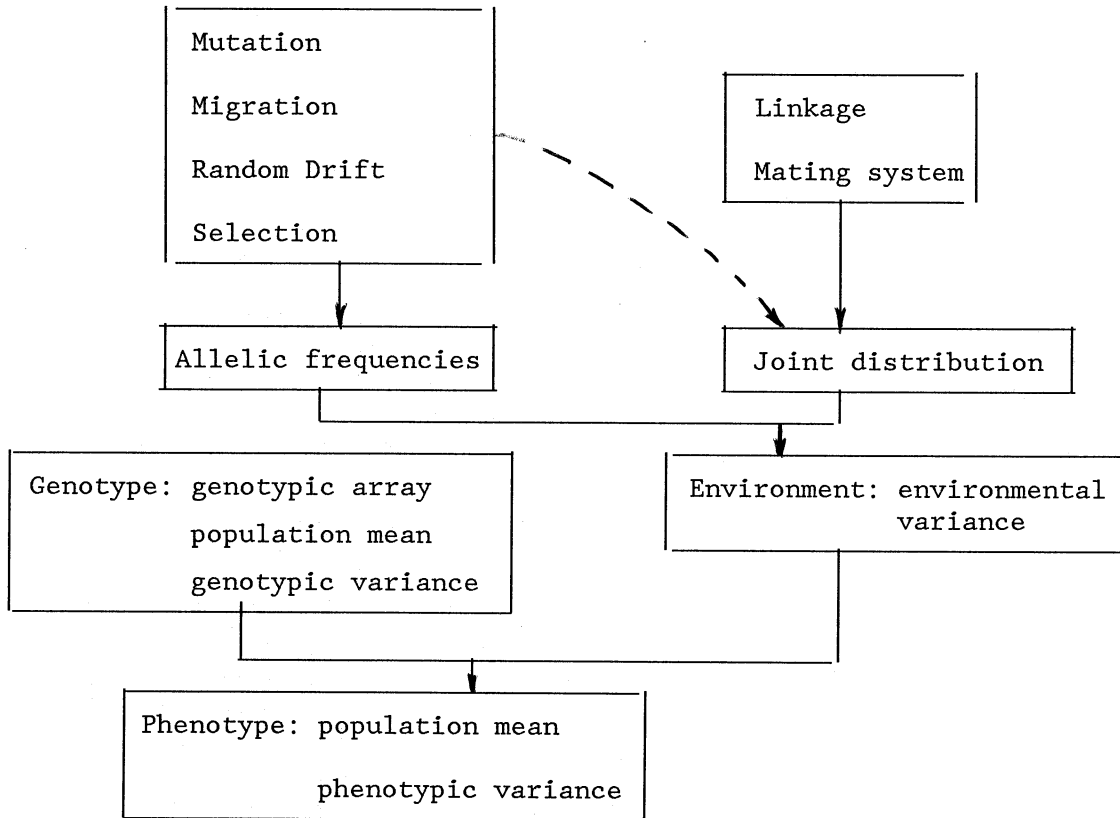


CHAPTER 1

GENERAL CONCEPTS

Population genetics can be defined as the extension of so called Mendelian genetics to the population level. It deals with frequencies of alleles and genotypes in a population -- a collection of individuals. It does not assign a genotypic or numerical value to each genotype. The possible exception to this is the assigning of "coefficients of selection" to genotypes. Quantitative genetics is that branch of genetics in which individual genotypes are unidentified and the traits or characteristics of individuals are measured. Genotypic values are assigned to genotypes. These are the broad areas in statistical genetics. Population genetics is basic to quantitative genetics. There is another term, biometrical genetics, which we shall attempt to define. It is a subdivision of quantitative genetics. Biometrical genetics relates to the measurement of traits of individuals in crosses which are commonly used to study qualitative characters in Mendelian genetics.

Lerner (1950, p. 80) presents the following overview of the subject. It is well to keep this diagram in mind as we discuss individual topics.



If neither mutation, migration, random drift, and selection are operating, allelic frequencies do not change. Allelic frequencies can be thought of as marginal distributions. Linkage and the mating system affect the joint distribution of alleles. The joint distribution of allelic frequencies gives the frequencies of genotypes. The joint distribution of alleles tells us how the alleles at one or more loci go together. In the following two examples, the marginal distributions are the same, but the joint distributions of alleles are different.

