11 Mating of Alleles

Since the struggle for existence is chiefly the struggle for subsistence, a careful comparative account of the food of various competing species and genera at different places and seasons and at all ages of the individual . . . cannot fail to throw much light upon the details, causes and effects of the struggle.

—S. Forbes, The Lake as Microcosm

11.1 Heterozygosity and Disease Resistance

Genetic theory is used in two basic commercial ways today: animal and plant breeding in agriculture and in the field of conservation biology. In the former, the basic strategy is to identify and eliminate undesirable, susceptible alleles by selective breeding. The susceptibility can be to a particular disease or perhaps it is manifested as a structural problem, such as weak anchor roots in corn plants.

Selection for particular alleles for agricultural purposes may decrease susceptibility to a particular disease or overcome some structural deficiency. However, such a selection process may also mean loss of some allele that was necessary to cope with some other problem. Thus, selective breeding may enhance susceptibility with regard to one problem but remove the ability to cope with another one. Conservation biologists see this path as one of walking the knife edge. Rather than increase the specialization of a plant or animal population, conservation biologists take just the opposite track. They want to maximize allele diversity in a locale of plants or herd of animals.

Let us distinguish two alleles, A and B. Suppose that the whole population was half AA and half BB. Then suppose that some disease hit this population and killed off the AA types. Half of the genetic history of the population would be gone. The same disease would not have so strongly affected the population had it also contained individuals of AB type, so-called heterozygotes. Not only does heterozygosity increase a population’s ability to cope with a variety of environmental influences, such as diseases, but a population is also more genetically adaptable in the face of an environmental challenge than are the AA or BB populations. More genetic information is retained in the heterozygote population, as a result of its history of natural selection, and therefore it is less prone to adverse conditions imposed by an altered environment.

Generally, conservation biologists want to maximize the number of AB type individuals because it increases the diversity and resilience of the population.
11.2 The Mating of Two Alleles into a Genotype: Proving the Hardy-Weinberg Law

Let us now model the process of genotype mixing, given two alleles, the fundamental experiment in genetics. In the next chapter we will then model the process of natural selection and mutation.

The process of genotype mixing can be illustrated for two alleles, A and B, which are drawn randomly from a pool of 100 A alleles and 200 B alleles. Each time step in the model is a drawing of an allele: we have 300 alleles so the total time for the mating process is 300 time steps (actually, 302 steps are needed to clear the very last allele choice into a genotype). The 300 steps represent a generation that resulted from a mating process in which the alleles were joining simultaneously. In STELLA, we could have chosen a time step of 1/300 so that \( t = 1, 2, 3, \ldots \) would represent 1, 2, 3, \ldots generations. The real time required for the run would not be shorter, of course. In this simple mating process, the genotype mix is set at the end of the first generation and remains fixed for all further ones.

The results of mating two alleles are explained by the Hardy-Weinberg law. This law states that the genotype frequencies are determined in a random mating process in the first generation. These genotype frequencies are for AA, \( p^2 \); for AB, \( 2pq \); for BB, \( q^2 \), where \( p \) and \( q \) are the A and B allele frequencies, respectively. In our sample problem, \( p = 100/300 \) or approximately 0.3333 and \( q = 200/300 \) or approximately 0.66667. From 300 alleles we can have 150 genotypes, so the Hardy-Weinberg law tells us that we should end up with 0.33333*0.33333*150 or 16.7 AA genotypes, 2*0.3333*0.666667*150 or 66.7 AB genotypes and finally, 0.66667*0.66667*150 or 66.7 BB genotypes.

There is another way to look at the problem of genotype mixing. If the A and B alleles were of equal frequency of occurrence, the chance of an AA genotype is .25. Since in our problem, the chance of an A choice is 0.33, the AA genotype frequency is .25*0.33333, or 1/12. The AB frequency is 2*.25*.66667, or 1/3. The relative frequency of AB to AA is therefore 4. We can check for the validity of this relationship in a graph generated by our model on the mating of two alleles.

To construct the model, we must set up a stock of 100 A alleles and another stock of 200 B alleles (Fig. 11.1). We use a random number generator to pick a number between 0 and 1 so that we can compare it to the frequency of the A allele in the total stock of alleles remaining to be chosen. Let's call that random number RAND.

The A frequency is just \( A/(A + B) \) and we make an initial and a running calculation of it in the variable A FREQ:

\[
A \text{ FREQ} = \frac{A}{A + B} \quad (1)
\]

If an A is randomly chosen we "store it" in a separate stock called A HOLD by adding a 1 to that stock: