

Analysis of testers with broad and narrow genetic base for topcrosses in popcorn breeding

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ABSTRACT - Three testers (three-way hybrid Zélia, single-cross hybrid IAC 112 and composite CMS 43) were compared in the evaluation of the combining ability of 36 popcorn S_2 families obtained from CMS 43. The performance per se of the families was evaluated in a randomized complete block and in 6 x 6 lattice design when in crossings with testers. Estimates of genetic parameters for grain yield and popping expansion were compared among the two sets of progenies (S_2 families per se and topcrosses). The general and specific combining abilities were estimated following Griffing's partial diallel model. The heterosis of each topcross was evaluated in relation to the performance per se of testers. The discrimination ability of testers was compared through the differentiation and performance index. Correlation estimates were obtained among four sets of means: the S_2 families and the three topcross sets. Results showed that Zélia was the most appropriate tester for both evaluated traits.

Key words: Popcorn, *Zea mays*, combining ability, tester, topcross.

INTRODUCTION

All breeding methods applicable to common maize could also be used for popcorn, including those to obtain hybrids. However, breeders should be aware of the lower vigor of popcorn plants and the double focus of selection - yield interests the producer while the consumer wants a quality product, expressed by the popping expansion index (Zinsly and Machado 1987).

A successful breeding program based on heterosis exploitation results in superior lines that are able to transmit the desirable characteristics to the hybrids. By the traditional method, the value of a line based on its ability to produce

good crosses only becomes apparent at the end of the slow and troublesome process of endogamy. Furthermore, the potential number of hybrids produced in all combinations of a set of lines becomes huge as the number of lines involved increases (Miranda Filho and Viégas 1987). To solve this problem, Davis (1927) suggested the use of topcrosses to assess the combining ability of the lines, crossing them with free pollinating varieties.

The topcross method aims to verify the relative merit of the lines in crosses with a tester to eliminate those that do not perform well. The test is applied in early generations to estimate the line potential in preliminary selfing stages.

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One of the most important decisions to be taken when obtaining the topcross is the choice of the appropriate tester. Theoretical and experimental studies have discussed the genetic base, number and efficiency of the tester, and correlation between the performances of lines assessed by different tester types (Paterniani and Miranda Filho 1987, Souza Junior 1989, Aguilar Moran 1990, Rissi and Hallauer 1991, Troyer 1994, Elias and Carvalho 2000). The research results have helped in the tester choice, but there are still doubts about certain points. Great care must be taken with the choice, because the use of a single tester can influence the expression ability of the characteristics of the test progeny (Aguilar Moran 1990).

MATERIAL AND METHODS

The topcross hybrids and their parents were obtained in Maringá, State of Paraná, Brazil, in the crop season 2000/2001. The topcross assessment experiments were carried out in winter 2001 on the Iguatemi Experimental Farm (FEI/UEM). Three testers (three-way hybrid Zélia, single cross hybrid IAC 112, and composite CMS 43) were compared in the evaluation of the general and specific combining ability of thirty-six S_2 popcorn families obtained from CMS 43, a population synthesized by the National Center for Maize and Sorghum Research (CNPMS) of the Brazilian Agricultural Research Corporation – EMBRAPA. Crosses were performed among the three testers and the 36 S_2 families, in a partial diallel scheme. A triple 6×6 lattice design was used to analyze the topcross derived from each of the testers. Due to plot loss, only thirty families were assessed in a randomized complete block design with three replications. Additionally, the three *per se* testers were included in each lattice block. Each experimental plot consisted of a 3m row, with 0.90m inter-row spacing and a density of five plants per meter.

A 30g grain sample of each material was submitted to constant 280 °C for 130s in order to obtain the popping expansion index data. Grain weight data were corrected to standard 15.5% moisture.

