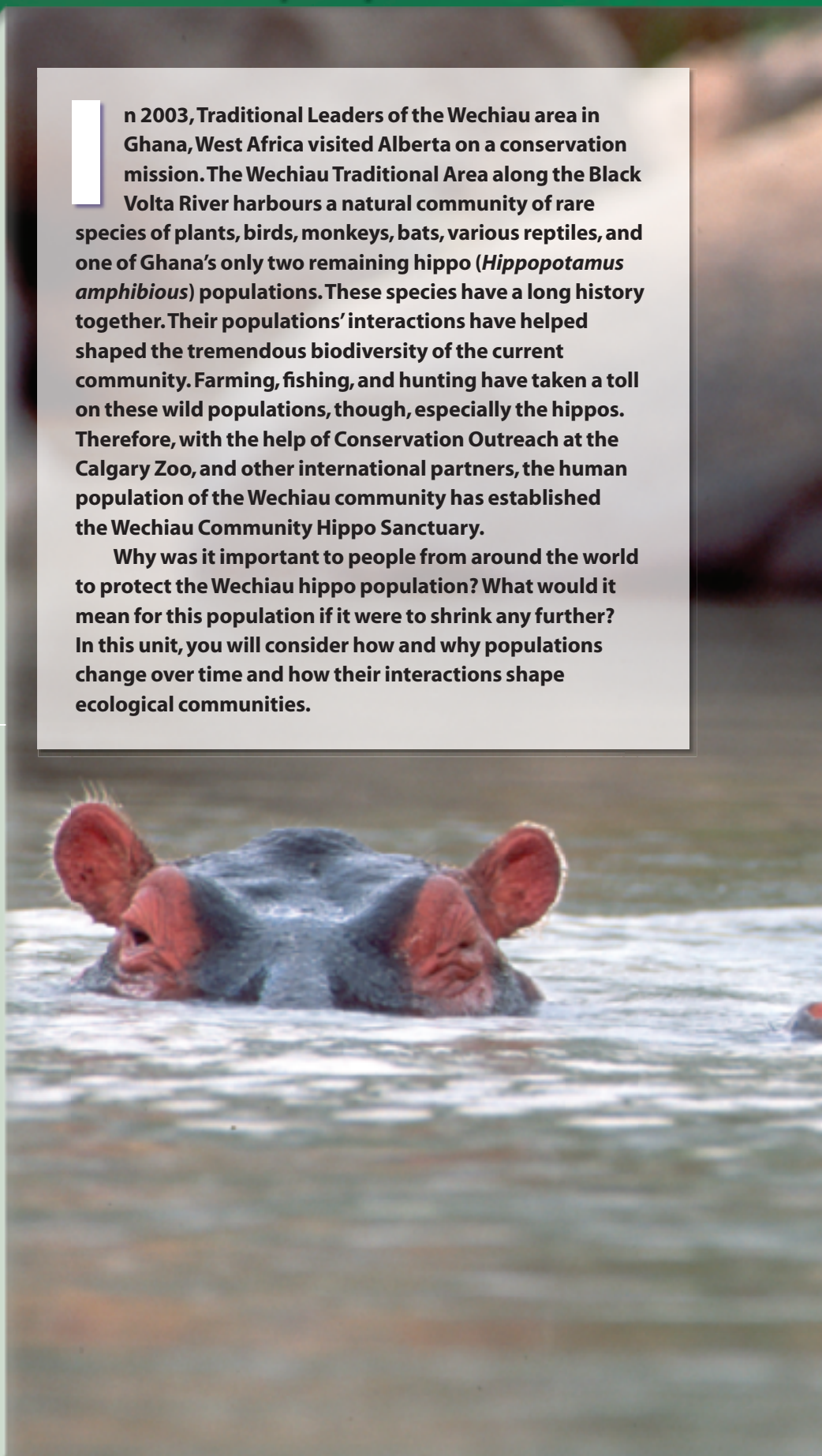
UNIT 8

Population and Community Dynamics



In 2003, Traditional Leaders of the Wechiau area in Ghana, West Africa visited Alberta on a conservation mission. The Wechiau Traditional Area along the Black Volta River harbours a natural community of rare species of plants, birds, monkeys, bats, various reptiles, and one of Ghana's only two remaining hippo (*Hippopotamus amphibious*) populations. These species have a long history together. Their populations' interactions have helped shaped the tremendous biodiversity of the current community. Farming, fishing, and hunting have taken a toll on these wild populations, though, especially the hippos. Therefore, with the help of Conservation Outreach at the Calgary Zoo, and other international partners, the human population of the Wechiau community has established the Wechiau Community Hippo Sanctuary.

Why was it important to people from around the world to protect the Wechiau hippo population? What would it mean for this population if it were to shrink any further? In this unit, you will consider how and why populations change over time and how their interactions shape ecological communities.

General Outcomes

In this unit, you will

- describe a community as a composite of populations in which individuals contribute to a gene pool that can change over time
- explain the interaction of individuals in populations with each other and with members of other populations
- explain, in quantitative terms, the changes in populations over time

Unit Contents

Focussing Questions

1. How is population change detected and measured over time?
2. What factors influence the degree and rate of growth or decline in a population's size?
3. In what ways do individual members of a population interact with one another and with members of other populations?

Unit PreQuiz ?
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UNIT 8

Preparation

Prerequisite Concepts

This unit draws and builds upon your understanding of genetics (from Unit 7), factors that affect populations (from Unit 4, Chapter 3), and the theory of evolution by natural selection (from Unit 4, Chapter 4).

Heredity and Evolution

In the theory of evolution by natural selection, new variants of species arise continually in populations. Some variants thrive and produce more offspring, thus slowly leading to change in a population, which may even lead to the development of new species over time. Other variants die off because they cannot thrive in their environment.

As scientists in the 1930s began to broaden their understanding of genetics, they demonstrated that there is substantial genetic variation within populations. These variations can arise in populations through mutations—permanent changes in the genetic material of an organism. Evolution, therefore, depends on both random genetic mutation (with provides variation) and mechanisms such as natural selection.

Reviewing the Language of Genetics

To understand and discuss genetic variation, it is helpful to review certain terms. Alleles are alternate forms of a gene. In humans, for example, there are three alleles—I^A, I^B, and i—that determine whether an individual has A, B, AB, or O blood type. Since individuals generally have two sets of chromosomes, one received from the male parent and one from the female parent, there are two alleles for each gene at each locus. A locus (plural loci) is the location of a gene on a chromosome. So humans could be I^AI^A, I^AI^B, I^Ai, I^BI^B, I^Bi, or ii at the locus for blood group. If the two alleles at a locus are identical (for example, I^AI^A or ii), the individual is called homozygous for that characteristic. An individual with two different alleles at the locus (for example, I^AI^B) is called heterozygous. The three blood type alleles, I^A, I^B, or i,

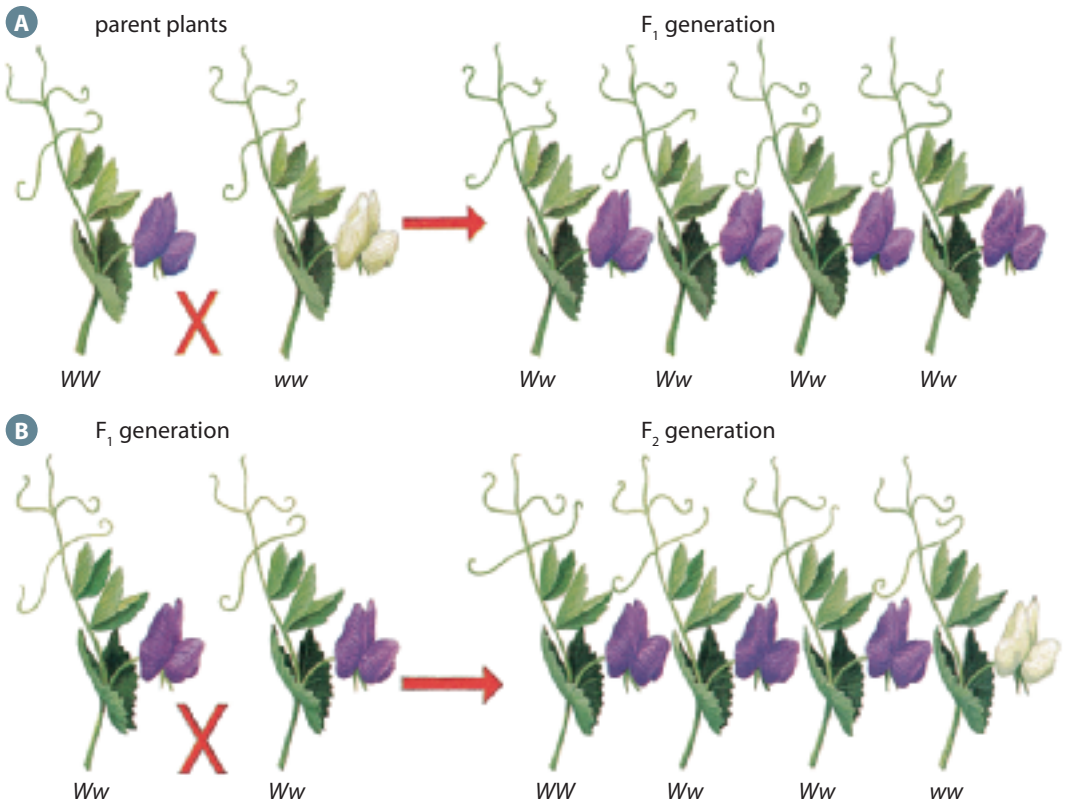

Figure P8.1 Two generations (**A** and **B**) resulting from the cross of a purple-flowered pea plant and a white-flowered pea plant.

exist in the population, but no single person can have all three. In some populations, the allele possibilities are even greater, and they far exceed the two possible alleles any human can have.

If the two alleles inherited from parents are different, one of them—the dominant allele—will be fully expressed in the individual's appearance and therefore will become the phenotype. The other allele, the recessive allele, has no noticeable effect on the organism's appearance, but it remains as part of the genotype of the organism. Figure P8.1 shows a cross between a pure purple-flowered pea plant and a pure white-flowered pea plant. The alleles for colour are represented by the letters *W* (for the dominant allele) and *w* (for the recessive allele). Since *W* is the dominant allele, the flowers can only be white when the two alleles are both recessive (that is, *ww*).

The genotype, or genetic makeup, of an individual remains constant throughout its life. However, over time, the alleles within a population may change. New alleles may arise and may be recombined, thus producing individuals with novel phenotypes. Phenotypes are the physical and physiological traits of an organism. A phenotype of an individual can be the product of both the environment and heredity. For example, environmental factors such as disease, crowding, injury, or the availability of food can all affect the appearance of an individual. But these acquired characteristics are not heritable; that is, they are not passed on to the next generation. Because of dominant and recessive alleles, an organism's appearance does not always reflect its genetic makeup. For example, Figure P8.2 shows a cross between two pea plants that have the alleles *W* or *w* at the locus for colour. The genotypes *WW* and *Ww* both result in a purple flower, while the genotype *ww* results in a white flower. Table P8.1 summarizes how genotype is related to phenotype.

Table P8.1 Genotype versus Phenotype

Genotype	Genotype	Phenotype
WW	homozygous dominant	purple flowers
Ww	heterozygous	purple flowers
ww	homozygous recessive	white flowers

Not all traits are totally dominant or totally recessive. Sometimes neither allele controlling a trait is dominant. In this case, blending of the two traits can occur—a situation called incomplete dominance. Occasionally both alleles for a trait may be dominant. These alleles are said to be co-dominant, and both alleles are expressed in the heterozygous individual. In some varieties of chickens, for example, two alleles for a trait may be expressed equally. A black rooster crossed with a white hen produces offspring that have some black feathers and some white feathers.

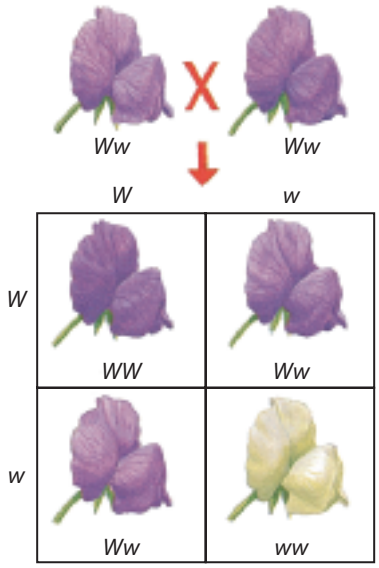

Figure P8.2 This cross between heterozygous pea plants (the same as the $F_1 \times F_1$ cross in Figure P8.1) is shown in a Punnett square.

CHAPTER
19

Genetic Diversity in Populations

Chapter Concepts

19.1 The Hardy-Weinberg Principle

- A gene pool is the sum of all the alleles for all the genes in a population. Population geneticists study gene pools.
- The Hardy-Weinberg principle is a mathematical model that is used to determine allele frequencies and genotype frequencies in a population.
- Sexual reproduction does not, by itself, cause allele frequencies to change from one generation to the next.
- Allele frequencies change over time in populations that are undergoing microevolution. The Hardy-Weinberg equation can be used to detect these changes.

19.2 The Causes of Gene Pool Change

- Genetic mutations, gene flow, non-random mating, chance events followed by genetic drift, and natural selection can lead to changes in gene pools.
- The formation of small isolated populations leads to inbreeding and a potential loss of genetic diversity from gene pools.
- Recessive alleles that are harmful in the homozygous state may remain in a gene pool if the heterozygous genotype provides a selective advantage.

Sage grouse (*Centrocercus urophasianus*, shown here), wood bison (*Bison bison athabascae*), and peregrine falcons (*Falco peregrinus*) were once abundant in the Prairies. As the human population in Canada grew and spread out, however, the habitats of many species became fragmented or polluted, and their populations declined. Ecologists are concerned about the lack of genetic diversity in these small populations. Small populations are more susceptible to disease, sudden changes in the environment, and competition from invasive non-native species.

In this chapter, you will learn how population genetics—the study of genetic diversity in populations—can be used to assess changes in populations over time. You will consider the factors that influence genetic diversity in populations, and learn why scientists consider these factors in order to develop effective conservation programs.

A male greater sage grouse inflates his air sacs to attract a female.

Launch Lab

Pick Your Plumage

The greater sage grouse is a subspecies of sage grouse that lives in the prairies of Canada and the United States. During mating season, groups of these ground-dwelling birds gather at breeding areas, called leks, where the males strut across bare ground in full view of the females. The males display their tail feathers and inflate their yellow air sacs, which are otherwise concealed under white chest feathers. Which males do the females choose? How does the selection of mates affect the next generation?

Materials

- paper silhouette of a greater sage grouse
- paper tail feathers of different lengths
- paper air sacs of different colours
- coloured felt pens
- stapler or clear tape

Procedure

1. Choose a paper silhouette of a greater sage grouse. Also choose five to ten paper tail feathers and a pair of paper air sacs. Attach the tail feathers and air sacs to the silhouette. Use a felt pen to add markings to the tail feathers.
2. Hold up your model bird so the other students can see it. At the same time, observe your classmates' model birds. Notice the variations among the model birds.
3. Your teacher will announce which greater sage grouse will reproduce and pass on their traits to the next generation.

Analysis

1. Identify three variations among the tail feathers and air sacs that you observed.
2. **a)** In step 3, what determined which male birds will reproduce? Which gender—male or female—influenced this more?
   b) What will the next generation of male birds look like?
3. In this activity, the selection of mates was based on two traits. In nature, many traits and other factors influence mate selection. Suggest three traits (not necessarily obvious to the human eye) that female greater sage grouse might use to select a mate.
4. Some of the male birds in this activity did not mate and pass on their genes to the next generation. Explain how that could be both an advantage and a disadvantage to the next generation.

SECTION 19.1

The Hardy-Weinberg Principle

Section Outcomes

In this section, you will

- **define** a gene pool as the sum of all the alleles for all the genes in a population
- **describe** the gene pool of a population at genetic equilibrium, as well as the molecular basis for gene pool change
- **summarize** the five conditions upon which the Hardy-Weinberg principle is based
- **describe** how the Hardy-Weinberg equation is used to determine whether a population is undergoing microevolution
- **calculate** allele and genotype frequencies in a population, as well as the number of individuals with specific genotypes, and **interpret** the data
- **conduct** an investigation to simulate gene pool change and **analyze** the data

Key Terms

population
genes
allele
gene pool
genotype frequency
phenotype frequency
allele frequency
Hardy-Weinberg principle
Hardy-Weinberg equation
genetic equilibrium
microevolution

Figure 19.1 The California ground squirrel is related to the Richardson's ground squirrel (*Spermophilus richardsonii*), also called a gopher in the Canadian Prairies. Both types of ground squirrel are small (less than 50 cm long), but dig extensive underground tunnels and mounds.

The California ground squirrel (*Spermophilus beecheyi*) may escape from predators by hiding in its burrows (Figure 19.1). While it has a key role in its ecosystem, humans often consider it to be a pest because of the digging it sometimes does in golf courses and farm fields. One of its ecological roles is as a food source for other species in the community. Scientists have observed that some populations of California ground squirrels are resistant to the venom of the northern Pacific rattlesnake (*Crotalus oreganus*), a ground squirrel predator. The venom-resistant ground squirrels are found in habitats where there are many northern Pacific rattlesnakes. Where the snakes are rare, the ground squirrels are less resistant to the snakes' venom. Are these populations of ground squirrels evolving?

As you may recall from Chapter 4, Charles Darwin and Alfred Wallace explained the mechanism by which species change over time as follows: *Individuals* with variations that make them better suited to their environment are more likely to survive and reproduce, and thereby pass on their favourable variations to the next generation.

Darwin and Wallace could not explain the source of these variations, however, or the way that traits were passed on from parents to offspring. The two naturalists were not aware of the work of Gregor Mendel, and other geneticists after him, who developed a basic understanding of inheritance. When scientists integrated the concepts of natural selection and inheritance, they were able to explain that evolution occurs when there are genetic changes in a population over time.

Thus, populations of venom-resistant ground squirrels would arise when ground squirrels with genes for venom-resistance pass on these genes to their offspring. In this section, you will learn how scientists measure changes in populations at the molecular level.

Describing Genetic Diversity in Populations

A **population** is a group of organisms of the same species that live together in a defined area and time. Thus, a group of ground squirrels that inhabit a particular field one summer make up a population, as do the Alberta wild rose bushes (*Rosa acicularis*) that grow in a particular valley

over one summer (Figure 19.2). Although the individuals in a population sometimes interbreed with members of a different population nearby, they usually breed among themselves. When a population becomes fragmented—for example, when a new road creates a barrier through a habitat—the individuals on either side of the barrier may form separate populations.

As you learned in Chapter 17, **genes** are carried on chromosomes and control the inheritance of traits such as flower colour in plants and fur colour in animals. A gene can have more than one form. Each form of a gene is called an **allele**. For example, one of the genes for coat colour in mice (*Mus musculus*) can take the form of either the black coat allele (*B*) or the white coat allele (*b*). The alleles that are carried by the sperm and the egg combine during fertilization to produce a genotype. Thus, three genotypes of coat colour are possible: *BB*, *Bb*, or *bb*.

A **gene pool** is the sum of all the alleles for all the genes in a population. In other words, a gene pool is the sum of all the genetic variation that can be passed on to the next generation. In general, the more variety there is in a gene pool, the better the population can survive in a changing environment.

Figure 19.2 The wild roses growing in a specific area during a particular time frame are an example of a population. Together, the alleles of all the plants in the population make up the population's gene pool.

Population geneticists study gene pools. As shown in Figure 19.3 on the next page, gene pools can be described in terms of genotypes and alleles. A **genotype frequency** is the proportion of a population with a particular genotype. It is usually expressed as a decimal. Suppose, for example, that a sample of a mouse population includes 72 black mice with the genotype *BB*, 96 black mice with the genotype *Bb*, and 32 white mice with the genotype *bb* (Figure 19.3). In this case, the allele for black coat colour is dominant to the allele for white coat colour. The genotype frequency of the *bb* genotype can therefore be determined by calculating the fraction of homozygous recessive mice in the sample. Since there are 200 mice in the sample, the genotype frequency of the *bb* genotype is $\frac{32}{200}$, or 0.16. The genotype frequency can also be expressed as the percentage of individuals with a particular genotype: $\frac{32}{200} \times 100 = 16$ percent.

Since the numbers of mice with *BB* and *Bb* genotypes are given, the frequencies of these genotypes can also be determined. The frequency of the *BB* genotype is $\frac{72}{200}$, or 0.36 (36 percent). The frequency of the heterozygous (*Bb*) genotype is $\frac{96}{200}$, or 0.48 (48 percent). Notice that the sum of all three genotype frequencies is 1.00, or 100 percent.

Similarly, a **phenotype frequency** is the proportion of a population with a particular phenotype, expressed as a decimal or percent. For the black and white mice, the phenotype frequency for white coat colour is the same as the genotype frequency for the *bb* genotype. This is because white coat colour is a recessive trait.

An **allele frequency** is the rate of occurrence of a particular allele in a population, with respect to a particular gene. An allele frequency is usually expressed as a decimal. Since diploid

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FYI

German-born scientist Ernst Mayr (1904–2005) was one of the first scientists to integrate the concepts of Mendelian genetics and Darwinian natural selection into a modern theory to explain evolutionary change. This theory became known as the theory of modern synthesis, or the synthetic theory of evolution. Mayr used this theory to explain how new species originate, a problem that Darwin and others had been unable to explain.

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Try This

Given the genotype frequencies for the *BB* and *Bb* genotypes, how would you calculate the phenotype frequency for black coat colour in a mouse population? How would you check your results?

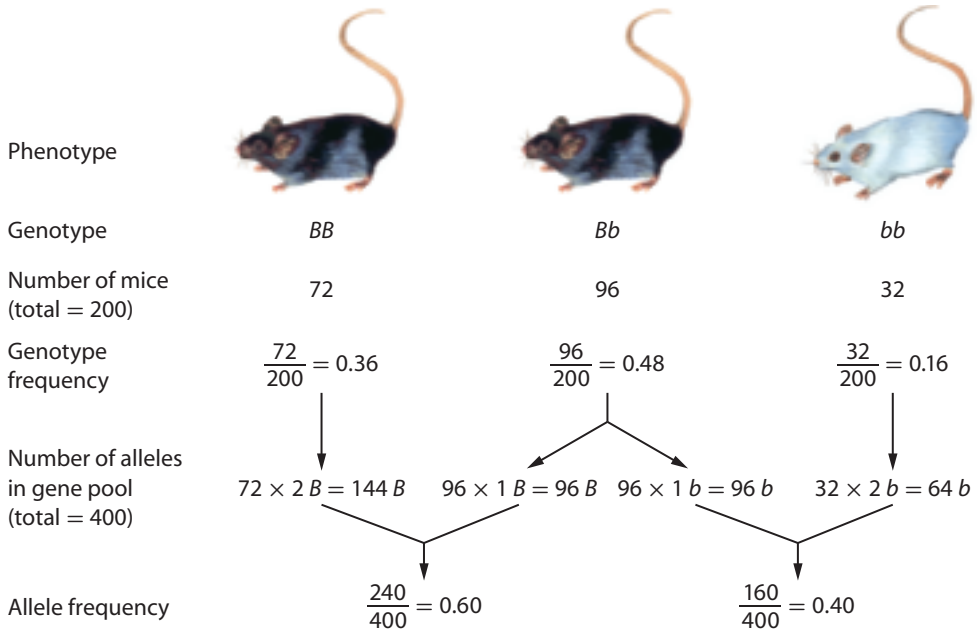


Figure 19.3 Determining the genotype and allele frequencies in a population sample by counting

organisms have two possible alleles for every gene, the total number of alleles in a population is twice the number of individuals. The sample of 200 mice, for example, has a total of 400 coat colour alleles.

