

Evaluation of inbred lines from two maize (*Zea mays* L.) brachytic populations in single crosses following the two-factor mating design

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ABSTRACT

Thirty dent and 15 flint inbred (S_5) lines from the brachytic maize (*Zea mays* L.) populations 'Piranão-VD2B' and 'Piranão-VF1B', respectively, were used for the evaluation of 120 single crosses. The factor design (partial diallel) of six 5 x 5 sets was used. The flint lines entered twice because each one was evaluated with two different sets of dent lines. Field evaluation was in 5 x 5 balanced lattice trials and the following traits were analyzed: TE, total ear weight in the plot; SE and SG, ear weight and grain weight in a sample of five ears; PH and EH, plant and ear height; TB, tassel branch number; ED and CD, ear and cob diameter, and MF and FF, days to male and female flowering. The 10% best single crosses yielded from 119.0% to 138.7% relative to check variety ('Piranão-VD2'). General combining ability (GCA) was more important than specific combining ability (SCA) as a source of variation, although SCA effects were relatively important in some specific crosses. The GCA mean squares for yield were higher for flint lines relative to dent lines in five of the six sets. High correlation coefficients were observed between g_j 's (GCA of flint lines) obtained from crosses with different sets of dent lines: 0.923, 0.904 and 0.907 for TE, SE and SG, respectively. The reduced model $\hat{Y}_{ij} = \hat{\mu} + \hat{g}_i + \hat{g}_j$ was used for prediction of single crosses that were not included in the field evaluation. For the yield traits (TE, SE and SG), the coefficients of determination (R^2) relative to the reduced model were in the range of 0.74 to 0.90. The use of the factor design for evaluating inbred lines in crosses and the reliability of predicted means as a guide for selection are discussed.

INTRODUCTION

Since the introduction of double crosses for maize hybrid production (Jones, 1918), the evaluation of inbred lines to be used in crosses has been an important task in hybrid breeding programs. The main constraint is the large number of lines and, consequently, the large number of crosses necessary for a complete evaluation. The top cross procedure (Davis, 1927; Jenkins and Brunson, 1932), in which the lines are first evaluated in crosses with a common tester, has been widely used. The choice of a good tester, however,

still remains a problem. Studies have been reported to provide the basis and guides to improve the efficiency in evaluation and selection of lines and hybrids (Rawlings and Thompson, 1962; Allison and Curnow, 1966; Hallauer and Lopez-Perez, 1979). Hallauer and Miranda Filho (1988) also provide a discussion on the use of testers in maize breeding programs.

Sprague and Tatum (1942) introduced the concept of general and specific combining ability (GCA and SCA, respectively) in evaluating inbred lines in all possible crosses among them (diallel crosses). The analysis of diallel crosses for evaluating inbred lines has been used, but its limitation is the great number of crosses, that increases rapidly with an increase in the

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number of parental lines. When two sets of lines or genotypes are available, the partial diallel cross (Vencovsky, 1987; Geraldi and Miranda Filho, 1988) has been suggested; crosses are made only between sets. The mating scheme is structurally similar to Design-II (Comstock and Robinson, 1948) and was designated "two-factor design" by Cockerham (1963). Although Design-II has been primarily suggested for estimating parameters in random samples from one reference population, it has also been used for the evaluation of combining ability of fixed or random sets of inbred lines (Hoegemeyer and Hallauer, 1976; Stangland et al., 1983; Lamkey and Hallauer, 1986).

The purpose of this paper is to report on the evaluation of random sets of inbred lines in single crosses obtained by use of Design-II or "two-factor" mating design.

MATERIAL AND METHODS

A sample of inbred lines from each of the populations 'Piranão-VD2B' and 'Piranão-VF1B' was used. The populations are brachytic versions (br_2br_2) of the composite varieties 'ESALQ-VD2' and 'ESALQ-VF1' (Paterniani *et al.*, 1977). The inbred lines were in the fifth generation of selfing with inbreeding coefficient $F = 0.969$, and in each population they were chosen so that each line came from a different S_0 plant. Because the lines were selected during the selfing generations, a relatively restricted sample of independent lines was obtained for each population: 30 from Piranão-VD2B and 15 from Piranão-VF1B. Each sample was partitioned into sets of five lines, thus resulting in six sets for 'Piranão-VD2B' and three sets for 'Piranão-VF1B'.