The data obtained in the lattices were submitted to variance analysis, using the linear model $Y_{ijk} = m + t_i + r_j + b_{k(j)} + e_{ijk}$ where Y_{ijk} = value observed of treatment i , in block k , within replication j ; m : general mean of the experiment; t_i = random effect of treatment i , $i = 1, 2, \dots, 36$; r_j = random effect of the replication j , $j=1, \dots, 3$; $b_{k(j)}$ = random effect of block k , within replication j ; e_{ijk} = experimental error associated to the Y_{ijk} observation. For the variance analysis of the data obtained in the parent evaluation experiment the linear model $Y_{ij} = m + t_i + r_j + e_{ij}$ was used, where Y_{ij} : value observed in treatment i within replication j ; m : general mean of the experiment; t_i : random effect of treatment i ; r_j : random effect

of j replication; e_{ij} : experimental error associated to the Y_{ij} observation. Data were analyzed using the software Genes (Cruz 2001). The mean square of the adjusted treatment and mean square of effective error were used for the F test. Whenever necessary, the obtained means were adjusted taking the recovery of the interblock information into consideration. Data were analyzed in randomized complete blocks for the evaluation of the parents and in the case where no efficiency was detected in the lattice design. The components of variance were estimated from the expected least squares, as described by Ferreira Neto (2002). The efficiency of the testers was first examined by the differentiation index (D) proposed by Fasoulas (1983). The Spearman classifying correlation estimate (Steel and Torrie 1980) was used to ascertain the degree of coincidence in the classification of S_2 in function of the applied tester.

The partial diallel was analyzed with adjusted treatment means, using the model proposed by Griffing (1956) adapted by Geraldi and Miranda Filho (1988). The pq hybrid combinations were evaluated, where p indicates the S_2 families (Group 1) and q the testers (Group 2). The adopted statistical model was $Y_{ij} = m + g_i + g_j + s_{ij} + e_{ij}$ where Y_{ij} : mean value of the hybrid combination between the i^{th} parent of group 1 and the j^{th} parent in group 2; m : general mean; g_i : general combining ability (GCA) effect of the i^{th} parent of group 1; g_j : GCA effect of the j^{th} parent of group 2; s_{ij} : specific combining ability (SCA) effect among parents of order i and j , of the groups 1 and 2, respectively; e_{ij} : mean experimental error. The effect of the S_2 families was considered random and the effect of the testers fixed.

The estimate of the relative heterosis of each topcross hybrid was obtained according to Ferreira Neto (2002) by the expression $h_{ij}(\%) = 100 \left[\frac{(\bar{S}_i - \bar{S}_{ij})}{\bar{S}_{ij}} \right]$ where h_{ij} : heterosis of the i^{th} family cross with the tester j ; \bar{S}_i : mean of each *per se* tester and \bar{S}_{ij} : mean of the topcross of the family i with tester j .

RESULTS AND DISCUSSION

The estimates of the coefficient of variation for grain yield and popping expansion varied from 19.69 to 23.23% and from 11.90 to 14.20%, respectively. These coefficients were relatively uniform and of acceptable size.

Table 1 shows that the genetic variance among topcrosses with Zélia was superior to that detected with the other testers for both traits. The heritability estimate values for grain yield and popping expansion were quite high. The proportionality between the genetic variation coefficient magnitude and the h^2 values was the expected. The estimates of genetic variance for popping expansion and grain yield

Table 1. Estimates of the genotypic (σ_G^2) and phenotypic (σ_P^2) variances among families S_2 x testers and S_2 *per se* families, genetic coefficient of variation (CV_g) and heritability ($h^2\%$) and its confidence interval (CI) for grain yield and popping expansion

