

# Predicting variety composite means without diallel crossing

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## ABSTRACT

Prediction of variety composite means was shown to be feasible without diallel crossing the parental varieties. Thus, the predicted mean for a quantitative trait of a composite is given by:  $Y_k = a_1 \Sigma V_j + a_2 \Sigma T_j + a_3 \bar{V} - a_4 \bar{T}$ , with coefficients  $a_1 = (n - 2k)/k^2(n - 2)$ ;  $a_2 = 2n(k - 1)/k^2(n - 2)$ ;  $a_3 = n(k - 1)/k(n - 1)(n - 2)$ ; and  $a_4 = n^2(k - 1)/k(n - 1)(n - 2)$ ; summation is for  $j = 1$  to  $k$ , where  $k$  is the size of the composite (number of parental varieties of a particular composite) and  $n$  is the total number of parent varieties.  $V_j$  is the mean of varieties and  $T_j$  is the mean of topcrosses (pool of varieties as tester), and  $\bar{V}$  and  $\bar{T}$  are the respective average values in the whole set. Yield data from a  $7 \times 7$  variety diallel cross were used for the variety means and for the "simulated" topcross means to illustrate the proposed procedure. The proposed prediction procedure was as effective as the prediction based on  $Y_k = \bar{H} - (\bar{H} - \bar{V})/k$ , where  $\bar{H}$  and  $\bar{V}$  refer to the mean of hybrids ( $F_1$ ) and parental varieties, respectively, in a variety diallel cross. It was also shown in the analysis of variance that the total sum of squares due to treatments (varieties and topcrosses) can be orthogonally partitioned following the reduced model  $Y_{ij} = \mu + \frac{1}{2}(v_j + v_j) + \bar{h} + h_j + h_j$ , thus making possible an F test for varieties, average heterosis and variety heterosis. Least square estimates of these effects are also given.

## INTRODUCTION

The synthesis of composite varieties to be used as base populations in recurrent selection programs has been recognized as an important procedure in modern maize breeding (Eberhart *et al.*, 1967; Hallauer and Miranda Filho, 1988). The number of possible composites from  $n$  parental varieties,  $N_{co} = 2^n - (n + 1)$ , increases rapidly with increasing  $n$  (Vencovsky and Miranda Filho, 1972). Synthesis and evaluation of all possible composites are not feasible and prediction procedures of their performance has been recommended and used (Eberhart *et al.*, 1967; Vencovsky and Miranda Filho, 1972; Miranda Filho, 1974; Carvalho, 1980; Vencovsky, 1987).

Miranda Filho (1974) provided a review of the applicability of the prediction procedures, and Hallauer and Miranda Filho (1988) presented many aspects of the use of predicted means in maize breeding. Wright (1922), Mather (1949) and Mather and Jinks (1971) provided the basic models for the prediction of means of quantitative traits in controlled crosses. Jenkins (1934) suggested procedures for predicting double-cross performance and Eberhart *et al.* (1967) extended Wright's basic statement for the prediction of composite varieties. Vencovsky (1970) extended the prediction theory to include means of composites where the parental varieties contribute unequally. Miranda Filho and Chaves (1991) emphasized the problem of the large number of possible composites and suggested an index ( $I_j = w_1 v_j + w_2 h_j$ ) as a criterion for selection among parental varieties for the synthesis of new populations; they also showed that  $I'_j = (2/k)I_j$  tends to  $g_j$  (general combining ability effect) by increasing the size ( $k$ ) of the composite.

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## MATERIAL AND METHODS

Eberhart *et al.* (1967) showed that the mean of a composite of  $k$  varieties can be predicted by  $Y_k = H - (H - V)/k$ , where  $V$  is the mean of parental varieties and  $H$  is the mean of the  $k(k-1)/2$  hybrids among them. Gardner and Eberhart (1966) suggested the model  $Y_{jj'} = \mu + \frac{1}{2}(v_j + v_{j'}) + \theta(h + h_j + h_{j'} + s_{jj'})$ , where  $\theta = 0$  for varieties ( $j = j'$ ) and  $\theta = 1$  for hybrids ( $j \neq j'$ ), to represent means in a diallel table. In the model,  $\mu$  is the mean of the  $n$  parental varieties,  $v_j$  is the variety effect,  $\bar{h}$  is the average heterosis,  $h_j$  is the variety heterosis, and  $s_{jj'}$  is the specific heterosis of the cross between varieties  $j$  and  $j'$ . Following the same model, for a given set of  $k$  varieties ( $2 \leq k \leq n$ ) it can be shown that:

$$\bar{V} = \frac{1}{k} \sum_{j=1}^k v_j = \mu + \frac{1}{k} \sum_{j=1}^k v_j \quad \text{and}$$

$$\bar{H} = \frac{2}{k(k-1)} \sum_{j < j'}^k H_{jj'} = \mu + \frac{1}{k} \sum_{j=1}^k v_j + \bar{h} + \frac{2}{k} \sum_{j=1}^k h_j + \frac{2}{k(k-1)} \sum_{j < j'}^k s_{jj'}$$

for a given size  $k$  of the composite ( $k = 2, 3, \dots, n$ ).

By replacing  $V$  and  $H$  in the formula of Eberhart *et al.* (1967), it follows that:

$$Y_k = \mu + \frac{1}{k} \sum_{j=1}^k v_j + \frac{k-1}{k} \bar{h} + \frac{2(k-1)}{k^2} \sum_{j=1}^k h_j + \frac{2}{k^2} \sum_{j < j'}^k s_{jj'} \quad (1)$$

(Miranda Filho and Chaves, 1991)

The estimates of components of means are obtained from the diallel table as follows (Gardner, 1967):

$$\hat{\mu} = \frac{1}{n} \sum_{j=1}^n Y_{jj} = \bar{Y}_v; \quad \hat{v}_j = Y_{jj} - \bar{Y}_v; \quad \hat{h} = \bar{Y}_H - \bar{Y}_v$$

$$\hat{h}_j = \left( \frac{n-1}{n-2} \right) (\bar{Y}_{h.} - \bar{Y}_H) - \frac{1}{2} (Y_{jj} - \bar{Y}_v) \quad \text{and}$$

$$\hat{s}_{jj'} = Y_{jj'} + \frac{n}{n-2} \bar{Y}_H - \left( \frac{n-1}{n-2} \right) (\bar{Y}_{h.} + \bar{Y}_{h'})$$

$$\text{where} \quad \bar{Y}_{h.} = \frac{1}{n-1} \sum_{j \neq j'}^n Y_{jj};$$

$j$  is replaced by  $h$  in  $Y_{h.}$ , indicating that summation is for hybrids, i.e.,  $Y_j = Y_{h.} + Y_{jj}$ .

A more detailed interpretation of the parameters of the diallel cross model is given by Eberhart and Gardner (1966).

It is readily seen that knowledge on individual crosses is required only for estimation of specific heterosis ( $s_{jj'}$ ). Therefore, neglecting

$$\frac{2}{k^2} \sum_{j < j'}^k s_{jj'}$$

in (1), the mean of a composite can be predicted on the basis of the performance of parental varieties, *per se*, and on the average of their crosses.

Formula (1) shows that among the parameters defined in the Gardner and Eberhart (1966) model, the mean ( $\mu$ ) and the average heterosis ( $\bar{h}$ ) are constants in their contribution to the mean of any composite of size  $k$ .

The parameters  $\mu$ ,  $v_j$ ,  $\bar{h}$  and  $h_j$  are estimable without knowledge of individual crosses, on the basis of the reduced model:

$$Y_{jj'} = \mu + \frac{1}{2} (v_j + v_{j'}) + \theta (\bar{h} + h_j + h_{j'}) + \bar{\epsilon}_{jj'}$$

Model 3 (Gardner, 1967).

The mean of the  $j$ th row (or column) in the diallel table is

$$\bar{Y}_j = \mu + \frac{1}{2} \hat{v}_j + \frac{n-1}{n} \bar{h} + \frac{n-2}{n} \hat{h}_j$$

and represents the average of crosses of the  $j$ th variety with the whole set of varieties, including itself. In this paper we suggest the use of the top-cross procedure, using the whole set of varieties as tester, to estimate  $\bar{Y}_j = T_j$ , i.e., the topcross means over  $r$  replications. The parental varieties are included in the experiment and their means are estimated by  $Y_{jj} = v_j$ . Both  $T_j$  and  $\bar{v}_j$  are used to estimate the components of means ( $\mu$ ,  $v_j$ ,  $\bar{h}$  and  $h_j$ ) and to perform the analysis of variance, according to the reduced model of Gardner (1967). The respective formulas were obtained through the least square procedure. The basic model is  $Y = X\beta + \epsilon$ , where  $Y$  is the vector of observations (means of varieties and topcrosses),  $X$  is the matrix of coefficients,  $\beta$  is the vector of parameters, and  $\epsilon$  is the vector representing the error term for the observed means. The estimates are then obtained by  $\hat{\beta} = (X'X)^{-1}X'Y$ .