The number of *B* or *b* alleles in the mouse population can be found by simply counting these alleles:

72 *BB* mice with 72 × 2 = 144 *B* alleles
and 0 × 72 = 0 *b* alleles

96 *Bb* mice with 96 × 1 = 96 *B* alleles
and 96 × 1 = 96 *b* alleles

32 *bb* mice with 32 × 0 = 0 *B* alleles
and 32 × 2 = 64 *b* alleles

Totals: 144 + 96 + 0 = 240 *B* alleles
and 0 + 96 + 64 = 160 *b* alleles

The frequency of each allele is found by dividing the incidence of the allele by the total number of alleles in the sample. Thus, the frequency of the *B* allele is $\frac{240}{400} = 0.60$, or 60 percent. The frequency of the *b* allele is $\frac{160}{400} = 0.40$, or 40 percent. This also means that 0.60 (60 percent) of the gametes produced will carry the *B* allele and 0.40 (40 percent) will carry the *b* allele. Because there are only two versions of the coat colour gene, the allele frequencies add up to 1.00—that is, 0.60 + 0.40 = 1.00 (100 percent).

Q1 What makes up a population's gene pool?

Q2 Distinguish among genotype frequency, phenotype frequency, and allele frequency.

Introducing the Hardy-Weinberg Principle

It might seem logical to assume that a recessive allele, such as the allele for albinism (lack of pigmentation), would eventually be eliminated from a population. This was the prevalent thinking among biologists in the early 1900s. In many populations, however, some recessive alleles are more common than the corresponding dominant alleles. Human blood type O, for example, is a recessive blood type, but it is the most common blood type among Albertans. How is this possible?

In 1908, two scientists, working independently, provided a mathematical model for studying population genetics. Godfrey Hardy, an English mathematician, and Wilhelm Weinberg, a German physician, each showed that allele frequencies in a population will remain

the same from one generation to the next, as long as five conditions are met:

1. The population is large enough that chance events will not alter allele frequencies.
2. Mates are chosen on a random basis.
3. There are no net mutations.
4. There is no migration.
5. There is no natural selection against any of the phenotypes.

The prediction based on these conditions is known as the **Hardy-Weinberg principle**.

The Hardy-Weinberg principle allows us to study one trait at a time. Consider the simplest case, a trait that is controlled by a dominant allele and a recessive allele. In this case, the letter p represents the frequency of the dominant allele in the population. The letter q represents the frequency of the recessive allele. Thus, p and q represent the proportion of these alleles in the population. Since there are only two alleles, when their frequencies are added together, the sum must be 1.00, or 100 percent of the alleles.

p	+	q	=	1.00
frequency of dominant allele		frequency of recessive allele		all the alleles (100 percent)

These allele frequencies also represent the genetic contribution that the population can make to the next generation. The Punnett square in Figure 19.4 on the next page shows the proportions of the two alleles in the gametes that can be produced by a population of black (*Bb* or *BB*) and white (*bb*) mice. Remember that each sperm and each egg is haploid and therefore carries only one of the alleles, dominant or recessive. In this example, the allele frequencies, p and q, are 0.70 and 0.30, respectively. This provides a general equation that can be used to determine the frequencies of different genotypes in a population. This equation, known as the **Hardy-Weinberg equation**, is highlighted to the right.

You know that the inner squares of a Punnett square represent the results of fertilization—the diploid offspring. Thus, a Punnett square takes into account all the possible recombinations of the given alleles. According to the product rule, if p represents the frequency of the dominant allele (*B*), then p^2 represents the frequency of the homozygous dominant offspring (*BB*). Similarly, if q represents the frequency the recessive allele (*b*), then q^2 represents the frequency of the homozygous recessive offspring (*bb*).

As shown in the Punnett square in Figure 19.4, there are two possible recombinations that will result in the heterozygous genotype (*Bb*). Therefore, the frequency of the heterozygous genotype is $pq + pq = 2pq$.

Given the allele frequencies, $p = 0.70$ and $q = 0.30$, we can calculate the frequencies of the different genotypes: p^2 is 0.49, q^2 is 0.09, and $2pq$ is 0.42. Thus, 49 percent of the individuals in the next generation will be homozygous for the dominant allele, 42 percent will be heterozygous, and 9 percent will be homozygous recessive.

Notice that the sum of all the genotypes is equal to 1.00, or 100 percent:

0.49	+	0.42	+	0.09	=	1.00
49 percent	+	42 percent	+	9 percent	=	100 percent
p^2	+	$2pq$	+	q^2	=	1.00

In other words, 70 percent of the mice in the study population have at least one dominant allele (*B*), while the other 30 percent have at least once recessive allele (*b*). Again, the sum of these allele frequences is 1.00, or 100 percent.

p^2	+	$2pq$	+	q^2	=	1.00
frequency of homozygous dominant genotype		frequency of heterozygous genotype		frequency of homozygous recessive genotype		all the individuals in the population (100 percent)

The Hardy-Weinberg equation can be used to calculate the proportion of a population that carries recessive alleles for genetic conditions, such as sickle cell anemia or cystic fibrosis. It can also

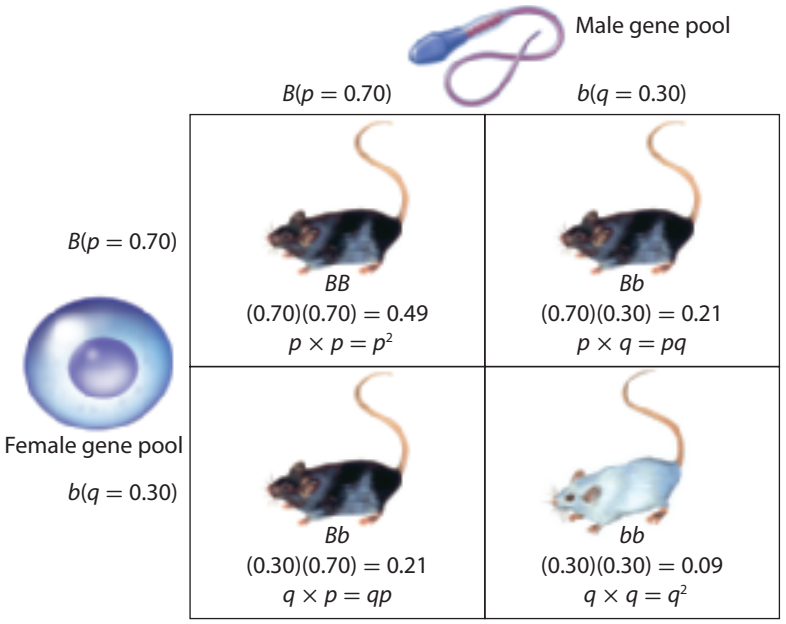


Figure 19.4 A Punnett square can be used to determine the expected genotype frequencies in the next generation. This Punnett square has been scaled up to represent the genotype frequencies for the gametes in an entire gene pool. In generic terms, p^2 represents the homozygous dominant offspring, $2pq$ represents the heterozygous offspring, and q^2 represents the homozygous recessive offspring.

be used to calculate the number of individuals with a specific genotype, such as the number of carriers of a genetic condition. To calculate the number of individuals, however, you need to know the population size, N:

$$p^2(N) + 2pq(N) + q^2(N) = N$$

Study the Sample Problems that follow. Then complete the Practice Problems and the Investigation that appear afterward.

3. What are the conditions of the Hardy-Weinberg principle?
4. Using the Hardy-Weinberg equation, distinguish between p and p^2 as used to describe a population.
5. How is it possible to find the number of heterozygotes in a sample population, given the allele frequencies?

Sample Problems

Sample Problem 1

Albinism in a Snake Population

In a randomly mating population of snakes, one out of 100 snakes counted is albino, a recessive trait. Determine the theoretical percentage of each of the genotypes in the population.

What Is Required?

To determine the values for p^2, $2pq$, and q^2, which represent the frequencies of the *AA*, *Aa*, and *aa* genotypes in the population

What Is Given?

The value of q^2: The proportion of snakes that are albino and thus have the *aa* genotype is $\frac{1.00}{100.00}$.
$p + q = 1.00$

Plan Your Strategy

Change the value of q^2 to a decimal.
Take the square root of the value of q^2 to find the value of q.
Subtract q from 1.00 to find the value of p.
Find the values of p^2 and $2pq$.
Express p^2 and $2pq$ as percents.

Act on Your Strategy

Step 1

$$q^2 = \frac{1.00}{100.00}$$
$$= 0.0100, \text{ or } 1.00\ \%$$

Step 2

$$\sqrt{q^2} = \sqrt{0.0100}$$
$$q = 0.100$$

Step 3

$$p + q = 1.00$$
$$p = 1.00 - q$$
$$= 1.00 - 0.100$$
$$= 0.900$$

Step 4

$$p^2 = (0.900)(0.900)$$
$$= 0.810, \text{ or } 81.0\ \%$$
$$2pq = 2(0.900)(0.100)$$
$$= 0.180, \text{ or } 18.0\ \%$$

The theoretical percentages of the genotypes are 81.0 percent *AA*, 18.0 percent *Aa*, and 1.00 percent *aa*.

Check Your Solution

$$p^2 + 2pq + q^2 = 1.00, \text{ or } 100\ \%$$
$$81.0\ \% + 18.0\ \% + 1.00\ \% = 100\ \%$$
$$100\ \% = 100\ \%$$

Sample Problem 2

Wing Length in Fruit Flies

A single pair of alleles codes for one of the genes that controls wing length in fruit flies (*Drosophila melanogaster*). The long wing allele (L) is dominant to the short wing allele (l). If 40 fruit flies out of 1000 that are counted have short wings, how many fruit flies out of 1000 would be expected to be heterozygotes?

What Is Required?

To determine the number of fruit flies that are heterozygous (Ll) for the wing length gene, given a population sample (N) of exactly 1000

What Is Given?

The proportion (q^2) of homozygous recessive (ll) fruit flies in the sample, $\frac{40}{1000}$

Plan Your Strategy

Change the frequency of q^2 to a decimal.
Take the square root of the value of q^2 to find the value of q.
Subtract q from 1.00 to find the value of p.
Find the value of $2pq$.
Multiply the population size (N) by the frequency of the heterozygous genotype ($2pq$).

Act on Your Strategy

Step 1

$$q^2 = \frac{40.0}{1000}$$
$$= 0.040$$

Step 2

$$\sqrt{q^2} = \sqrt{0.0400}$$
$$q = 0.200$$

Step 3

$$p + q = 1.00$$
$$p = 1.00 - q$$
$$= 1.00 - 0.200$$
$$= 0.800$$

Step 4

$$2pq = 2(0.800)(0.200)$$
$$= 0.320$$

Step 5

$$\text{number of heterozygotes} = (2pq)(N)$$
$$= (0.320)(1000.0)$$
$$= 3.2 \times 10^2$$

The population sample would be expected to contain exactly 320 fruit flies that are heterozygous (Ll) for the wing length gene.

Check Your Solution

$$p^2 + 2pq + q^2 = 1.00$$
$$(0.800)^2 + 0.320 + 0.0400 = 1.00$$
$$0.640 + 0.320 + 0.0400 = 1.00$$
$$1.00 = 1.00$$

Fruit fly with long wings

Fruit fly with short wings

Practice Problems

1. Suppose that in a fruit fly population the frequency of the recessive allele that codes for short wings (l) is 0.30. What would be the expected genotype frequencies in the next generation?

2. In a pea plant population, the dominant allele for tallness (T) has a frequency of 0.64. What percent of the population would be expected to be heterozygous (Tt) for the height alleles?

3. In a randomly mating population of mice, 25.0 out of every 100.0 mice born have white fur, a recessive trait.

a) Calculate the frequency of each allele in the population.

b) Calculate the genotype frequencies for the population.

4. A dominant allele, T, codes for the ability to taste the compound phenylthiocarbamide (PTC). People who are homozygous for the recessive allele, t, are unable to taste PTC. In a genetics class of 125 students, 88 students can taste PTC and 37 cannot.

a) Calculate the expected frequencies of the T and t alleles in the student population.

b) How many students would you expect to be heterozygous for the tasting gene?

c) How many students would you expect to be homozygous dominant for the tasting gene?

d) How could you check your answers for parts (b) and (c)?

5. In the Caucasian population of North America, one out of every 10 000 babies is born with a recessive condition known as phenylketonuria (PKU). This condition is controlled by a single pair of alleles. People who are homozygous recessive for the PKU gene completely lack the enzyme that is necessary to metabolize the amino acid phenylalanine into harmless by-products. The presence of this amino acid in a baby's diet can slow the development of the baby's brain. What percentage of the Caucasian population of North America would you expect to be heterozygous for the PKU allele?

