

Who Am I?

Species and Races

Individual Census Report



U.S. Department of Commerce
Bureau of the Census

6

What is your race? Mark one or more races to indicate what you consider yourself to be.

- White
- Black, African Am., or Negro
- American Indian or Alaska Native, enrolled or principally



black or blue pen.

How should a woman who has Asian, black, white, and Native American grandparents respond to this question?

MI

- Asian Indian
- Chinese
- Filipino
- Japanese

MOST OF

11.1 What Is a Species? 284
The Biological Species Concept
The Process of Speciation

11.2 The Race Concept in Biology 293

11.3 Humans and the Race Concept 295

The Morphological Species Concept
Modern Humans: A History
Genetic Evidence of Divergence
Human Races Are Not Biological Groups
Human Races Have Never Been Truly Isolated

11.4 Why Human Groups Differ 306

Natural Selection
Convergent Evolution
Genetic Drift
Sexual Selection
Assortative Mating

11.5 Race in Human Society 313



What race is Indigo?



Do the races on Indigo's census form represent different "basic types" of humans?

Indigo pondered the choices in front of her: White, Black, American Indian or Alaskan Native, Vietnamese, Other Asian. As the daughter of a man with African American and Choctaw ancestry, and a woman with a white American father and a Laotian mother, Indigo was not sure what race she should report on the U.S. census form.

The 2000 census was different from all previous censuses in that it allowed people to check multiple boxes under the category, "race." While this change satisfied many multiracial individuals who felt that it was impossible to classify themselves as one particular race, the opportunity to do so was disquieting to others. In Indigo's case, despite having a half-Asian mother, she knew that most people saw her as black, and her connection to her mother's white father was weak at best; she didn't feel a kinship to other whites at all. And while her dad was proud of his Choctaw heritage, Indigo did not know a single Native American. Indigo did not see herself as belonging to any of the races on the census form. Maybe "human" was what she was looking for. She wondered, "Why do I need to specify my racial category? And what does it mean? If I'm part white and part black, am I somehow different from each group?"

Indigo's questions reflect those posed by many people over the years. Why do human groups differ from each other in skin color, eye shape, and stature?



Are we more similar to people of the same race than to people of different races?

Do these physical differences reveal underlying basic biological differences among these groups?

11.1 What Is a Species?

All humans belong to the same species. Before we can understand the concept of race, we first need to understand both what is meant by this statement and what is known about how species originate.

In the mid-1700s, the Swedish scientist Carolus Linnaeus began the task of cataloging all of nature. As described in Chapter 9, Linnaeus developed a classification scheme that grouped organisms according to shared structural traits. The primary category in his classification system was the **species**, a group whose members have the greatest resemblance. Linnaeus assigned a two-part name to each species—the first part of the name indicates the **genus**, or broader group to which the species belongs; the second part is specific to a particular species within that genus. For example, lions, the species *Panthera leo*, are classified in the same genus with other species of roaring cats such as the leopard, *Panthera pardus*. Linnaeus coined the binomial name *Homo sapiens* (*Homo* meaning “man,” and *sapiens* meaning “knowing or wise”) to describe the human species. Although Linnaeus recognized the impressive variability among humans, by placing all of us in the same species he acknowledged our basic unity. Linnaeus did classify humans into different varieties within *Homo sapiens*, a point we will return to in Section 11.3.

Modern biologists have kept the basic Linnaean classification, although they have added a **subspecies** name, *Homo sapiens sapiens*, to distinguish modern humans from earlier humans who appeared approximately 250,000 years ago.

The Biological Species Concept

While most people intuitively grasp the differences between most species—lions and leopards are both definitely cats but not the same species—biologists have had difficulty finding a single, objective definition that can be applied to all situations at all times. Several useful concepts have been proposed and used. The concept most commonly used by biologists interested in the process of species formation is called the biological species concept.

Biological Species Are Reproductively Isolated. According to the **biological species concept**, a species is defined as a group of individuals that, in nature, can interbreed and produce fertile offspring but cannot reproduce with members of other species. In practice, this definition can be difficult to apply. Species that do not overlap in space and so have no opportunity to interbreed, species that do not undergo sexual reproduction (for example, some bacteria), and species known only by their fossils do not easily fit into the biological species concept. However, this definition does provide a basis for us to understand why species generally maintain their distinctness from each other.

Recall that differences in traits among individuals arise partly from differences in their genes. New alleles of a gene occur when the DNA that makes up the gene mutates. By the process of evolution, a particular allele can become more common in a species. If individuals of that species are unable to breed with individuals of another species, then the allele cannot spread from one species to the other. In this way, two species can evolve differences from each other. For example, imagine the common ancestor of lions and leopards. Evidence of the relationship among all large cats indicates that this ancestor had a spotted coat. The allele that eliminated the spots from adult lion coats arose and spread within this species, but it is not found in leopards because lions

and leopards cannot interbreed. Scientists refer to the sum total of the alleles found in all the individuals of a species as the species' **gene pool**. Therefore, we can think of a single species as making up an impermeable container for that species' gene pool—a change in the frequency of an allele in a gene pool can take place only within a biological species.

The Nature of Reproductive Isolation. The spread of an allele throughout a species' gene pool is called **gene flow**. Gene flow cannot occur between different biological species because a pairing between them fails to produce fertile offspring. The inability of pairs of individuals from different species to produce fertile offspring is known as **reproductive isolation**. Reproductive barriers can take two general forms: pre-fertilization barriers or post-fertilization barriers.

