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Modified full-sib selection and estimation of genetic parameters

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Summary. A cycle of full-sib selection is completed in three seasons while that of a modified method is completed in two seasons. In modified full-sib selection, selected families can be recombined and new families generated following a partial-diallel cross. The components of genetic variance can be estimated from the partial-diallel analysis of such families. Thus, in addition to performing selection, genetic parameters can be estimated.

Key words: Partial-diallel cross – Components of genetic variance – *Zea mays* L. – Maize

Introduction

In maize (*Zea mays* L.), full-sib selection is a common method of intrapopulation improvement (Hallauer and Miranda 1981).

A cycle of full-sib selection requires three seasons: season 1 to generate full-sib families, season 2 to evaluate the families, and season 3 to intermate the selected families in order to develop the population for initiating the next cycle of selection. Recently, a modified method was developed wherein the recombination of the selected families and generation of new families were combined. Thus, a cycle of selection can be completed in a year if the facility of an off-season breeding nursery is available. This enhances genetic advance per unit time. Modified full-sib selection was adopted by CIMMYT, Mexico (Anonymous 1974), and is being used extensively by the All-India Coordinated Maize Improvement Project and by others (Compton and Lonnquist 1982; Zorilla and Crane 1982).

The plants in the selected full-sib families are involved in plant-to-plant inter-family crosses, as shown in Fig. 1, assuming that 50 families are selected and 250 families are generated for evaluation in the next cycle of selection. In an optimal crossing plan, $2N_2/N_1$ plants of a selected family are used in crossing where N_1 is the number of families selected and N_2 is the number of families to be generated for evaluation in next cycle (reciprocal crosses are considered equiva-

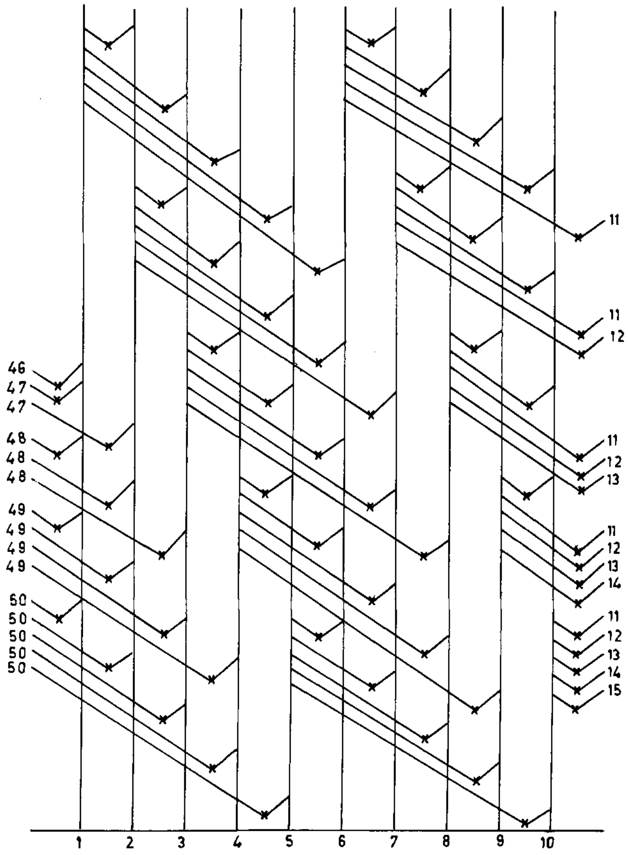

Fig. 1. Schematic representation of the recombination of selected families (50) and generation of new families (250) in modified full-sib selection

lent). Each plant of a family is crossed to a plant from a different family, thus involving a family in cross combinations with $2N_2/N_1$ different families. In practice, however, the crossing plan is modified depending upon performance of selected families, the number of plants available, and the synchronisation of flowering.

Estimation of genetic parameters

The selected full-sib families can be crossed following the partial-diallel cross mating design to generate families for evaluation in the next cycle. Plans of partial-diallel crosses are available (Dhillon 1975; Arya 1983). Some of these have specific requirements with respect to the number of parents (p) and number of crosses per parent (s), but the algorithms given by Kempthorne and Curnow (1961) and Federer (1967) have general applicability. These can easily be used in modified full-sib selection. The families thus generated will offer an additional advantage of being amenable to partial-diallel analysis, thereby providing estimates of components of genetic variance. The genetic parameters thus obtained will provide information about the nature and magnitude of variability in a hypothesized population in linkage equilibrium generated by random mating of the parental full-sib families.

