

## BIOMETRICAL GENETICS

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WE are grateful to Professor Falconer for his review of our book *Biometrical Genetics* (*Heredity*, 29, 111) and for the kind things that he has to say. We hope, therefore, that he will not think us unappreciative or ungracious if we comment further on two points that he makes.

The first emerges in the opening paragraph of the review where Professor Falconer says "The subject (of the book) is the analysis of the genetic differences between homozygous strains, and of the variation in segregating generations derived from crosses between the strains". He goes on to say later in the review that "Unfortunately these methods (for studying the properties of genes in crosses between homozygous strains) powerful though they are, are not entirely suitable for the study of randomly breeding populations even if highly inbred strains can be obtained . . .". These and indeed other passages in the review may combine to give the impression that our approach has nothing to offer the study of randomly breeding populations and that we neglect them. This would be a misconception—though not a new one. While it is true that we deal most extensively with crosses among true-breeding lines, where the partitioning of the variation is easier, can be taken further and is more informative, we go on to devote a complete chapter of some 40 pages to the extension of our approach to the analysis chiefly of randomly breeding populations, but also to populations with partial inbreeding. We discuss the analysis of such as human populations, where no experimental tests are possible, as well as populations where experimental breeding methods can be used; we compare the efficiency of experimental methods, originating chiefly from North Carolina, for the partitioning of variation in randomly breeding populations, none of which involves the production of inbred lines or even partial inbreeding; and we comment on the applications of these methods to animals as well as plants, besides using *Tribolium* data for illustrative analyses. True, by the very nature of the problem, the analysis is less penetrating than in crosses between true-breeding lines, but we know of no other approach that would enable it to be taken further. Indeed we believe that our approach, based firmly as it is on the fuller analysis of crosses between inbred lines, permits a clearer perception of the needs of effective experimental design and confident interpretation than do others. And we would claim that our extensions of the approach to cover the analysis and interpretation of maternal inheritance and sex-linkage in randomly mating populations, both natural and experimental, and to deal with populations of haploid organisms is vindication of our view.

The second point on which we would like to comment arises in Professor Falconer's last paragraph, where he expresses some disappointment that we have not discussed the results obtained by applications of our methodology in plant breeding as well as in the general understanding of genetical architecture. Useful applications had indeed been made in plant breeding

and we believe that more will come. We also have views on the genetical architecture of continuous variation and we have written extensively elsewhere on this subject: in fact our fig. 18, which is used to illustrate the properties of effective factors, is taken from such a study of the impact of past selection on the present architecture of a character. To have included such material would have made the book unduly long—as indeed Professor Falconer recognises—and we thank him for the valuable suggestion of writing further on these matters.

In conclusion, may we reiterate our thanks to Professor Falconer for his views and hope that he will not take these further comments amiss, but find them to be of interest and use as we found his?