

Population genetics, a short introduction

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Population genetics is mainly concerned with the study of the nature and the source of inherited differences of individuals belonging to the same species (for review, see e.g. Cavalli-Sforza and Bodmer 1971). Investigations in population genetics analyse the changes of the frequencies of the different phenotypes found in a population and the conditions causing an equilibrium between the various forces influencing these phenotypes.

Populations can be described by the distribution of the frequencies of the various phenotypes, that means by the gene frequencies in the different polymorphisms.

In Mendelian populations, i.e. infinitely large populations of interbreeding subjects with a common pool of genes, these genes are transmitted from one generation to the other according to the laws discovered by Gregor Mendel in 1865. The genetic composition of such populations undisturbed by evolutionary forces will not change and correspond to the Hardy-Weinberg law. This Hardy-Weinberg law shows that under random mating a biallelic autosomal locus with the genes A_1 and A_2 (relative frequencies of the alleles: p_1 and p_2) reaches in one generation a distribution of the genotype frequencies given by the expansion of the formula $(p_1 + p_2)^2$, that means the terms p_1^2 , $2 p_1 p_2$ and p_2^2 which give the relative frequencies of the genotypes $A_1 A_1$, $A_1 A_2$ and $A_2 A_2$, respectively. Based on the phenotype frequencies, the allele frequencies can be calculated by using the Hardy-Weinberg law.

Departures from the Hardy-Weinberg equilibrium are rare, but can be due to several reasons. A deficiency of heterozygotes is sometimes seen in the following cases: heterogeneity of the population (e.g. very recent mixture of populations), inbreeding,

selection against heterozygotes, existence of a silent allele (which makes homozygotes indistinguishable from heterozygotes carrying this silent allele), misclassification of phenotypes or positive assorting mating (tendency of individuals with similar phenotype to mate with each other); an excess of heterozygotes can be due to: selection in favour of heterozygotes, errors in the classification of phenotypes or negative assorting mating.

The Hardy-Weinberg law can be easily extended to multiple alleles, polyploids, sex-linked genes or several closely linked loci. Evolution can be seen through the changes of the frequencies of the genes. The major forces of evolutionary processes are: natural selection, mutation, migration and random genetic drift.

Random genetic drift is the random change of gene frequencies in a population with small size. Without selection, mutation or migration, the ultimate outcome of random genetic drift is the fixation of one allele and the disappearance of the other ones. In humans, migrations can be subdivided in at least three kinds: individual migrations, massive migrations and demic expansions (migration and extreme population growth). Migration is the major force against the effects of random genetic drift. The main factors with regard to evolution are mutation and selection. Mutation produces new alleles and, therefore, is the basis for the development and existence of polymorphisms (i.e. the state in which a mutant gene is rather frequent - frequency higher than 0.01 - and in which more than one phenotype can be distinguished). Most of the mutations, however, are deleterious, so that they are selected against. At equilibrium, a balance between mutation and selection (equilibrium between new mutations and elimination of the mutants by selection) exists. This equilibrium depends on several factors, e.g. whether the mutant is autosomal or sex-linked, or on the fitness of the genotypes carrying the mutant genes. In some cases, heterozygotes for a normal and a mutant gene show in a given environment a higher fitness than homozygote carriers of the normal allele. The best known of such situations is the relationship between the sickle-cell polymorphism and malaria which is an excellent example for a balanced polymorphism with heterozygote advantage.

This very short introductory remarks should show the extreme complexity of population genetics. Many problems which arise during the study of populations are due to the facts that the true populations are finite in size, that generations overlap and that the evolutionary forces vary rapidly. It is clear that this complexity has some influence of the gene frequencies which are currently used for the biostatistical evaluation of paternity; in the practical use, however, if enough genetic markers - especially the HLA system - are used, these factors will not influence the biostatistical opinions in a major degree.

REFERENCE

Cavalli-Sforza LL, Bodmer WF (1971) The genetics of human populations. WH Freeman and Company, San Francisco