Estimates	Topcrosses			Families S_2 <i>per se</i>
	Zélia	IAC 112	CMS 43	
Grain yield (kg ha ⁻¹)				
σ_G^2	88028.16	80972.03	68988.81	220132.05
σ_P^2	92722.27	118019.72	115002.32	227465.14
CV_g	49.23	18.48	16.42	69.18
$h^2\%$	94.94	68.61	59.99	96.78
CI(95%) of h^2	(90.58-97.16)	(41.61-82.36)	(25.57-77.52)	(93.75-98.23)
Popping expansion (mL g ⁻¹)				
σ_G^2	25.84	6.75	6.55	34.47
σ_P^2	27.98	8.97	7.80	35.39
CV_g	26.99	14.09	15.41	44.60
$h^2\%$	92.35	75.25	83.97	97.40
CI(95%) of h^2	(85.74-95.64)	(54.00-85.95)	(70.14-90.88)	(94.95-98.57)

for the topcrosses involving Zélia and IAC 112 were superior to the σ_G^2 values detected in the topcrosses with CMS 43. This result suggests that the release of variability was greater when using an unrelated tester than when the population itself was used as tester.

The combining ability estimates of the assessed genotypes were obtained by a partial diallel. Means in the partial diallel were 1247 kg ha⁻¹ for grain yield and 17.833 mL g⁻¹ for popping expansion. The effect of all variation sources was highly significant, indicating that there were differences among families and testers for both combining abilities.

Table 2 shows a large variation among the S_2 families in relation to their respective values of the g_i estimates, coherently with the high significance for the GCA effect within group I. Except for family 3, the families with greater GCA for grain yield were not the same as those that performed well for popping expansion. Progenies 3, 14 and 15 were outstanding in specific attributes and had positive GCA values for both traits. Regarding the testers, the CMS 43 GCA was slightly superior to that detected in IAC 112 for grain yield and both were much superior to the Zélia GCA. The results for popping expansion were inverse to those detected for grain yield.

There was a great variability in the topcross SCA estimates for each S_2 cross x tester (Table 3). No S_2 progeny was outstanding with more than one tester, at the same time.

The study of the tester discrimination ability showed that Zélia presented a superior D value to that of the IAC 112 and CMS testers, suggesting that Zélia discriminated more contrasts (Tables 4 and 5). When the results for grain yield in Tables 3 and 4 are compared, the families with greater GCA were generally among those with greater means when crossed with the 3 testers.

The findings for grain yield were also observed for popping expansion by comparing the results in Tables 2 and 5. Families 3, 21, 33, 15, 5, and 14 occupied the best positions when crossed with the testers (Table 5) and showed the greatest GCA (Table 2).

Families 3 and 7 were classified similarly for grain yield when crossed with Zélia, IAC 112, and CMS 43 (Tables 4 and 5). However, several families received variable classification with different testers. The coincidence among the testers for S_2 family classification was quantified by the Spearman classifying correlation coefficient (Table 6).

The Spearman classifying correlation showed that the association between the family *per se* and the topcross performance was practically nil for grain yield in all cases, and very low for popping expansion. Results suggest that the additive component of the topcross genetic variance was expressive in both traits, although accompanied by appreciable levels of dominance, especially in grain yield.

Table 2. Estimates of the general combining ability (GCA) effects associated to groups I and II for grain yield and popping expansion, according to the model by Griffing (1956)

Families	GCA effects		Families	GCA effects	
	Grain yield	Popping expansion		Grain yield	Popping expansion
1	-238.134	-2.743	19	-4.373	-0.010
2	-152.091	-2.450	20	-275.934	-3.373
3	695.743	7.504	21	-437.416	5.640
4	21.180	-5.740	22	52.693	1.857
5	-133.044	3.680	23	-323.148	-4.253
6	174.259	1.547	24	-13.752	0.260
7	464.310	-1.030	25	-76.704	0.770
8	-103.047	1.904	26	-113.178	1.950
9	-185.269	1.417	27	-214.560	3.014
10	-60.592	-1.693	28	-266.088	0.350
11	-162.840	-6.140	29	441.670	-1.210
12	-91.770	-2.543	30	405.122	-1.163
13	-85.482	1.190	31	-243.447	0.967
14	409.413	2.837	32	196.763	-2.807
15	104.234	4.040	33	-171.309	4.260
16	-7.589	-2.120	34	180.374	0.660
17	46.626	-2.966	35	-17.839	1.024
18	226.227	-1.696	36	-41.100	-2.940