Pre-fertilization barriers to reproduction occur when individuals from different species either do not attempt to mate with each other, or if they do, they fail to produce a fertilized egg. The most obvious impediment to mating is that individuals from different biological species simply never contact each other; that is, they are separated by distance, a reproductive barrier known as **spatial isolation**. Among species that are close in space, one barrier to mating is differences in mating behaviors, a mechanism known as **behavioral isolation**. For example, many of the songs and displays produced by birds serve as pre-fertilization barriers. Male blue-footed boobies, sea birds that look almost as goofy as their name implies, perform an elaborate dance for the female before they mate (Figure 11.1a). This dance involves wagging and displaying their electric blue feet and differs from the dances performed by males of other, related booby species. A female blue-footed booby will not respond until she has witnessed several rounds of the dance, at which time she will engage the male in a pointing display (Figure 11.1b). In this display, both birds point their bills skyward, drop their wings, and call out their mating song. The male's dance and the pairs' pointing display presumably provide a way for both birds to recognize that they belong to the same booby species. If a female is courted by a male that cannot perform the "Blue-footed Booby Dance," she will not mate with him. Another barrier to mating results from the physical incompatibility between the sexual organs of two different individuals, a mechanism known as **mechanical isolation**. The genitals of male and female insects of the same species often fit together as specifically as a lock and a key, making matings between two members of different species impossible.

(a) Courting dance



(b) Pointing display

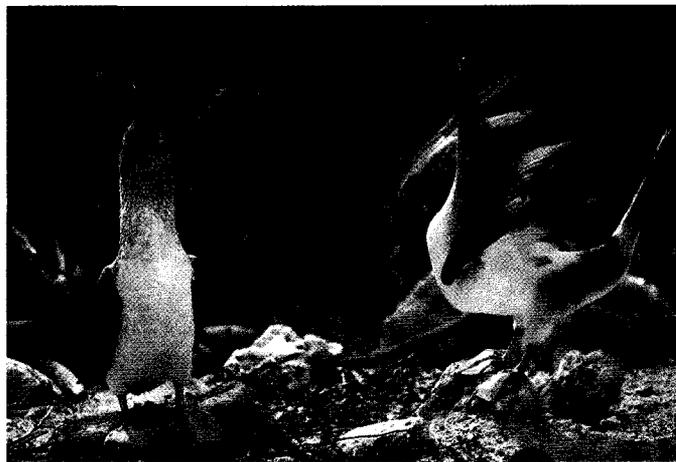


Figure 11.1 A behavioral pre-fertilization barrier to reproduction. (a) Female blue-footed boobies will not mate with males who fail to perform this dance. (b) Male blue-footed boobies will not mate with females who do not engage in the pointing display with them. These behaviors prevent reproduction between unrelated booby species.

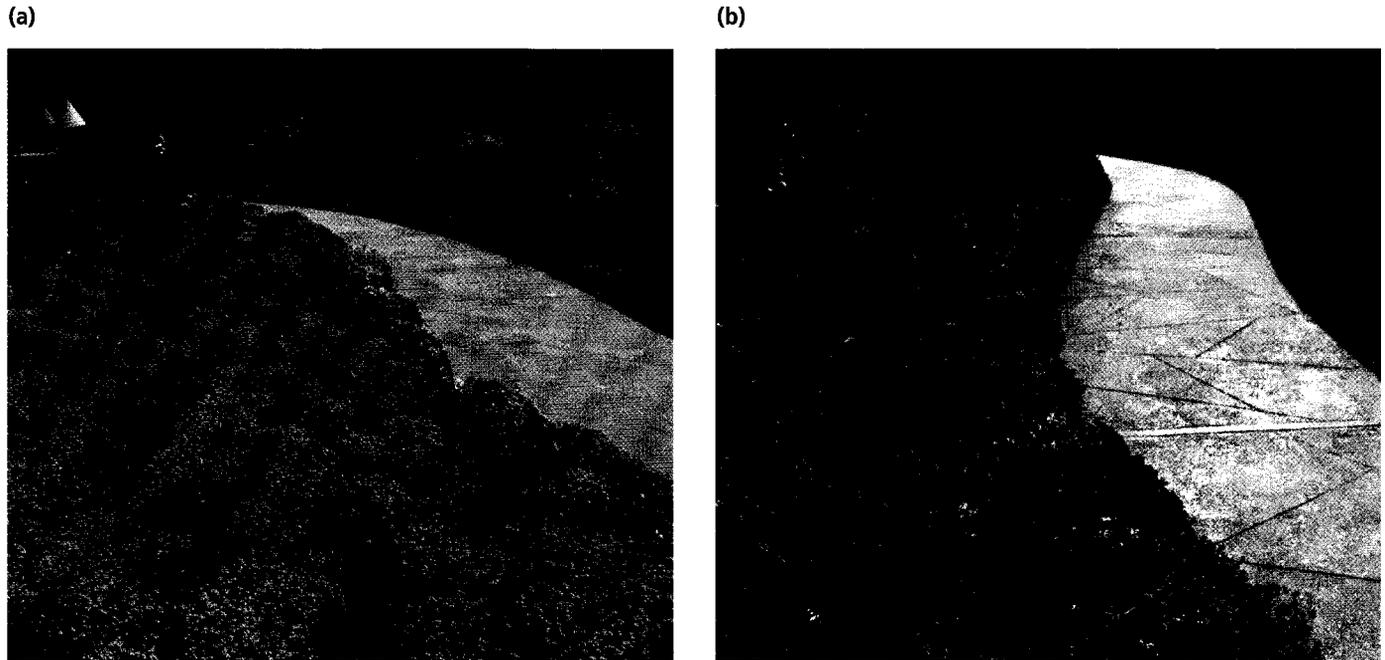


Figure 11.2 A temporal pre-fertilization barrier to reproduction. If different species of flowering plants bloom at different times of the year, they are effectively reproductively isolated. These photos show the completely different suite of species present in (a) spring and (b) summer.