(1) Random mating

	A	a	
	0.6	0.4	
A	AA	Aa	
0.6	0.36	0.24	0.6
a	Aa	aa	
0.4	0.24	0.16	0.4
	0.6	0.4	

(2) Nonrandom mating

	A	a	
	0.6	0.4	
A	AA	Aa	
0.6	0.30	0.30	0.6
a	Aa	aa	
0.4	0.30	0.10	0.4
	0.6	0.4	

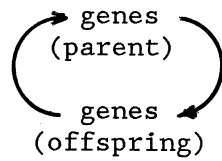
Mutation, migration, random drift, and selection also affect the joint distribution indirectly (hence the dotted line), because any change in allelic frequencies also brings about a change in the joint distribution. The quantitative geneticist observes the phenotype. Before he can deal effectively with these observations, he must make some assumptions about the upper part. This is a very important point. The above diagram presents a very simple schematic overview. It omits many things, e.g., competition or interaction between phenotypes.

The following basic units may be recognized: gene, block of genes, chromosome, gamete (a set of chromosomes), individual (union of two gametes), population (a collection of noninteracting or interacting individuals), ecosystem (a collection of noninteracting or interacting populations). We will stop at the population level and will assume no competition or no interaction between

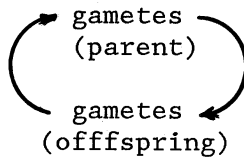
individuals. A general theory, I suppose, could be written, but I fear no one would understand it. We simply have bits and pieces at the present. For example, theory has been worked out considering the role of random drift with selection, migration and mutation held constant.

Plant and animal improvement may be regarded as evolution in the short term. In considering such cyclic phenomena one may use the gene, the gamete, or the individual as the basic unit.

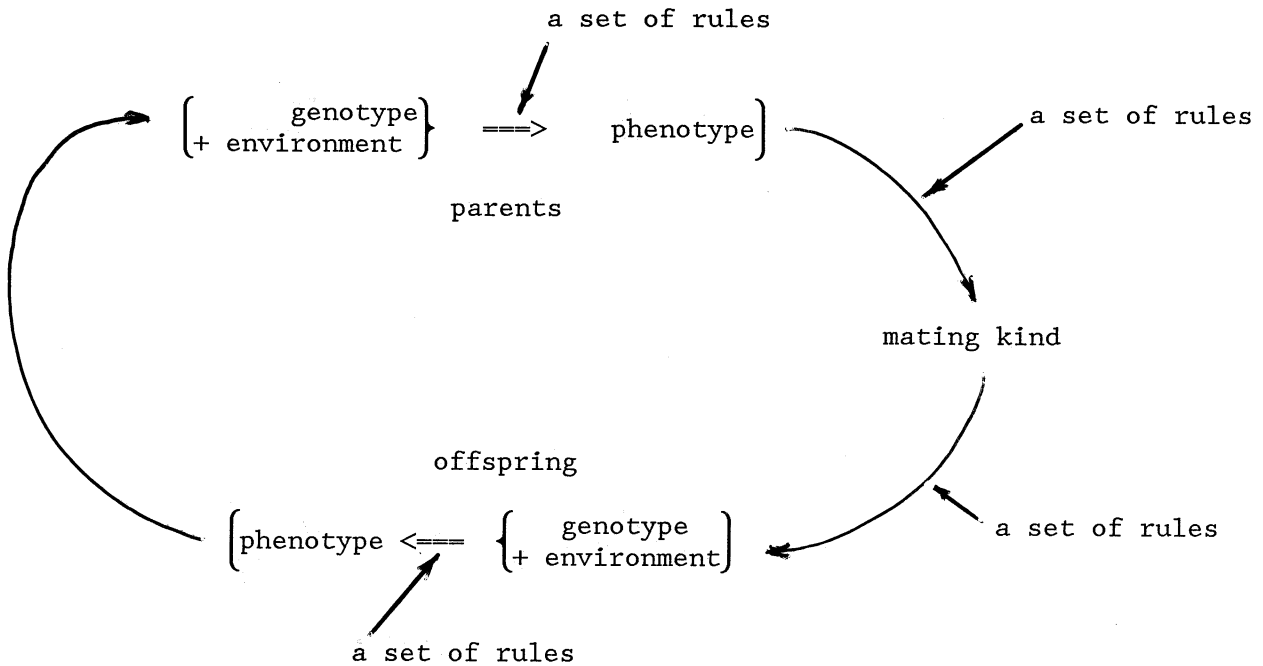
(1) Gene



(2) Gamete



(3) Individual



In some situations, working at the gametic level may be simpler than the individual level. In other cases, working at the genic level may be simpler than either the gametic or individual level. These kinds of systems can obviously be programmed for an electronic computer and can be evolved from generation to generation.

REFERENCES

- Lerner, I. M.
1950 Population genetics and animal improvement. Cambridge University Press, London.