Minding *p* and *q*

The Hardy-Weinberg principle not only provides a method for measuring the amount of variation within a gene pool, but also allows geneticists to compare allele frequencies in a population at different times. If there is no change in allele frequencies over time, then the population is said to be at **genetic equilibrium** (also called *Hardy-Weinberg equilibrium*). A population at genetic equilibrium is not changing or evolving. If, on the other hand, there *is* a change in allele frequencies over time, then one of the conditions of the Hardy-Weinberg principle is not being met and the population may be evolving. For example, if the first four conditions are being met, then we can conclude that natural selection is occurring.

The gradual change in allele frequencies in a population is called **microevolution**. An example of microevolution is the development of DDT-resistance in *Anopheles* mosquito populations. The females of 30 to 40 species of *Anopheles* mosquitoes carry the parasitic protozoan, *Plasmodium*. This single-celled parasite causes malaria, a disease responsible for at least one million deaths worldwide annually. The pesticide DDT has been used successfully for decades in tropical and subtropical countries to reduce *Anopheles* numbers in the past, but resistance in some species has limited the effectiveness of DDT over time. Look for signs of microevolution in two populations as you complete Investigation 19.B.

Q6 How can you tell if a population is at genetic equilibrium or undergoing microevolution?

INVESTIGATION 19.A

Applying the Hardy-Weinberg Equation

Target Skills

Asking questions about genotype frequencies based on observable phenotypes, and **investigating** these frequencies

Applying, quantitatively, the Hardy-Weinberg principle to observed data

Interpreting data, and **communicating** results and ideas

Some human traits are controlled by a single gene, with one pair of alleles. These traits can easily be studied to measure genetic variability in a population. The presence of freckles, for example, is generally dominant to the absence of freckles. Unattached earlobes are dominant to attached earlobes. A pointed hairline on the forehead when the hair is pulled back is dominant to a straight hairline. What are the frequencies of the various genotypes in your class?

Procedure

1. Work with a partner. Your teacher will tell you which three single-gene traits to investigate.
2. Survey the class to find out the number of students with each phenotype for the traits you are investigating. For example, survey the class to find out how many students have attached earlobes and how many do not. Alternatively, your teacher will provide you with data to use.

Analysis

1. Using the Hardy-Weinberg equation, determine the frequency of the dominant and recessive alleles for each trait in the class.

Conclusions

2. Determine the frequency of each genotype in the class. (Remember that there are three genotypes for each trait that you investigated.)
3. How closely would you expect your class results to match the genotype frequencies for the population of North America? Explain your answer.

Expanding the Hardy-Weinberg Equation

You have learned how to use the Hardy-Weinberg equation to study pairs of dominant and recessive alleles. The Hardy-Weinberg equation can also be used to study co-dominant alleles, alleles that show incomplete dominance, or alleles that do not produce observable phenotypic differences.

Population ecologists often use DNA testing to find out which allele an individual carries. They can test DNA from several individuals in a population to determine allele frequencies for the sample. Then they can use these frequencies to predict the allele frequencies for the total population. For example, DNA testing was used to find the allele frequencies in the gene pool of a collared pika population (*Ochotona collaris*) over time (Figure 19.5).

In addition, the Hardy-Weinberg equation can be expanded to study genes with multiple alleles. Examine Figure 19.5, for example. Each line in Figure 19.5 represents the frequency of an allele at different points in time, and all the alleles are for the same gene. The sum of the frequencies for all the alleles at any point in time equals 1.00, or 100 percent of the alleles. Changes in the frequencies over time indicate that something is happening to cause microevolution in this vulnerable population.

Q 7 Describe how the two equations based on the Hardy-Weinberg principle can be used to detect gene pool changes over time.

Section 19.1 Summary

- A gene pool contains all the alleles for all the genes in a population that can be passed on to the next generation.
- The Hardy-Weinberg principle provides a basis for studying allele frequencies and genotype frequencies in a gene pool.

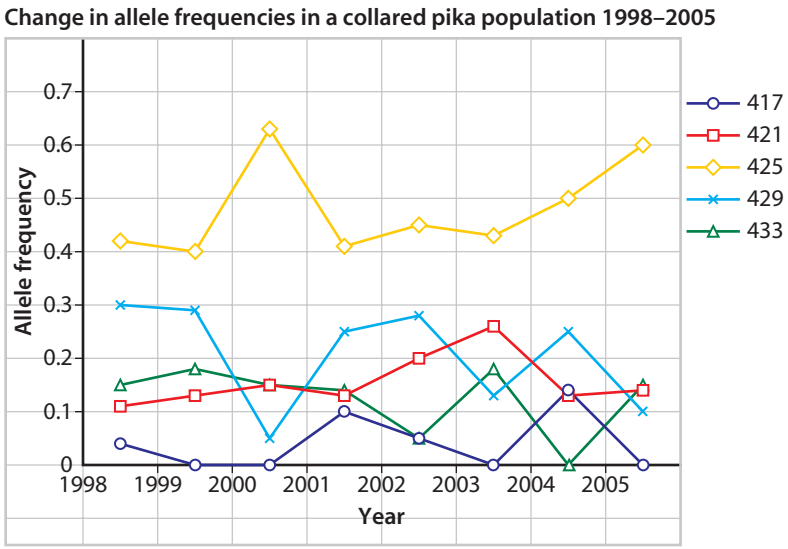


Figure 19.5 The change in frequencies of five alleles (identified by different numbers in the legend) in a collared pika population over eight years. This population, which has been declining in size, appears to be undergoing microevolution. The sum of the allele frequencies estimated for each year of the study is 1.00 (or very close to 1.00 due to rounding and estimation). (Data provided by Jessie Zgurski, University of Alberta.)

- According to the Hardy-Weinberg principle, a population can be at genetic equilibrium only if the population is large enough that chance events do not alter allele frequencies, there is random mating among all individuals in the population, there are no net mutations, there is no migration, and natural selection is not occurring. If any of these conditions are not met, microevolution will occur.
- The total of the allele frequencies, p and q, for one gene locus always equals 1.00, or 100 percent of the alleles.
- According to the Hardy-Weinberg equation, $p^2 + 2pq + q^2 = 1.00$. The letters p and q represent the frequencies of the dominant and recessive alleles, respectively.
- The genotypes in the gene pool are represented by p^2 (frequency of homozygous dominant genotype), $2pq$ (frequency of heterozygous genotype), and q^2 (frequency of homozygous recessive genotype).
- If the population size, N, is known, the number of individuals with a particular genotype can be calculated using the equation, $p^2(N) + 2pq(N) + q^2(N) = N$.

INVESTIGATION 19.B

Testing the Hardy-Weinberg Principle

Target Skills

Predicting what will affect allele and genotype frequencies over time in two model populations

Performing simulations to demonstrate genetic equilibrium and possible gene pool change

Applying, quantitatively, the Hardy-Weinberg principle to observed data

Interpreting data, and **communicating** results and ideas

The Hardy-Weinberg principle states that the allele frequencies in a population will not change from generation to generation, as long as five conditions are met. In this investigation, you will focus on the first two conditions:

- The population is large enough that chance events will not alter allele frequencies.
- Mates are chosen on a random basis.

Part 1 of this investigation involves simulating the effect of random mating on allele frequencies in a large population. Part 2 involves testing to find out if a model population is at genetic equilibrium. You will work with a partner. One of you will carry out the procedure for Part 1, while the other carries out the procedure for Part 2. You will work together to complete the hypothesis and prediction for each part, and the analysis and conclusions.

Question

What processes affect the genetic equilibrium of a population?

Part 1: Demonstrating Genetic Equilibrium

Hypothesis

Make a hypothesis about the effects of random mating on allele and genotype frequencies in a population over time.

Prediction

In a model simulation using 80 beads, the proportion of corresponding alleles in a population undergoing random mating are $\frac{48}{80}$ for *D*, the dominant allele, and $\frac{32}{80}$ for *L*, the recessive allele. Calculate the allele frequencies for *L* and *D*. Use the Hardy-Weinberg equation to predict the expected frequency of each genotype *DD*, *DL*, and *LL*. Then predict the allele and genotype frequencies for future generations.

Materials

- 2 paper cups (or similar containers)
- 48 dark-coloured beads
- 32 light-coloured beads

Procedure

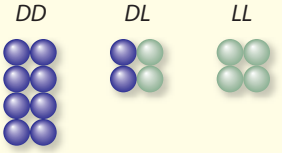
1. Prepare two data tables like the following one. Use one table for your data and the other table for class data.

Number of Each Genotype in a Population Undergoing Random Mating

Generation	Number of *DD*	Number of *DL*	Number of *LL*	Total number of individuals

2. Label one paper cup "male gene pool" and the other paper cup "female gene pool." Put 24 dark-coloured (*D*) and 16 light-coloured (*L*) beads in each cup. The beads represent the alleles for a specific trait.

3. Gently shake the cups to mix the beads. To simulate random mating, without looking, select one bead (allele) from each cup. Place the pair of beads (the genotype of the offspring) on the table. Repeat this process, lining up the genotypes (*DD*, *DL*, and *LL*) in separate columns until you have used all the beads.



4. In your data table, record the number of offspring with each genotype for this generation.

5. To establish the gene pool for the next generation, assume that half the population in each column of beads is male and the other half is female. Place the beads representing the male genotypes in the male gene pool and the beads representing the female genotypes in the female gene pool. Remember that genotypes are made up of two alleles, so each male and female must contribute two beads to the gene pool. (You should end up with an equal number of alleles in each gene pool. If there is an odd number of genotypes in a column, assume that the last genotype belongs to a male. The next time this happens,

assume that the last genotype belongs to a female. Switch from male to female every time there is an odd number of genotypes in a column.)

6. Repeat steps 3 to 5 three more times to obtain data for a total of four generations.
7. Pool your data with the data obtained by the rest of the class and record the class data.

Part 2: Testing for Genetic Equilibrium

Hypothesis

Make a hypothesis about the effects of a recessive lethal allele on allele frequencies and genotype frequencies in a population over time.

Prediction

The proportions of corresponding alleles in a population are $\frac{48}{80}$ for *D* (the dominant allele for a healthy phenotype) and $\frac{32}{80}$ for *L* (the recessive lethal allele). Calculate the allele frequencies for *L* and *D*. Use the Hardy-Weinberg equation to predict the expected frequency of each genotype *DD*, *DL*, and *LL*. Then predict the allele and genotype frequencies for future generations.

Materials

- 3 paper cups (or similar containers)
- 48 dark-coloured beads
- 32 light-coloured beads

Procedure

1. Prepare a data table like the one below. Use one table for your data and the other table for class data.

Number of Each Genotype in a Population with a Lethal Allele, *L*

Generation	Number of *DD*	Number of *DL*	Number of *LL*	Total number of individuals

2. Complete steps 2 to 4 as described in Part 1.
3. Assume that the light bead (*L*) is the recessive lethal allele. Therefore, none of the organisms with the *LL* genotype will survive to reproduce. Remove the *LL* genotypes from the population on the table, and place them in a separate cup. You now have two columns of beads on the table: *DD* and *DL*.
4. Complete step 5 as described in Part 1.
5. Repeat steps 2 to 4 three more times to obtain data for a total of four generations.
6. Pool your data with the data obtained by the rest of the class and record the class data.

Analysis

1. **a)** Use the class data from Part 1 to graph the genotype frequencies over four generations. Compare your results with your prediction.
   b) Use the class data from Part 1 to determine the allele frequencies for the fourth generation. (**Hint**: Use the Hardy-Weinberg equation and the equation $p + q = 1.00$.) Compare your results with your prediction.
2. **a)** Use the class data from Part 2 to graph the genotype frequencies over four generations. Compare your results with your prediction.
   b) Use the class data from Part 2 to determine the allele frequencies for the fourth generation. Compare your results with your prediction.
   c) What happened to the total number of alleles in the population over the course of the investigation? Did this affect the results of the investigation? Explain your answer.
3. Explain why data from the whole class were pooled.
4. In reality, each individual contributes one allele to the next generation. Identify any false assumptions that were made when choosing alleles in this investigation.

Conclusions

5. Account for the allele and genotype frequencies observed over time in Part 1. Were the conditions of the Hardy-Weinberg principle met in this population? Explain your answer.
6. Account for the allele and genotype frequencies observed over time in Part 2. Were the conditions of the Hardy-Weinberg principle met in this population? Explain your answer.

