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Efficiency of circulant diallels as compared to complete diallels for the estimation of combining ability

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ABSTRACT - *The efficiency of circulant and complete diallels was compared regarding the estimation of the general (GCA) and specific (SCA) combining ability. Maize population ear yield data from a 28 x 28 diallel were used. The circulant diallels were formed by resampling data from the complete diallel. Each circulant diallel was represented by s crosses per parent, and s by an odd number between 3 and 25. A thousand circulant diallels were generated for each s value. Estimators for genetic parameters were defined to study the diallels' efficiency. GCA and SCA estimates from the circulant diallels were close to those from the complete diallel, except for a few of the parents (s=3). Best results in terms of selecting parents and hybrid combinations were obtained with s=19. The feasibility of using circulant diallels depends on the genetic background of the populations as well as on the goals of the breeding program.*

Key words: combining ability, diallel analysis, simulations by resampling, genetic breeding.

INTRODUCTION

In breeding programs, it is necessary to use adequate methodologies to deal with phenotypic data in order to correctly interpret the estimates of genetic parameters and hence, rank the genotypes correctly. Diallel crossing is a widely used method by which the performance of a group of parents can be evaluated on an individual basis and also in hybrid combinations, and in addition one can study the gene action determining the quantitative traits (Cruz and Regazzi 2001). This method can be used at the beginning, middle, or final stages of a breeding program.

A limiting aspect for the use of diallel crosses is the

multitude of parents that have to be evaluated in some cases. An alternative would be to evaluate only a sample of these parents in a so-called circulant diallel scheme. The circulant diallel proposed by Kempthorne and Curnow (1961) deserves special attention because it allows the use of a reduced number of parents, although questionable estimates of GCA and SCA may result when the number of crosses per parent (s) is too small (Cruz and Regazzi 2001).

Kempthorne and Curnow (1961) mentioned that more detailed studies concerning statistical, economical, and genetic aspects of circulant diallel crosses are needed. Quite a bit of research has been done dealing with these issues (Murty and Anand 1966, Murty et al. 1967, Anand and Murty

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1969, Bray 1971, Dhillon and Singh 1978, Veiga et al. 2000, Fuzzato 2003). Nevertheless, the circulant diallel scheme is a method seldom used in breeding programs because many breeders still have doubts concerning its efficiency when compared to a complete diallel.

The main goal of the present study was to compare GCA and SCA estimates obtained from circulant and complete diallels. We used data from a complete diallel to simulate circulant diallels by resampling techniques.

MATERIAL AND METHODS

The circulant diallels were generated by resampling data (mean ear yield in tons ha^{-1}) from a complete diallel conducted by Pacheco (1997) at Embrapa Maize and Sorghum, in Sete Lagoas, State of Minas Gerais, in 1992/93. This complete diallel had p = 28 open-pollinated maize populations and their respective 378 F_1 hybrids.

We simulated circulant diallels with all possible odd **s** values (from s=3 to s=25), following the algorithm proposed by Kempthorne and Curnow (1961). We used method 2, model 1, for fixed effects, proposed by Griffing (1956), given by

