REVIEW

BIOMETRICAL GENETICS. By K. Mather. London : Methuen, 1949. Pp. ix+162. 18s

Professor Mather commences by reviewing the historical development leading up to the fusion of Biometry and Mendelism in biometrical genetics. Genetics has concerned itself mainly with the study of discontinuous variation, and in the wide variety of instances where the phenotypic classes can be shown to have an obvious correspondence with the inheritance of relatively unchanging and independently assorting units, the success of the Mendelian approach and analysis has been enormous. Prior to the rediscovery of Mendel's work in 1900 genetical investigations had been started by Galton and continued by Pearson. But the concentration on human material with its small families of doubtful ancestry, as well as the choice of quantitative characters, prevented discovery of the method of transmission. Galton and Pearson had shown that some continuous variation was partly inherited and Darwin had stressed the importance of small cumulative changes for the theory of evolution. The problem of continuous variation could not be ignored. With the new recognition of the importance of Mendel's work there was some initial rivalry between the Biometricians and the Mendelians which delayed synthesis of the two approaches. The multiple factor hypothesis, already considered by Mendel, was advocated as early as 1907 by G. U. Yule, and in 1910 by E. M. East ; while Nilsson-Ehle's work (1909-11) on the trifactorial inheritance of grain colour in wheat was a case of special influence in the matter. In 1909 Johannsen showed that both heritable and non-heritable factors contributed to the variation of seed weight in beans, and that the effects were of the same order of magnitude. The stage was then set for the emergence of a polygenic theory of inheritance embodying both the Mendelian basic assumptions and the biometrical or statistical method of analysis. In 1918 an important step forward was made when Professor R. A. Fisher showed how the results of the biometricians, particularly the correlations observed in human families, followed from the new approach ; Fisher also produced evidence of dominance relationships. At this point Mather goes on to discuss in some detail the evidence for polygenic segregation and linkage, and the relation between polygenes and the "major" genes of Mendelian genetics.

In the second chapter, entitled "Characters," the relations between genotype and phenotype in polygenic systems are considered, and a method is described of finding a function of a number of metrical characters which shall be "best" in the sense of being as sensitive as possible to *genetical* variation. This is followed by a chapter devoted to the fundamentally important question of "Scaling." It is obvious that with a metrical character there must be a variety of scales of measurement to choose from. A satisfactory scale will be one for which both the non-heritable effects and the individual genic contributions are additive, or approximately so. Tests are given for the adequacy of a given scale, based on the homogeneity of different estimates of the residual error variance.

A certain amount of statistical knowledge is essential in the treatment of the subject, though it need not be extensive. Mather assumes some acquaintance with both genetics and statistics, but is careful to introduce the mathematics gradually. It is not until the fourth chapter that he embarks upon the fundamental method of analysis developed in 1932 by Fisher, Immer and Tedin. This is a procedure for partitioning the variation in filial and backcross generations into genetic and environmental portions by considering certain functions of means, variances, covariances, etc. This leads on to the question of linkage, which is dealt with in the succeeding chapter. Although linkage does not influence mean values it does affect the second degree statistics. Thus the test for linkage is essentially a test of homogeneity of the genetic components of variation among the available filial and backcross data.

Mather then proceeds to a discussion of the rather more sophisticated concept of "Effective Factors." The actual number of genes operating in a polygenic system is somewhat difficult to arrive at. Its estimate is complicated by the incomplete concentration of "similar" allelomorphs in the parents; by the incomplete reinforcement of "unfixable" components; by the inequality of the genetic increments; and by the presence of linkage. In 1940 Panse devised a method of coping with the first three difficulties; he has also used his analysis to tackle the vitally important problem of the speed of advance under selection. If linkage is very tight or very loose then evidence of its existence may be hard to come by. In ordinary Mendelian genetics the linkage of two genes, previously considered to be a single gene of pleiotropic effect, may be suggested by a single rare instance of recombination. But in biometrical genetics recombination can only be detected if its consequences admit of *statistical* recognition. The upshot is that the biometrical units in terms of which the data are described may easily be not actual genes but a certain number of *effective* factors.

In the final chapter Mather concludes with a discussion of experimental design, and of the general ideas involved in the subject.

Mather's book, which is the first of its kind, will be welcomed by all geneticists as showing just how the basic ideas of Mendelian genetics, so appropriate to discrete variation, can also be used to lay the foundations of a biometrical genetics of quantitative characters. The many worked examples and the references to the literature, including the pioneer work of Mather himself, will be found especially useful. The great value of the book lies in its making more widely known methods of dealing with continuous variation, which is of cardinal importance for a variety of subjects such as: the social consequences of the conditions of inheritance of human intelligence; the theory of evolution; and the practical problems of plant and animal breeding.

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