1. Is the frequency of a homozygous dominant genotype equal to the proportion of individuals that show the dominant trait? Explain your answer.

2. Suppose that the frequency of a recessive allele is found to be 0.30. When the same population is sampled five years later, the frequency of the recessive allele is found to be 0.20. Do these findings indicate that the Hardy-Weinberg principle is false? Justify your response.

3. Cystic fibrosis is an inherited recessive disorder that causes especially thick mucus to build up in the lungs and digestive tract. The mucus makes it difficult to clear micro-organisms from the airways, so people with cystic fibrosis are prone to dangerous respiratory infections. Among Caucasians, about one in every 3000 newborns is affected by this condition. Determine the frequency of the cystic fibrosis allele among Caucasians. What proportion of this population would you expect to be heterozygous carriers of the cystic fibrosis allele? Express your answers as decimals.

4. The M and N factors are glycoproteins that are found on the surface of red blood cells. Unlike other types of red blood cell antigens, the M and N factors do not cause antibody reactions in human blood transfusions. People with type M blood are homozygous for the M allele, and people with type N blood are homozygous for the N allele. Heterozygous individuals have type MN blood. In a study of a population of Inuit living in the Northwest Territories, 512 people had blood type M, 256 had blood type MN, and 32 had blood type N.

a) Calculate the frequency of each allele, M and N, in the population studied.

b) What would be the expected frequency of each genotype in the next generation, assuming that this population is in genetic equilibrium for the trait.

c) In a second study group, the frequencies of the genotypes were 0.306 MM, 0.491 MN, and 0.203 NN. Could this second study group have, in fact, come from the previously described Inuit population? Explain your answer.

5. In Japan, the incidence of recessive homozygosity for PKU is one in every 119 000 newborns. What percent of the Japanese population is heterozygous for this allele?

6. If 85 percent of the population of Alberta has Rh^+ blood, a dominant trait, what percentage of Albertans would you expect to be heterozygous for this trait?

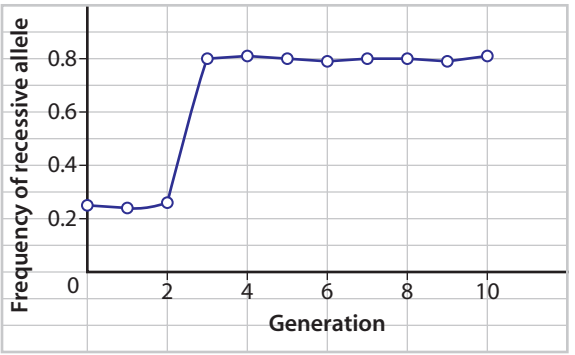
7. A farmer planted some bean seeds. When the seeds germinated, 192 of the seedlings were albino, a recessive trait, and 2880 were green.

a) Determine the proportion of the seedlings that you would expect to be homozygous for the production of chlorophyll. Express your answer as a decimal.

b) Determine the number of seedlings that you would expect to be carriers of the albino allele.

8. The following graph shows the frequency of a recessive allele in the parental generation (0 on the *x*-axis) of a hypothetical fruit fly population and throughout 10 subsequent generations.

Frequency of recessive allele in fruit fly population over time



a) Based on the graph, determine whether or not the fruit fly population is evolving. Justify your response.

b) Describe the frequency of the recessive allele over time. Make a hypothesis to explain what has affected the frequency of the recessive allele over time.

SECTION 19.2

The Causes of Gene Pool Change

Section Outcomes

In this section, you will

- **outline** the conditions that are required in order to maintain genetic equilibrium in a population
- **identify** and **compare** the effects of mutations, gene flow, non-random mating, and genetic drift on gene pool diversity
- **apply**, quantitatively, the Hardy-Weinberg principle to published data, and **infer** the significance of your results
- **distinguish** between the founder effect and the bottleneck effect on gene pools
- **explain** how the process of natural selection is related to the microevolution of a population
- **explain** the cause of heterozygote advantage and how it affects a gene pool
- **describe** strategies that are used in captive breeding and population management
- **explain** that genetic engineering may have both intended and unintended effects on gene pools

Key Terms

genetic diversity
mutation
gene flow
non-random mating
genetic drift
founder effect
bottleneck effect
natural selection
heterozygote advantage

Figure 19.6 Although most mallard ducks migrate south for the winter, some populations stay in Alberta and even Alaska as long as they can find open water and enough food. Male mallard ducks are recognizable by their green heads. Female mallard ducks are brown with white spots.

To most people, the mallard ducks (*Anas platyrhynchos*) shown in Figure 19.6 look much the same as mallards always have. Over time, however, the population these mallards belong to has probably undergone microevolution. For example, a mallard population that stays in Alberta year-round will have occasionally been joined by migrating mallards, which have contributed to the gene pool. On the other hand, an especially cold winter a few years ago might have killed many of the less resilient ducks, reducing **genetic diversity**, the degree of genetic variation within a species or population. Clearly, the conditions of the Hardy-Weinberg principle do not hold true in this population.

The conditions of the Hardy-Weinberg principle represent an ideal situation that rarely, if ever, occurs in natural populations. The principle is valuable, however, because the Hardy-Weinberg equation can be used to measure the amount of change in the allele frequencies of a population over time. Processes such as genetic mutations, gene flow, non-random mating, genetic drift, and natural selection all cause changes in gene pools (Figure 19.7 on page 688). These processes are discussed separately in this section, but they tend to be interacting. Together, over a few generations, they can expand or limit genetic variation in a population.

Q8 What is the relationship between the conditions of the Hardy-Weinberg principle and gene pool change?

Mutations

A **mutation** is a change that occurs in the DNA of an individual. An inheritable mutation, however, has the potential to affect an entire gene pool. While most mutations are neutral, some are harmful and a few are even beneficial. A small number of people, for example, have a rare mutation in a gene that codes for a protein receptor on the surface of the white blood cells. In people without the mutation, HIV can use the protein receptor to enter the white blood cells. Some people who are homozygous for the mutation lack the functioning

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FYI

A major difficulty in developing effective anti-HIV drugs is HIV's ability to rapidly mutate. This ability is partly due to the fact that HIV is a retrovirus and must therefore change its genetic material (RNA) into DNA and then back into RNA before its proteins can be translated. Copying errors before translation are common.

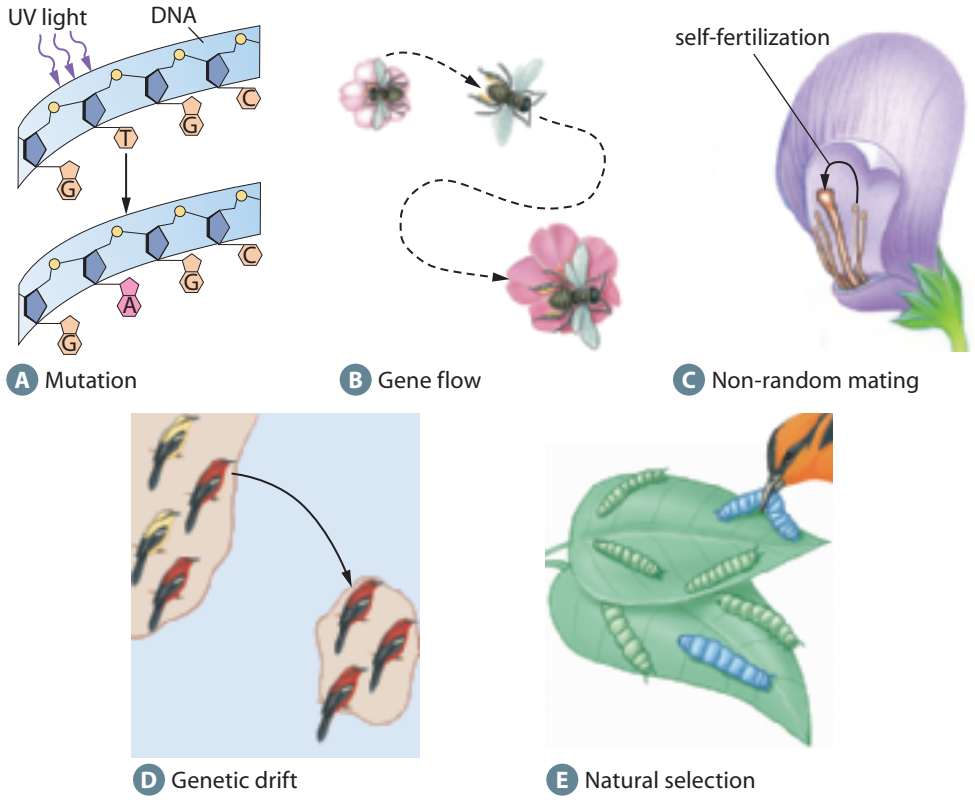

Figure 19.7 The five agents of evolutionary change are **(A)** mutation, a change in DNA; **(B)** gene flow, the migration of alleles from one population to another; **(C)** non-random mating, such as self-fertilization in flowers; **(D)** genetic drift, a change in allele frequencies in a small population due to a chance event; and **(E)** natural selection for favourable variations.

receptor and are therefore resistant to HIV infection (Figure 19.8).

Sometimes *back mutations* occur. These mutations reverse the effects of former mutations. If the number of mutations from *A* to *a* are equal to the number of back mutations from *a* to *A*, then there are no net mutations.

Initially, however, inheritable mutations may diversify a gene pool. The more genetic variation there is in a population, the greater the chance that a variation will be present and provide a selective advantage in a changing environment. Resistance to HIV might be considered an example of a selective advantage.

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Web Link

Scientists are not sure why resistance to HIV would have been a favourable variation in the past. Some scientists have hypothesized that a mutation in the CCR5 receptor helped people resist a form of bubonic plague. Other scientists have suggested that the mutation provided protection against the smallpox virus. Analyze the evidence for these hypotheses, and draw your own conclusions.

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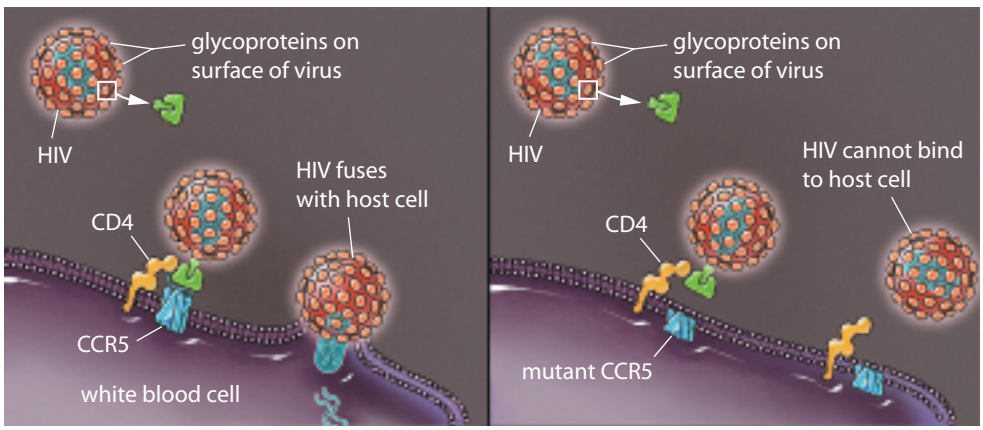

Figure 19.8 In healthy white blood cells, CCR5 is a receptor for chemical messages of the immune system. Along with the receptor CD4, CCR5 acts as a receptor for HIV. Some people who are homozygous for a mutation in the CCR5 gene are resistant to HIV infection.

Another example is poison resistance in the Norway rat (*Rattus norvegicus*). The compound Warfarin has been widely used to control rat populations since the 1950s. Warfarin is a blood thinner, which means that it prevents the blood from clotting and can therefore cause internal bleeding. Before Warfarin was introduced as a rat poison, it is likely that a few rats already had a mutation that made them resistant to Warfarin's effects. These rats survived applications of Warfarin, mated, and passed on the mutation for Warfarin resistance to their offspring. By the 1960s, there were many Warfarin-resistant rat populations in Europe.