Differences in the timing of reproduction, called **temporal isolation**, can also form a pre-fertilization barrier between species. This is common in flowering plants, different species of which have distinct flowering periods (Figure 11.2). Different species of periodical cicadas, insects that spend most of their lives as larvae in the soil and emerge as adults on a 13- or 17-year cycle, are also isolated temporally. Individuals of the species of cicadas that emerged throughout the eastern United States in the summer of 2004 could not possibly mate with individuals from a species that emerges anytime in the next 12 years.

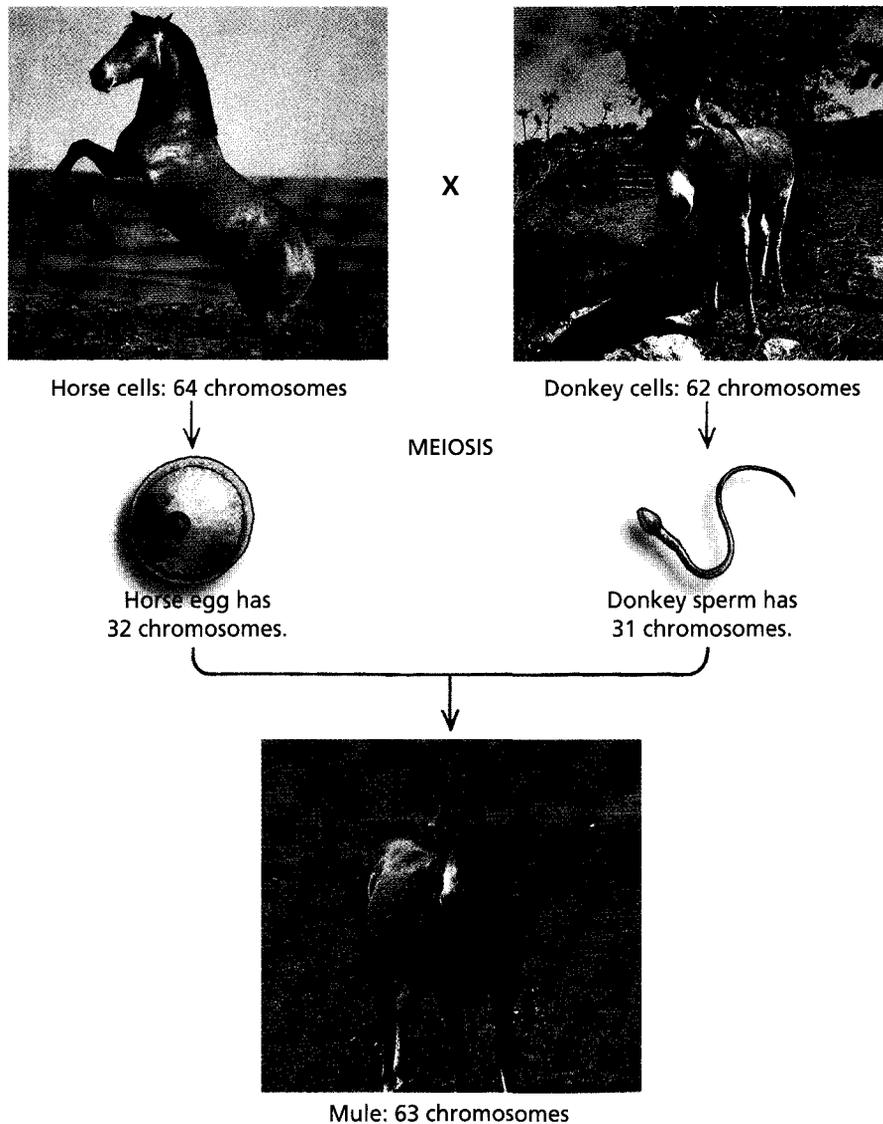
The most common pre-fertilization barrier between species that *will* mate with each other is an incompatibility between eggs and sperm. For fertilization to occur, a sperm cell must bind to a protein on the surface of an egg cell. If the egg does not recognize the sperm (that is, if the egg does not have a protein that will bind to the sperm), fertilization cannot occur. Among animal species that utilize external fertilization and release their sperm and eggs into the environment—such as fish, amphibians, and sponges—this method of reproductive isolation, called **gamete incompatibility**, is widespread. Plants often have a similar incompatibility—pollen from one species cannot fertilize the ovules of another species.

Post-fertilization barriers occur when fertilization happens as a result of mating between two members of different species, but the resulting offspring does not survive or is sterile. Leopons are the result of matings between a male leopard and a female lion—an event that occurs rarely, if ever, in the wild but has been observed in captive cats. Leopons are apparently sterile, although few have been observed, so it is difficult to know the nature of the reproductive barrier. A better-known example of an offspring of a mating between two species is the mule, resulting from a cross between a horse and a donkey. Mules have a well-earned reputation as tough and sturdy farm animals, but they are also sterile and cannot produce their own offspring. Most instances of post-fertilization barriers are less obvious; most **interspecies hybrids**—that is, the offspring of parents from two different species—do not survive long after fertilization. This inability to develop is primarily a result of an incompatibility between the genes of different species. Since different species have different versions of the genes that direct the development of their bodies, placing these genes in combination

often provides a hybrid offspring with incomprehensible information about how to build a body.

In the case of leopons, mules, and other sterile hybrids, the genetic incompatibility is not so large that the offspring cannot develop. Instead, the post-fertilization barrier of hybrid sterility occurs because these hybrids cannot produce proper sperm or egg cells. Recall from Chapters 5 and 6 that during the production of eggs and sperm, compatible genetic sequences called chromosomes pair up and separate during the first cell division of meiosis. Since a hybrid forms from the chromosome sets of two different species, the chromosomes cannot pair up correctly during this process, and the sperm or eggs that are produced in these animals will have too many or too few chromosomes. In the case of mules, the horse parent has 64 chromosomes and therefore produces eggs or sperm with 32; the donkey parent has 62 chromosomes, producing eggs or sperm with 31. The offspring of a cross between a horse and a donkey will therefore have 63 chromosomes and no way to effectively sort these into pairs during the first division of meiosis (Figure 11.3). As a result,

(a) A mule results from the mating of a horse and a donkey.