In 1981/82, single crosses at the interpopulation level were obtained by randomly combining the sets from each population. Because of the different numbers, the flint lines were crossed twice and, hence, six sets of single crosses were obtained (D and F stand for dent and flint lines, respectively):

- Set 1: [D₁.D₂.D₃.D₄.D₅] × [F₁.F₂.F₃.F₄.F₅]
 Set 2: [D₆.D₇.D₈.D₉.D₁₀] × [F₆.F₇.F₈.F₉.F₁₀]
 Set 3: [D₁₁.D₁₂.D₁₃.D₁₄.D₁₅] × [F₁₁.F₁₂.F₁₃.F₁₄.F₁₅]
 Set 4: [D₁₆.D₁₇.D₁₈.D₁₉.D₂₀] × [F₁.F₂.F₃.F₄.F₅]
 Set 5: [D₂₁.D₂₂.D₂₃.D₂₄.D₂₅] × [F₆.F₇.F₈.F₉.F₁₀]
 Set 6: [D₂₆.D₂₇.D₂₈.D₂₉.D₃₀] × [F₁₁.F₁₂.F₁₃.F₁₄.F₁₅]

Each set of single crosses represented a 5 × 5 partial diallel cross, according to terminology used by Vencovsky (1987) and Geraldi and Miranda Filho (1988). Because of failures in some crosses due to

differences in flowering date or no production of hybrid seeds as a consequence of extremely reduced height of some brachytic lines, the number of single crosses in the six sets was not always the same; one or more plots in each replication included a check to complete the 25 entries in each set. The single crosses and checks in each set were evaluated in a 5 × 5 balanced lattice experiment, with six replications in one location (ESALQ/USP-Piracicaba, SP). Plots were 5.0 m long, spaced 1.0 m apart with 25 plants per plot after thinning. The variety 'Piranão-VD2' was used as check; it has the same origin as 'Piranão-VD2B', except that it has undergone several cycles of recurrent selection and was released as an open-pollinated variety. The number of single cross and check plots within replications were in the following proportions: 24:1, 20:5, 17:8, 17:8, 21:4, and 21:4, from the 1st to the 6th set, respectively.

The following traits were analyzed: TE, total ear weight (except husks) in the plot, corrected for stand variation; SE, weight (kg) of a sample of five well developed ears, taken at random after discarding the abnormally developed or diseased ones; SG, weight (kg) of grains of the five ears sampled for SE; PH, plant height (m); EH, ear height (m); TB, tassel branch number; ED, ear diameter; CD, cob diameter; MF, days to male flowering, and FF, days to female flowering.

Because of the low efficiency of the lattice design relative to randomized complete block (RCB) design, the preliminary analysis of variance was as RCB. The analysis of the partial diallel cross (Design-II) was performed only for the yield traits (TE, SE and SG), according to the factorial model:

$$Y_{ij} = \mu + g_i + g_j + s_{ij} + \bar{e}_{ij}$$

where Y_{ij} is the mean over six replications for the cross between the i th line of Piranão-VD2B and the j th line of Piranão-VF1B; μ is the general mean of the diallel table; g_i and g_j are the GCA; and s_{ij} is the SCA; \bar{e}_{ij} is the error term for treatment means. Because of the failure of some crosses, the analyses were performed following the least square procedure, as given by Harvey (1979) for the unbalanced factorial design. The estimates of GCA and SCA effects were also obtained.

The reduced model $\hat{Y}_{ij} = \hat{\mu} + \hat{g}_i + \hat{g}_j$ was used to estimate the single cross means. The coefficient of determination (R^2) was used to infer on the effectiveness of the reduced model to predict single cross means.

RESULTS AND DISCUSSION

Among the 10 traits evaluated, three refer to yield measurements: TE is the total ear weight (kg) of

the plot with 25 plants; SE and SG are weight of ear and grain, respectively, of a sample of five ears. The purpose of including SE and SG in the study was to investigate the effectiveness of such a procedure in evaluating the potential yield of single crosses.

Five of six sets of single crosses outyielded the variety check 'Piranão-VD2' (Table I). No difference was observed between the average yield of single crosses and the check variety averaged for the six sets. For SE and SG the single crosses yields were about 5% less than the check variety. Single crosses had shorter plants and lower ear placement when compared with the check variety: 98.2% and 96.8%, respectively, in an average of six sets. A consistent difference between single crosses and the check was for tassel branch number. Soares Filho (1987) reported 19.8 and 28.3 as the average number of branches per tassel in the base populations, Piranão-VD2B and Piranão-VF1B, respectively. The overall mean for ED and CD in the single crosses was similar to the check variety and the base populations Piranão-VD2B (4.39 and 2.67) and Piranão-VF1B (4.44 and 2.61), respectively (Soares Filho, 1987). Days to male and female flowering indicated that the single crosses were about 5% earlier than the check. The coefficients of variation were consistent among experiments (sets) (Table I). For SE and SG evaluated in the sample, the CV's were 2% higher than for yield evaluated in the whole plot; the CV's were 11.6% (TE), 13.3% (SE), and 13.6% (SG), for the average of six trials.

The frequency distribution of TE means for 120 single crosses shows that about 40% outyielded the check variety (Figure 1). The 10% best single crosses are identified in Table II, with their means for the 10 traits. The superiority of the 12 best single crosses for TE varied from 19.0% to 38.7%, averaging 24.9% relative to the check mean. The check variety (Piranão-VD2) is a high yielding cultivar in the regional trials. It is thus apparent that inbred lines from Piranão-VD2B and Piranão-VF1B have good genetic potential for use in hybrids. The highly inbred lines of the brachytic populations, however, had a strong inbreeding depression that would limit their commercial use in single crosses. However, their potential for use in three-way and double crosses should be investigated. Mota (1984), working with the same brachytic populations, evaluated crosses (interpopulation level) between half-sib families and found that the best hybrid combinations outyielded the check mean by 32.5 to 54.5%.