$$Y_{ij} = m + g_i + g_j + s_{ij} + \varepsilon_{ij}$$

Y_{ij} is the observed mean where i=j denotes the parent and $i \neq j$ denotes the hybrid, with i, j = 1, 2,..., p in the complete diallel and, i = 1, 2,..., p and j = k+i, k+i+1, ..., k+i-1+s in the circulant diallels, with k = (p + 1 - s)/2. The overall mean is m; g_i and g_j are the general combining ability (GCA) effects; s_{ij} the specific combining ability (SCA) effect; and ε_{ij} the non-observable experimental random error. Restrictions in the parameters of the model are necessary in order to obtain unique solutions for the estimators (see for example Cruz and Regazzi 2001), which results in the following estimators: $\hat{m} = 2Y_{..} / p(p-1)$ or $\hat{m} = 2Y_{..} / p(s+2)$, the overall mean of the complete or circulant diallels, respectively. The GCA effect of the ith parent in the complete diallel is $\hat{g}_i = [Y_{ii} + Y_{i.} - 2Y_{..}/p]/(p+2)$; with $\hat{g}_i$ for circulant diallels given by the equations (in matrix notation) $A\hat{G} = \hat{Q}$, where $\hat{G}$ is the p x 1 vector of GCA estimators, whose i[th] element is given by $\hat{Q}_i = 2Y_{ii} + \sum_{j(i) \neq i} Y_{ij} - (s+2)\hat{m}$. The p x p matrix A from the circulant diallel has the elements $a_{ii} = s+4$, $a_{ij} = 1$ for $j = k+i, k+i+1, ..., k+i-1+s$ ($1 \leq j \leq p$) and $a_{ij} = 0$ when the cross ij is not present; $\hat{s}_{ij} = Y_{ij} - \hat{m} - \hat{g}_i - \hat{g}_j$ is the SCA of the ith parent with itself.

Kempthorne and Curnow (1961) defined an algorithm that allows the establishment of a genetically balanced circulant diallel. That is, every parent participates in **s** crosses. With p parents it is possible to obtain $p!/2$ circulant diallels for every value of s. In our study, we randomly generated 1000 circulant diallels for each one of the 12 considered s values and hence a total of 12 thousand circulant diallels were generated.

The following estimators ($\hat{\theta}$), mainly associated to GCA, were used in our study to compare the estimates obtained from circulant diallels to those obtained from complete diallels: $\hat{g}_i$; $\hat{m}$; $\hat{V}_g = \sum_{i=1}^{p} \hat{g}_i^2 / (p-1)$; $R^2 = SSGCA / (SSGCA + SSSCA)$ the coefficient of determination of the GCA sums of squares, and r, the Pearson correlation coefficient among the 28 estimates from complete and circulant diallels.

Let $\hat{\theta}_{(b)}$ be the estimator of parameter θ obtained with the bth circulant diallel, for b=1,2,...,B, with B=1000 for each value of s. Also, consider $\hat{\theta}$ one the previously defined estimators obtained with a circulant diallel and let θ be the parameter value or reference value, the value obtained from the complete diallel (s=27). The bootstrap methodology establishes that $\hat{E}(\hat{\theta}) = \bar{\hat{\theta}} = \sum_{b=1}^{B} \hat{\theta}_b / B$ and $\hat{\sigma}_b^2 = \sum_{b=1}^{B} (\hat{\theta}_b - \bar{\hat{\theta}})^2 / (B-1)$ are, respectively, the estimators of the mean and variance of the genetic parameter estimators ($\hat{\theta}$).

These estimators were used to establish an s value that would provide reliable estimates of GCA in circulant diallels. For this purpose we defined two criteria: An acceptance limit (AL) given by $-1 \leq z \leq 1$, where $z = (\theta - \bar{\hat{\theta}})/\hat{\sigma}_b$, was defined for each estimator, and $r \geq 0.90$ was considered an acceptable value.

For s=19 we obtained reasonable estimates and hence chose this value to conduct an additional simulation study in which we calculated the following estimators: evaluation of relative importance of GCA and SCA given by $2\hat{\phi}_g /(2\hat{\phi}_g + \hat{\phi}_s)$, where $\hat{\phi}_g$ and $\hat{\phi}_s$ are the respective quadratic components of GCA and SCA, expressed by $\hat{\phi}_g = (MSGA - MSE)/(P+2)$ and $\bar{\phi}_g = p - 1/s(P+2)(MSGCA - MSE)$ for the complete and circulant diallel, respectively, and $\bar{\phi}_s = (MSSCA - MSE)$ for both diallel types; the Pearson correlation coefficient (r) and the coincidence coefficient between $\hat{g}_i$, and $\hat{s}_{ii}$ and the $\hat{s}_{ij}$, obtained with the circulant and complete diallel; Pearson correlation coefficient (r) between the hybrid mean values (predicted and non predicted) from the circulant diallel with the ones from the complete diallel.