Standard error (SE)

Grain yield

Popping expansion

 $SE(G_i)$

97.364

0.779

 $SE(G_i - G'_i)$

139.647

1.117

GCA effects associated to group II

Testers

Grain yield

Popping expansion

Zélia

-644.540

0.983

IAC 112

292.414

0.447

CMS 43

352.127

-1.430

 $SE(G_i)$

23.274

0.186

 $SE(G_i - G'_i)$

40.313

0.322

Table 3. Estimates of the specific combining ability (SCA) effects of each S_2 cross x tester and estimates of the standard error for grain yield and popping expansion

Group I (S_2)	Group II (testers)					
	Grain yield			Popping expansion		
	Zélia	IAC 112	CMS 43	Zélia	IAC 112	CMS 43
1	-100.991	177.885	-76.894	-3.473	2.333	1.140
2	-44.257	42.692	1.565	-1.426	2.040	-0.613
3	39.903	-294.354	254.450	5.550	-2.044	-3.507
4	-278.903	275.804	3.098	-5.336	1.730	3.607
5	-20.961	45.418	-24.457	3.244	-2.360	-0.883
6	163.380	-40.906	-122.474	1.107	-3.827	2.720
7	-40.549	172.653	-132.104	1.814	-0.180	-1.633
8	-45.469	228.890	-183.421	0.080	-0.444	0.363
9	-73.893	84.031	-10.138	-1.693	3.243	-1.550
10	-227.010	-99.749	326.759	-6.183	3.953	2.230
11	496.191	-395.060	-101.131	-0.536	1.060	-0.523
12	404.845	-136.813	-268.032	0.797	0.263	-1.060
13	192.331	-123.318	-69.013	0.794	-0.400	-0.393
14	-136.723	272.149	-135.426	-2.313	2.753	-0.440
15	45.421	-508.057	462.636	1.284	-0.980	-0.303
16	-1.502	-7.873	9.375	-0.956	1.640	-0.683
17	171.499	115.656	-287.156	0.150	1.286	-1.437
18	-354.476	272.757	81.720	-1.250	0.216	1.033
19	320.885	-292.374	-28.512	0.264	0.529	-0.793
20	149.700	-185.113	35.413	2.027	-4.337	2.310
21	10.932	29.132	-40.064	0.084	-0.180	0.097
22	-139.980	340.080	-200.102	1.597	-0.937	-0.660
23	-152.228	327.462	-175.235	-10.093	5.043	5.050
24	-253.737	-240.264	494.001	4.394	-3.070	-1.323
25	-47.831	-94.232	142.063	0.954	-3.250	2.297
26	-4.535	-76.673	81.208	1.504	-0.890	-0.613
27	70.343	392.476	-462.819	1.770	0.176	-1.947
28	-13.813	10.876	2.937	0.174	0.440	-0.613
29	275.617	18.689	-294.306	1.194	-0.400	-0.793
30	-34.253	156.371	-122.118	1.147	-0.977	-0.170
31	326.435	-506.800	180.365	0.617	-0.047	-0.570
32	-295.358	86.043	209.315	-0.270	-0.404	0.676
33	-99.887	8.269	91.619	-0.676	-0.400	1.077
34	-105.841	-79.872	185.713	1.464	-1.200	-0.263
35	116.344	92.726	-209.070	4.730	-2.104	-2.627
36	-311.626	-68.605	380.231	-2.536	1.730	0.807
Standard error (SE)	Grain yield			Popping expansion		
SE	137.693			1.101		
SE	238.492			1.908		
SE ($S_{ij} - S_{kj}$)	197.490			1.580		
SE ($S_{ij} - S_{kl}$)	193.332			1.546		

