PHYSIOLOGY- 6th SEM

Topic: POPULATION GENETICS

Submitted by: Mousumi Mitra

BASIC CONCEPT

The field of population genetics is concerned with changes in genetic variation within a group of individuals over time. Population geneticists want to know the extent of genetic variation within populations, why it exists, and how it changes over the course of many generations. Its mathematical foundations were developed by theoreticians who extended the principles of Gregor Mendel and Charles Darwin by deriving formulas to explain the occurrence of genotypes within populations.

GENES IN POPULATIONS AND THE HARDY-WEINBERG EQUATION

Population genetics may seem like a significant departure from other topics in this textbook, but it is a direct extension of our understanding of Mendel's laws of inheritance, molecular genetics, and the ideas of Darwin. In the field of population genetics, the focus shifts away from the individual and toward the population of which the individual is a member. Conceptually, all of the alleles of every gene in a population make up the gene pool. In this regard, each member of the population is viewed as receiving its genes from its parents, which, in turn, are members of the gene pool.

A. Population Is a Group of Interbreeding Individuals That Share a Gene Pool

In genetics, the term population has a very specific meaning. With regard to sexually reproducing species, a population is a group of individuals of the same species that occupy the same region and can interbreed with one another. Many species occupy a wide geographic range and are divided into discrete populations. For example, distinct populations of a given species may be located on different continents, or populations on the same continent could be divided by a geographical feature such as a large mountain range.

A large population usually is composed of smaller groups called local populations, or demes. The members of a local population are far more likely to breed among themselves than with other members of the general population. Local populations are often separated from each other by moderate geographic barriers.

Populations typically are dynamic units that change from one generation to the next. A population may change its size, geographic location, and genetic composition. With regard to size, natural populations commonly go through cycles of "feast or famine," during which environmental factors cause the population to swell or shrink. In addition, natural predators or disease may periodically decrease the size of a population to significantly lower levels; the population later may rebound to its original size. Populations or individuals within populations may migrate to a new site and establish a distinct population in this location.

B. At the Population Level, Some Genes May Be Monomorphic, But Most Are Polymorphic

In population genetics, the term polymorphism (meaning many forms) refers to the observation that many traits display variation within a population. Historically, **polymorphism** first referred to the variation in traits that are observable with the naked eye. Polymorphisms in color and pattern have long attracted the attention of population geneticists.

At the DNA level, polymorphism may be due to two or more alleles that influence the phenotype of the individual that inherits them. In other words, it is due to genetic variation. Geneticists also use the term polymorphic to describe a gene that commonly exists as two or more alleles in a population. By comparison, a monomorphic gene exists predominantly as a single allele in a population. By convention, when a single allele is found in at least 99% of all cases, the gene is considered **monomorphic**. (Some geneticists view an allele frequency of 95% or greater to be monomorphic.)

At the level of a particular gene, a polymorphism may involve various types of changes such as a deletion of a significant region of the gene, a duplication of a region, or a change in a single nucleotide. This last phenomenon is called a **single nucleotide polymorphism (SNP)**. SNPs are the smallest type of genetic change that can occur within a given gene and are also the most common. In humans, for example, SNPs represent 90% of all the variation in DNA sequences that occurs among different people. SNPs are found very frequently in genes. In the human population, a gene that is 2000 to 3000 bp in length, on average, contains 10 different sites that are polymorphic. The high frequency of SNPs indicates that polymorphism is the norm for most human genes.

C. Population Genetics Is Concerned with Allele and Genotype Frequencies

As we have seen, population geneticists want to understand the prevalence of polymorphic genes within populations. Their goal is to identify the causative factors that govern changes in genetic variation. Much of their work evaluates the frequency of alleles in a quantitative way. Two fundamental calculations are central to population genetics: allele frequencies and genotype frequencies. The allele and genotype frequencies are defined as

$$\text{Allele frequency} = \frac{\text{Number of copies of an allele in a population}}{\text{Total number of all alleles for that gene in a population}}$$

$$\text{Genotype frequency} = \frac{\text{Number of individuals with a particular genotype in a population}}{\text{Total number of individuals in a population}}$$

D. The Hardy-Weinberg Equation Can Be Used to Calculate Genotype Frequencies Based on Allele Frequencies

Now that we have a general understanding of genes in populations, we can begin to relate these concepts to mathematical expressions as a way to examine whether allele and genotype frequencies are changing over the course of many generations. In 1908, a British mathematician, Godfrey Harold Hardy, and a German physician, Wilhelm Weinberg, independently derived a simple mathematical expression that predicts stability of allele and genotype frequencies from one generation to the next. It is called the Hardy-Weinberg equilibrium, because (under a given set of conditions, described later) the allele and genotype frequencies do not change over the course of many generations.

