrosses, suggesting that there was variability between the topcrosses and between the technology levels.

Table 2. Results of a combined diallel analysis for plant height (PH), ear height (EH), and ear weight (EW).

SV	d.f.	Mean Square		
		PH	EH	EW
Technological level (TL)	1	7.2629**	18027.5714**	713,399,611.42**
Topcrosses (TC)	787	0.0462**	178.3639**	4,243,680.93**
GCA Progenies	393	0.0529**	220.6154**	4,622,548.79**
GCA Controls	1	2.2310**	645.9940 ^{ns}	134,753,782.86 ^{ns}
SCA Controls x Progenies	393	0.0338 ^{ns}	134.9226**	3,532,726.30**
TC x TL	787	0.0276**	103.2789**	2,115,017.20 ^{ns}
GCA (Progenies) x TL	393	0.0222**	104.1143**	1,765,240.49 ^{ns}
GCA (Controls) x TL	1	0.2319**	4.4420 ^{ns}	218,357,602.98**
SCA (Controls x Progenies) x TL	393	0.0324**	102.6950 ^{ns}	1,914,558.33 ^{ns}
Residue	80	0.0134	76.8552	1,824,100.5

^{ns}Not significant; **Significant at 5% by F-test; SV, source of variation; d.f., degrees of freedom; GCA, general combining ability; SCA, specific combining ability.

The general combining ability (GCA) estimates of the progenies were significant for the characteristics studied, indicating that there was genetic divergence between the progenies and that additive gene effects were important in the expressions of these characteristics. The testers were less divergent between themselves than were the progenies, which is shown by the non-significant GCA estimates for EH and EW, with only PH being significant.

The SCA, regarding non-additive gene effects, was fundamental for the expression of EH and EW. This indicates that the hybrids may have exhibited performances that were different from those expected because of the GCA effects of their parents, and that heterosis was important for their phenotypic expression; however, it was not very important for the

expression of PH. Both GCA and SCA effects were significant for EW, which shows that additive and non-additive gene effects were important. Therefore, the number of favorable alleles provided by the progenies and the allelic complementation obtained in the specific crosses were important for the formation of superior hybrids.

The estimates for the topcross x technological level interaction for PH and EH were significant in relation to the response variable EW. It can be inferred that the topcrosses exhibited performances that were similar in the two technological levels. In the breakdown of this interaction for the PH trait, GCA (progenies) x technological level, GCA (controls) x technological level, and SCA (controls x progenies) x technological level were all significant, indicating that the environment could change the expression of the favorable alleles provided by the parents. Regarding EH, breaking down the interaction showed that only GCA (progenies) x technological level was significant, indicating that the alleles of the progenies were of greater importance than those of the testers in EH determination.

Tester 2 (dent heterotic group) that belonged to group I exhibited positive GCA values for all of the variables studied (Table 3). This tester had effective alleles that provided a positive increase in these variables in the crosses in which it participated. In group II, of the 20 best progenies, the progenies '9307', '9592', and '9321' exhibited the greatest GCA estimate for EW.

Table 3. General combining ability (GCA) estimates of the parents of group II (GCA Controls) and the 25 best progenies of group I (GCA Progenies) for the mean values of plant height (PH), ear height (EH), and ear weight (EW) in the two environments.

GROUP II	Progeny	Effect of GCA		
		PH	EH	EW
Tester 1		-0.038**	-0.64 ^{ns}	-292.41 ^{ns}
Tester 2		0.038**	0.64 ^{ns}	292.41 ^{ns}
DP (G _i)		0.004	0.309	46.971
DP (G _i -G _j ')		0.008	0.619	93.102
GROUP I		GCA	GCA	GCA
1	9307	0.188	13.029	3093.261
2	9592	-0.012	7.612	2404.427
3	9321	0.113	0.529	2326.595
4	9302	0.226	11.779	2109.928
5	9143	0.226	10.112	2009.928
6	9310	0.238	13.029	1993.262
7	9145	0.301	12.612	1976.595
8	9507	0.018	10.112	1976.595
9	9603	0.088	5.112	1954.427
10	9200	0.247	6.362	1876.595
11	9441	0.018	0.112	1826.595
12	9184	0.122	6.362	1809.928
13	9105	0.038	4.696	1798.817
14	9083	0.030	1.112	1798.817
15	9379	0.072	16.362	1759.929
16	9126	0.038	9.696	1732.151
17	9322	0.088	3.029	1709.929
18	9440	0.030	-7.388	1659.929
19	9232	-0.032	-1.971	1637.706
20	9283	0.088	4.279	1626.595
21	9315	-0.037	0.529	1626.595
22	9294	-0.087	-1.971	1609.929
23	9449	-0.020	-2.388	1559.929
24	9201	0.147	10.112	1559.929
25	9135	0.238	7.612	1543.262
DP (G _i)		0.082	6.132	931.163
DP (G _i -G _j ')		0.116	8.683	1318.538

^{ns}Not significant; **significant at 5% by F-test.