9 Explain how inheritable mutations may add to the diversity of a gene pool.

Gene Flow

Gene flow describes the net movement of alleles from one population to another due to the migration of individuals (Figure 19.9). Grey wolves (*Canis lupis*), for example, have large territories. In addition, a lone grey wolf may travel over 800 km in search of a new territory or breeding partner. Very often, a grey wolf from one population will mate with members of a nearby population and may bring new alleles into the gene pool of the nearby population (Figure 19.10). As a result, genetic diversity in the nearby population may increase. Having greater genetic diversity may help this population survive.

Wolf conservationists considered the importance of genetic diversity when they reintroduced the grey wolf to Yellowstone National Park in the United States in the mid-1990s. Grey wolves from different populations in Alberta, and later British Columbia, were captured and brought to Yellowstone. These 32 wolves formed the basis of a new, successful population that grew to 148 individuals by 2003.

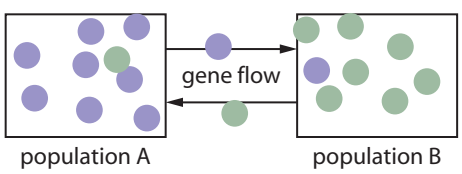

Figure 19.9 Gene flow between nearby populations

Figure 19.10 Gene flow between grey wolf populations is quite common because individuals travel long distances. Why might scientists have difficulty in defining distinct grey wolf populations in North America?

While gene flow increases genetic diversity in one population, it reduces genetic differences among populations. As a result, adjacent populations tend to share many of the same alleles. In the past, for example, local human populations tended to be isolated from one another and probably had distinct gene pools. As cultural and geographic barriers have dissolved, gene flow between human populations has increased. This has reduced genetic differences between local human populations.

10 How does gene flow into a population affect the population's gene pool?

11 Describe the outcomes of two situations that result in gene flow between populations.

Non-Random Mating

Random mating in a population means that there is no way to predict which males will mate with which females, or which females will mate with which males. The probability of any individual with a specific genotype mating with another

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Web Link

The Yukon to Yellowstone Conservation Initiative (Y2Y) combines land stewardship with scientific research to protect habitat within the numerous mountain corridors spanning these two regions. How does the preservation of critical mountain corridors influence gene flow within the Yukon to Yellowstone region?

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FYI

Scientists estimate that everyone carries four to six lethal recessive alleles. When close relatives have children together, the likelihood that these children will receive two copies of the same lethal allele is higher than it is in the general population, resulting in above average rates of infant mortality.

individual with a specific genotype depends on the allele frequencies in the population. Random mating is much like a lottery in which breeding partners are randomly selected by drawing names out of a hat. Unrestricted random mating is probably uncommon in natural populations for two main reasons: preferred phenotypes and inbreeding.

In animal populations, individuals may choose mates based on their physical and behavioural traits. Female greater sage grouse, for example, choose mates based on their phenotypes. In caribou (*Rangifer tarandus*) herds, males compete for mates by using their antlers to spar against other males, chasing one another, and fighting. This is a form of **non-random mating** because it prevents individuals with particular phenotypes from breeding. Only the individuals that mate will contribute to the gene pool of the next generation.

Inbreeding is another example of non-random mating. Inbreeding occurs when closely related individuals breed together. An extreme example of inbreeding is the self-fertilization of some flowers (Figure 19.7). Since close relatives share similar genotypes, inbreeding increases the frequency of homozygous genotypes. Although inbreeding does not directly affect allele frequencies, as homozygous genotypes become more common, harmful recessive alleles are more likely to be expressed. The negative effects of inbreeding are sometimes seen in purebred

Thought Lab 19.1 The Spirit Bear

Target Skills

Describing the factors that cause gene pool diversity to change

Applying, quantitatively, the Hardy-Weinberg principle to published data, and **inferring** the significance of the results

Assessing the role of the Hardy-Weinberg principle in explaining natural phenomena

A Kermode black bear mother and her cubs

The Kermode bear (*Ursus americanus kermodei*) is a white variety of black bear that is found only in small island populations and in populations on the coastal mainland of British Columbia. Known to local Aboriginal peoples as the spirit bear, the Kermode is rare and people are unclear about how best to ensure its survival. Scientists know that its white coat colour is due to a recessive allele. They rely on bear counts and DNA testing of hair samples to estimate the frequency and distribution of this allele.

Estimated Frequency of White Kermode Bears on Two British Columbia Islands

Location	Gribbell Island	Princess Royal Island
Frequency of white bears	0.3	0.1

Procedure

Use the information and preceding table to answer the following Analysis questions.

Analysis

1. Predict the frequency of the white coat allele in the Kermode bear population of
   - **a)** Gribbell Island
   - **b)** Princess Royal Island
2. Predict the frequency of the heterozygous genotype for coat colour in the Kermode bear population of
   - **a)** Gribbell Island
   - **b)** Princess Royal Island
3. Suggest why the frequency of the white coat allele is different on Gribbell Island and Princess Royal Island.
4. Suggest why some conservationists are concerned about inland black bears having access to the coastal bears' territories.
5. Scientists are unsure if Kermode bears select mates based on coat colour. Suggest how this form of non-random mating might affect coastal black bear populations.

Figure 19.11 A domestic goat (*Capra aegagrus hircus*) with an underbite. Underbites in goats are commonly due to inbreeding.

farm animals and pets, which tend to have a higher incidence of deformities and health problems compared to outbred animals (Figure 19.11). For some purebred animals, fertility rates are very low and offspring die at a young age.

Inbreeding can also have a positive effect on a population, however. If homozygous recessive individuals fail to breed, and there are fewer heterozygous individuals each generation, harmful recessive alleles will be eliminated from the gene pool over time. In wild plant populations, self-fertilization may allow individual plants to reproduce even when they are isolated from one another or there are few pollinators in the area. In addition, artificial selection is often used to produce varieties of crops that consistently express desirable traits.

12 Why is most mating in populations non-random?

13 Describe one effect of non-random mating in plants and one effect in animals.

Genetic Drift

In moments of frustration, older siblings may sometimes say that they are "never going to have children." In biological terms, this means that they will not contribute genetic material to the next generation. Any unique alleles they may have will therefore be lost from the gene pool.

A small population is more likely to lose alleles from its gene pool than a large population is. A change in allele frequencies due to chance events in a small breeding population is called **genetic drift**. The roses (*Rosa* sp.) shown in Figure 19.12 form a small population, and, in each generation, only a few individuals reproduce. Due to random chance, none of the light pink roses (*aa*) or roses heterozygous for this colour (*Aa*) in the second generation reproduced. As a result, the pink petal allele was lost from the population in only three generations.

In general, large populations do not experience genetic drift, because chance events are unlikely to affect overall allele frequencies. For example, in a large population of ground squirrels, predators are unlikely to kill all the ground squirrels with a particular allele. If the population size decreases relatively quickly, however, due to disease, climatic change, or extensive habitat fragmentation, genetic drift can occur.

BiologyFile

Web Link

Africa's Ngorongoro Crater in Tanzania is home to a population of lions (*Panthera leo*) that exhibit little genetic variation. Although the steep crater walls prevent easy movement of animals in and out, migrations of lions have occured over time. Why is there so little genetic diversity in this lion population and what is the population's current status?

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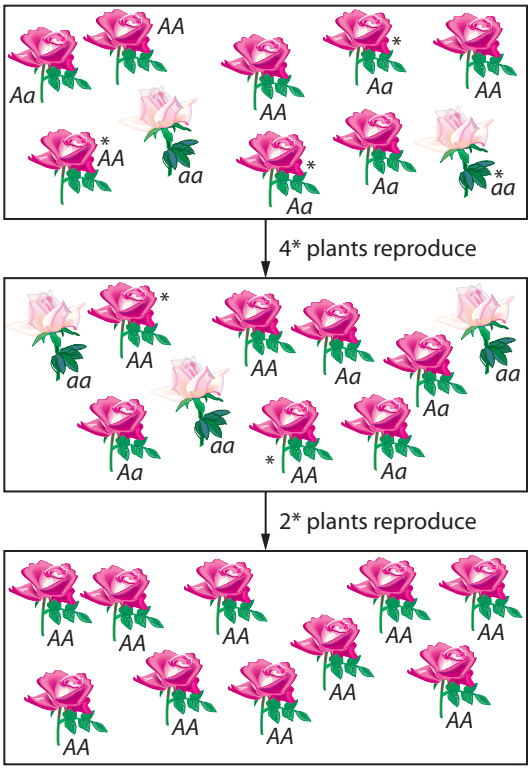


First generation
p (frequency of A) = 0.6
q (frequency of a) = 0.4

Second generation
p = 0.5
q = 0.5

Third generation
p = 1.0
q = 0.0

Figure 19.12 In every generation, only some of the plants in this population reproduce. When the light pink and heterozygous roses in the second generation did not reproduce, the allele for light pink petals was quickly lost from the gene pool.

Q14 Why are small populations more susceptible to genetic drift than large populations are?

The Founder Effect

Often, new populations are formed by only a few individuals, or *founders*. For example, strong winds may carry a single, pregnant fruit fly to a previously unpopulated island, where the fruit fly and her offspring may found a new colony. The founders will carry some, but not all, of the alleles in the original population's gene pool. Diversity in the new gene pool will therefore be limited. Furthermore, the founders may not be typical of the population they came from, and so previously rare alleles may increase in frequency. The gene pool change that occurs when a few individuals start a new, isolated population is called the **founder effect**. The founder effect occurs frequently on islands, and probably occurred when various plants, insects, birds, and reptiles first colonized the islands of Hawaii and the Galápagos.

The founder effect also occurs in human populations, and the lack of genetic diversity in these populations can be a medical concern. Due to the founder effect, the incidence of inherited health conditions in these populations is much higher than average. The Amish population of Philadelphia, Pennsylvania, for example was founded in the 1700s by just a few families. One of the couples carried a recessive allele for Ellis Van Creveld syndrome, a form of dwarfism that also causes bone and heart malformations. This syndrome is nearly 300 times more common in the current Pennsylvania Amish population than in the general U.S. population.

Q15 Describe two possible gene pool changes that could result from the founder effect.

Q16 Why might the founder effect cause inbreeding?

The Bottleneck Effect

Starvation, disease, human activities, or natural disasters, such as severe weather, can quickly reduce a large population. Since the survivors have only a subset of the alleles that were present before the population declined, the gene pool will lose diversity. Gene pool change that results from a rapid decrease in population size is known as the **bottleneck effect** (Figure 19.13).

This phenomenon is often seen in species driven to the edge of extinction. By the 1890s, overhunting had reduced the number of northern elephant seals (*Mirounga angustirostris*) to as few as 20 (Figure 19.14). Today, there are tens of thousands of northern elephant seals, but, due to the bottleneck effect followed by genetic drift, their genetic diversity is very low. Similarly, DNA analysis of cheetahs (*Acinonyx jubotus*) shows little to no genetic variation among individuals. This evidence suggests that their populations declined dramatically in the past, and all the cheetahs that are alive today are descendants of the survivors. As a result, the fertility rates of cheetahs are extremely low, making the work of conservationists very difficult.

Q17 Describe two situations that might result in the bottleneck effect.

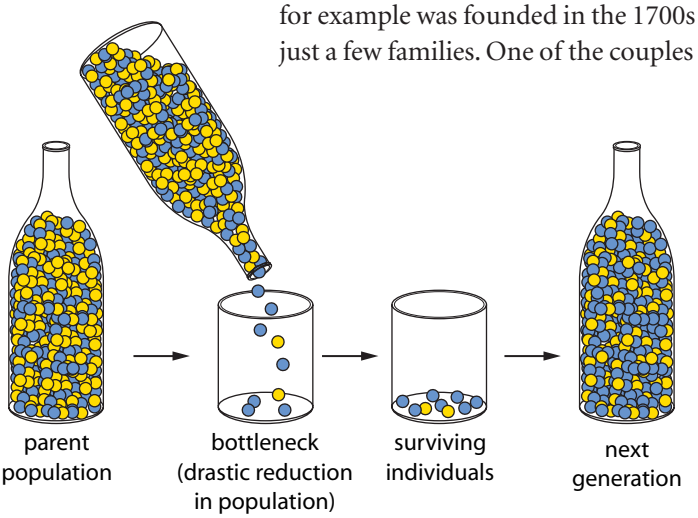


Figure 19.13 Modelling the bottleneck effect. The parent population contains roughly equal numbers of yellow and blue alleles. A catastrophe occurs and there are only a few survivors. Most of these survivors have blue alleles. Due to genetic drift, the gene pool of the next generation will contain mostly blue alleles.