Why is Hardy-Weinberg equilibrium a useful concept?

An equilibrium is a null hypothesis, which suggests that evolutionary change is not occurring. In reality, however, populations rarely achieve an equilibrium. Therefore, the main usefulness of the Hardy-Weinberg equilibrium is that it provides a framework on which to understand changes in allele frequencies within a population when such an equilibrium is violated.

To appreciate the Hardy-Weinberg equilibrium, let's return to our hypothetical frog example in which a gene is polymorphic and exists as two different alleles: G and g. If the allele frequency of G is denoted by the variable p, and the allele frequency of g by q, then

$$p + q = 1$$

For example, if p = 0.8, then q must be 0.2. In other words, if the allele frequency of G equals 80%, the remaining 20% of alleles must be g, because together they equal 100%. The Hardy-Weinberg equilibrium relates allele frequencies and genotype frequencies. For a diploid species, each individual inherits two copies of most genes. The Hardy-Weinberg equilibrium assumes that the alleles for the next generation for any given individual are chosen randomly and independently of each other. Therefore, we can use the product rule and multiply the sum, p + q, together. Because p + q = 1, we also know that their product also equals 1:

$$(p + q)(p + q) = 1$$

$$p2 + 2pq + q2 = 1 \text{ (Hardy-Weinberg equation)}$$

In the absence of evolutionary changes, the Hardy-Weinberg equation predicts an equilibrium—unchanging allele and genotype frequencies from generation to generation—if certain conditions are met in a population. With regard to the gene of interest, these conditions are as follows:

1. No new mutations: The gene of interest does not incur any new mutations.

2. No genetic drift: The population is so large that allele frequencies do not change due to random sampling effects.

3. No migration: Individuals do not travel between different populations.

4. No natural selection: All of the genotypes have the same reproductive success.

5. Random mating: With respect to the gene of interest, the members of the population mate with each other without regard to their phenotypes and genotypes.

The Hardy-Weinberg equation provides a quantitative relationship between allele and genotype frequencies in a population.

E. FACTORS THAT CHANGE ALLELE AND GENOTYPE FREQUENCIES IN POPULATIONS

The genetic variation in natural populations typically changes over the course of many generations. The term microevolution describes changes in a population's gene pool from generation to generation. Such change is rooted in two related phenomena (Table 24.1). First, the introduction of new genetic variation into a population is one essential aspect of microevolution. As discussed later in this chapter, gene variation can originate by a variety of molecular mechanisms. For example, new alleles of preexisting genes can arise by random mutations. Such events provide a continuous source of new variation to populations. However, due to their low rate of occurrence, mutations do not act as a major factor in promoting widespread changes in a population. If mutations were the only type of change occurring in a population, that population would not evolve at a significant rate because mutations are so rare.

Microevolution also involves the action of evolutionary mechanisms that alter the prevalence of a given allele or genotype in a population. These mechanisms are random genetic drift, migration, natural selection, and nonrandom mating (see Table 24.1). The collective contributions of these evolutionary mechanisms over the course of many generations have the potential to promote widespread genetic changes in a population. In this section, we will examine how random genetic drift, migration, natural selection, and nonrandom mating can affect the type of genetic variation that occurs when a gene exists in two or more alleles in a population. As you will learn, these mechanisms may cause a particular allele to be favored, or they may create a balance where two or more alleles are maintained in a population.

TABLE 24.1
Factors That Govern Microevolution

Source of New Allelic Variation*	
Mutation	In this section, we consider allelic variation. Random mutations within preexisting genes introduce new alleles into populations, but at a very low rate. New mutations may be beneficial, neutral, or deleterious. For new alleles to rise to a significant percentage in a population, evolutionary mechanisms (i.e., random genetic drift, migration, natural selection) must operate on them.
Mechanisms That Alter Existing Genetic Variation	
Random genetic drift	This is a change in genetic variation from generation to generation due to random sampling error. Allele frequencies may change as a matter of chance from one generation to the next. This tends to have a greater effect in a small population.
Migration	Migration can occur between two different populations. The introduction of migrants into a recipient population may change the allele frequencies of that population.
Natural selection	This is the phenomenon in which the environment selects for individuals that possess certain traits that favor reproductive success. For example, natural selection may be related to the survival of members to reproductive age.
Nonrandom mating	This is the phenomenon in which individuals select mates based on their phenotypes or genetic lineage. This can alter the relative proportion of homozygotes and heterozygotes predicted by the Hardy-Weinberg equation but does not change allele frequencies.