(b) Why mules are sterile

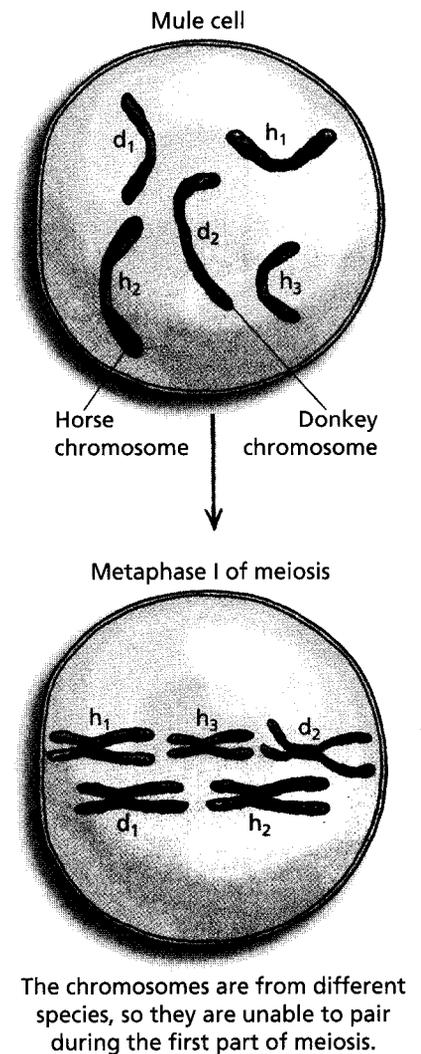


Figure 11.3 Reproductive isolation between horses and donkeys. (a) A female horse produces an egg carrying 32 chromosomes, and a male donkey produces sperm containing 31 chromosomes. A cross between these two animals produces a mule with 63 chromosomes. (b) Mules produce only very few eggs or sperm because their chromosomes cannot pair properly during meiosis. Fewer chromosomes are illustrated to simplify the drawing.

male mules produce few or no sperm, and females release eggs rarely. Despite this low gamete production, a small number of mules have produced offspring, but this event is so rare that the gene pools of donkeys and horses have remained separate despite the mule's popularity as a work animal.

Given the definition of species just discussed, we can see that all humans belong to the same biological species. There is no evidence of post-fertilization barriers to reproduction between different human groups, and Indigo's diverse ancestry clearly demonstrates that no pre-fertilization barriers exist that prohibit mating among the races listed on her census form. To understand the concept of races *within* a species, however, we must first examine how species form.

The Process of Speciation

According to the theory of common descent discussed in Chapter 9, all modern organisms descended from a common ancestral species. This evolution of one or more species from an ancestral form is called **speciation**.

For one species to give rise to a new species, most biologists agree that three steps are necessary:

1. Isolation of the gene pools of subgroups, or **populations**, of the species;
2. Evolutionary changes in the gene pools of one or both of the isolated populations; and
3. The evolution of reproductive isolation between these populations, preventing any future gene flow.

Recall that gene flow occurs when reproduction is occurring within a species. Now imagine what would happen if two populations of a species became *physically* isolated from each other, so that the movement of individuals between these two populations was impossible. Even without genetic or behavioral barriers to mating between these two populations, gene flow between them would cease.

What is the consequence of eliminating gene flow between two populations? It is identical to what occurs in separate biological species. New alleles that arise in one population may not arise in the other. Thus, a new allele may become common in one population, but it may not exist in the other. Even among existing alleles, one may increase in frequency in one population but not in the other. In this way, each population would be evolving independently. Over time, the traits found in one population begin to differ from the traits found in the other population. In other words, the populations begin to **diverge** (Figure 11.4). When the

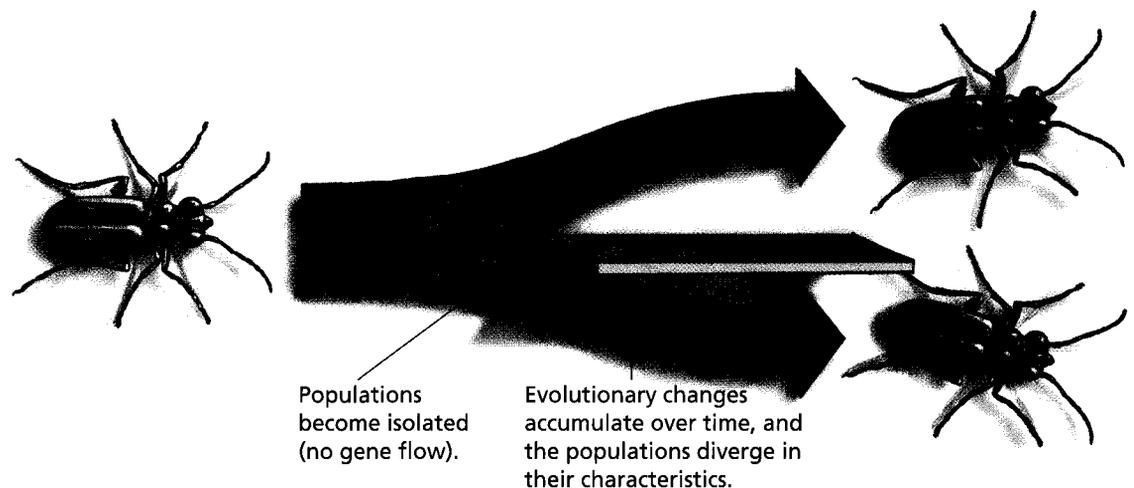


Figure 11.4 Isolation of populations leads to divergence of traits. In this hypothetical situation, populations of beetles diverge as each adapts to its own particular environmental conditions.

