Theoretical and Applied Genetics 43, 335–336 (1973)

Brief Notices / Kurze Mitteilung

Estimation of Genetic Parameters by Fractionating the Diallel Experiment: A Proposed Computerized Procedure

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After a set of data from an $N \times N$ diallel experiment have been analyzed and the estimates of the various genetic parameters obtained, the investigator often poses one or more of the following questions:

1. Supposing some particular array(s) were eliminated from the original diallel experiment, would the estimates of the genetic parameters be substantially different from those of the original diallel? Elimination of which array(s) resulted in these differences?

2. Supposing the original diallel experiment were divided into two or more sub-diallels according to the relative genetic divergence of the parents, say, as measured by Mahalanobis' D^2-statistic (Lee and Kaltsikes: The application of Mahalanobis' generalized statistical distance to measure genetic divergence in durum wheat. 1973, Euphytica **22**, 124–131), how would the estimates of the genetic parameters compare amongst the sub-diallels and with the original diallel? For instance, the sub-diallels might be grouped such that the genetic divergence amongst the parents within group is less than those between groups, or a sub-diallel could be extracted to include the parents which showed greatest divergence amongst each other.

3. Supposing all possible combinations of R arrays were eliminated from the N-array diallel, i.e. $\frac{N!}{R!\,(N-R)!}$, will the mean of the estimates of each of the genetic parameters significantly differ from those of the original diallel? Furthermore, an investigator may wish to know what is the smallest possible diallel which will give him essentially the same information as those in the original diallel. This he can do by systematically eliminating all possible combinations of arrays from 1 through R, inclusive; that is,

$$\frac{N!}{1!\,(N-1)!},\quad \frac{N!}{2!\,(N-2)!},\cdots,\quad \frac{N!}{R!\,(N-R)!}.$$

The mean and the standard error of the mean for each genetic parameter is calculated at each successive stage. For example, to test whether $\hat{D}_{n-2}$ (the additive genetic variance) obtained from systematically eliminating two arrays is significantly different from that of the original diallel (D_n), the procedure is

$$t = \frac{\hat{D}_{n-2} - D_n}{S\,E_{\hat{D}_{n-2}}} \quad \text{with} \quad \left[\frac{N!}{2!\,(N-2)!}\right] - 1,$$

degrees of freedom.

It is not difficult to visualize that in order to provide information to these questions requires a Herculean task in terms of calculational efforts. For example, systematically eliminating 1 through 5 arrays in a 10-array diallel experiment requires processing the diallel data for the estimation of the various genetic parameters for 637 times! More explicitly,

$$\frac{10!}{1!\,(10-1)!} + \frac{10!}{2!\,(10-2)!} + \cdots + \frac{10!}{5!\,(10-5)!}.$$

Even using a computer program specifically designed to do the diallel analysis (Lee and Kaltsikes, 1972, Crop Science 12: 133) becomes impractical for these analyses since no provision was made to reduce the original N-square matrix of diallel input data into the numerous required sub-matrices for processing. It is then apparent why the analyses of diallel data in the afore-mentioned manner (particularly referenced to question 3) has never been reported in the literature.

We have developed a computer program (Fortran IV, I.B.M. System 360) to handle all of the aforementioned analyses. The program can accommodate data from the F_1, F_2 and F_3 generations with or without reciprocal families. The analysis of the data from the two segregating generations is carried out by considering each filial generation (g) individually as if it were F_1. That is, by taking the effect of the heterozygote, $A\,a$, as $(1/2)^{g-1}\,h = h$. Thus, effect $A\,a$ in $F_1 = h$; $F_2 = h/2$; $F_3 = h/4$. (We have prepared a set of mimeographed copies showing the algebraic derivations of the various genetic parameters for the 3 generations with or without reciprocal families.)

The computer program provides two major options: The first option handles questions (1) and (2). That is, it will process the sub-diallel data with the specified array (s) eliminated from the original diallel and prints out $\hat{D}$, $\hat{F}$, $\hat{H}_1$, $\hat{H}_2$, $\hat{h}^2$, $(\hat{H}_1/\hat{D})^{1/2}$, $\hat{H}_2/4\,\hat{H}_1$,

$(4\hat{D}\hat{H}_1)^{1/2} + \hat{F}/(4\hat{D}\hat{H}_1)^{1/2} - \hat{F}$, and $\hat{h}/\hat{H}_2$ (Hayman, 1954: The theory and analysis of diallel crosses. Genetics **39**, 789—809). It also prints out the narrow-sense heritability estimate, defined as the ratio of additive and/or additive × additive genetic variance to the phenotypic variance (Crumpacker and Allard, 1962: A diallel cross analysis of heading date in wheat. Hilgardia **32**, 275—318). The second option handles question (3). That is, it will process the subdiallel data eliminating R array(s) in all possible combinations and prints out the mean and standard error of each of the above genetic parameters.

The program is extremely easy to use. For example, under option 1, the user merely specifies on the header card(s) which array(s) he wishes to eliminate; under option 2, he need only to specify on the header card(s) how many array(s) he wishes to eliminate — the computer will automatically eliminate the array(s) in all possible combinations. Parenthetically, a word of caution is in order: Option 2 may consume a substantial amount of computer time.

A listing of the source program with the necessary supporting information may be obtained upon request from the first author.

Received October 2, 1972

Communicated by W. Seyffert

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