F. In Small Populations, Allele Frequencies Can Be Altered by Random Genetic Drift

In the 1930s, geneticist Sewall Wright played a key role in developing the concept of **random genetic drift**, or simply**, genetic drift**, which refers to changes in allele frequencies in a population due to random fluctuations. As a matter of chance, the frequencies of alleles found in gametes that unite to form zygotes vary from generation to generation. Over the long run, genetic drift usually results in either the loss of an allele or its fixation at 100% in the population. The rate at which this occurs depends on the population size and on the initial allele frequencies.

Bottleneck Effect: Changes in population size may influence genetic drift via the bottleneck effect. In nature, a population can be reduced dramatically in size by events such as earthquakes, floods, drought, or human destruction of habitat. Such events may randomly eliminate most of the members of the population without regard to genetic composition. The initial bottleneck may be greatly influenced by genetic drift because the surviving members may have allele frequencies that differ from those of the original population. In addition, allele frequencies are expected to drift substantially during the generations when the population size is small. In extreme cases, alleles may even be eliminated. Eventually, the population with the bottleneck may regain its original size.

Founder Effect: Geography and population size may also influence genetic drift via the founder effect. Compared to the bottleneck effect, the key difference is that the founder effect involves migration; a small group of individuals separates from a larger population and

establishes a colony in a new location. For example, a few individuals may migrate from a large continental population and become the founders of an island population. The founder effect has two important consequences. First, the founding population is expected to have less genetic variation than the original population from which it was derived. Second, as a matter of chance, the allele frequencies in the founding population may differ markedly from those of the original population.

G. Natural Selection Is Based on the Relative Reproductive Success of Genotypes

In the 1850s, Charles Darwin and Alfred Russel Wallace independently proposed the theory of evolution by natural selection. According to this theory, the conditions found in nature result in the selective survival and reproduction of individuals whose characteristics make them better adapted to their environment. These surviving individuals are more likely to reproduce and contribute offspring to the next generation. Natural selection can be related not only to differential survival but also to mating efficiency and fertility. A modern restatement of the principles of natural selection can relate our knowledge of molecular genetics to the phenotypes of individuals.

1. Within a population, allelic variation arises in various ways, such as through random mutations that cause differences in DNA sequences. A mutation that creates a new allele may alter the amino acid sequence of the encoded protein, which, in turn, may alter the function of the protein.

2. Some alleles may encode proteins that enhance an individual's survival or reproductive capability compared with that of other members of the population. For example, an allele may produce a protein that is more efficient at a higher temperature, conferring on the individual a greater probability of survival in a hot climate.

3. Individuals with beneficial alleles are more likely to survive and contribute to the gene pool of the next generation.

4. Over the course of many generations, allele frequencies of many different genes may change through this process, thereby significantly altering the characteristics of a species. The net result of natural selection is a population that is better adapted to its environment and more successful at reproduction. Even so, it should be emphasized that species are not perfectly adapted to their environments, because mutations are random events and because the environment tends to change from generation to generation.

H. Directional Selection Favors the Extreme Phenotype

Directional selection favors individuals at one extreme of a phenotypic distribution that are more likely to survive and reproduce in a particular environment. Different phenomena may initiate the process of directional selection. One way that directional selection may arise is that a new allele may be introduced into a population by mutation, and the new allele may promote a higher fitness in individuals that carry it. If the homozygote carrying the favored allele has the highest fitness value, directional selection may cause this favored allele to

eventually become the predominant allele in the population, perhaps even becoming a monomorphic allele.

