

## A COMPUTER PROGRAMME FOR ANALYSING TWO-LEVEL DIALLEL EXPERIMENTS WITH PARENTS INCLUDED

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### SUMMARY

A computer programme for analysing two-level diallel experiments involving parental lines and one set of F<sub>1</sub>'s is provided in FORTRAN-4 language†.

**Keywords :** Two-level diallel experiments, General and specific combining abilities, Heterosis.

### Introduction

Two-level diallel experiments have been discussed by Hinkelmann [1] where diverse populations (or groups) consisting of inbred lines (individuals) are intermated. Yadav [2] and Yadav and Arya [3] enhanced the scope of these designs by including parental lines which are desirable for studying the heterotic responses of the crosses directly. Such designs furnish information regarding general and specific combining abilities on population as well as on individual levels and the heterosis of the crosses involved.

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†The programme can be obtained from the first author.

In order to make an easy access to these experiments a computer programme written in Fortran-4 language is presented in what follows.

2. Crossing Pattern and the Model

Consider  $M$  diverse populations ( $P_i, i = 1, 2, \dots, M$ ) each consisting of  $N$  homozygous individuals. The  $p$ th individual belonging to  $i$ th population will be denoted by  $I_{ip}$  ( $i = 1, 2, \dots, M; p = 1, \dots, N$ ). The crossing pattern for the design is exhibited in Table 1 for  $M = 3$  and  $N = 4$ , wherein a dash refers to no cross.

TABLE 1—CROSSING PATTERN FOR TWO-LEVEL DIALLEL EXPERIMENT WITH  $M = 3$  AND  $N = 4$

	$P_1$				$P_2$				$P_3$			
	$I_{11}$	$I_{12}$	$I_{13}$	$I_{14}$	$I_{21}$	$I_{22}$	$I_{23}$	$I_{24}$	$I_{31}$	$I_{32}$	$I_{33}$	$I_{34}$
$I_{11}$	X	—	—	—	X	X	X	X	X	X	X	X
$I_{12}$		X	—	—	X	X	X	X	X	X	X	X
$I_{13}$			X	—	X	X	X	X	X	X	X	X
$I_{14}$				X	X	X	X	X	X	X	X	X
				$I_{21}$	X	—	—	—	X	X	X	X
				$I_{22}$		X	—	—	X	X	X	X
		$P_2$		$I_{23}$			X	—	X	X	X	X
				$I_{24}$				X	X	X	X	X
								$I_{31}$	X	—	—	—
								$I_{32}$		X	—	—
						$P_3$		$I_{33}$			X	—
								$I_{34}$				X

Thus the material consists of  $MN + M(M - 1)N^2/2$  crosses including  $MN$  selfs of the type  $I_{ip} \times I_{ip}$  in all the  $M$  populations and  $M(M - 1)N^2/2$  crosses of the type  $I_{ip} \times I_{jq}$  relating to crosses between different populations.

Under the set up of randomized block design with  $R$  replicates, let  $Y_{(ip)(jq)z}$  be the observation on the progeny of a cross  $I_{ip} \times I_{jq}$  in  $z$ th

replicate ( $z = 1, 2, \dots, R$ ). The appropriate linear model for this environmental design is then given by

$$Y_{(i_p)(j_q)z} = u + B_z + G_i + G_j + S_{ij} + g_{i_p} + g_{j_q} + s_{(i_p)(j_q)} + e_{(i_p)(j_q)z}$$

where  $u$  = general mean,  $B_z$  =  $z$ th block effect,  $G_i$  = general combining ability (GCA) effect of population  $P_i$ ,  $S_{ij}$  = specific combining ability (SCA) effect of the population cross  $P_i \times P_j$ ,  $g_{i_p}$  = GCA of individual  $I_{i_p}$ ,  $s_{(i_p)(j_q)}$  = SCA of the cross  $I_{i_p} \times I_{j_q}$ , and  $e_{(i_p)(j_q)z}$  is a random error assumed to be distributed normally with mean zero and variance  $\sigma^2$ .

### 3. The Computer Programme

The programme, written primarily for TDC-16, in Fortran-4 accommodates data for  $M = 3$  populations and  $N = 4$  individuals in each population collected from 4 randomized complete blocks. Change in the values of  $M$ ,  $N$  etc. will require change in dimension and format etc.

#### Input

The following is the order of the data requirements :

(i) First card contains  $M$  (No. of populations),  $N$  (No. of individuals per population) and  $IR$  (No. of replicates) entered each in I3 format.

(ii) Second card carries the title, such as character name and may run from 5th through 80th column. A non-negative number, such as 9999, is punched in first 4 columns.

(iii) Next are the data cards. Observations on  $M \times N$  parental lines are entered first, followed by those on their crosses in exactly the order of Table 1. Thus first 12 entries relate to parents which appear in diagonal position and then row by row accounting for 48 crosses. Hence there are 60 entries in all in one replication which are to be punched in continuation. Data on second replicate should start from fresh card and so on. Observations for another character should be preceded by a corresponding title. Any number of characters can be analysed sequentially for the same experiment or as long as  $N$ ,  $M$  and  $IR$  remain the same. A blank card should follow the data cards to end the compilation.

#### Output

The following is rendered as printed output :

(i) Title.

(ii) Population GCA in sequential order, i.e.,  $G_1, G_2, \dots, G_M$ .

(iii) Population SCA in the following manner,  $S_{11}$  in first line,  $S_{21}, S_{22}$  in second line,  $S_{31}, S_{32}, S_{33}$  in third line and so on.

(iv) Individual GCA in the form of elements of a  $M \times N$  matrix.

(v) Individual SCA with identification of crosses and fresh numbering for further identification in (vi).

(vi) Individual SCA arranged ascendingly with serial number as in (v) for purpose of selecting the extreme crosses.

(vii) Analysis of variance accounting variations for : blocks; treatments = parents + crosses + parents vs crosses; parents =  $P_1 + P_2 + P_3$  + possible contrasts among populations; population GCA; population SCA; individual GCA; individual SCA and error.

(viii) Treatment means in the form of input (iii).

(ix) Standard error of difference between two means.

(x) Standard errors of GCA and SCA estimates for comparing their values against a hypothesized value zero (1) at population level, (2) at individual level.

(xi) Standard errors of the differences between two estimates as in (x).

(xii) Heterotic responses.

1. Best parental mean.
2. Absolute heterosis of crosses over mid-parents for purpose of testing their significance.
3. Percent heterosis over mid-parents as per customary.
4. Identification of crosses showing heterosis over best parent.
5. Standard error of absolute heterosis.
6. Best lower 10% and best upper 10% crosses showing heterosis over mid-parents (arrangement is in ascending order of magnitude) with identification.

The programme has been illustrated with live data on tiller number in wheat (*Triticum aestivum* L.).

#### REFERENCES

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