The analysis of variance for all traits and sets indicated that the variation due to hybrid crosses was significant in nearly all instances (Martins, 1988 and data not shown). The variation among hybrids for yield

Table I - Observed means of single crosses (upper) and check (middle) and coefficients of variation (CV%, lower) for 10 maize traits in six sets.

Trait	Set-1	Set-2	Set-3	Set-4	Set-5	Set-6	Combined	
							Mean	%
TE	3.187	2.997	3.142	3.213	2.989	3.046	3.093	100.8
	3.140	2.860	3.114	3.165	2.899	3.203	3.069	100.0
	11.5	12.2	12.9	9.4	11.0	12.0	11.6	-
SE	0.759	0.778	0.792	0.817	0.755	0.758	0.774	94.3
	0.814	0.763	0.834	0.850	0.793	0.837	0.821	100.0
	14.0	13.5	12.9	10.7	13.0	15.8	13.3	-
SG	0.637	0.639	0.663	0.691	0.644	0.646	0.651	95.0
	0.674	0.635	0.692	0.711	0.668	0.705	0.685	100.0
	14.4	13.5	13.0	10.7	13.6	16.4	13.6	-
PH	1.62	1.74	1.63	1.68	1.93	1.49	1.68	98.2
	1.73	1.67	1.69	1.75	1.79	1.66	1.71	100.0
	7.4	5.7	6.4	7.0	6.2	7.8	6.7	-
EH	0.86	0.94	0.86	0.91	1.11	0.74	0.91	96.8
	0.90	0.93	0.92	0.97	0.97	0.91	0.94	100.0
	10.0	8.7	7.7	9.1	8.1	10.0	8.9	-
TB	19.1	20.8	19.3	21.7	21.9	18.5	20.2	125.5
	15.2	14.9	15.1	17.5	17.4	15.5	16.1	100.0
	12.5	11.7	14.1	14.9	14.3	16.4	14.0	-
ED	4.40	4.36	4.29	4.45	4.41	4.35	4.38	97.8
	4.40	4.37	4.47	4.55	4.45	4.52	4.48	100.0
	3.6	3.6	3.2	3.3	3.7	4.4	3.6	-
CD	2.65	2.67	2.53	2.66	2.60	2.50	2.60	102.4
	2.44	2.51	2.55	2.57	2.51	2.54	2.54	100.0
	3.2	3.8	3.0	3.8	3.3	3.6	3.5	-
MF	70.5	67.7	67.5	66.6	67.5	68.8	68.2	94.6
	73.8	72.9	72.9	71.0	71.0	72.2	72.1	100.0
	2.2	2.5	2.6	2.2	2.8	3.2	2.1	-
FF	73.4	72.8	71.4	71.5	70.7	74.5	72.5	95.4
	76.8	76.9	77.1	74.4	74.7	77.0	76.0	100.0
	2.6	2.6	2.3	3.2	3.4	3.8	3.1	-

TE, Total plot ear weight (kg); SE, sample ear weight (kg); SG, sample grain weight (kg); PH, plant height (m); EH, ear height (m); TB, tassel branch number; ED, ear diameter (cm); CD, cob diameter (cm); MF, days to male flowering; FF, days to female flowering.

traits (TE, SE and SG) was partitioned according to the partial diallel (two-factor) model and the analysis of variance is summarized in Table III. The sources of variation designated as dent and flint are for GCA of lines from Piranão-VD2B and Piranão-VF1B, respectively; the source D x F is the SCA. For TE, GCA was highly significant for both groups in all sets. Mean squares due to flint lines, however, were generally higher than for dent lines (except in set 6), indicating a

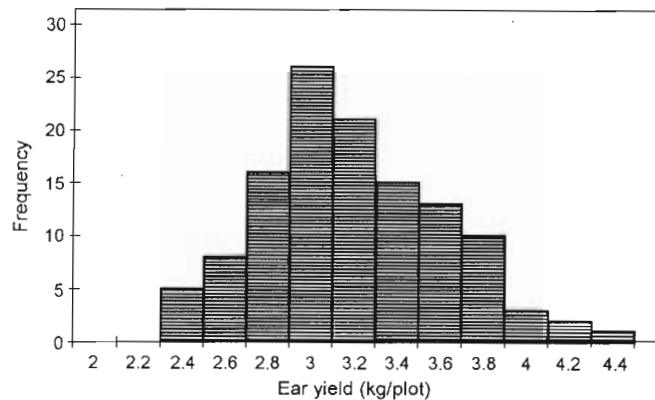


Figure 1 - Frequency distribution of 120 single crosses for ear yield (kg/4 m²).

greater variation among GCA effects (g_j) for lines derived from Piranão-VF1B. There are greater opportunities for selection among flint lines for GCA differences than for selection among dent lines. This finding agrees with the estimates of the additive genetic variance, which was much higher for Piranão-VF1B (879.9) than for Piranão-VD2B (422.8), expressed in g/plant² (Soares Filho, 1987). The flint lines in sets 1, 2, and 3 are the same as in sets 4, 5 and 6, respectively. In the first three sets the smallest mean square for flint lines is in set 3, corresponding to set 6, that also showed the smallest mean square for flint lines among the last three sets. It was concluded that the variation among flint lines did not change much when different sets of dent lines were used as testers.