Table 4. Tester discrimination ability according to the D index and P performance test (Fasoulas 1983) for topcross hybrids grain yield, based on Duncan's test (0.05)

Order	Zélia			IAC 112			CMS 43		
	S ₂	Grain yield	P	S ₂	Grain yield	P	S ₂	Grain yield	P
1	3	1338.368	34	14	2221.238	21	3	2549.582	25
2	29	1320.008	34	7	2176.638	19	15	2166.259	12
3	7	1026.482	26	30	2101.168	16	24	2079.638	6
4	30	973.591	25	18	2038.659	12	32	2005.467	4
5	6	940.361	25	29	2000.034	10	34	1965.475	3
6	11	936.073	25	3	1941.065	6	36	1938.611	3
7	19	919.235	23	22	1932.449	6	7	1931.595	3
8	12	915.797	23	4	1836.660	5	18	1907.336	3
9	14	875.412	21	32	1822.482	5	30	1882.393	3
10	17	820.847	21	27	1717.591	2	14	1873.375	3
11	15	752.377	20	17	1701.957	2	10	1865.555	2
12	13	709.571	17	6	1673.029	2	29	1746.753	1
13	35	701.227	14	8	1665.519	2	25	1664.748	0
14	31	685.711	13	34	1640.178	1	6	1651.174	0
15	34	677.254	11	35	1614.563	1	4	1623.667	0
16	16	593.631	10	23	1543.990	1	16	1601.174	0
17	22	515.436	4	16	1524.214	1	26	1567.419	0
18	32	504.128	4	1	1479.426	1	19	1566.504	0
19	26	485.008	2	5	1452.050	0	31	1536.306	0
20	25	478.187	2	9	1438.437	0	33	1519.698	0
21	20	476.488	2	2	1430.277	0	22	1451.980	0
22	18	474.473	2	36	1430.061	0	2	1448.862	0
23	27	458.504	2	10	1379.335	0	13	1444.894	0
24	8	454.205	2	33	1376.635	0	5	1441.888	0
25	5	448.717	2	25	1368.739	0	9	1403.982	0
26	2	406.374	2	26	1349.824	0	35	1372.480	0
27	4	344.999	0	13	1330.876	0	20	1358.868	0
28	9	343.559	0	12	1311.093	0	17	1358.859	0
29	24	335.234	0	24	1285.660	0	28	1336.237	0
30	33	331.525	0	28	1284.463	0	11	1335.417	0
31	28	322.820	0	19	1242.929	0	8	1312.920	0
32	10	315.119	0	15	1135.853	0	1	1284.360	0
33	1	263.597	0	21	1131.392	0	12	1239.586	0
34	36	250.087	0	20	1078.629	0	21	1121.908	0
35	21	176.237	0	11	981.776	0	23	1101.006	0
36	23	127.347	0	31	789.429	0	27	922.009	0

D = 20.91 (Zélia) D = 6.45 (IAC 112) D = 3.88 (CMS 43)

Table 5. Tester discrimination ability, according to the D index and P performance test (Fasoulas 1983) for popping expansion of the topcross hybrids, based on Duncan's test (0.05)