Yield data from a  $7 \times 7$  variety diallel cross were used for illustration of the proposed methodology (Miranda Filho and Vencovsky, 1984). The values for  $T_j$  were obtained by using the marginal means of the diallel table, i.e., by considering  $T_j = \bar{Y}_j$ , or the average of  $n$  entries [ $j$ th variety and  $(n-1)$  crosses with the remaining ones] represents the mean of the cross between the  $j$ th variety with the set of varieties, including itself. In the example, the original data are

represented by yields of variety and varietal crosses. For comparisons, the analysis of the diallel table is shown for both the complete and reduced models (models 4 and 3 of Gardner, 1967).

## RESULTS AND DISCUSSION

The use of Gardner's (1967) reduced model to explain the means of varieties and varietal crosses, used for prediction of composite means, is supported by: a) specific heterosis seems to be a less important source of variation in varietal diallel crosses (Vencovsky, 1970) and has shown to be nonsignificant in the analysis of variance in most studies (Hallauer and Miranda Filho, 1988); b) the summation  $\sum s_{ij}$  tends to cancel out for increasing  $k$  (size of a composite) and equals zero for  $k = n$  and  $k = n - 1$ , and c) the coefficient  $2/k^2$  tends rapidly to zero by increasing  $k$ . Therefore, reducing the prediction formula (1) by neglecting specific heterosis or taking

$$\frac{2}{k^2} \sum_{j < j'}^k s_{ijj'} = 0, \quad \text{it follows that:}$$

$$Y_k = \hat{\mu} + \frac{1}{k} \sum_{j=1}^k \hat{v}_j + \frac{k-1}{k} \bar{h} + \frac{2(k-1)}{k^2} \sum_{j=1}^k \hat{h}_j \quad (2)$$

From model 3 of Gardner (1967), the estimates of parameters are obtained through the least square procedure, under the following restrictions:  $\sum v_j = \sum h_j = 0$ .

The estimates are:

$$\hat{\mu} = \bar{V}; \quad \hat{v}_j = V_j - \bar{V}; \quad \bar{h} = \frac{n}{n-1} (\bar{T} - \bar{V}); \quad \text{and}$$

$$\hat{h}_j = \frac{n}{n-2} \left[ (T_j - \bar{T}) - \frac{1}{2} (V_j - \bar{V}) \right]$$

A simpler notation was used in the above formulas, so that:

$$V_j = Y_{jj}; \quad \bar{V} = \frac{1}{n} \sum V_j; \quad T_j = \frac{1}{n} \sum_{j \leq j'} Y_{jj'}; \quad \bar{T} = \frac{1}{n} \sum T_j$$

where the observed values (means) are  $V_j$  and  $T_j$ .

The corresponding sources of variation in the analysis of variance are shown in Table I, with their respective sums of squares that represent an orthogonal partition of the treatment sum of squares.

From formula (2), and replacing the parameters by their estimates as functions of  $V_j$ ,  $T_j$ ,  $V$  and  $T$ , it follows that:

$$Y_k = \frac{n-2k}{k^2(n-2)} \sum_{j=1}^k V_j + \frac{2n(k-1)}{k^2(n-2)} \sum_{j=1}^k T_j + \frac{n(k-1)}{k(n-1)(n-2)} \bar{V} - \frac{n^2(k-1)}{k(n-1)(n-2)} \bar{T}; \quad \text{or}$$

$$Y_k = \frac{1}{k(n-2)} \left\{ \frac{1}{k} \left[ (n-2k) \sum_{j=1}^k V_j + 2n(k-1) \sum_{j=1}^k T_j \right] + \frac{n(k-1)}{n-1} (\bar{V} - n\bar{T}) \right\} \quad (3)$$