The mean squares for SCA (D x F) were smaller than for GCA and was nonsignificant only in set 3. It seems that SCA is a non-negligible source of variation when considering selection among single crosses from the two brachytic populations. Hoegemeyer and Hallauer (1976) studied selected and unselected lines from two maize populations (BS-10 and BS-11), using the Design-II mating scheme, that is essentially the same as the partial diallel in the present study. They found significance for GCA for lines from both BS-10 and BS-11 and SCA was nonsignificant in only two of the six 4 x 4 sets of crosses. The selected lines were developed from "cryptic" double crosses ($S_0 \times S_0$) which are characterized by continuous selection among full-sib families with increasing inbreeding of parents (Hallauer, 1967; Lonquist and Williams, 1967). Therefore, each selected line was developed on the basis of combining ability with one line of the opposite population. Hoegemeyer and Hallauer (1976) found a higher frequency of positive and significant SCA effects in the crosses ($S_4 \times S_4$) representing the original $S_0 \times S_0$ crosses (diagonal in the 4 x 4 factorial mating scheme) than in random crosses (off-diagonal in the 4 x 4 mating scheme).

The estimates of the mean and GCA effects are shown for the three yield traits (Table IV). The highest \hat{g}_i (best dent line) in each set were in the range of 6.1% to 11.9% of the mean ($\hat{\mu}$). The highest g_j (best flint line) in the first three sets varied from 10.9% to 20.1% of the mean. In sets 4, 5 and 6, the best lines were the same as

Table II - Means of 10 traits for 12 (10%) highest yielding maize single crosses.

Single crosses	TE		SE	SG	PH	EH	TB	ED	CD	MF	FF
	kg/plot	%									
D ₁ x F ₅	4.256	138.7	0.925	0.764	1.64	1.05	18.6	4.6	2.7	69.6	70.8
D ₅ x F ₅	4.026	131.2	0.997	0.796	1.67	0.96	23.2	4.7	3.0	71.0	75.5
D ₁₃ x F ₁₄	4.014	130.8	0.888	0.744	1.85	1.01	15.8	4.3	2.5	69.9	72.5
D ₂₉ x F ₁₄	3.983	129.8	0.935	0.792	1.74	0.85	20.0	4.7	2.6	70.9	73.7
D ₁₈ x F ₅	3.845	125.3	1.060	0.891	1.88	1.10	19.1	4.7	2.8	66.9	71.0
D ₁₉ x F ₅	3.810	124.1	0.959	0.785	1.91	1.06	21.4	4.6	2.9	66.2	71.5
D ₂ x F ₂	3.712	120.9	0.839	0.717	1.94	0.87	19.5	4.3	2.6	69.5	71.3
D ₃ x F ₅	3.708	120.8	0.964	0.792	1.82	0.99	24.5	4.8	2.9	71.7	73.8
D ₁₇ x F ₁	3.677	119.8	0.989	0.819	1.94	1.21	24.4	4.5	2.6	72.1	76.8
D ₁₀ x F ₉	3.664	119.4	0.845	0.728	1.96	1.12	18.4	4.3	2.4	63.7	67.7
D ₁₉ x F ₂	3.655	119.1	0.972	0.795	1.70	0.73	20.3	4.6	2.7	66.0	70.8
D ₂ x F ₅	3.652	119.0	0.881	0.701	1.88	1.02	17.5	4.5	2.7	69.3	73.2
Mean	3.834	124.9	0.938	0.777	1.83	1.00	20.2	4.5	2.7	68.9	72.4
Whole set	3.093	100.8	0.774	0.651	1.68	0.91	20.2	4.4	2.6	68.2	72.5
Highest	4.256	138.7	1.060	0.891	2.33	1.45	30.2	4.9	3.0	74.6	79.2
Lowest	2.263	73.7	0.562	0.466	1.06	0.41	12.8	3.9	2.3	61.8	64.3
Check	3.069	100.0	0.821	0.685	1.71	0.94	16.1	4.5	2.5	72.1	76.0

For abbreviations see Table I.

Table III - Analysis of variance with partition of the variation among single crosses into general combining ability due to lines of Piranão-VD2B (dent) and Piranão-VF1B (flint) and specific combining ability (dent x flint interaction) for yield traits in six sets.