Order	Zélia			IAC 112			CMS 43		
	S ₂	Expansion	P	S ₂	Expansion	P	S ₂	Expansion	P
1	3	31.867	35	14	23.866	28	21	22.133	27
2	5	25.733	26	3	23.733	27	33	21.733	27
3	35	24.567	21	21	23.733	27	6	20.666	19
4	21	24.533	21	9	22.933	19	3	20.400	19
5	15	24.133	20	33	22.133	19	15	20.133	18
6	27	23.600	19	27	21.466	14	25	19.466	15
7	24	23.467	19	15	21.333	12	5	19.200	13
8	33	22.400	13	10	20.533	9	14	18.800	12
9	22	22.267	13	8	19.733	4	8	18.666	10
10	26	22.267	13	5	19.600	4	26	17.733	6
11	6	21.467	12	26	19.333	3	22	17.600	5
12	34	20.933	11	22	19.200	3	27	17.466	4
13	8	20.800	11	31	19.200	3	13	17.200	3
14	13	20.800	11	13	19.066	3	23	17.200	3
15	25	20.533	11	23	19.066	3	10	16.933	3
16	31	20.400	11	28	19.066	3	31	16.800	3
17	7	19.600	7	19	18.800	3	34	16.800	3
18	14	19.333	7	1	17.866	2	9	16.266	2
19	28	19.333	7	2	17.866	2	28	16.133	2
20	19	19.067	7	16	17.800	2	18	15.733	1
21	29	18.800	6	34	17.733	2	19	15.600	1
22	30	18.800	6	35	17.200	1	20	15.333	1
23	9	18.533	6	7	17.066	1	24	15.333	1
24	20	17.467	6	36	17.066	1	30	15.066	1
25	12	17.067	5	18	16.800	1	1	14.800	1
26	17	16.000	3	29	16.666	1	35	14.800	1
27	18	15.867	3	17	16.600	1	29	14.400	1
28	16	15.733	3	30	16.133	1	4	14.266	1
29	32	15.733	3	6	16.000	1	32	14.266	1
30	2	14.933	3	12	16.000	1	36	14.266	1
31	36	13.333	2	25	15.800	1	7	13.733	1
32	1	12.600	2	24	15.466	1	16	13.600	1
33	11	12.133	2	32	15.066	1	2	13.333	1
34	10	10.933	1	4	14.266	1	12	12.800	0
35	4	7.733	0	11	13.200	0	17	12.000	0
36	23	4.467	0	20	10.566	0	11	9.733	0

D = 20.91 (Zélia) D = 6.45 (IAC 112) D = 3.88 (CMS 43)

Table 6. Spearman classifying correlations data for grain yield and popping expansion: (a) in the classification of the S₂ families according to the tester analyzed and (b) between the family *per se* and the topcross performance

Traits	(a)				(b)	
	Grain yield		Popping expansion		Grain yield	Popping expansion
	Zélia	IAC 112	Zélia	IAC 112		
CMS 43	0.40	0.34	0.69	0.68	0.26	0.16
Zélia	-	0.34	-	0.50	0.18	0.45
IAC 112					0.01	0.22

Table 7 shows that the topcross heterotic mean for grain yield was negative for all testers. This result had been expected because it would be unlikely that the topcross could surpass the performance of a bred variety or of commercial hybrids. Family 3 with cross CMS 43 was the only true heterotic topcross detected for grain yield. Family 15 presented an exceptional *per se* yield, but this performance was usually not repeated when crossed with the testers. The heterosis values for popping expansion were generally positive for the topcrosses with CMS 43 and negative for the topcrosses with Zélia and IAC 112, possibly because of the low endogamic depression of the S₂ families and the popping expansion in *per se* CMS 43. Families 3, 7, and 30 had a better *per se* performance. The families involved in the most heterotic topcrosses (3 and 7 for grain yield, 3 and 21 for popping expansion) are those with greatest GCA, possessing, therefore, a greater frequency of favorable alleles.

Theoretically, a tester is considered to be useful when the results of its crosses are useful to identify the best evaluated families. The adoption of this agreement criterion for ranking suggested again that, for grain yield, Zélia was a better tester than CMS43 which, in turn, was superior to IAC 112. The results in Table 7, however, did not identify superiority of one tester over the others, which is why this criterion was not suitable for the choice of a tester for greater popping expansion.