Natural Selection

Natural selection is the only process that leads directly to evolutionary adaptation. In a given environment, some individuals are better able to survive and reproduce than others are. Those individuals with greater fitness breed and pass on their favourable variations to the next generation.

The environment is what makes certain mutations relatively beneficial, neutral, or detrimental. Natural selection occurs when a mutation produces a phenotype that gives one individual a survival advantage over another. Ultimately, if a population's gene pool is small and lacks diversity due to genetic drift, the population may not be able to adapt to environmental change and may become extinct.

You learned about various examples of natural selection in Chapter 4. With the use of antibiotics, a few bacterial cells with genes for antibiotic-resistance had a *selective advantage* over other bacterial cells, resulting in new populations of bacteria that were antibiotic resistant. The frequency of the allele for dark wings in the peppered moth changed as levels of air pollution changed. It is possible that human resistance to HIV, the Ebola virus, the West Nile virus, and other viruses will increase in frequency as these viruses become more widespread in the population.

Sexual selection, which results from a form of non-random mating, is related to natural selection. If a male greater sage grouse can attract more mates as a result of his bright air sacs and extravagant tail feathers, then his phenotype gives him a reproductive advantage over the other males in his population. Furthermore, scientists hypothesize that female greater sage grouse may associate his looks and behaviour with being strong and healthy—both important survival advantages.

Survival advantages also explain why some lethal recessive alleles remain in the human gene pool rather than being eliminated over time. Several alleles that are related to genetic health conditions are thought to provide a **heterozygote advantage**. For example, an allele for cystic fibrosis may help carriers better resist diarrheal diseases such as cholera. The allele for Tay-Sachs disease may protect against tuberculosis, a bacterial infection of the lungs, while the allele for PKU may protect against miscarriages caused by fungal toxins.

Figure 19.14 The northern elephant seal became protected in the early 20th century, and, since then, its populations have recovered. Why might the lack of genetic variation in current northern elephant seal populations put them at risk once again?

Q18 What is the relationship between mutations and natural selection?

Q19 Define heterozygote advantage.

Human Activities and Genetic Diversity

Human activities can affect the genetic diversity of populations in various ways. Habitats may become fragmented when people convert large stretches of wilderness into croplands or when they develop wild areas, construct dams, or build roads. These human-made barriers may prevent gene flow between the split populations. Over time, the isolated populations may undergo adaptive radiation if their environments are very different. Due to genetic drift, however, each population will likely have little genetic diversity within it.

Unregulated hunting, habitat removal, and other human activities that cause populations to decline abruptly can cause a bottleneck effect followed by genetic drift. The sudden large-scale loss

of genetic diversity results in inbreeding, which may cause fertility rates to decline. Populations that lack genetic diversity are more susceptible to new diseases and other environmental changes, too (Figure 19.15). As you will learn in Thought Lab 19.2, conservation and wildlife management programs must take into account the processes affecting gene pools in order to ensure that wild populations remain large enough and have sufficient genetic diversity to survive.

Q20 In what ways can habitat fragmentation affect gene pools of natural populations?

Thought Lab 19.2 Maintaining Genetic Diversity in the Whooping Crane

Target Skills

Describing the factors that affect the genetic diversity of an endangered species

Assessing the value of captive breeding programs in preserving the genetic diversity of an endangered species

Whooping cranes

The whooping crane (*Grus americana*) is the tallest bird in North America. Standing 1.5 m high, this graceful white bird has a wingspan of 2.5 m. The whooping crane—affectionately referred to as the whooper—lives and breeds in shallow wetlands surrounded by bulrushes (*Scirpus* sp.) and other sedges. Its diet includes plant roots, crustaceans, mollusks, and insects. At age 3 to 4, it reaches sexual maturity. The adult whooper is known for its magnificent mating behaviour, which involves displays of plumage, courtship dances, and synchronized honking to signal its choice of a life mate. The female lays two eggs a year, but the couple will raise only one, usually the first to hatch, and may push the other from the nest.

The largest current population of whooping cranes migrates between Wood Buffalo National Park in northern Alberta and Aransas National Wildlife Refuge in southern Texas. Scientists estimate that there were 1400 migrating whooping cranes in the late 1800s. The total population fell to about 15 in the 1940s. Loss of habitat, excessive hunting, avian disease, and lead poisoning were some of the factors that contributed to their decline. The discovery and preservation of the whoopers' nesting and over-wintering grounds has helped to reverse this trend. The introduction of hunting regulations and the establishment of captive breeding programs, one of which is at the Calgary Zoo, has also helped. The world population of whoopers has now increased to over 300.

Procedure

Use the preceding information to answer the following Analysis questions. You may also use library, Internet, or other resources to help you answer the questions.

Analysis

1. All the whooping cranes that are alive today are descendants of the 15 or so that remained in the 1940s. Make a hypothesis about the degree of genetic diversity within current whooping crane populations, and justify your thinking.
2. Does the fact that pairs bond for life help or hinder captive breeding programs? Explain your answer.
3. DNA technologies, such as DNA sequencing, are being used to determine the relatedness of all the whooping cranes in the main migrating population. How could conservationists use this information to assess the vulnerability of the population to environmental change?
4. To re-establish another wild population of whooping cranes, conservationists placed whooping crane eggs in the nests of sandhill cranes (*Grus canadensis*). The whooping cranes reared by the sandhill cranes feed normally and migrate, but are not breeding. Suggest a reason why the breeding program has not been successful.
5. Suggest a method, other than captive breeding programs, that could be used to protect wild whooping cranes. Explain how this method works and how it would affect the world's population of whooping cranes.

Extensions

6. Evaluate the role of gene banks in helping to preserve endangered species, such as the whooping crane, and in helping to maintain genetic diversity within populations.
7. Identify and describe technologies that are being used by whooping crane breeders to improve the success of captive egg hatching and chick rearing.

Figure 19.15 During the last century, the chestnut blight fungus (*Cryphonectria parasitica*), an introduced species, decimated populations of the American chestnut tree (*Castanea dentate*). As a result, the current populations of American chestnut trees have little genetic variation.

Section 19.2 Summary

The Hardy-Weinberg equation is used to detect microevolution (changes in the diversity of a gene pool). Microevolution in a population is caused by one or more of the following five processes:

1. Inheritable mutations that arise may be beneficial, neutral, or detrimental in a given environment.
2. Gene flow due to the emigration and immigration of individuals increases the genetic diversity of a population that receives new members, but decreases the genetic diversity among populations.
3. Non-random mating can result in sexual selection for preferred phenotypes, or inbreeding. Inbreeding can severely limit genetic diversity in gene pools, making populations more vulnerable to environmental change.
4. Genetic drift can result in the loss of alleles from small populations, and an increase in the frequency of previously rare alleles. The founder effect and the bottleneck effect are two extreme causes of genetic drift.
5. Natural selection for favourable phenotypes interacts with the other microevolutionary processes and leads to the evolution of adaptations. Various human activities can affect the amount of gene flow and genetic drift in natural populations.

BiologyFile

Web Link
What do you do when you re-establish a bird population that migrates, but has no parents to learn from? Whooping crane conservationists have become very creative!

www.albertabiology.ca
WWW

Section 19.2 Review

1. Draw a two-column table. In the first column, list the five conditions that are associated with the equilibrium of allele frequencies, as identified by the Hardy-Weinberg principle. In the second column, describe the possible effects on a population's genetic diversity if each condition is not met.
2. How can mutations help populations survive?
3. Predict what might happen to the diversity of a gene pool if individuals with rare alleles emigrated from the population.
4. Compare and contrast the founder effect with the bottleneck effect. Specifically, how do these effects occur and how can they change a gene pool?
5. In what ways might the lack of genetic diversity in cheetahs put their populations at risk? Provide an example of a human action that could be taken to increase the genetic diversity of cheetahs.
6. What could prevent a lethal recessive allele from being entirely eliminated from a population?
7. Why is inbreeding in animals unlikely to lead to evolutionary adaptations?
8. HIV mutates and reproduces faster than the body can produce antibodies against it. Some antiviral medications slow HIV's reproductive rate. This changes the environment in favour of the immune system, allowing it time to produce antibodies against HIV before it mutates. As a result, these medications can help to delay the progression of HIV to acquired immunodeficiency syndrome (AIDS). Explain how anti-HIV medications impede microevolution of the virus.

Biotechnology and Gene Pools

Genetic variation is the raw material of evolution. Natural sources of variation include genetic mutations, the recombination of alleles during sexual reproduction, gene flow, genetic drift, and various methods of gene transfer between bacteria. Biotechnology now adds genetic engineering to this list of processes. Will biotechnology result in the evolution of new species? Can biotechnology help us preserve species?

Engineering New Species?

Biotechnology—the use of organisms to benefit humanity—includes methods as old as artificial selection and as current as genetic engineering. Modern artificial breeding techniques have been used to develop plant crosses, such as triticale, which is a hybrid of wheat (*Triticum aestivum*) and rye (*Secale cereale*). Genetic engineering allows scientists to combine traits from different species that are incapable of breeding with one another. A gene from a bacterium, for example, can be made to function in a corn (*Zea mays*) plant. This does not mean that bacteria and corn share a breeding population, nor that the transgenic organism is a hybrid. But is the transgenic corn a different species because it has characteristics that are not shared by other corn plants?

All members of a species—interbreeding populations of similar organisms—share a common gene pool. By altering a gene pool, is biotechnology altering the course of evolution? Unlike biotechnology, natural selection acts on individuals, not on isolated genes, and it results in adaptive traits. Genes function in interlocking relationships with other genes in a cell. As a result, biotechnology—in particular, genetic engineering—can have unexpected effects on non-target genes. For example, adding a trait, such as herbicide resistance, to a plant may produce offsetting physiological changes in the plant that will reduce its overall survival rate. For this reason, engineering a transgenic organism that will be useful in industry or agriculture can be a challenge.

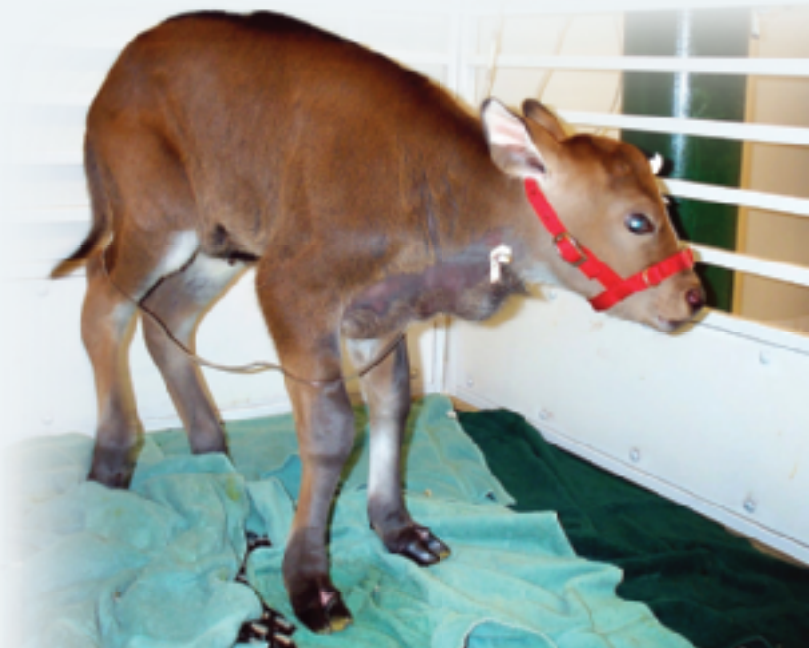
Some forms of biotechnology have the potential to affect wild populations, as well. In Canada, nearly 90 percent of the field tests of genetically engineered plants involve crop plants with introduced genes for herbicide tolerance. Studies show that the added genes can spread to populations of related wild plants by cross-pollination. Should cross-pollination occur, it could result in new populations of herbicide-tolerant weeds.