The predicted hybrid mean values are those from the non-evaluated crosses and are given by $\hat{Y}_{ij} = \hat{m} + \hat{g}_i + \hat{g}_j$ (Cruz and Regazzi 2001), and the non-predicted means are those obtained from the evaluated crosses.

The resampling procedures and statistical analyses were all performed on software Genes (Cruz 1997).

RESULTS AND DISCUSSION

In diallel analysis, the classification and characterization of the parents based on the GCA ($\hat{g}_i$) estimates yields information on the concentration of genes whose effects are predominantly additive. This method has been widely used to select parents for breeding programs (Cruz and Regazzi 2001).

Table 1 presents the z statistic values for the GCA estimates. Based on our acceptance limit (AL), we observe that even with s=3, the most extreme reduction, most s values were considered acceptable, with the exception of $\hat{g}_6$, $\hat{g}_8$, $\hat{g}_{12}$, $\hat{g}_{15}$, $\hat{g}_{16}$, $\hat{g}_{17}$, and $\hat{g}_{28}$, for which the smallest acceptable s values were 11, 7, 5, 7, 7, 7, 11 and 5, respectively.

As aforementioned, we use the method of Kempthorne and Curnow (1961) for parents assumed to have fixed effects. When we establish s crosses for a parent (circulant diallel) there is a conceptual conflict, because this in fact implies a random effect for the parents, since we use a sample of s crosses among the p-1 possible ones. Hence, this might explain the observed differences among the acceptable s

Table 1. Statistical z values of the 28 estimates of GCA obtained in 1000 circulant diallels for each value of s, considering the variable ear yield of maize (t ha^{-1})

s	z_1	z_2	z_3	z_4	z_5	z_6	z_7	z_8	z_9	z_{10}	z_{11}
3	0.311	-0.085	0.081	-0.746	-0.324	-2.105	0.781	-1.445	-0.910	0.958	0.889
5	0.139	-0.043	0.078	-0.615	-0.323	-1.540	0.589	-1.096	-0.629	0.791	0.588
7	0.112	-0.061	0.078	-0.426	-0.209	-1.277	0.480	-0.915	-0.597	0.631	0.547
9	0.017	-0.083	0.142	-0.332	-0.232	-1.000	0.409	-0.714	-0.536	0.444	0.492
11	0.015	-0.068	0.140	-0.300	-0.172	-0.867	0.368	-0.676	-0.532	0.487	0.417
13	0.007	-0.056	0.086	-0.208	-0.206	-0.741	0.275	-0.563	-0.344	0.379	0.402
15	-0.015	-0.023	0.081	-0.163	-0.129	-0.642	0.173	-0.410	-0.348	0.245	0.341
17	0.000	-0.057	0.055	-0.192	-0.075	-0.407	0.155	-0.416	-0.280	0.290	0.296
19	0.025	-0.068	0.100	-0.154	-0.011	-0.349	0.141	-0.332	-0.217	0.204	0.286
21	-0.003	-0.057	0.062	-0.117	-0.019	-0.318	0.192	-0.311	-0.251	0.148	0.259
23	0.047	-0.077	0.000	-0.023	0.054	-0.201	0.137	-0.199	-0.196	0.089	0.179
25	0.036	0.000	0.022	0.000	0.070	-0.114	0.110	-0.096	-0.181	0.112	0.146