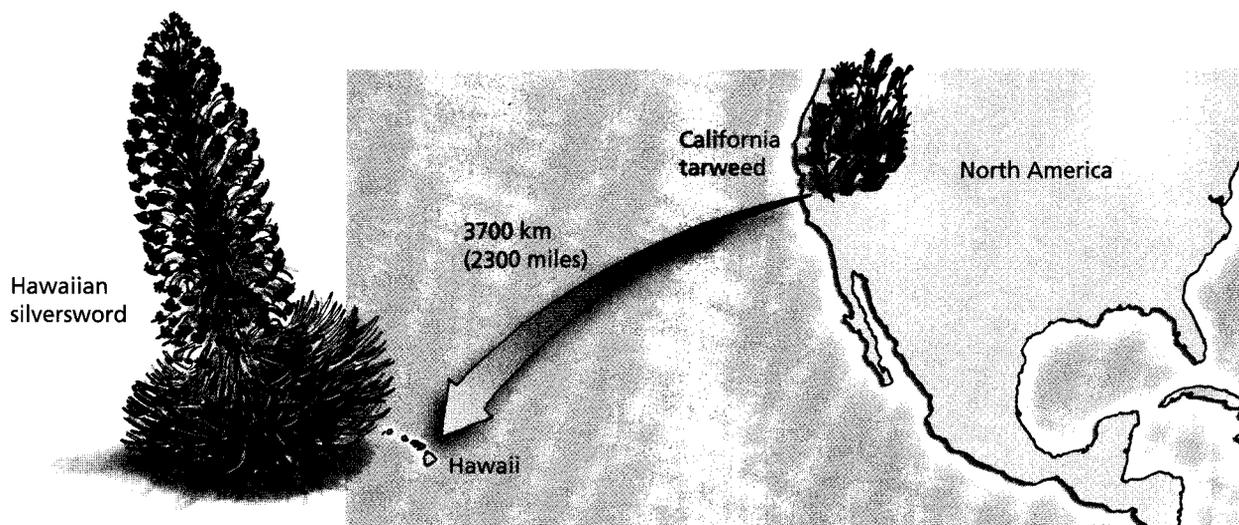


Figure 11.5 Migration leads to speciation. The ancestor of Hawaiian silverswords was the much smaller and less dramatic California tarweed. Tarweed seeds were blown or carried by birds to the Hawaiian Islands, creating an isolated population. With no gene flow between the two populations, Hawaiian silverswords evolved into a very different group of species.

divergence is great enough, reproductive isolation can occur. The three steps of speciation are discussed in detail below.

Isolation and Divergence of Gene Pools. The gene pools of populations may become isolated from each other for several reasons. Often a small population becomes isolated when it migrates to a location far from the main population. This is the case on many oceanic islands, including the Galápagos and Hawaiian islands. Bird, reptile, plant, and insect species on these islands appear to be the descendants of species from the nearest mainland. The original ancestral migrants arrived on the islands by chance. Because it is rare for organisms from the mainland to find their way across hundreds of miles of open ocean to these islands, populations at each site are nearly completely isolated from each other (Figure 11.5). In addition, because migrant populations are often small, their gene pools can change rapidly and dramatically via the process of genetic drift, as described in Section 11.5. Migration of populations from nearby sources appears to have resulted in the evolution of most species in newly emerged or unusual habitats—an idea known as the **founder hypothesis**. According to this hypothesis, the diversity of unique species on oceanic islands, as well as in isolated bogs, caves, and lakes, resulted from colonization of these once “empty” environments by small populations of migrants. Because these habitats had few competitors for resources, variants in a founding population having traits that allowed them to exploit a different resource than that used by other individuals would have had increased fitness. The advantage these different variants had caused the population to diversify and eventually to split into numerous species. For example, the large diversity of fish species once found in Africa’s Lake Victoria resulted from rapid divergence from a founding population (Figure 11.6).

Populations may also be isolated from each other by the intrusion of a geologic barrier. This could be an event as slow as the rise of a mountain range or as rapid as a sudden change in the course of a river. The emergence of the Isthmus of Panama between 3 and 6 million years ago represents one such intrusion event. This land bridge connected the formerly separate continents of South and North America but *divided* the ocean gulf between them. Scientists have described at least 6 pairs of biological species of snapping shrimp on both sides of the isthmus that diverged during and after this event. These shrimp species appear to be related to each other because of similarities in appearance, protein structure, and lifestyle. In each case,



Figure 11.6 Support for the founder hypothesis. Lake Victoria contains over 500 species of cichlid fish found nowhere else in the world. A small sampling of this diversity is shown in this tank. This huge diversity appears to have evolved from one or two ancestral species that colonized this “empty” lake less than 20,000 years ago.