Set	Source	d.f.	TE ⁽¹⁾	SE ⁽²⁾	SG ⁽²⁾
1	Hybrids	23	11.836**	6.706**	3.921**
	Dent	4	9.975**	2.207	1.279
	Flint	4	50.336**	30.806**	16.707**
	D x F	15	2.504*	1.635	1.245
	Error#	120	1.362	1.135	0.841
2	Hybrids	19	13.204**	7.156**	5.985**
	Dent	4	6.616**	4.795**	3.693**
	Flint	4	44.347**	19.451**	17.955**
	D x F	11	3.684*	2.050	1.371
	Error	124	1.336	1.118	0.770
3	Hybrids	16	8.652**	5.435**	3.973**
	Dent	3	13.209**	2.836*	1.072
	Flint	4	20.281**	12.570**	9.616**
	D x F	8	1.671	2.025**	2.157**
	Error	127	1.594	1.039	0.745
4	Hybrids	16	10.866**	9.714**	6.303**
	Dent	4	18.904**	12.126**	8.026**
	Flint	3	20.294**	25.837**	16.050**
	D x F	8	3.860**	3.858**	2.892**
	Error	127	0.895	0.802	0.570
5	Hybrids	20	8.032**	3.632**	3.383**
	Dent	4	4.729**	1.977	1.843
	Flint	4	24.464**	9.957**	9.731**
	D x F	12	2.721*	1.626	1.320
	Error	123	1.064	0.955	0.755
6	Hybrids	20	7.816**	5.267**	4.287**
	Dent	4	18.643**	7.114**	4.585**
	Flint	4	11.749**	15.537**	13.451**
	D x F	12	2.701**	1.005	0.798
	Error	123	1.347	1.468	1.395

^{(1), (2)}Mean squares multiplied by 10 and 10², respectively. #For TE d.f. is one less than shown, because of correction for stand variation through linear regression; in all instances the error d.f. include r(t-1) d.f. due to variation of check plots(t) within replications(r). **, *Significance levels for the F test at P < 0.01 and P < 0.05, respectively. For abbreviations see Table I.

those identified in the first three sets and the \hat{g}_j effects varied from 10.8 to 13.3% of the mean. Therefore, for the flint lines there was a high consistency between the \hat{g}_j effects evaluated with different sets of dent lines; the correlation coefficients between the two estimates of \hat{g}_j effects for TE, SE and SG were larger than 0.9 (diagonal in Table V). Table V also includes the correlation coefficients between \hat{g}_i 's (and \hat{g}_j 's) for combinations of traits (TE, SE and SG). The high observed correlations indicate that in the evaluation of GCA of inbred lines in single crosses, a sample of five ears may be fairly effective for that purpose. Such information can be helpful in situations that force the use of smaller plots or when some kind of damage may compromise only a part of a plot, so that a sample of ears can be saved for evaluation.

Table IV - Estimates of the mean ($\hat{\mu}$) and general combining ability effects for TE, SE and SG.

Set	Dent	TE	SE	SG	Flint	TE	SE	SG
1	1	0.204	0.010	0.009	1	-0.123	-0.020	0.015
	2	0.191	0.040	0.033	2	0.188	0.024	0.025
	3	-0.152	-0.003	-0.009	3	-0.342	-0.072	-0.042
	4	-0.199	-0.039	-0.017	4	-0.358	-0.096	-0.083
	5	-0.044	-0.008	-0.017	5	0.636	0.164	0.115
	μ_1	3.164	0.755	0.635	μ_1	3.164	0.755	0.635
2	6	0.014	-0.021	-0.020	6	0.301	0.102	0.085
	7	-0.101	-0.040	-0.032	7	-0.493	-0.109	-0.105
	8	0.245	0.073	0.062	8	-0.406	-0.097	-0.090
	9	-0.125	-0.005	-0.015	9	0.418	0.041	0.049
	10	-0.035	-0.007	0.005	10	0.180	0.062	0.060
	μ_2	3.024	0.787	0.648	μ_2	3.024	0.787	0.648
3	11	-0.273	-0.050	-0.030	11	0.349	0.089	0.090
	12	-	-	-	12	-0.435	-0.062	-0.059
	13	0.332	0.028	0.022	13	-0.259	-0.107	-0.088
	14	-0.068	0.000	-0.001	14	0.197	0.055	0.046
	15	0.008	0.023	0.009	15	0.148	0.024	0.010
	μ_3	3.199	0.802	0.671	μ_3	3.199	0.802	0.671
4	16	-0.488	-0.124	-0.102	1	0.112	0.028	0.021
	17	0.207	0.100	0.080	2	-	-	-
	18	0.067	-0.025	-0.020	3	-0.163	-0.065	-0.040
	19	0.277	0.031	0.019	4	-0.321	-0.107	-0.092
	20	-0.062	0.019	0.023	5	0.372	0.144	0.111
	μ_4	3.268	0.839	0.710	μ_4	3.268	0.839	0.710
5	21	-0.170	-0.036	-0.033	6	0.244	0.033	0.034
	22	0.203	0.031	0.038	7	-0.264	-0.060	-0.060
	23	0.009	0.022	0.012	8	-0.303	-0.078	-0.076
	24	0.021	0.000	-0.003	9	0.396	0.061	0.062
	25	-0.064	-0.018	-0.015	10	-0.073	0.044	0.040
	μ_5	2.978	0.753	0.642	μ_5	2.978	0.753	0.642
6	26	-0.140	0.023	0.017	11	0.344	0.073	0.073
	27	-0.103	-0.042	-0.026	12	-0.226	-0.123	-0.116
	28	0.152	0.010	0.004	13	-0.239	-0.043	-0.037
	29	0.370	0.065	0.054	14	0.099	0.052	0.044
	30	-0.280	-0.056	-0.048	15	0.033	0.040	0.035
	μ_6	3.098	0.772	0.659	μ_6	3.098	0.772	0.659
Overall mean	3.116	0.782	0.658		3.116	0.782	0.658	

For abbreviations see Table I.

