

TABLE 5.1 Example of Allele Frequency Computation

Imagine you have just collected information on MN blood group genotypes for 250 humans in a given population. Your data are as follows:

Number of MM genotype = 40  
 Number of MN genotype = 120  
 Number of NN genotype = 90

The allele frequencies are computed as follows:

GENOTYPE	NUMBER OF PEOPLE	TOTAL NUMBER OF ALLELES	NUMBER OF M ALLELES	NUMBER OF N ALLELES
MM	40	80	80	0
MN	120	240	120	120
NN	90	180	0	180
Total	250	500	200	300

The relative frequency of the M allele is computed as the number of M alleles divided by the total number of alleles:  $200/500 = 0.4$ .

The relative frequency of the N allele is computed as the number of N alleles divided by the total number of alleles:  $300/500 = 0.6$ .

As a check, note that the relative frequencies of the alleles must add up to 1.0 ( $0.4 + 0.6 = 1.0$ ).

Source: Relethford 1996, 66.

of the **gene pool**, which includes all of the genes in the bodies of all members of a given species (or a population of a species). Using mathematical models, evolutionary theorists can estimate the **gene frequency** of particular genes—that is, the frequency of occurrence of gene variants or alleles within a particular gene pool. Measuring the stability or change of gene frequencies in populations over time allowed geneticists to trace short-term evolutionary change in a new field called **population genetics**. Once population geneticists had identified a target population, they analyzed its gene pool by calculating the frequencies of various alleles within that gene pool and trying to figure out what would happen to those frequencies if the carriers of the various alleles were subjected to particular selection pressures (Table 5.1). Some evolutionary geneticists tested these predictions on such organisms as fruit flies, but others concentrated on human beings.

The ability of human beings from anywhere in the world to interbreed successfully is one measure of membership in a single species. Comparing our genotypes provides additional evidence of our biological closeness. As we have seen, most alleles come in a range of different forms (i.e., are **polymorphous**), and known polymorphous variants fall into one of two groups. The first group, *polymorphic alleles*, accounts for most genetic variation across populations. Populations differ not because they have mutually exclusive sets of alleles but because they possess different *proportions* of the same set of alleles. An example is the ABO blood groups: the

polymorphic alleles A, B, and O are found in all human populations, but the frequency of each allele differs from population to population. The second group, *private polymorphisms*, includes alleles that are found in the genotypes of some, but usually not all, members of a particular population. One example is a genetically determined blood cell antigen known as the “Diego antigen.” The Diego antigen occurs only in Asian and African populations, but 60 to 90% of the members of the populations where it is found do not have it (Marks 1995, 165). This work leads to the inescapable conclusion that the traditional Western concept of “race” makes no sense in terms of genetics. Racial thinking is essentialistic. However, evolutionary geneticist Richard Lewontin demonstrated more than four decades ago that more genetic variation could be found within conventionally identified racial groups than could be found between them (Lewontin 1972). These results, based on population thinking, make it clear that “humankind . . . is not divided into a series of genetically distinct units” (Jones 1986, 324). Ian Tattersall and Rob Desalle (2011) point out that Lewontin’s claims have successfully withstood attempts to reject

**gene pool** All the genes in the bodies of all members of a given species (or a population of a species).

**gene frequency** The frequency of occurrence of the variants of particular genes (i.e., of alleles) within the gene pool.

**population genetics** A field that uses statistical analysis to study short-term evolutionary change in large populations.

**polymorphous** Describes alleles that come in a range of different forms.