The SCA was significant for EW (Table 1), confirming that there were certain combinations that proved to be relatively better or worse than would be expected based on the mean performance of the parents. Considering the 25 best progenies in regard to the mean values for EW, the highest SCAs were obtained in the crosses ‘9307’ x L1, ‘9302’ x L1, and ‘9592’ x L1 (Table 4). The best hybrid combinations were those with high SCA values and at least one of the parents with a high GCA value.

Table 4. Specific combining ability (SCA) estimates obtained in a partial diallel between the testers of the 20 best progenies for plant height (m), ear height (cm), and ear weight (kg/ha).

Progeny	Plant height		Ear height		Ear weight	
	L1	L2	L1	L2	L1	L2
9307	0.005	-0.02	-1.86	1.86	109.077	-109.077
9592	-0.053	0.038	-7.277	7.277	1431.243	-1431.24
9321	0.03	-0.045	0.64	-0.64	-224.256	224.256
9302	0.143	-0.158	4.39	-4.39	2525.741	-2525.74
9143	-0.082	0.067	-6.443	6.443	681.299	-681.299
9310	0.055	-0.07	3.14	-3.14	-1090.92	1090.92
9145	0.018	-0.033	-1.443	1.443	81.299	-81.299
9507	0.118	-0.133	3.557	-3.557	1414.631	-1414.63
9603	-0.078	0.063	0.223	-0.223	914.577	-914.577
9200	0.013	-0.029	9.807	-9.807	-52.034	52.034
9441	-0.007	-0.008	-6.443	6.443	331.299	-331.299
9184	-0.012	-0.004	-0.193	0.193	-885.366	885.366
9105	-0.045	0.03	3.974	-3.974	225.744	-225.744
9083	-0.028	0.013	5.89	-5.89	1159.076	-1159.08
9379	-0.095	0.08	-16.026	16.026	886.854	-886.854
9126	0.005	-0.02	-1.026	1.026	-1307.59	1307.588
9322	0.105	-0.12	3.14	-3.14	59.077	-59.077
9440	0.03	-0.045	6.057	-6.057	1197.965	-1197.97
9232	0.001	-0.016	-9.36	9.36	464.632	-464.632
9283	-0.02	0.005	-5.61	5.61	-890.922	890.922
9315	0.105	-0.12	5.64	-5.64	1542.409	-1542.409
9294	0.03	-0.045	3.14	-3.14	1925.74	-1925.74
9449	-0.02	0.005	-3.94	3.94	797.97	-797.97
9201	-0.162	0.146	-3.94	3.94	-2002.032	2002.032
9135	0.005	-0.02	-3.94	3.94	-585.37	585.37

Although Tester 2 had higher GCAs, the highest SCAs were obtained in the crosses between the progenies and Tester 1, which was in the flint heterotic group. This indicates that line 1 probably had greater allelic complementation than the dent line 2, and that the most productive progenies were of the dent heterotic group.

A classification of the topcrosses with regard to production, based on their efficiency in the use of nutrients at low availability and their ability to respond to high nutrient availability, is presented in Figures 1 and 2 for Testers 1 and 2, respectively. Regarding the topcross with Tester 1, 18.8% of the progenies were classified as efficient and responsive, and in the topcross with Tester 2, 14.2% of the progenies were classified in the same quadrant. In both topcrosses, there was wide dispersion in the progenies, with segregation in all types of performance. Similar results were found by Fidelis et al. (2010) when analyzing maize populations with regard to P-use efficiency and response.

The partially inbred progenies that were classified as efficient at a low level of technology and responsive at a high level of technology were located in quadrant I (Figures 1A and 2A). Prominent among the progenies were ‘9268’, ‘9495’, ‘9309’, ‘9083’, ‘9315’, and ‘9507’ crossed with Tester 1 of the flint heterotic group (Figure 1B), and progenies ‘9617’,

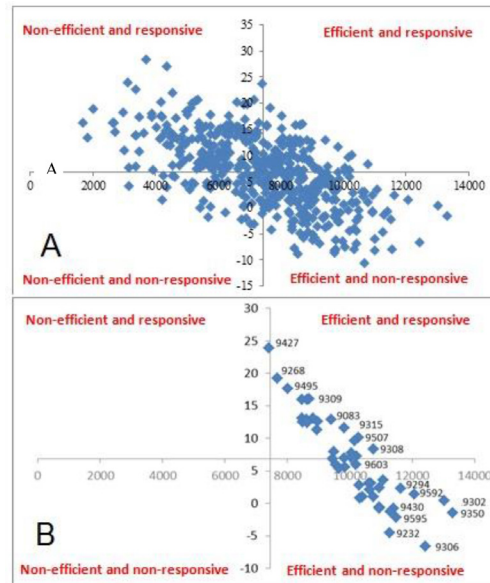


Figure 1. A. Efficiency at the low-technological level and response to the high-technological level of the topcrosses with Tester 1. **B.** Efficiency at the low-technological level and response to the high-technological level of the 48 topcrosses with Tester 1.

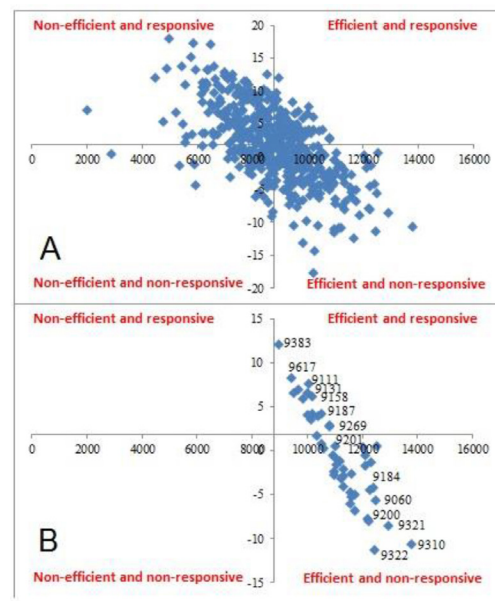


Figure 2. A. Efficiency at the low-technological level and response to the high-technological level of the topcrosses with Tester 2. **B.** Efficiency at the low-technological level and response to the high-technological level of the 48 topcrosses with Tester 2.

'9111', '9131', '9158', and '9187' crossed with Tester 2 of the dent heterotic group (Figure 2B). Based on their performances in the crosses with the two testers, it can be inferred that the progenies that combined best with Tester 1 were of the dent heterotic group, whereas the progenies that combined best with Tester 2 were of the flint heterotic group.

These progenies exhibited the best mean values for EW at the low-technological level and the highest mean values of alpha, and were the most efficient in using N, P, and K even at moderately low concentrations, indicating their efficacy both in N-, P-, and K-deficient environments and in environments with optimal levels of N, P, and K. The efficiency of these genotypes in relation to the others in the uptake and use of nutrients in grain production means that the processes associated with the uptake, translocation, assimilation, and redistribution of nutrients were more efficient in these than in the other genotypes. Therefore, these progenies can be used in breeding programs with the aim of obtaining cultivars that take up and use nutrients in an efficient manner.

CONCLUSION

There were no differences in grain yield between the progenies at the two technological levels, and the testers did not differ in mean progeny grain yield at the two technological levels. Although the performances of the progenies were similar to those of the controls, it was possible to select progenies that were derived from commercial hybrids that were responsive and efficient with regard to fertilization.

Conflicts of interest

The authors declare no conflict of interest.

REFERENCES

- Balestre M, Von Pinho RG, Souza JC and Oliveira RL (2009). Genotypic stability and adaptability in tropical maize based on AMMI and GGE biplot analysis. *Genet. Mol. Res.* 8: 1311-1322. <http://dx.doi.org/10.4238/vol8-4gmr658>
- Fageria NK and Kluthcouski J (1980). Metodologia para avaliação das cultivares de arroz e feijão para condições adversas de solo. Circular Técnica No. 8, EMBRAPA/CNPAP 22, Brasília.
- Federer WT (1956). Augmented (hoonuiaku) designs. *Hawaiian Planters' Record. Aica* 55: 191-208.
- Ferreira DF, Rezende GDSP and Ramalho MAP (1993). An adaptation of Griffing's Method IV of complete diallel cross analysis for experiments repeated in several environments. *Rev. Bras. Genet.* 16: 357-366.
- Fidelis RR, Miranda GV, Pelúzio M and Galvão JCC (2010). Classificação de populações de milho quanto à eficiência e resposta ao uso de fósforo. *Acta Sci. Agron.* 32: 241-246. <http://dx.doi.org/10.4025/actasciagron.v32i2.2632>
- Griffing B (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Aust. J. Biol. Sci.* 9: 463-493.
- Hallauer A and Carena MJ (2009). Maize breeding. In: Handbook of plant breeding: cereals (Carena MJ, eds.). Springer, New York, 3-98.
- Hallauer AR and Miranda Filho JB (1988). Quantitative genetics in maize breeding 2nd edn. Iowa State University Press, Ames, 468.
- Pimentel-Gomes F (1990). Curso de estatística experimental 13th edn. Nobel, Piracicaba, 468.
- Rodrigues CS, Pacheco CAP, Carvalho HWL and Castro CR (2013). Metodologia para a seleção de cultivares de milho eficientes e responsivas em dois níveis de tecnologia. In: Congresso Brasileiro de melhoramento de plantas 7. SBMP, Uberlândia.
- Silva AC (1984). Comparação entre linhagens e híbridos de milho (*Zea mays* L.) de portenormal e suas versões braquíticas. 100.
- Vencovsky R (1987). Herança quantitativa. In: Melhoramento e produção do milho 2nd edn. (Paterniani E and Viegas GP, eds.). Fundação Cargill, Campinas, 137-214.