In general terms, several authors (Rawlings and Thompson 1962, Comstock 1964, Allison and Curnow 1966) have indicated that the recessive homozygote lines and populations with low favorable allele frequencies in important loci are the most effective testers to discriminate lines in hybrid maize programs and population breeding by recurrent selection. In the present case, the fact that CMS 43 presented a greater GCA than the other testers for grain yield (Table 2) suggests that its favorable allele frequency is relatively high, and does therefore not present best conditions as a good tester for this trait. Furthermore, the ability of CMS 43 to

discriminate topcross means was lower than that obtained with Zélia, for both grain yield and for popping expansion (Tables 4 and 5). This finding is important because the best tester is the one that, when crossed with the families, can classify them coherently with the GCA of these same families. Thus the lower discrimination of CMS 43 also impaired its qualification as a really useful tester for grain yield assessment of future lines.

The D index was adequate for information on grain yield, coinciding with the GCA. CMS 43 was not the best tester because it was practically limited to identifying the best family (progeny 3). The superiority of Zélia as a tester was justified by its ability to identify four out of six best families and because the families not identified by Zélia (14 and 18) were not outstanding for GCA.

The results for popping expansion are not as clear as those for grain yield, where Zélia had lower GCA and greater D values. IAC 112 was the worst tester because it only identified three out of the five families with greater GCA. The choice of the best tester for popping expansion between Zélia and CMS 43 seems to be more difficult, because in this case it is likely that Zélia strongly influenced the GCA of these five best families.

The greater GCA of Zélia for popping expansion indicated its greater favorable allele frequency, daunting its prospects as a good line tester for popcorn quality. However, the merits of Zélia were effective for the crucial point of the discussion: the accuracy level of the tester in the material classification. Furthermore, the use of Zélia as tester for popping expansion was more advantageous in practically all aspects: variability among topcrosses, heritability, coefficient of genetic variation, ability to discriminate the topcross hybrids and the Spearman correlation for a comparison among the performances of the *per se* families and the performance of their topcrosses. Regarding this latter criterion, the Spearman classifying correlation for CMS 43 was almost three times lower than the Zélia coefficients. This confirmed

Table 7. Estimate of heterosis percentage in relation to the testers *per se* and mean of the S₂ families and the topcross hybrids in each cross, for grain yield and popping expansion

Family	Grain yield				Popping expansion			
	S ₂	Zélia	IAC 112	CMS 43	S ₂	Zélia	IAC 112	CMS 43
1	265	-88.02	-50.17	-46.19	2.40	-57.08	-34.56	5.71
2	704	-81.50	-51.82	-39.31	7.70	-48.91	-34.56	-4.29
3	747	-39.04	-34.60	6.83	21.80	8.31	-12.87	45.71
4	1043	-84.33	-38.14	-31.98	8.40	-73.77	-47.79	1.43
5	898	-79.59	-51.08	-39.61	20.80	-12.47	-27.94	37.14
6	1379	-57.18	-43.63	-30.80	7.00	-27.11	-41.18	47.86
7	649	-53.26	-26.68	-19.07	21.30	-33.24	-37.50	-1.43
8	676	-79.32	-43.90	-45.01	18.50	-29.16	-27.57	33.57
9	241	-84.37	-51.55	-41.20	14.40	-36.99	-15.44	15.71
10	843	-85.65	-53.54	-21.84	6.50	-62.87	-24.63	21.43
11	750	-57.36	-66.95	-44.05	6.20	-58.45	-51.47	-30.00
12	167	-58.31	-55.83	-48.07	16.80	-42.10	-41.18	-8.57
13	815	-67.70	-55.19	-39.48	17.80	-29.16	-30.15	22.86
15	2481	-65.74	-61.76	-9.22	15.30	-17.57	-21.32	44.29
16	435	-72.98	-48.65	-32.90	10.00	-46.53	-34.56	-2.86
17	302	-62.64	-42.69	-43.08	15.40	-45.50	-38.97	-14.29
19	953	-58.13	-58.15	-34.37	18.40	-35.29	-30.88	11.43
20	203	-78.31	-63.68	-43.08	7.10	-40.74	-61.40	10.00
21	277	-91.98	-61.89	-53.02	12.20	-16.55	-12.87	58.57
22	407	-76.54	-34.91	-39.19	22.50	-24.39	-29.41	25.71
23	879	-94.21	-48.01	-53.86	13.40	-84.67	-30.15	22.86
24	120	-84.74	-56.70	-12.87	20.30	-19.96	-43.38	10.00
25	573	-78.22	-53.91	-30.26	14.10	-30.18	-41.91	39.29
26	991	-77.90	-54.55	-34.33	8.20	-24.05	-29.04	26.43
27	605	-79.13	-42.15	-61.36	4.90	-19.62	-21.32	24.29
28	389	-85.33	-56.74	-44.01	14.20	-33.92	-30.15	15.71
29	290	-39.86	-32.61	-26.82	12.00	-35.97	-38.60	3.57
30	1268	-55.67	-29.21	-21.12	21.20	-35.97	-40.44	7.14
32	228	-77.04	-38.61	-15.97	4.80	-46.53	-44.85	1.43
33	759	-84.92	-53.64	-36.34	10.80	-23.71	-18.38	55.00
Mean*	678.16	-72.63	-48.70	-34.39	13.16	-36.14	-33.15	17.52
Material	Means <i>per se</i> *							
	Grain yield				Popping expansion			
S ₂	678				13.16			
Zélia	2195				29.36			
IAC 112	2968				27.20			
CMS 43	2386				14.00			

