

## 1. Efficient experiments in multigenetics.

Inbred lines which may be repeatedly crossed in various or all combinations may provide sets of offspring and parents which may be tested year after year and in various situations sufficiently with almost identical genotypes to determine genetic-environment interactions. (Is the degree of dominance the same at all yield levels of corn, or at one intermediate level whether nitrogen, phosphorus or water is the main limiting factor?) Or the test may be repeated simply for more data on a questionable conclusion. Insofar as the parents are homozygous the offspring are of one genotype within one single cross, with no limit on number of such offspring; and dominance occurs only in offspring -- parents are free of it.

Other "constant" parents such as clones and  $F_1$ 's of homozygous lines if they may be often crossed, may also provide sets of offspring and parents with all of the above advantages, except, (1) offspring within one single cross are heterogeneous not homogenous in genotype, (2) parents are heterozygous -- dominance must be counted in the phenotypes of parents -- theoretical offspring-parent regression is much more complex than with homozygous parents.

These latter two points were apparently entirely obscure to Griffing (Gen. 35:303-321. 1950) and his Iowa advisors, or they would not have attempted to introduce the very inappropriate "constant parent regression" for what I have labeled bp in the regression of offspring on homozygous parents.

$F_1 = b_1P_i + b_1P_i - b_2P_iP_j$  is easily established as the theoretical function of Mendelian Multigenetics, with dominance bias. Previous to Hull the 3rd term was ignored in studies of regression of  $F_1$  corn on inbred parents. The general form  $y = ax + bz + cxz$  is a familiar one. Simplifying the analysis by holding either x or z constant must have been a common place in mathematics for more than a hundred years. I have not intended to claim originality for that even though Bruce and his advisors give it first rank over, (1) including the 3rd term of the function i.e. product of parents, and (2) using homozygous parents not just constant parents.

Hayman (Gen. 39:789-809. 1954) has recently stressed the diallel approach as the powerful one, largely ignoring points outlined here above.

I have used diallel data (Hull, MGNL 1946; "Heterosis", Chap. 28, 1952), simply because it was the only data available, and I think satisfactory enough. But we might draw a sample of 45  $F_1$ 's from many homozygous parents with any one parent included more than once being a rarity (nearly 90 parents) and thus obtain greater efficiency in some respects than with a diallel of only 10 parents and 45  $F_1$ 's. Analysis would be to fit the above multiple regression function and estimate k from  $b_1$  and  $b_2$  as before. Partial regression coefficients for specific common parents would be inaccessible directly, but they could be estimated from  $b_1$  and  $b_2$  by commonplace procedures. Sorry I have failed to note before that the diallel is not a bulwark, just incidental, in my approach, which I supposed was obvious.

Without epistasis, but with any variation of dominance from locus to locus, partial regression of offspring on homozygous parent in a set of one common parent is linear in the Mendelian scheme or even with linkage. Hayman (lc. page 795) has introduced non-linearity of partial regression and perhaps other bias by including parents on the diallel diagonal among offspring. This seems to be a very unlikely departure from random sampling. It may simplify the mathematics and the bias may then come out easily enough, but I am presently frustrated, though willing to be shown, if this be true. Anyhow, the partial regressions calculated by Hull from diallel data omitting parent diagonal are theoretically linear except for epistasis, but it is not clear if Hayman means to imply that they are not.