Using expression (3), the mean of a composite of size  $k$  can be predicted on the basis of the performance of the parental varieties ( $V_j$ ) and their topcrosses ( $T_j$ ). Thus, the prediction procedure, as proposed, will require  $2n$  means (varieties and topcrosses) instead of  $n(n+1)/2$ , as in the original procedure. The reduced number of entries in the experimental trials is particularly important when the number of parental varieties ( $n$ ) is large. For example, for  $n = 20$  the usual prediction procedure based on diallel crosses would require 210 entries in the yield trials, and 40 entries in the proposed procedure. Thus, for the same experimental area, the number of replications could be increased, thus increasing the precision of the estimated means. The relative efficiency of the two procedures is measured as the ratio between the variance of the estimated treatment means for the same experimental area and is  $\lambda = (n+1)/4$ , e.g., for  $n = 7$  the variance of means in the diallel table will be twice as large as the variance of means of varieties and topcrosses in the proposed procedure. In other words, the number of replications ( $r_2$ ) in the topcross procedure should be  $\lambda$  times the number of replications

**Table I** - Analysis of variance\* based on varieties and topcrosses according to the reduced model for diallel crosses.

Source	d.f.	Sums of squares
Populations	$2n - 1$	$\sum_{j=1}^n V_j^2 + \sum_{j=1}^n T_j^2 - \frac{(V. + T.)^2}{2n}$
Varieties	$n - 1$	$\frac{1}{5} \sum_{j=1}^n [2(V_j - \bar{V}) + (T_j - \bar{T})]^2$
Average heterosis	1	$\frac{1}{2n} (V. - T.)^2$
Variety heterosis	$n - 1$	$\frac{1}{5} \sum_{j=1}^n [(V_j - \bar{V}) - 2(T_j - \bar{T})]^2$
Error	$(r-1)(2n-1)$	---

\*Analysis with treatment means over  $r$  replications.

( $r_1$ ) in the diallel, or  $r_2 = \lambda r_1$ ; because  $r_2$  must be an integer, that ratio is exact only for  $n = 3, 7, 11, 15, \dots$

The topcrosses can be obtained in an ordinary isolation block where the parental varieties are planted as female rows (detasseled) and the male rows (pollinator) are represented by a balanced mixture of all varieties. This is the easiest procedure and is based on natural and random pollination; however, unequal pollination among the parental varieties is expected to occur, which would increase the bias of the predicted means. Control of the number of effective male gametes contributed by each parental variety can be obtained partially by using hand pollination and blending samples of pollen collected from the male rows. Control of the number of female gametes is obtained by sampling the same number of ears (mother plants) and kernels per ear of each cross.

Table II shows the means of varieties and crosses (diallel table) and estimated topcross means (marginal means of the diallel table); it also includes estimates of parameters according to both models: diallel (complete model) and topcross (reduced model). It can be seen that the estimates  $\mu$ ,  $\bar{h}$ ,  $v_j$  and  $h_j$  are exactly the same for both models.

The predicted means of some composites of size  $k$  ( $k = 2, 3, \dots, n$ ) are shown in Table III for grain yield, following the two prediction procedures (I: diallel and II: topcross). The difference between the two procedures ( $Y_{kI} - Y_{kII}$ ) decreases by increasing  $k$ , thus increasing the correlation coefficient ( $r_{I,II}$ ). For  $k = n$  and  $k = n - 1$ ,  $Y_{kI}$  and  $Y_{kII}$  have exactly the same value. The average ( $m$ ) of composites of the same size ( $k$ ) is also the same for

Table II - Mean yield of varieties and crosses (diallel table) and estimates of the components of means ( $\mu$ ,  $v_j$ ,  $h$  and  $h_j$ ) under two models.

	1	2	3	4	5	6	7	Estimates*		
								$Y_j = T_j$	$\hat{v}_j$	$\hat{h}_j$
1	4.47	5.08	4.84	5.16	5.52	5.13	4.72	4.989	0.611	0.060
2		4.20	5.33	4.96	5.25	4.70	4.66	4.883	0.341	0.101
3			4.30	5.04	4.95	4.72	3.72	4.700	0.441	-0.225
4				4.22	5.25	4.66	4.20	4.784	0.361	-0.051
5					3.74	4.40	3.98	4.727	-0.119	0.205
6						3.19	3.90	4.386	-0.669	0.112
7							2.89	4.010	-0.969	-0.204
								$\hat{\mu} = 3.8586$		
								$\bar{h} = 0.9114$		