* The means of the S₂ families *per se* and the average heterosis were calculated from 30 observations

the observations that when using CMS 43 as a tester, a lower identity was obtained between the classification of the best *per se* families and the classification of its best topcross hybrids.

Results of the present study showed that family 3 best joined favorable alleles for the two assessed characteristics grain yield and popping expansion and that it could be selected as a tester for new progenies extracted from CMS 43, Zélia, and IAC 112.

CONCLUSIONS

Generally, the performance of the topcross families varied with the tester and their *per se* performance did not permit a performance prediction for the hybrid combinations. However some progenies were outstanding both *per se* and in hybrid combinations.

The criterion used to define the best tester for each

trait was based on the results of the different genetic and phenotypic parameters for grain yield and popping expansion, especially of the heterosis levels, correlation between family performance and their respective topcross, the Fasoulas D differentiation index, and combining abilities. Results indicated that the most appropriate tester for grain yield and popping expansion was the triple hybrid Zélia, given its greater discriminatory ability, its indexes and the greater release of variability when using an unrelated tester than that observed when the population itself was used as tester. However, our conclusion should be handled carefully, since data were obtained at a single location. Performance data from more than one location or year shall be provided in further research.

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Análise de testadores de base genética ampla e restrita para topcrosses em melhoramento de milho-pipoca

RESUMO - Três testadores (híbrido triplo Zélia, híbrido simples IAC 112 e composto CMS 43) foram comparados na avaliação da capacidade combinatória de 36 famílias S_2 de milho-pipoca provenientes de CMS 43. As famílias foram avaliadas em blocos ao acaso por seu desempenho *per se* e em látice 6 x 6 quando em cruzamentos com os testadores (topcrosses). Foram comparadas entre si as estimativas dos parâmetros genéticos para rendimento e capacidade de expansão de grãos referentes aos dois conjuntos de progênies (famílias S_2 *per se* e topcrosses). As capacidades de combinação geral e específica foram estimadas segundo o modelo de dialelo parcial de Griffing. Avaliou-se a heterose dos topcrosses em relação aos testadores *per se*. A capacidade de discriminação dos testadores foi avaliada através do índice de diferenciação e desempenho. Foram estimadas as correlações entre o desempenho médio das famílias e dos três conjuntos topcrosses. Os resultados indicaram Zélia como o testador mais apropriado para ambos os caracteres avaliados.

Palavras-chave: Milho pipoca, *Zea mays*, capacidade combinatória, testador, topcross.

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