Table V - Correlation coefficients between g_i 's (above diagonal) and between g_j 's (below diagonal) for combinations of traits; and between g_i 's (flint lines) evaluated in two sets of dent lines for the same traits (diagonal).

Traits	TE	SE	SG
TE	0.923	0.832	0.818
SE	0.926	0.904	0.983
SG	0.929	0.990	0.907

For abbreviations see Table I.

Figure 2 represents the frequency distribution of SCA (\hat{s}_{ij}) effects for ear yield. The ranges for \hat{g}_i , \hat{g}_j , and \hat{s}_{ij} are shown in Table VI. The range for \hat{g}_i effects (dent lines) are equivalent to -0.98 to 0.74 t/ha, and for \hat{g}_j effects (flint lines) a greater range (-0.99 to 1.27 t/ha) was observed. The range for SCA effects (Table VI) is equivalent to (-0.84 to 0.83 t/ha). Hoegemeyer and Hallauer (1976) reported \hat{s}_{ij} effects varying from -1.54 to 0.91 t/ha; their lines had, however, undergone selection for both GCA and SCA, so that a greater range for \hat{s}_{ij} was expected. In specific crosses ($S_4 \times S_4$) that were selected from the corresponding $S_0 \times S_0$ crosses, the SCA showed a higher frequency of positive values than for nonspecific crosses (off diagonal in the 4×4 mating scheme) leading the authors to conclude that the method of selection permitted the development of elite lines with higher SCA for specific crosses and with higher GCA with other nonspecific mates. Stangland *et al.* (1983) also found highly significant s_{ij} effects, ranging from -0.88 to 1.05 t/ha in crosses involving S_2 lines from four different populations arranged in six crosses according to the Design-II.

Although the mean squares for SCA have been shown to be less important than GCA as a source of variation, the s_{ij} effect may turn out to be an important component in the single cross mean. Table VII includes the components of means for the ten best single crosses for ear yield. In all crosses, except for $D_{19} \times F_5$, the \hat{s}_{ij} 's were positive and had values as high as 0.416 kg/plot (10.4% of the single cross mean). Hoegemeyer and

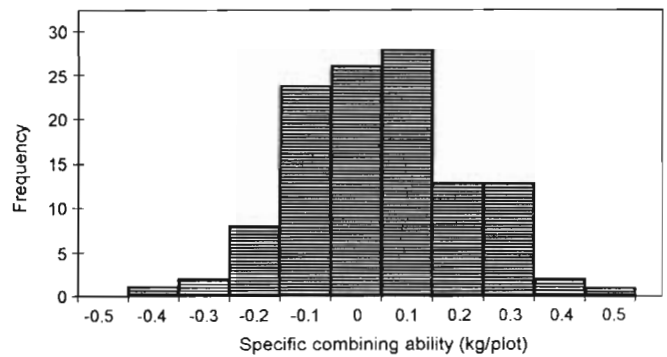


Figure 2 - Frequency distribution of specific combining ability for ear yield in single crosses.

Hallauer (1976) also found that specifically mated crosses (diagonal in their mating scheme) yielded 4.2% more than nonspecific crosses and that in the former most of the specific effects were positive. Their results clearly indicated that \hat{s}_{ij} may contribute to increase the yield of the outstanding hybrids. Although the lines used in this project were not previously selected for combining ability, the positive estimates of the s_{ij} 's in the outstanding crosses may lead to a similar conclusion.

The use of a reduced model to predict the mean of single crosses that were not directly evaluated would increase the range of information for the set of inbred lines to identify outstanding crosses. The reduced model does not include the SCA effect, which implies that SCA is not an important source of variation for an

Table VI - Maximum (upper) and minimum (lower) estimates of general combining ability (\hat{g}_i , \hat{g}_j) and specific combining ability (s_{ij}) for ear yield (TE) in each set.