s	z_{12}	z_{13}	z_{14}	z_{15}	z_{16}	z_{17}	Z_{18}	z_{19}	z_{20}	z_{21}	z_{22}
3	-1.342	-0.326	-0.020	1.664	1.359	-1.483	-0.551	0.326	0.508	2.097	0.217
5	-0.983	-0.184	0.061	1.238	1.040	-1.041	-0.452	0.280	0.364	1.575	0.144
7	-0.818	-0.191	-0.012	0.967	0.803	-0.845	-0.336	0.251	0.252	1.262	0.083
9	-0.631	-0.190	0.060	0.790	0.691	-0.697	-0.259	0.228	0.200	1.023	0.165
11	-0.578	-0.170	0.031	0.684	0.650	-0.606	-0.206	0.190	0.157	0.836	0.096
13	-0.415	-0.182	0.067	0.557	0.561	-0.577	-0.257	0.186	0.186	0.660	0.080
15	-0.330	-0.183	0.081	0.442	0.513	-0.513	-0.193	0.134	0.147	0.654	0.042
17	-0.261	-0.117	0.010	0.349	0.381	-0.330	-0.152	0.111	0.136	0.527	-0.049
19	-0.274	-0.065	0.000	0.263	0.345	-0.320	-0.146	0.127	0.057	0.454	0.035
21	-0.217	-0.072	-0.011	0.192	0.338	-0.213	-0.115	0.144	0.072	0.418	0.047
23	-0.234	-0.070	-0.024	0.153	0.259	-0.169	-0.107	0.114	0.023	0.329	0.097
25	-0.120	-0.024	-0.041	0.128	0.133	-0.181	-0.141	0.074	0.037	0.246	0.000

s	z_{23}	z_{24}	z_{25}	z_{26}	z_{27}	z_{28}
3	0.485	0.335	0.997	-0.287	-0.045	-1.150
5	0.385	0.238	0.809	-0.244	-0.048	-0.797
7	0.356	0.172	0.640	-0.168	-0.034	-0.648
9	0.242	0.133	0.484	-0.156	-0.030	-0.547
11	0.310	0.107	0.419	-0.129	-0.041	-0.453
13	0.201	0.079	0.382	-0.118	0.001	-0.382
15	0.161	0.103	0.316	-0.099	0.048	-0.335
17	0.125	0.092	0.176	-0.002	-0.035	-0.289
19	0.057	0.064	0.170	-0.100	-0.016	-0.262
21	0.015	-0.017	0.190	-0.130	0.000	-0.191
23	0.057	0.029	0.104	-0.085	-0.003	-0.243
25	0.031	0.040	0.019	-0.099	-0.003	-0.156

s = number of crossings per parent
Acceptance limit for the statistic z is $-1 \leq z \leq 1$.

values for GCA estimation for some of the parents. Many references in literature cite adaptations of this method to fixed effect models for the estimation of GCA and SCA (see Dhillon and Singh 1978, Silva et al. 1999).

We conclude that the parents involved in a diallel may require different s values for acceptable GCA estimates. Using a minimum s value for a circulant diallel may result in biased GCA estimates when compared to the estimates obtained in the complete diallel. Consequently, the breeder will rank the parents incorrectly (Bray 1971). In our simulation, we observed that the sample variance of the estimators () increased with the decrease in the s values.

Table 2 presents the mean estimates of the overall diallel mean ($\hat{m}$) and also the mean values of the variances of the GCA estimates ($\hat{v}_g$). Results for the estimator indicate the s=19 as an acceptable value based on the AL. S values smaller than 19 yield $\hat{m}$ estimates that are smaller in the mean than the overall diallel mean and hence do not represent the p-1=27 possible crosses for each parent. On the other hand, results presented in Table 2 show that the estimates of $\hat{v}_g$ and correlation (r) that did not seem to vary much with the reduction in the s values. We observed that s=3 did not result

in reliable estimates for all the g_i, although for these parameters, s=3 only estimated GCA well.

A high correlation between GCA estimates of circulant (with s=3) and complete diallels was observed by Veiga et al. (2000) when heritability was higher than 50%. The authors used both simulated and real data reported in the literature. With real experimental data reported in the literature, the same authors mention that the proportion of GCA estimates from a circulant diallel that were contained in the corresponding confidence interval, obtained from a complete diallel, were approximately 50% with 28 parents and 70% with 18 parents, when the heritability was 39.28% and 63.11%, respectively.

Results presented in Table 2 show that larger s values are related to larger dominance effects represented by the SCA. Hence, a reduction in the number of hybrid combinations increases the R^2 value. This result means that the smaller the s value, the smaller is the variability among the evaluated hybrid combinations. For this parameter, s=15 was the acceptable limit.

In a simulation study, Pederson (1972) concluded that circulant diallels yield good estimates of heritability. Results by other authors (Bray 1971, Dhillon and Singh 1978) showed that when a small number of crosses was used, the

Table 2. Estimates associated to $\hat{m}$, $\hat{v}_g$, R^2 and r for the variable ear yield (t ha^{-1}), obtained by different numbers of crosses (s) for a set of 28 parents of maize based on 1000 simulations

s	$\hat{m}$ Mean	$\hat{\sigma}$	z	$\hat{V}_g$ Mean	$\hat{\sigma}$	z	R^2 Mean	$\hat{\sigma}$	z	r Mean	$\hat{\sigma}$
3	8.609	0.071	3.739	0.414	0.044	-0.797	0.695	0.041	-3.220	0.928	0.016
5	8.699	0.061	2.870	0.408	0.040	-0.722	0.653	0.036	-2.475	0.945	0.013
7	8.752	0.051	2.403	0.401	0.039	-0.567	0.628	0.033	-1.973	0.956	0.012
9	8.784	0.044	2.031	0.394	0.035	-0.426	0.609	0.029	-1.553	0.966	0.009
11	8.806	0.037	1.820	0.391	0.031	-0.403	0.598	0.026	-1.329	0.973	0.008
13	8.821	0.033	1.584	0.389	0.029	-0.344	0.591	0.023	-1.195	0.979	0.006
15	8.836	0.029	1.287	0.386	0.025	-0.289	0.583	0.021	-0.924	0.984	0.004
17	8.845	0.026	1.104	0.384	0.023	-0.232	0.579	0.019	-0.825	0.988	0.004
19	8.852	0.023	0.926	0.382	0.019	-0.178	0.574	0.015	-0.686	0.991	0.003
21	8.860	0.019	0.727	0.380	0.016	-0.107	0.571	0.013	-0.591	0.994	0.000
23	8.866	0.015	0.535	0.379	0.013	-0.052	0.568	0.010	-0.424	0.996	0.000
25	8.869	0.010	0.391	0.379	0.009	0.003	0.565	0.007	-0.273	0.998	0.000
27	8.874			0.379			0.563			1.000	
AL		$-1 \leq z \leq 1$			$-1 \leq z \leq 1$			$-1 \leq z \leq 1$			

Mean = $\hat{E}(\hat{\theta}) = \bar{\bar{\theta}} = \sum_{b=1}^{B} \hat{\theta}_b / B$; $\hat{\sigma} = \left[\sum_{b=1}^{B} (\hat{\theta}_b - \bar{\bar{\theta}})^2 /(B-1) \right]^{1/2}$; $z = (\theta - \bar{\bar{\theta}})/\hat{\sigma}$; AL = Acceptance limit;

$\hat{\theta}$ = Estimates associated to $\hat{m}$, $\hat{v}_g$, R^2, and r, for s from 3 to 25; θ = Estimates associated to $\hat{m}$, $\hat{v}_g$, R^2, and r for s = 27

heritability values are less reliable because the estimates tend to be farther away from the parametric values. Results reported in the literature concerning the number of crosses per parent (s) in circulant diallels are quite different. Anand and Murty (1969) mention that s should not be smaller than half the number of parents (p). However, they also state that if p is large, this rule does not apply and s < p/2 is acceptable. Bray (1971) did not find an optimal s value but concluded that more than eight or ten crosses per parent are unnecessary. According to Veiga et al. (2000), the estimation efficiency of GCA and SCA effects in a circulant diallel increases with the increase in s up to s=p/2, independently of the heritability value.