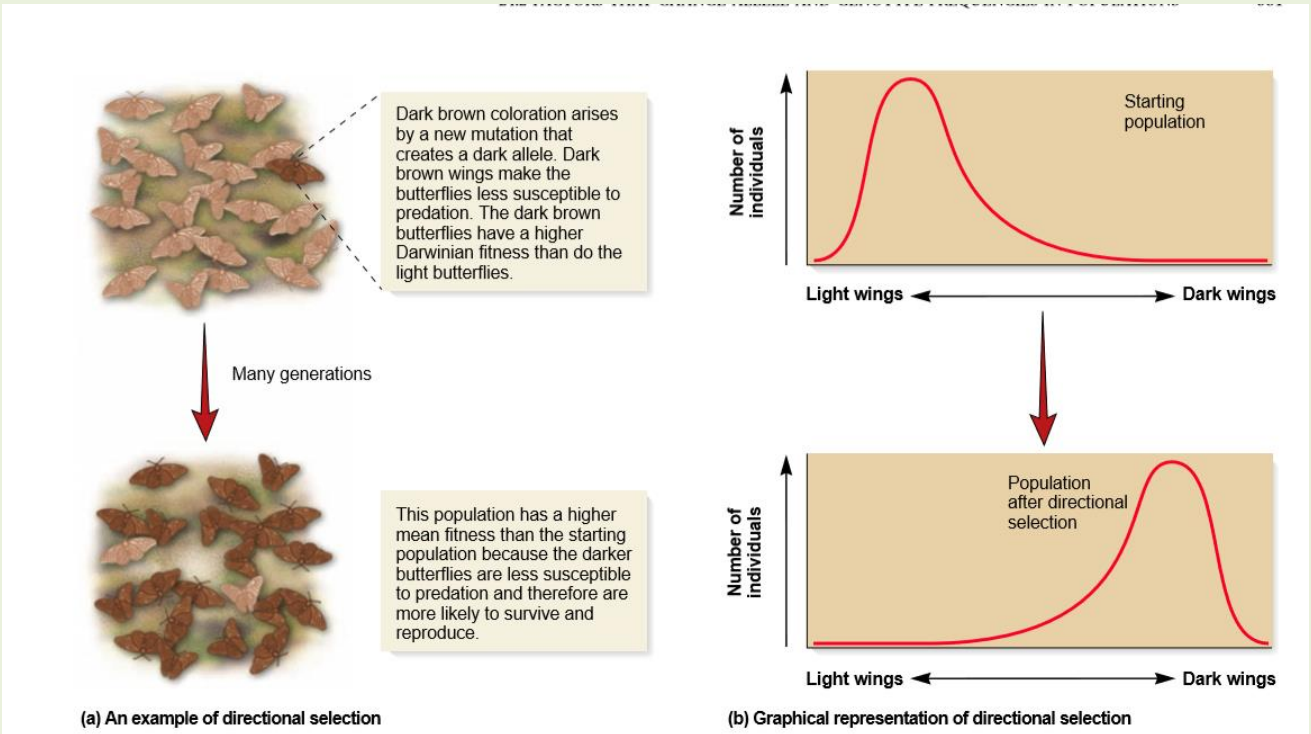

FIGURE 24.8 **Directional selection.** (a) A new mutation arises in a population that confers higher Darwinian fitness. In this example, butterflies with darker individuals.

I.Stabilizing Selection Favors Individuals with Intermediate Phenotypes

In stabilizing selection, the extreme phenotypes for a trait are selected against, and those individuals with the intermediate phenotypes have the highest fitness values. Stabilizing selection tends to decrease genetic diversity for a particular gene because it eliminates alleles that cause a greater variation in phenotypes. An example of stabilizing selection involves clutch size in birds, which was first proposed by British biologist David Lack in 1947. Under stabilizing selection, birds that lay too many or too few eggs have lower fitness values than those that lay an intermediate value.

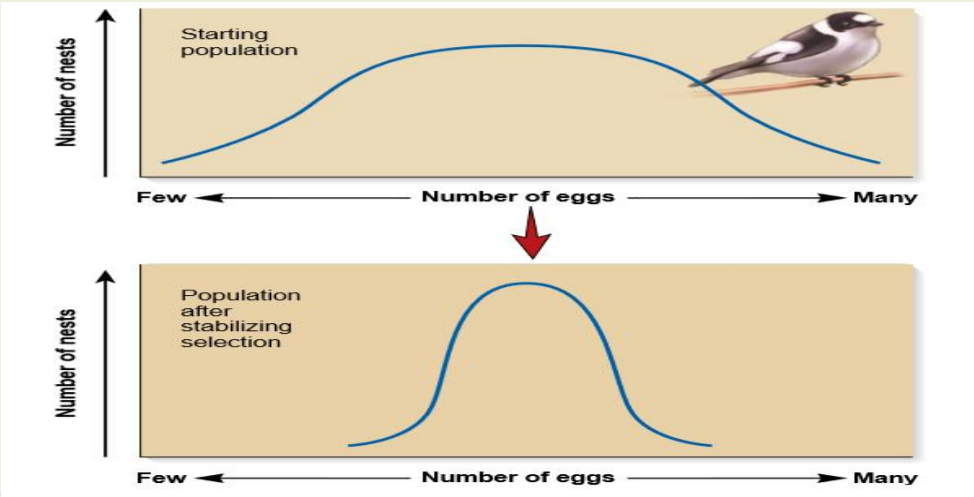

FIGURE 24.11 **Stabilizing selection.** In this pattern of natural selection, the extremes of a phenotypic distribution are selected against. Those individuals with intermediate traits have the highest fitness. This results in a population with less diversity and more uniform traits.

