

The Evolution of Populations I

Slide 2 When we discuss evolution, we often equate evolution and natural selection. However, natural selection is only an agent of evolution, it is not evolution itself. We define evolution as a change in the genetic constitution of a population. Most simply, then, evolution may occur in two ways: 1) by changing the frequency of the existing alleles of a gene or genes in a population, or 2) by changing the alleles themselves, for example by mutation or by introducing new alleles into a population. There are many ways by which populations may evolve, or by which the genetic makeup of populations may change. These mechanisms of evolutionary change, including natural selection, will be discussed in the following lesson. In this lesson, however, we will consider the characteristics of a hypothetical population that is not evolving. Such populations are said to be in Hardy-Weinberg equilibrium.

Slide 3 Consider a large, isolated population of a diploid species. A particular gene, called gene A, is present in all members of this population. Further, gene A has two alleles – big A and little a – so that there are homozygous individuals (AA and aa) and heterozygous individuals (Aa or aA) within the population. Now, imagine if all of the individuals in the population mated randomly with other individuals in the population to produce many offspring. Essentially, this would be akin to putting all of the alleles of gene A from all of the individuals in the population into a hat, and pulling out two at a time to represent new, diploid offspring. If enough offspring were produced, eventually the same frequency of alleles present in the parental population would be present in the offspring population.

Slide 4 We can show this to be true by calculating the allele frequencies from generation to generation. For example, the frequency of each allele, big A or little a, may be calculated as the total number of that type of allele, divided by the total number of both alleles. Say our population has 40 AA individuals, 40 Aa individuals, and 20 aa individuals. In total, we have 100 individuals, but 200 alleles, since each individual has two alleles. The frequency of the big A allele would simply be 40×2 (since 40 homozygous individuals have two copies of big A) plus 40 (since the 40 heterozygous individuals carry only one copy of big A), divided by 200 total alleles. This gives an allele frequency of 0.6, or 60%, for big A. The same calculation can be performed for little a, in this case to give a frequency of 0.4, or 40%. At this point, you may notice that the frequencies of the two alleles, A and a, add to equal one. When the frequencies of the different alleles of a gene in a population are added, they will always add to equal one. Take a moment and think about why this is true...

When our hypothetical population reproduces at random, i.e., when the gametes carrying one or the other allele are 'drawn out of the hat,' there is a 60% chance for big A to be drawn, and a 40% chance for little a to be drawn. As more and more offspring are produced, then, the new allele frequencies will tend toward the frequencies of the original population.

Slide 5 While it is not difficult to see how the allele frequencies remain the same, it is also true that the genotype frequencies will remain the same from generation to generation. This occurs because the genotype frequencies in large, randomly mating populations are determined by the frequencies of alleles. If the allele frequencies do not change, genotype frequencies also will not change. For example, the odds in our population of producing a homozygous dominant offspring are equal to the odds of receiving two big A alleles. There is a 60% chance that any offspring will receive one big A allele, and a 60% chance that they will receive a second big A allele. The odds of receiving both big A alleles are then 60% times 60%, or 36%. Alternatively, the odds of producing a homozygous recessive offspring are obtained by multiplying the frequencies of little a and little a, in this case to give 0.16, or 16%. Genotype frequencies for entire populations are calculated using a special equation, called the Hardy-Weinberg equation. This equation is written as $p^2 + 2pq + q^2 = 1$, where p^2 and q^2 are the frequency of homozygous genotypes, and $2pq$ is the frequency of heterozygotes. As you might guess, p and q represent the allele frequencies of any gene with two alleles, like gene A that we have been considering. For example, if p equals the frequency of the big A allele, the frequency of the AA genotype is p times p , or p^2 . The same holds true when q equals the frequency of the little a allele. To determine the frequency of heterozygotes, we multiply the allele frequencies of the big A allele by the frequencies of the little a allele, and then multiply that by two, since heterozygous individuals could be either Aa or aA.

As we have seen previously, the allele frequencies in our hypothetical population are not changing from generation to generation. It follows, then, by the Hardy-Weinberg equation, that the genotype frequencies also will not change, because the same allele frequencies will be plugged into the equation, generation after generation. Since allele and genotype frequencies are not changing from generation to generation, our population is not evolving. Populations in these cases are said to be in Hardy-Weinberg equilibrium.

Slide 6 So, how do we use the Hardy-Weinberg equation for real populations? Scientists use Hardy-Weinberg equilibrium as a baseline, or a null hypothesis, against which to measure the genetic change of real populations. As a null hypothesis, Hardy-Weinberg equilibrium is usually considered to rest on five assumptions:

- 1) population size is large
- 2) mating is random
- 3) there is no migration into or out of the population
- 4) there is no mutation
- 5) there are no selective forces on the alleles under consideration

If the frequencies of the alleles of a gene are changing, it is clear that one or more of the above assumptions is incorrect.

Slide 7 As you might guess, many characters in populations are evolving. In fact, Hardy-Weinberg equilibrium is more often the exception, rather than the rule, when investigating the genetic structure of populations. What factors cause populations to evolve, or drive populations away from Hardy-Weinberg equilibrium? Any factor that

causes the assumptions of Hardy-Weinberg equilibrium to be violated can be considered an agent of evolutionary change. As we mentioned before, natural selection is one factor that can cause populations to evolve. There are others, too, such as mutation, sexual selection, gene flow and genetic drift that also play important roles in the evolution of populations. We will discuss these mechanisms of evolutionary change in the following lesson.