Miranda Filho and Vencovsky (1999) is an original paper dealing with partial circulant diallels. Many other quality studies concerning the s value are available. Miranda Filho (1995), cited by Fuzzato (2003), concluded that s=4 gave a good precision to the GCA estimates. According to Fuzzato (2003), for s ≥ 5 values it provided good estimates as much of GCA as of SCA, mainly when one works with heterotic groups.

In the present study, s=19 was found to be the smallest reasonable value based on the acceptance limit. It is important to mention that Veiga et al. (2000) found higher Spearman correlation coefficients for SCA than for GCA at every s value investigated, when estimating correlations between circulant and complete diallel estimates. Hence, s values that yield good estimates for GCA should also yield good or even better SCA estimates.

In an additional simulation (Table 3) study, we compared GCA and SCA estimates, as well as predictions of hybrid combinations, obtained with only one simulated circulant diallel to those from a complete diallel. The ANOVA results (Table 3) show that both additive and non-additive genetic variability are present since GCA and SCA were significant (P < 0.01) in the circulant and also in the complete diallel.

Baker (1978) showed that the total genetic variance among the hybrid combinations is twice the GCA component of variance plus the SCA component of variance. Hence, in a fixed model where ϕ are quadratic components, the relation $2\hat{\phi}_g/(2\hat{\phi}_g + \hat{\phi}_s)$ is also valid to assess the relative importance of GCA and SCA in the hybrid performances when the SCA effects are significant. The non-additive genetic effects were important, with $2\hat{\phi}_g/(2\hat{\phi}_g + \hat{\phi}_s)$ = 0.76 and 0.78 for complete and circulant diallel, respectively (Table 3). This result also shows that the use of a fixed model does not affect the relation between GCA and SCA effects, and a 30% reduction in the number of crosses did not affect the genetic variability among the evaluated parents and hybrid combinations.

Matzinger et al. (1959) suggested that the relation among additive and non-additive effects depends on the population as well as on the variable under study. Pacheco (1997) showed that the relation $\hat{\phi}_g/\hat{\phi}_s$ for the same 28 populations used in this study was greatly altered by environmental effects.

The Pearson correlation coefficient among the 28 GCA estimates from circulant and complete diallels was r=0.99. Additionally, the 20% higher GCA values (six parents) and 10% lower GCA values (three parents) were exactly the same in both diallel schemes.

The SCA estimate of a parent with itself ($\hat{s}_{ii}$) plays an important role when discriminating parents with respect to

Table 3. Analyses of variance of a 28 x 28 complete diallel performed by Pacheco (1997) and of a circulant diallel (s=19) for ear yield (t ha^{-1})

Sources of variation	Complete diallel			Circulant diallel (s = 19)		
	df	MS	F[1]	df	MS	F[1]
Treatments	(405)			(293)		
GCA	27	22.7194	28.1253**	27	18.5016	22.9038**
SCA	378	1.2574	1.5566**	266	1.3141	1.6268**
Error	400	0.8078		400	0.8078	
$\hat{\phi}_g$		0.7304			0.9002	
$\hat{\phi}_s$		0.4496			0.5063	
$2\hat{\phi}_g/(2\hat{\phi}_g + \hat{\phi}_s)$		0.7646			0.7805	

[1]Fixed model
**P<0.01 by F test

varietal heterosis (Cruz and Vencovsky 1989). It is an important parameter in order to discriminate the genetic divergence of a parent with respect to all the others, and to determine the direction of the dominance deviations. A correlation equal to 0.97 among the $\hat{s}_{ii}$ values for the two diallels was observed. In addition, only one parent among the six with highest absolute $\hat{s}_{ii}$ value was different from the ones in the complete diallel (coincidence of 83.33%).