Set	\hat{g}_i		\hat{g}_j		\hat{s}_{ij}				
	Line	kg/plot	g/pl	Line	kg/plot	g/pl	Cross	kg/plot	g/pl
1	D ₁	0.204	8.16	F ₅	0.636	25.44	D ₅ × F ₅	0.270	10.80
	D ₄	-0.199	-7.96	F ₄	-0.358	-14.32	D ₂ × F ₅	-0.339	-13.56
2	D ₈	0.245	9.80	F ₉	0.418	16.72	D ₇ × F ₇	0.363	14.52
	D ₉	-0.125	-5.00	F ₇	-0.493	-19.72	D ₁₀ × F ₁₀	-0.285	-11.40
3	D ₁₃	0.332	13.28	F ₁₁	0.349	13.96	D ₁₃ × F ₁₄	0.287	11.48
	D ₁₁	-0.273	-10.92	F ₁₂	-0.435	-17.40	D ₁₅ × F ₁₄	-0.241	-9.64
4	D ₁₉	0.277	11.08	F ₅	0.372	14.88	D ₁₆ × F ₁	0.325	13.00
	D ₁₆	-0.488	-19.52	F ₄	-0.321	-12.84	D ₁₈ × F ₁	-0.422	-16.88
5	D ₂₂	0.203	8.12	F ₉	0.396	15.84	D ₂₃ × F ₇	0.284	11.36
	D ₂₁	-0.170	-6.80	F ₈	-0.303	-12.12	D ₂₁ × F ₉	-0.244	-9.76
6	D ₂₉	0.370	14.80	F ₁₁	0.334	13.36	D ₂₉ × F ₁₄	0.416	16.64
	D ₃₀	-0.280	-11.20	F ₁₃	-0.239	-9.56	D ₂₉ × F ₁₂	-0.307	-12.28

Table VII - Components of the best single cross means (TE) over all sets.

Single crosses	TE kg/plot	kg/plot				%			
		$\hat{\mu}$	\hat{g}_i	\hat{g}_j	\hat{s}_{ij}	$\hat{\mu}$	\hat{g}_i	\hat{g}_j	\hat{s}_{ij}
D ₁ × F ₅	4.256	3.164	0.204	0.636	0.252	74.3	4.8	14.9	5.9
D ₅ × F ₅	4.026	3.164	-0.044	0.636	0.270	78.6	-1.1	15.8	6.7
D ₁₃ × F ₁₄	4.014	3.199	0.332	0.197	0.287	79.7	8.3	4.9	7.1
D ₂₉ × F ₁₄	3.983	3.098	0.370	0.099	0.416	77.8	9.3	2.5	10.4
D ₁₈ × F ₅	3.845	3.268	0.067	0.372	0.138	85.0	1.7	9.7	3.6
D ₁₉ × F ₅	3.810	3.268	0.277	0.372	-0.107	85.8	7.3	9.8	-2.8
D ₂ × F ₂	3.712	3.164	0.191	0.188	0.169	85.2	5.1	5.1	4.6
D ₃ × F ₅	3.708	3.164	-0.152	0.636	0.060	85.3	-4.1	17.2	1.6
D ₁₇ × F ₁	3.677	3.268	0.207	0.112	0.091	88.9	5.6	3.0	2.5
D ₁₀ × F ₉	3.664	3.024	-0.033	0.418	0.256	82.5	-0.9	11.4	7.0

effective prediction of cross performance. Although it has been emphasized that specific effects may be important in some crosses, it was also shown in the analysis of variance that the mean squares for SCA were smaller than for GCA. A direct measure of the effectiveness of the reduced model to explain the total variation is by means of the coefficient of determination (R^2) (Table VIII). For TE, SE, and SG, R^2 varied from 0.73 to 0.90, which ensures a fairly high level of confidence in predicting means with the reduced model. Table IX includes the predicted means for ear yield (TE) for nine single crosses selected on the basis of the three highest values of \hat{g}_i and \hat{g}_j . The predicted means varied from 121.9% to 134.3% of the check mean. Among the selected single crosses, only one (D₁₉ × F₅) was among those directly evaluated; its predicted mean was slightly higher than the observed mean because a negative SCA was detected in that cross (Table VII). The selected crosses shown in Table IX represent a selection intensity of 9/450, because 450 is the total number of possible single crosses with 30 dent and 15 flint lines.

The method used herein for the evaluation of inbred lines is adequate when two sets of lines are available, so that the factorial arrangement (Design-II) may be feasible. If we have N lines (random sample) from each source, it can be partitioned into n sets of k lines (N = nk). The sample of lines should be random to permit the random distribution of lines within sets and random combination between sets. The total number of possible crosses is $N^2 = n^2k^2$. The sets are combined randomly, forming n sets of k × k crosses; therefore, nk^2 single crosses are evaluated directly in yield trials, which will provide information on GCA of all lines and SCA of the nk^2 single crosses. They also allow the analysis of variance to infer on the magnitude and

Table VIII - Coefficients of determination relative to the reduced model[#] for 10 traits in six sets of single crosses.

Traits	Set 1	Set 2	Set 3	Set 4	Set 5	Set 6
TE	0.862	0.838	0.904	0.822	0.797	0.793
SE	0.841	0.834	0.731	0.807	0.731	0.885
SG	0.792	0.868	0.729	0.771	0.767	0.888
PH	0.882	0.893	0.968	0.898	0.854	0.933
EH	0.943	0.898	0.983	0.901	0.865	0.949
TB	0.719	0.900	0.816	0.737	0.896	0.698
ED	0.913	0.768	0.870	0.854	0.631	0.931
CD	0.922	0.922	0.842	0.778	0.932	0.693
MF	0.883	0.831	0.971	0.864	0.898	0.855
FF	0.806	0.892	0.987	0.786	0.872	0.679

[#]Reduced model: $\hat{Y}_{ij} = \hat{\mu} + \hat{g}_i + \hat{g}_j$. For abbreviations see Table I.

