

SOME GENETIC PROBLEMS IN CONTROLLED POPULATIONS

EVERETT R. DEMPSTER

GENETICS DEPARTMENT, UNIVERSITY OF CALIFORNIA

The titles of this talk and of the succeeding one do not divide genetics into two fundamental categories. At the present stage of development, it may be more profitable to emphasize the common features rather than the differences between wild populations on the one hand, and domestic and laboratory populations on the other. The division indicated by the titles was adopted chiefly as a convenience for the purpose of preventing overlap in subject matter. Within what I take as my half of this subject, limitations of time prevent an over-all review and dictate a selection from the many interesting developments of a mathematical nature that have recently appeared. I am restricting myself therefore to a consideration of nonadditive genetic variance, a condition that must lie near the heart of the currently unpredictable behaviors of populations subjected to prolonged selection, or to inbreeding and subsequent crossing. It is on this particular field of nonadditive variance that a new method of attack has very recently been conceived and developed independently at three different research centers. The different but quite compatible developments of this new idea are themselves very interesting; in addition there may be value in a comparative study of the separate pathways by which individuals of different propensities and backgrounds can exploit the same basic idea. All this work is very recent and I am greatly indebted to the authors for permission to discuss their contributions prior to their appearance in print, although it will be possible to insert full references in the published version of this talk.

In studies of the variance of measurements of organisms, the measurement of each individual is considered to be the sum of a genotypic value, defined as the average measurement that replicates of individuals of the given genetic constitution would have if exposed to the whole array of environments, and of an environmental or nongenetic deviation from the genotypic value. In the present discussion only genotypic values will be considered. In order to subdivide the genotypic variance it is necessary to consider the general features of Mendelian heredity. The genotype of an individual consists of two alleles (related genes) at each of a large but fixed number of loci. One allele at each locus comes from the male parent, and one from the female parent. If the two alleles are the same at a particular locus, the individual is said to be homozygous at this locus; if the two alleles are different, the individual is heterozygous at this locus. The distributions of alleles at different loci, for the most part in the following discussion, are assumed to be independent, although deviations from this condition due to linkage or to linkage in combination with inbreeding are considered by two of the authors.

With this background we can consider the usual subdivision of genotypic values