One of the main purposes of the $\hat{s}_{ij}$ values is to be of help at the identification of hybrid pair combinations which can produce promising lines and are complementary about contrasting heterotic groups, in order to gain efficiency in breeding programs for obtaining hybrids (Ramalho et al. 1993). The correlation among 266 $\hat{s}_{ij}$ values for circulant and complete diallels was also high (0.99), showing that s=19 brought forth reasonable estimates. When selecting the 20% best, which included the 54 hybrids with highest $\hat{s}_{ij}$ values, the 22 best always included at least one of six parents selected based on the GCA estimates. Of the 22 hybrids with $\hat{s}_{ij}$ values coinciding with the complete diallel, only one was not present in the circulant diallel (coincidence of 95.45%).

Cruz and Regazzi (2001) stated that in breeding programs the most favorable SCA that involves at least one parent with the most favorable GCA value ($\hat{g}_i$) is of interest. However, Pacheco et al. (2002) stated that this rule applies when the $\hat{g}_i$ value of this parent is due to positive effects for both, mean varietal effects and varietal heterosis. It is not possible to estimate all p(p-1)/2 possible SCA effects of the p parents in a circulant diallel. A complete diallel with p=28 yields 378 SCA estimates, and a circulant diallel with s=19 only allow the estimation of 266 SCA effects. Many alternatives have been proposed to deal with this issue, among them the use of mixed models and BLUP prediction (Bernardo 1995, Charcosset et al. 1998).

In general, the mean values of the hybrids in the complete diallel were superior to the predicted ones. The correlation among the means of all hybrids in the circulant diallel (including predicted ones) with the complete diallel

was equal to 0.93. A correlation equal to 0.69 was observed among the predicted hybrids and those in the complete diallel. The GCA effects include dominance deviations but the totality of the SCA effects are not estimated with the GCA. That is, only a small fraction was captured and hence this smaller correlation, compared to the one obtained from both diallels (r=0.99), is an evidence that there is loss in predicting hybrid combinations and also that dominance effects are indeed important.

The use of diallels with a reduced number of hybrid combinations depends on the breeder's interest to evaluate all possible hybrids or not (Miranda Filho and Geraldi 1984). When the lack of resources is a restricting factor for field experiments, as for example with hybrid seeds for oat and common beans, circulant diallels may be an alternative. Prior knowledge of genetic divergence among the populations can be used to select the promising crosses and thus reduce the number of combinations.

In self-pollinating species, Kurek et al. (2001) mention that selection is carried out at more advanced stages of the segregating populations in which pure lines with additive gene effects are already present. In this case, circulant diallels also offer a good alternative.

CONCLUSIONS

1. Circulant diallels are comparable to complete diallels in terms of efficiency to estimate the GCA and SCA effects, but the efficiency depends on the choice of the s value.

2. When genitor effects are considered fixed, small s values may yield non-reliable estimates for the GCA and SCA effects.

3. A 30% reduction in the number of crosses did not affect the choice of the best parents and hybrid combinations when we studied ear yield of maize.

4. The feasibility of using circulant diallels depends on the genetic background of the populations under study and also on the goals of the breeding program.

Eficiência dos dialelos circulantes em relação aos dialelos completos para a estimação da capacidade combinatória

RESUMO - *Comparou-se a eficiência dos dialelos circulante e completo para estimar as capacidades geral (CGC) e específica (CEC) de combinação. Foram utilizados dados de produção de espigas de um dialelo completo de 28 populações de milho. Os dialelos circulantes foram obtidos por reamostragem do dialelo completo, sendo cada um deles representado*

por s cruzamentos ímpares, variando de 3 a 25. Foram gerados 1000 dialelos circulantes para cada valor de s e definidos alguns estimadores.As estimativas de CGC e CEC dos dialelos circulantes foram semelhantes às do dialelo completo, exceto para alguns genitores, para o valor s=3. O dialelo circulante com s=19 permitiu selecionar os melhores genitores e combinações híbridas. Constatou-se que a viabilidade dos dialelos circulantes depende das populações estudadas e do objetivo do programa de melhoramento.

Palavras-chave: capacidade combinatória, análise dialélica, simulações por reamostragem, melhoramento genético.

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