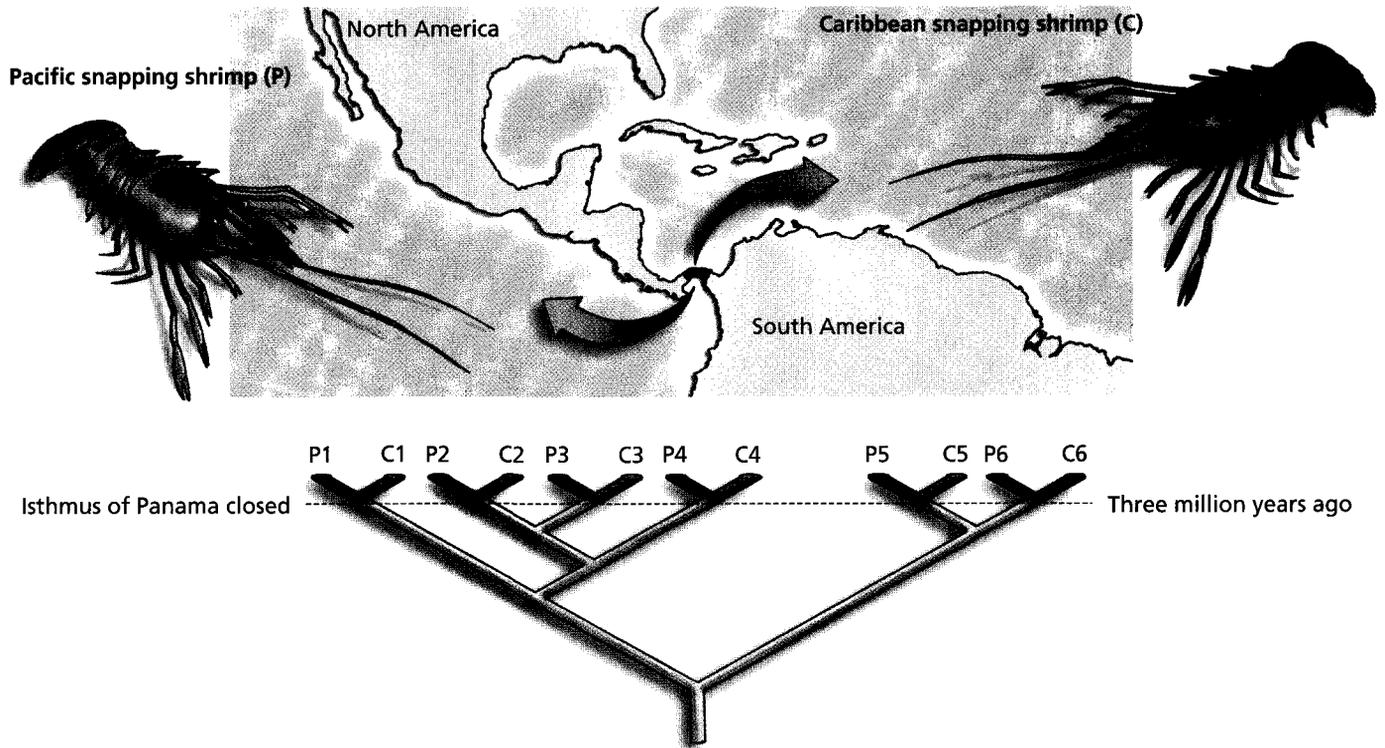


Figure 11.7 Physical separation leads to speciation. Species of snapping shrimp on either side of the Isthmus of Panama can be paired according to similarities in appearance and habit. Pairs are numbered for simplicity—the letter C before the number indicates the species is found on the Caribbean side of the Isthmus, while a P indicates a Pacific species. This pattern indicates that recent speciation in this group occurred during the period that the isthmus was emerging and therefore was dividing formerly continuous populations of ancestral species.

1 member of each of the 6 pairs is found on the Caribbean side of the land bridge, while the other member of each pair is found on the Pacific side (Figure 11.7). This geographic pattern indicates that the two species in each pair descended from a single species. Each original species was most likely found throughout the gulf before the isthmus arose, and each was divided into two isolated populations during the time that the land bridge was arising. Once in isolation, the separated populations of each species diverged into different biological species.

Populations that are isolated from each other by distance or a barrier are known as **allopatric** (meaning “different countries”). However, separation between two populations’ gene pools may also occur even if the populations are living in physical proximity to each other, that is, if they are **sympatric** (“same country”). This appears to be the case in populations of the apple maggot fly, a species that may provide one of the clearest examples of speciation “in action.”

Apple maggot flies are so named because they are notorious pests of apples grown in northeastern North America. However, apple trees are not native to North America; they were first introduced to this continent less than 300 years ago. Apple maggot flies also infest the fruit of hawthorn shrubs, a group of species that *are* native to North America. Apple-infesting flies appear to have descended from hawthorn-infesting ancestors that began to use the novel food source of apples after the fruit began to be cultivated in their home range. Apples and hawthorns live in close proximity, and apple maggot flies clearly have the ability to fly between apple orchards and hawthorn shrubs. At first glance, it does not appear that the apple maggot flies that eat apples and those that eat hawthorn fruit are isolated from each other.

Figure 11.8 Differences in the timing of reproduction can lead to speciation. This graph illustrates the life cycle of two populations of the apple maggot fly: one that lives on apple trees and another that lives on hawthorn shrubs. The mating period for these two populations differs by a month, resulting in little gene flow between them.

However, upon closer inspection, scientists determined that populations of apple maggot flies on apples and those on hawthorns actually have little opportunity for gene flow between them. Flies mate on the fruit where they will lay their eggs, and hawthorns produce fruit approximately 1 month after apples do. Each population of fly has a strong preference regarding which fruit it will mate on, and flies that lay eggs on hawthorns develop much faster than flies that lay eggs on apples. There appears to be little mixing between the apple-preferring and hawthorn-preferring populations.

Scientists who have examined the gene pools of the two groups of apple maggot flies find that they differ strongly in the frequency of some alleles. Thus it appears that divergence of two populations can occur even if those populations are in contact with each other, as long as some other factor—in this case, the timing of mating and reproduction as a result of variation in fruit preference—is keeping their gene pools relatively isolated (Figure 11.8). While the small amount of mating that still occurs between apple flies and hawthorn flies means that they are still considered the same biological species, the divergence that has occurred between these two populations in the past 300 years indicates that these flies may be headed toward complete reproductive isolation.