\*Estimates are exactly the same in both procedures.

both procedures, i.e.,  $m_I = m_{II}$  (Table IV). The correlation coefficients ( $r_{I,II}$ ) are also shown in Table IV and varied from 0.9621 for  $k = 2$  to 1.0000 for  $k = 6$ ; the correlation does not apply for  $k = 7$ . Therefore, the equivalence between the two procedures is closer for composites of larger sizes. Miranda Filho and Chaves (1991) showed that within the set of composites of the same size ( $k$ ), the overall mean increases and the variance decreases so that the highest yielding composites should be those with smaller sizes. Nevertheless, composites are particularly useful as base populations for recurrent selection, and in this sense the potential genetic variability must be taken into account. Although it is difficult to predict the genetic variability in the

Table III - Predicted means of some composites for varying sizes ( $k = 2, 3, \dots, 7$ ) under two prediction procedures: diallel (upper) and topcross (lower).

k = 2		k = 3		k = 4		k = 5		k = 6	
#	t/ha	#	t/ha	#	t/ha	#	t/ha	#	t/ha
12	4.708	123	4.830	1234	4.876	12345	4.948	123456	4.836
	4.872		4.903		4.938		4.944		4.836
13	4.613	124	4.810	1235	4.916	12346	4.785	123457	4.698
	4.759		4.954		4.915		4.805		4.698
	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮	⋮
67	3.470	567	3.820	4567	4.176	34567	4.319	234567	4.499
	3.450		3.932		4.217		4.345		4.499
								Composite (1234567) with predicted means:	
								4.640	
								4.640	

#, Number of identification of parental varieties.

**Table IV** - Mean ( $m$ ), variance ( $\sigma^2$ ) and coefficient of correlation ( $r$ ) between predicted means of composites of size  $k$  under two procedures (I: diallel; II: topcross).

$k$	$m_I = m_{II}$	$\sigma_I^2$	$\sigma_{II}^2$	$r_{I,II}$
2	4.3143	0.16758	0.15512	0.9621
3	4.4662	0.09073	0.08639	0.9758
4	4.5421	0.05170	0.05033	0.9866
5	4.5877	0.02831	0.02799	0.9944
6	4.6181	0.01315	0.01315	1
7	4.6398	0	0	1*
Overall	4.5280	0.08352	0.07975	0.9771

\*Actually the correlation coefficient is not estimable.

newly formed population, it is reasonable to assume that, in general, higher genetic variability would result in composites of larger sizes (Miranda Filho and Chaves, 1991). Under a breeding viewpoint, values of  $k \geq 4$  should be acceptable in most cases. Anyway, the greater the number chosen by the breeder, the closer the two procedures will be for predicting means. In addition, the topcross procedure should be particularly useful when the number of varieties (accessions) is too large to permit producing and testing diallel crosses. In some species the synthesis of new populations is guided by previous knowledge of the germplasm to be handled. The germplasm of many species (e.g., forage crops) has not been widely studied and a greater

number of accessions is usually available, making it practically impossible to make crosses in all possible combinations.

We have emphasized the use of the topcross procedure for making predictions of composite means. However, an important aspect to be discussed is that the model and the statistical procedure used herein also allows an analysis of variance where tests of hypothesis are allowed to be made in relation to the effects described for the diallel model (reduced model, excluding specific heterosis). The formulae for the analysis of variance, according to the orthogonal partition of the total sum of squares, are shown (Table I). The complete analysis of variance for the example given is in Table V; for comparison the analyses were performed under the two models: diallel (complete model) and topcross (reduced model). A comparison should be made between the sources of variation that are common to both models, and it is readily seen that the mean squares are different. However, in this example the topcross means were not obtained directly from the experiment, but rather were taken as the marginal means of the diallel table, i.e.,

$$T_j = \frac{1}{n} \sum_{j \leq j} Y_{ij}$$

Therefore, the error associated with the "topcross" mean is not the same as if it had been obtained directly from the experiment. For this reason, a correction factor