Cloning to Save Species

Although the tools of biotechnology can change gene pools in both intended and unintended ways, some of these tools can also be used to preserve gene pools. Cloning is one method that may help reverse the threat to endangered species. The first endangered animal to be cloned was the Asian gaur (*Bos gaurus*), a rare, ox-like mammal native to India and Southeast Asia. The animal was cloned from a dead gaur's skin cells, which were fused with a domestic cow's egg cell from which the nucleus had been removed. The egg was then transplanted into a surrogate mother, also a domestic cow (*Bos taurus*). The cloned gaur was born in November 2000, in Iowa in the United States. The same technique may one day be used to resurrect species that have already become extinct.

• • •

1. Are transgenic organisms new species? Explain your answer.
2. How might genetic engineers prevent the spread of introduced genes into wild populations?
3. How might the release of transgenic organisms into the wild affect natural populations?
4. Discuss the benefits and disadvantages of using cloning as a method for protecting endangered species.



This baby gaur was the first endangered species to be cloned. It died a few days after birth. Scientists continue their work to clone mammals, such as the gaur, successfully.

Chapter 19 SUMMARY

A gene pool contains all the alleles for all the genes in a population that can be passed on to the next generation. Population geneticists study gene pools. The Hardy-Weinberg principle is a mathematical model that population geneticists use to determine allele frequencies and genotype frequencies in a population. According to the principle, allele frequencies in a population will remain constant in succeeding generations unless acted upon by outside forces.

The total of the allele frequencies, p and q, for one gene always equals 1.00, or 100 percent of the alleles. A change in the allele frequencies over time indicates that a population is undergoing microevolution. The Hardy-Weinberg equation is $p^2 + 2pq + q^2 = 1.00$, in which the letters p and q represent the frequencies of the dominant and recessive alleles, respectively. The frequency of the homozygous dominant genotype is represented by p^2, the frequency of the heterozygous genotype is represented by $2pq$, and the frequency of the homozygous recessive genotype is represented by q^2. If the population size (N) is known, the number of individuals with a particular genotype can be calculated using the equation, $p^2(N) + 2pq(N) + q^2(N) = N$. The more diverse the gene pool of a population, the better is the population's chance of survival should the environment change.

Inheritable mutations can be neutral, beneficial, or detrimental, depending on the environment. Mutations that provide a selective advantage will increase in frequency due to natural selection.

Gene flow due to emigration and immigration of individuals increases the genetic diversity of a population that receives new members, but decreases the genetic diversity among populations.

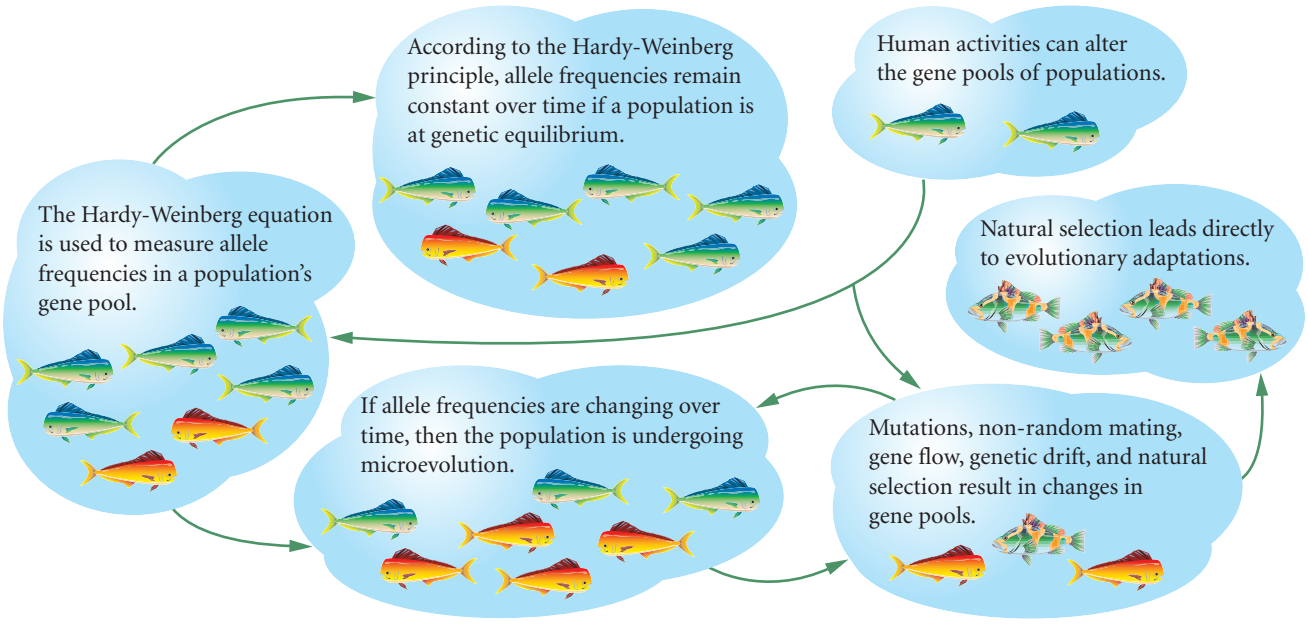
Non-random mating due to mate selection based on phenotypic differences leads to sexual selection. Inbreeding, another form of non-random mating, increases the frequency of homozygous genotypes in a gene pool.

Genetic drift can result in the loss of alleles from small populations due to chance events, as well as an increase in the frequency of previously rare alleles. The formation of an isolated population from a small founding population or population bottleneck may lead to inbreeding and a loss of genetic diversity in the population.

The process of natural selection selects for favourable variations and directly leads to the adaptation of species to their environments. Harmful recessive alleles may be maintained in a population by heterozygous carriers, particularly if the carrier state has greater fitness (called heterozygote advantage) compared with homozygous individuals, under certain environmental conditions.

Human activities can affect the amount of gene flow between and genetic drift within natural populations.

Chapter 19 Graphic Organizer



Understanding Concepts

1. An individual fly has a mutation that allows it to survive being sprayed by an insecticide. Is the mutation itself an example of microevolution? Justify your answer.

2. A population has two alleles for a particular gene (*B* and *b*), and the allele frequency of *B* is 0.70. Calculate the frequency of the heterozygous genotype, assuming that the population is at genetic equilibrium.

3. If 16 out of 100 people in a population have a recessive trait, calculate the frequency of the dominant allele in the population. Assume that the population is at genetic equilibrium. Express your final answer as a decimal.

4. About 11 percent of Canadians have a recessive condition called lactose intolerance, which makes it difficult for them to digest milk and milk products. Calculate the percentage of heterozygous carriers of the lactose intolerance allele and the percentage of individuals homozygous for lactose tolerance. Assume that the population is at genetic equilibrium.

5. In a species of salamander, yellow tail colour (*Y*) is dominant to brown tail colour (*y*). In a sample of 400 of these salamanders, 44 percent are homozygous dominant, 38 percent are heterozygous, and 18 percent are homozygous recessive.

a) Calculate the frequency of each tail colour allele in the population.

b) Calculate the number of salamanders with each genotype in the sample.

6. In a population of ferns at genetic equilibrium, 0.60 of all the gametes carry the dominant allele for curly leaves (*C*). In recessive homozygotes, the recessive allele (*l*) produces straight leaves. Calculate the frequency of the recessive allele in the population and the expected frequency of each genotype in the next generation.

7. Why does genetic drift occur more frequently in small populations than in large populations?

8. If a human population has a higher-than-usual percentage of individuals with a genetic health problem, is the most likely explanation gene flow or genetic drift? Explain your answer.

9. Recall from your studies of Mendelian genetics that the sickle cell allele shows incomplete dominance when inherited with the allele for healthy red blood cells. The incidence of sickle cell anemia was estimated in two human populations, both of which were at genetic equilibrium for this trait. The condition occurred in one out of every 1000 births in the first population, and in three out of every 1000 births in the second population.

a) Determine the expected frequency of the heterozygous genotype in each population.

b) Infer which population most likely originated in Africa. Explain your answer.

c) Sickle cell anemia is often fatal. What accounts for the higher incidence of the condition in the second population?

Applying Concepts

10. Use the following table to answer the questions below.

Change in Genotype Frequencies for a Single Gene in a Collard Pika (*Ochotona collaris*) Population

Year	Number of pikas with each genotype		
	170/170	170/172	172/172
1998	9	6	0
1999	16	6	0
2000	6	6	0
2001	no data	no data	no data
2002	28	4	0
2003	4	0	1
2004	27	6	1
2005	42	9	1

Note: The alleles for the gene under study are called 170 and 172.
Source: Data provided by Jessie Zgurski, University of Alberta

a) Based on the 1998 data, calculate the expected frequencies of the 170 and 172 alleles.

b) Based on the 2005 data, calculate the expected frequencies of the 170 and 172 alleles.

c) Does this collard pika population appear to be at genetic equilibrium? Explain your answer.

d) No individuals that were homozygous for the 172 allele were detected between 1998 and 2002. How did the 172 allele remain in the population?

e) Populations of collard pika in Canada have been declining since 1995. How would you expect this to affect genetic diversity in collard pika populations?

11. In Eastern grey squirrels (*Sciurus carolinensis*), the allele for black fur is dominant to the allele for grey fur. One afternoon, a student observed 10 Eastern grey squirrels in the school yard, and counted eight black squirrels and two grey squirrels.

a) Based on the student's data, calculate the frequency of each fur colour allele in the local Eastern grey squirrel population.

b) Based on the student's data, calculate the percentage of the local squirrel population that you would expect to be heterozygous for fur colour.

c) A credible Internet source stated that the frequency of the grey fur allele is 0.80. How does this value compare with the value you calculated in part (a), based on the student's data?

d) How could the student's sampling method be improved?

e) Account for any differences between the student's data and the other source.

12. In a sample of 1100 Japanese people from Tokyo, 356 individuals belonged to blood group M, 519 belonged to blood group MN, and 225 belonged to blood group N.

a) Calculate the frequency of each allele in the population.

b) Calculate the expected frequency of each genotype in the next generation.

c) Suppose that a small group of people, mostly with blood group N, emigrated from Tokyo to a distant island, where they founded a new colony. Predict how the gene pool for the new population might change.

13. Six out of 2400 babies that were born at a maternity hospital died shortly after birth from colonic obstruction due to a recessive allele.

a) Determine the frequency of the lethal allele in the population, expressed as a percent.

b) What percent of the population would you expect to be carriers of the lethal allele?

c) The population is closely knit and isolated. Explain why the incidence of infant mortality due to the recessive lethal allele is relatively high.

14. A recessive lethal allele in domestic chickens (*Gallus domesticus*) causes circulatory failure and death of the embryo within 70 h. A commercial hatchery finds that a hatching failure greater than 4 percent due to this allele is commercially unacceptable. What is the upper limit of the frequency of this allele that would be acceptable to the hatchery managers? Express your answers as percents.

15. The process of natural selection leads to adaptive phenotypic changes in populations. Compare and contrast the process of natural selection with the process of genetic drift.

16. Draw a pedigree to show how inbreeding could lead to the elimination of the heterozygous genotype for an allele and increase the homozygous genotypes in a small population.

Making Connections

17. Scientists have been using DNA testing to determine the lineage of wild polar bears (*Ursus maritimus*). Their research is helping them learn how far polar bears range and what type of males are most successful at breeding. Because some polar bear populations are declining, the polar bears in these populations are probably becoming less selective about the mates they choose. Suggest how genetic analysis of polar bear populations could be used to help preserve the species. What microevolutionary processes are likely to be occurring in the current populations of polar bears?

18. Phenylketonuria (PKU) is a condition of newborns caused by a recessive allele. The incidence of PKU is one in 160 000 births in China, one in 2600 births in Turkey, and one in 119 000 births in Japan.

a) Calculate the frequency of carriers of the PKU allele in each population. Express your answer as a decimal.

b) There is evidence that the PKU allele is advantageous in the heterozygous state, because it seems to offer protection against miscarriage caused by certain fungal toxins. Make an hypothesis about the relative amounts of the toxin-producing fungi in various regions of the world.

19. Advances in medical technology have greatly improved the quality of life for people with inherited conditions, such as cystic fibrosis, as well as their ability to have children. Over time, what might happen to the frequency of the alleles for such conditions? Justify your answer.

20. A Russian geneticist, Sergi Tshetverikov had this to say about mutations: "Mutations can provide the raw material for evolution but do not constitute evolution itself." Evaluate his comment in the light of what you have learned in this chapter.