Interestingly, in plants, the formation of isolated gene pools can happen instantaneously and without any geographic or temporal barriers between populations. Most plants can undergo **asexual reproduction**; that is, a new plant can form from part of the body of a parent plant. This is often how gardeners propagate their favorite roses, for instance, by taking cutting of a stem and placing the ends of these cuttings in soil, where they will develop roots. Because hybrid plants can perform asexual reproduction, hybrid sterility as a result of an inability to produce eggs or sperm does not doom such plants to only a single generation. A population of many hybrid plants can arise from a single hybrid parent plant via asexual reproduction. However, because the hybrids cannot form eggs and sperm (for the same reason as described earlier for mules), this population is reproductively isolated from its parent populations and can travel its own evolutionary trajectory.

Amazingly, some hybrid plants can become fertile again—if a mistake during mitosis produces a cell containing duplicated chromosomes. Because these cells now contain two of each kind of chromosome, meiosis can proceed, and a plant with these cells can produce eggs and sperm. Since most plants do produce both types of gametes, such an individual can self-fertilize and give rise to a brand new species. One example of such a species is canola, an important agricultural crop grown primarily for the oil that can be extracted from its seeds. Canola developed as a result of chromosome duplication in a hybrid of kale (*Brassica oleracea*) and turnip (*Brassica campestris*); see Figure 11.9 on page 292. In fact, the same process of chromosome duplication, called **polyploidy**, that allows the production of fertile hybrids can also occur in nonhybrid plants. For example, the geneticist Hugo de Vries discovered individual evening primrose plants that had 28 chromosomes—twice as many as other plants in the same population. Upon investigation, he found that these plants were unable to produce viable offspring with evening primrose having only 14 chromosomes. Apparently, a mistake during cell division caused the number of chromosomes to double in an individual plant and led to its immediate reproductive isolation. Recent research suggests that this process of “instantaneous speciation” may have been a key factor in the evolution of diversity in plants. As many as 50% of flowering plant species may have resulted from polyploidy. It appears to occur in some animal groups, such as frogs, as well.

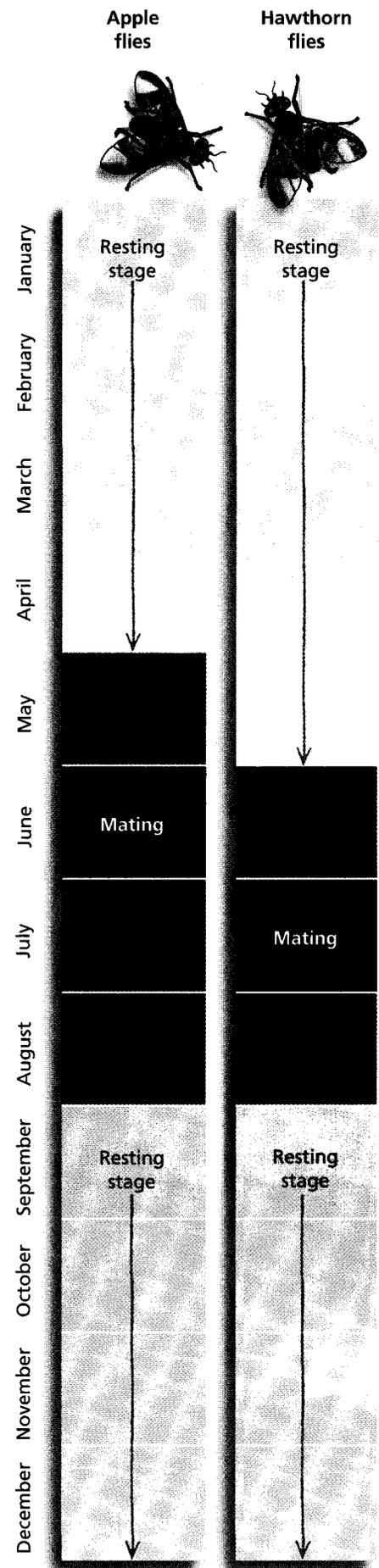
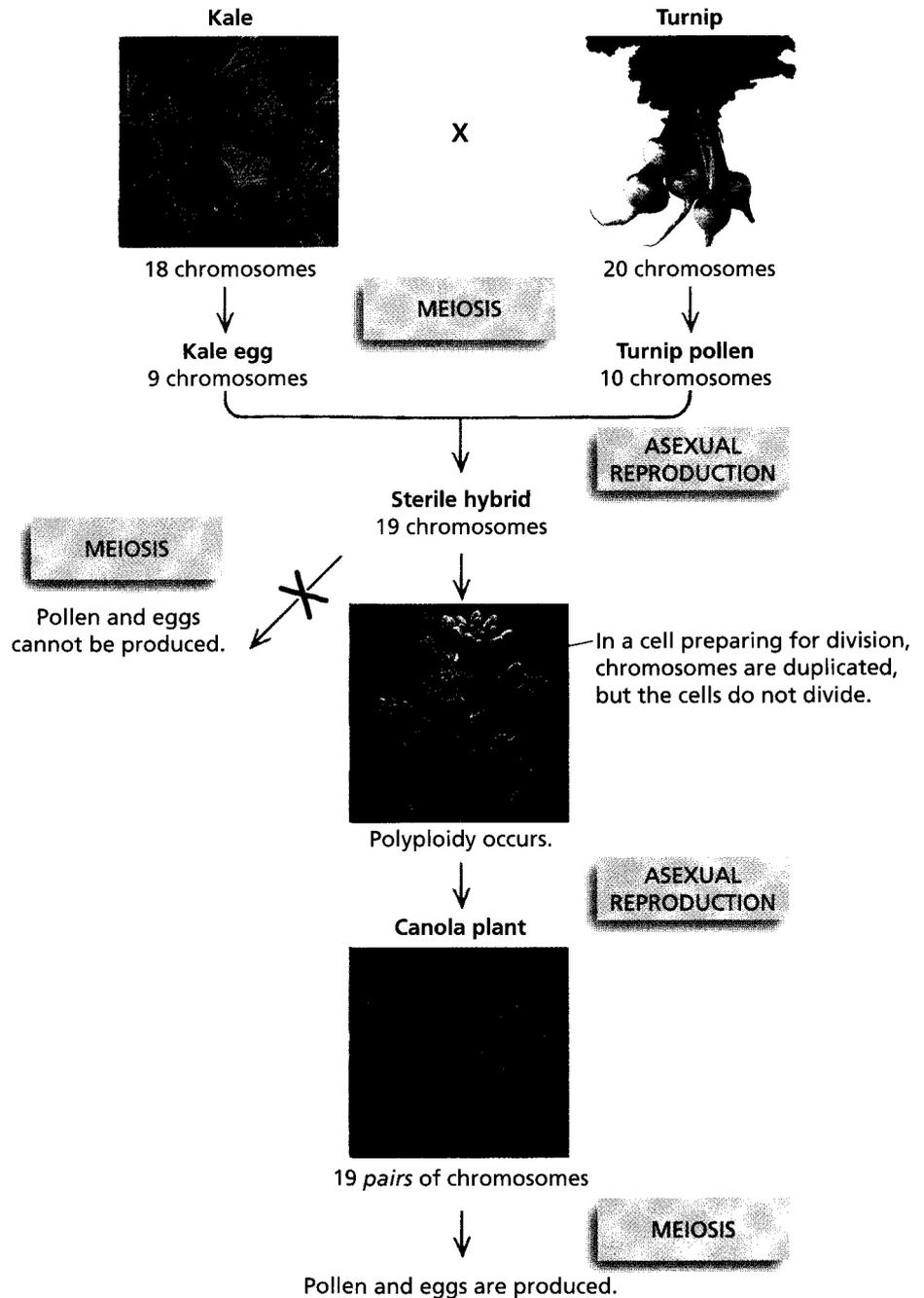