The analysis of the variance of combining ability of a partial-diallel cross can be calculated following Kempthorne and Curnow (1961) and Dhillon (1978). The components of general combining ability (Φ_g^2), specific combining ability (Φ_s^2) and interactions of combining abilities with the environments (Φ_{ge}^2, Φ_{se}^2) can be interpreted in the terms of the genetic variances (Φ_A^2, Φ_D^2, Φ_{AE}^2, Φ_{DE}^2), using the relationships based on covariances between relatives (Kempthorne and Curnow 1961). The relationship of covariance half sibs (Cov HS) and covariance full sibs (Cov FS) with observational components is $\mathrm{Cov(HS)} = \Phi_g^2$, and $\mathrm{Cov(FS)} - 2\,\mathrm{Cov(HS)} = \Phi_s^2$. These covariances in terms of genetic variances, assuming an absence of epistasis, are: $\mathrm{Cov(HS)} = \left(\frac{1+F}{4}\right)\Phi_A^2$, and $\mathrm{Cov(FS)} = \left(\frac{1+F}{2}\right)\Phi_A^2 + \left(\frac{1+F}{2}\right)^2 \Phi_D^2$, where Φ_A^2 is the additive genetic variance and Φ_D^2 is the dominance variance of the population generated from random mating of the parental full-sib families. Similar relationships can be derived for Φ_{ge}^2, Φ_{se}^2, Φ_{AE}^2, and Φ_{DE}^2.

Table 1. Analysis of variance for combining ability of partial-diallel cross and estimates of components of variance for number of ears in maize

Source	df	Mean squares	Estimates of variance components	
GCA	25	0.122**	$\Phi_g^2 = 0.0045 \pm 0.0015$	$\Phi_A^2 = 0.0176 \pm 0.0059$
SCA	130	0.056**	$\Phi_s^2 = 0.0190 \pm 0.0036$	$\Phi_D^2 = 0.0725 \pm 0.0138$
Error	155	0.018		

** Significant at the 0.01 level

To translate observational components into genetic variance, an estimate of F, inbreeding coefficient of full-sib families, in required. This can be worked out following Curnow (1983). If N_1 families are selected in the $(n-1)$th generation for recombination and generation of N_2 families for evaluation in the nth cycle, the inbreeding coefficient in nth generation (F_n) will be $F_n = \frac{1}{8}P + \left(1 - \frac{P}{4}\right)F_{n-1} + \frac{1}{8}PF_{n-2}$, where P is the probability that two full-sib families have a parental full-sib family in common. It is obtained as $P = 2\left(\frac{2N_2}{N_1} - 1\right)/(N_2 - 1)$.

Example

An intrapopulation improvement programme for number of ears was undertaken in a random-mating population of maize, 'Partap'. In the first cycle 140 full-sib families were evaluated and 20 families were selected for recombination. The selected families were involved in plant-to-plant inter-family crosses, as shown in Fig. 1, to recombine the selected families and generate 200 full-sib families. These 200 families were evaluated in the second cycle. Twenty-six families were selected and involved in plant-to-plant inter-family crosses following the algorithm of partial-diallel cross given by Federer (1967), taking $p = 26$ and $s = 12$. The 156 families developed were evaluated in a randomized complete block design with two replications. A plot included one row 6 m long. Row-to-row and plant-to-plant spacings were 75 and 30 cm, respectively. The plots were overplanted and thinned to maintain a perfect plant stand. Data were recorded on number of ears per plant on a plot basis. Analysis of partial-diallel cross was conducted following Kempthorne and Curnow (1961). The standard errors (SE) of various components were estimated using the formula: $\mathrm{SE}(\hat{\sigma}_i^2) = \sqrt{\frac{2}{C^2}\sum\left(\frac{M_i^2}{df_i}\right)}$, where M_i are the mean squares involved in the function, df_i are the corresponding degrees of freedom, and C is the divisor.

The inbreeding coefficient of the population (F_0) was zero. The inbreeding coefficient of the full-sib families evaluated in the first cycle (F_1) was also zero as each of these families was developed by crossing a pair of randomly selected plants in the population. No plant was involved in more than one cross. F and P in the second cycle, to which the parental 26 full-sib families belonged, were calculated as follows:

$P_2 = 2\left(\frac{2 \times 200}{20} - 1\right)/199 = \frac{38}{199} = 0.1910$; and

$$F_2 = \frac{1}{8} \times \frac{38}{199} + 0 + 0 = \frac{19}{796} = 0.0239\,.$$

Analysis of variance indicated significant variation due to general (GCA) and specific (SCA) combining ability (Table 1). Variance components (Φ_g^2) and (Φ_s^2) were derived from the observed and expected mean squares. These variance components were interpretable in terms of Φ_A^2 and Φ_D^2 using the above discussed relationships. The estimates of Φ_A^2 and Φ_D^2 were significant and represented variation in the hypothesized population resulting from random mating of the 26 parental full-sib families. The significance of Φ_A^2 indicated that the population should be amenable to further intra-population improvement.

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