2. Definitions and basic formulae.

A diallel table is an arrangement in a square of n^2 observations from a set of diallel crosses among n parents, the rows and columns of the square corresponding to the offspring of each parent. The n homozygous parents themselves form the diagonal of the table. It is easy to test whether there are significant differences between the reciprocal crosses, and, whether these exist or not, reciprocals may be averaged so that rows and columns contain the same figures and will be termed arrays.

Following Mather (Mather, K. Biometrical Genetics. Methuen. London. 1949) we suppose that the quantitative character is polygenically controlled and there are in fact g genes represented by more than one allele in the parents. If each gene has just two alleles then for the ith locus we define

$2d_i$ = a difference between the homozygotes

h_i = difference between the heterozygote and the mid-homozygote

$u_i:v_i$ = ratio of numbers of positive and negative homozygotes in the parents

($d_i > 0$; h_i may take sign; $u_i + v_i = 1$; $I = 1,2…g$)

The dominant homozygote is that which deviates from the mid homozygote in the same direction as the heterozygote.

When the g genes have independent actions and are distributed independently in the parents the following statistics may be obtained from the diallel table.

F_1 mean - parental mean, $F_1 - p$ = $\Sigma 2u_i v_i h_i$

Variance of parents, Vp   = $\Sigma 4u_i v_i d_i^2$

Variance of the families of the rth array (including   = $\Sigma u_i v_i (d_i^2 - h_i)^2 + \Sigma 2u_i v_i (d_i + h_i)^2$
the common parent), Vr
and its mean value, V   = $\Sigma u_i v_i (d_i^2 - 2(u_i - v_i)d_i h_i + h_i^2)$

Covariance between the families of the rth array and   = $\Sigma_1 2u_i v_i d_i (d_i - h_i) + \Sigma_2 2u_i v_i d_i (d_I \div h_i)$
their non-recurrent parents, Wr
and its mean value, W   = $\Sigma 2u_i v_i d_i (d_i - (u_i - v_i)h_i)$

which is also the covariance between parents and their offspring means.

Variance of the array means, $V_M = \Sigma u_i v_i (d_i - (u_i - v_i)h_i)^2$ (Σ is over i = 1 … g, $\Sigma 1$ over genes with positive homozygotes in the rth parent, $\Sigma 2$ the negative ditto). There is also an environmental component of these statistics which will be given later.