Table IX - Predicted mean yield (TE) of the best single crosses over all sets.

Single crosses	Reduced model			Predicted mean			
	$\hat{\mu}$	\hat{g}_i	\hat{g}_j	kg/plot	g/pl	t/ha	%
D ₂₉ × F ₅	3.116	0.370	0.636	4.122	164.9	8.24	134.3
D ₁₃ × F ₅	3.116	0.332	0.636	4.084	163.4	8.17	133.1
D ₁₉ × F ₅	3.116	0.277	0.636	4.029	161.2	8.10	131.3
D ₂₉ × F ₉	3.116	0.370	0.418	3.904	156.2	7.81	127.2
D ₁₃ × F ₉	3.116	0.332	0.418	3.866	154.6	7.73	126.0
D ₁₉ × F ₉	3.116	0.277	0.418	3.811	152.4	7.62	124.2
D ₂₉ × F ₁₁	3.116	0.370	0.349	3.835	153.4	7.67	125.0
D ₁₃ × F ₁₁	3.116	0.332	0.349	3.797	151.9	7.59	123.7
D ₁₉ × F ₁₁	3.116	0.277	0.349	3.742	149.7	7.48	121.9

$\hat{\mu}$: Estimated mean, weighted by the number of crosses in each set.
 %: Percent of the check mean (3.069 kg/plot), weighted by the number of check plots in each set.

significance of variation due to GCA and SCA, and also on the effectiveness (R^2) of the reduced model for prediction of single cross means. With nk^2 observed means it will be possible to predict the remaining $n(n-1)k^2$ crosses; the accuracy of prediction will depend on the relative importance of SCA and also on the precision of means used for prediction. For example, with 50 inbred lines from each source, we would have 2,500 possible single crosses. Using 10 sets of 5×5 crosses, then 250 single crosses will be experimentally evaluated; this represents 10% of the total number of crosses, or a proportion of $1/n$. The remaining $(n-1)/n$ (2,250 in the example) will be predicted with the reduced model. For selecting the best hybrid cross, the selection intensity will be $1/N^2$ or $1/n^2k^2$.

The inbred lines from each population were unrelated in the sense that they came from different S_0 plants. There are other lines, however, that are related to them to some extent, with common ancestors in S_1 , S_2 , and S_3 generations. So once the best single crosses are identified based either on observed or predicted means, or both, it is possible to include in the second stage of evaluation the relatives of the selected lines in crosses guided by specific selected pairs. Hence, if the outstanding cross $D_1 \times F_5$ has some other relative inbred lines, say D_{1a} , D_{1b} ,... and F_{5a} , F_{5b} ,..., the maximization of the genetic effects in the single cross would be attained by evaluating those relative lines in a partial diallel or Design-II mating scheme, i.e., $[D_{1a}, D_{1b}, \dots] \times [F_{5a}, F_{5b}, \dots]$. Further experimental results to evaluate the effectiveness of the proposed scheme would be straightforward.

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RESUMO

Foram utilizadas 30 linhagens de 'Piranão-VD2B' (tipo dentado) e 15 linhagens de 'Piranão-VF1B' (tipo duro) para a obtenção e avaliação de 120 híbridos simples, segundo o delineamento fatorial (dialélico parcial) em seis conjuntos 5×5 . As linhagens tipo duro entraram duas vezes nos cruzamentos, porque cada conjunto foi cruzado com dois conjuntos do tipo dente. A avaliação foi feita em látice balanceado 5×5 para 10 caracteres. Os 10% melhores híbridos produziram de 119% a 138,7% em relação à testemunha (variedade 'Piranão-VD2'). A capacidade geral de combinação (GCA) foi mais importante do que a capacidade específica de combinação (SCA) como fonte de variação, embora o efeito de SCA tenha sido importante em alguns cruzamentos específicos. Os quadrados médios de GCA para

produção foram maiores para linhagens tipo flint do que entre linhagens tipo dente em cinco dos seis conjuntos. Uma alta correlação foi observada entre g_j 's (GCA para linhagens de Piranão-VF1B) estimados em cruzamentos com diferentes conjuntos de linhagens de Piranão-VD2B.

O modelo reduzido $\hat{Y}_{ij} = \hat{\mu} + \hat{g}_i + \hat{g}_j$ foi usado para predição de híbridos simples que não foram incluídos na avaliação. Para os caracteres de produção, os coeficientes de determinação (R^2) relativos ao modelo reduzido variaram de 0,74 a 0,90. O uso do delineamento fatorial para a avaliação de linhagens em cruzamentos e a possibilidade de predição de médias para auxiliar na seleção de híbridos são discutidos.

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