J. Disruptive Selection Favors Multiple Phenotypes

Disruptive selection, also known as diversifying selection, favors the survival of two or more different genotypes that produce different phenotypes (Figure 24.12). In disruptive selection, the fitness values of a particular genotype are higher in one environment and lower in a different one. Disruptive selection is likely to occur in populations that occupy diverse environments so that some members of the species survive in each type of environmental condition.

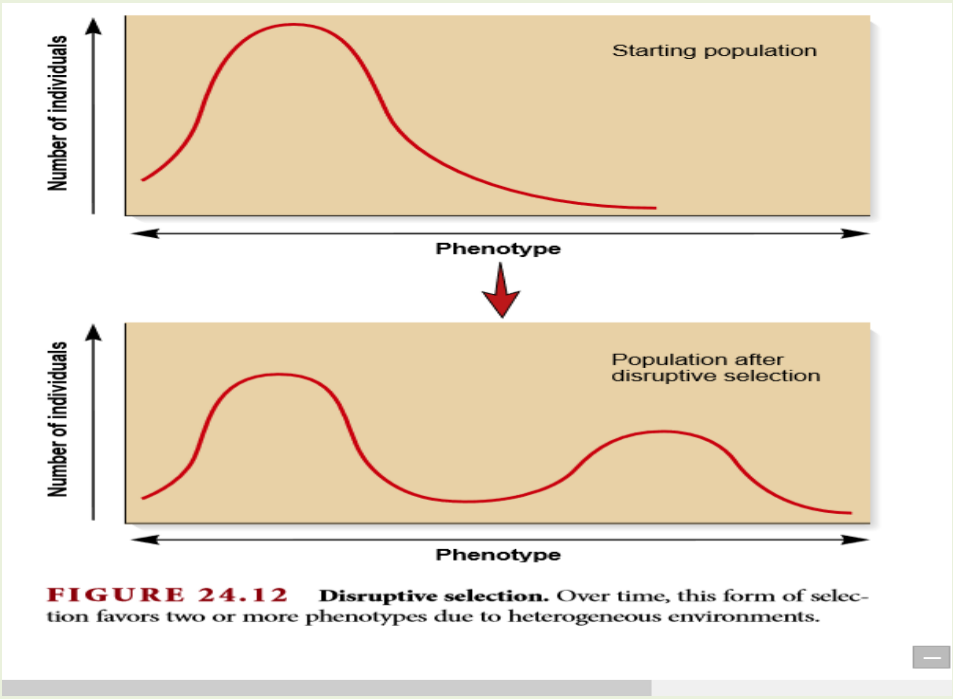

FIGURE 24.12 **Disruptive selection.** Over time, this form of selection favors two or more phenotypes due to heterogeneous environments.

Conceptual Questions

1. What is the gene pool? How is a gene pool described in a quantitative way?

2. In genetics, what does the term population mean? Pick any species you like and describe how its population might change over the course of many generations.

3. What is a genetic polymorphism? What is the source of genetic variation?

4. State for each of the following whether it is an example of an allele, genotype, and/or phenotype frequency: A. Approximately 1 in 2500 Caucasians is born with cystic fibrosis. B. The percentage of carriers of the sickle cell allele in West Africa is approximately 13%. C. The number of new mutations for achondroplasia, a genetic disorder, is approximately 5×10^{-5}.

5. The term polymorphism can refer to both genes and traits. Explain the meaning of a polymorphic gene and a polymorphic trait. If a gene is polymorphic, does the trait that the gene affects also have to be polymorphic? Explain why or why not.

6. In the term genetic drift, what is drifting? Why is this an appropriate term to describe this phenomenon?

7. Why is genetic drift more significant in small populations? Why does it take longer for genetic drift to cause allele fixation in large populations than in small ones?

8. Describe what happens to allele frequencies as a result of the bottleneck effect. Discuss the relevance of this effect with regard to species that are approaching extinction.

9. Discuss the similarities and differences among directional, disruptive, balancing, and stabilizing selection.