**Table V** - Analysis of variance under two models: diallel and topcross.

Source	I. Diallel			II. Topcross			
	d.f.	MS	$F_I$	d.f.	MS	$\beta$	$F_{II}$
Populations*	27	0.422838	9.04**	13	0.386556	0.5553	14.88**
Varieties	6	0.949363	20.29**	6	0.470421	0.9388	10.71**
Heterosis	21	0.272402	5.82**	—	—	—	—
Average heterosis	1	4.361171	93.20**	1	2.136091	0.4898	93.20**
Variety heterosis	6	0.060443	1.29	6	0.011103	0.18367	1.29
Specific heterosis	14	0.071187	1.52	—	—	—	—
Error	498	0.046795		498	0.046795	—	—

\*I - Varieties and crosses. Model:  $Y_{ij} = \mu + \frac{1}{2}(v_i + v_j) + \theta(\bar{h} + h_i + h_j + s_{ij}) + \bar{e}_{ij}$ .

II - Varieties and topcrosses. Model:  $Y_{ij} = \mu + \frac{1}{2}(v_i + v_j) + \theta(\bar{h} + h_i + h_j) + \bar{e}_{ij}$

$F_{II} = M_i / \beta M_e$ ;  $M_i$ : mean squares of several sources;  $M_e$ : error mean square.

$$\beta: \beta_p = \frac{2n^3 + n^2 - 4n + 1}{2n^2(2n-1)}, \beta_v = \frac{4n^2 + 5n - 1}{5n^2}, \beta_{\bar{h}} = \frac{n^2 - 1}{2n^2} \text{ and } \beta_{v_h} = \frac{n^2 - 4}{5n^2}$$

for populations, varieties, average heterosis and variety heterosis, respectively. \*\*Significance level:  $P < 0.01$ .

( $\beta$ ) for the error term must be included for each source of variation in the topcross analysis of variance to make the F tests comparable for the two analyses. After correction, it is shown that the F tests are exactly the same for average heterosis and variety heterosis sources of variation. A difference in the F test appears for the variety effects, although the estimates of variety effects are the same for both models (Table II).

When using the topcross procedure, no correction is necessary if the variety means and the topcross means are obtained directly from the field data, so that in the analysis of variance all sources of variation have the same error term ( $\sigma^2$ ) in the expected mean squares. If the topcross means are not seriously biased by unequal pollination or some other unknown disturbing factor or, in other words, if the topcross means fairly represents the marginal means of the diallel table, then the proposed procedure would be superior to the diallel procedure.

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## RESUMO

Foi demonstrado que a predição da média de compostos pode ser feita sem o cruzamento dialélico das variedades parentais. Assim, a média predita para um caráter quantitativo de um composto é dada por:  $Y_k = a_1 + \Sigma V_j + a_2 \Sigma T_j + a_3 \bar{V} - a_4 \bar{T}$ , com  $a_1 = (n - 2k)/k^2(n - 2)$ ;  $a_2 = 2n(k - 1)/k^2(n - 2)$ ;  $a_3 = n(k - 1)/k(n - 1)(n - 2)$  e  $a_4 = n^2(k - 1)/k(n - 1)(n - 2)$ ; somatório é para  $j = 1$  a  $j = k$ , onde  $k$  é o tamanho do composto (número de variedades de um composto em particular) e  $n$  é o número total de variedades.  $V_j$  e  $T_j$  se referem a médias de variedades e dos seus "topcrosses" (mistura das variedades como testador), e  $\bar{V}$  e  $\bar{T}$  aos seus respectivos valores médios de todo o conjunto. O método de predição proposto mostrou-se eficiente em comparação com a predição baseada em  $Y_k = \bar{H} - (\bar{H} - \bar{V})/k$ , onde  $\bar{H}$  e  $\bar{V}$  se referem às médias dos híbridos ( $F_1$ ) e das variedades parentais, respectivamente, em um cruzamento dialélico de variedades. Também mostrou-se que, na análise da variância, a soma de quadrados total devida a tratamentos pode ser decomposta ortogonalmente de acordo com o modelo reduzido  $Y_{ij} = \mu + \frac{1}{2}(v_j + v_i) + \bar{h} + h_j + h_i$ , assim tornando possível o teste F para variedades, heterose média e heterose de variedades; são apresentadas estimativas de quadrados mínimos desses efeitos. Os dados de produção de um cruzamento dialélico 7 x 7 foi usado para extrair as médias de variedades e as médias simuladas dos "topcrosses" a fim de ilustrar o procedimento proposto.

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