Figure 11.9 Instantaneous speciation. Canola evolved from a hybrid of kale and turnip. Although canola was initially a sterile hybrid, a variant that had duplicated chromosomes must have appeared via asexual reproduction. This plant could perform meiosis and is capable of sexual reproduction. Because canola is a new species, its pollen cannot fertilize kale or turnip plant eggs, and vice versa.



The Evolution of Reproductive Isolation. For populations that have diverged in isolation to become truly distinct biological species, they must become reproductively isolated either by their behavior or by genetic incompatibility. In the case of canola, genetic incompatibility occurs immediately—a cross between canola and kale does not result in fertilization. In animals, the process may be more gradual, occurring when the amount of divergence has caused numerous genetic differences between two populations. There is no hard-and-fast rule about how much divergence is required; sometimes a difference in a single gene can lead to incompatibility, while at other times, populations demonstrating great physical differences can produce healthy and fertile hybrids (Figure 11.10). Exactly how reproductive isolation evolves on a genetic level is still unknown and is an actively researched and intriguing question in biology.

Of course, once reproductive isolation occurs, each species may take radically different evolutionary paths because gene flow between the two species is impossible. Once separated, species that derived from a common ancestor can

accumulate many differences, even completely new genes. How rapidly and smoothly different forms evolve is another intriguing question in biology. Darwin assumed that speciation occurred over millions of years as tiny changes gradually accumulated. This hypothesis is known as **gradualism**. Other biologists, most notably the late Stephen Jay Gould, have argued that most speciation events are sudden, result in dramatic changes in form (via natural selection and other mechanisms of evolutionary change) within the course of a few thousand years, and are followed by many thousands or millions of years of little change—a hypothesis known as **punctuated equilibrium**. The hypothesis of punctuated equilibrium is supported by observations of the fossil record, which seems to reflect just this pattern (Figure 11.11).

The period after the separation of the gene pools of two populations but before the evolution of reproductive isolation, could be thought of as a period during which races of a species may form. Determining if the racial groupings on Indigo's census form came about via this process is our focus in the next section.

11.2 The Race Concept in Biology

Biologists do not agree on a standard definition of *biological race*. In fact, not all biologists feel that *race* is a useful term; many prefer to use the term *subspecies* to describe subgroups within a species, and others feel that race is not a useful biological concept at all. When the term is applied, it is often inconsistent. For example, populations of birds with slightly different colorations might be called different races by some bird biologists, while other biologists would argue that the same contrasts in color are meaningless. However, Indigo's question about how the racial group with which she identifies matters leads us to a definition of race that does have a specific meaning. What Indigo wants to know is: If she identifies herself as a member of a particular race, does that mean she is more closely related and thus biologically more similar to other members of the same race than she is to members of other races? The definition of **biological race** that addresses this question is the following: Races are populations of a single species that have diverged from each other. With little gene flow among them, evolutionary changes that occur in one race may not occur in a different race.

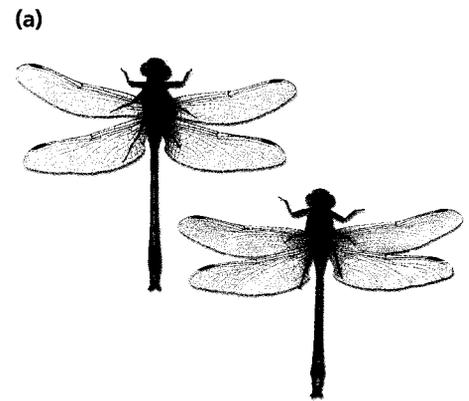
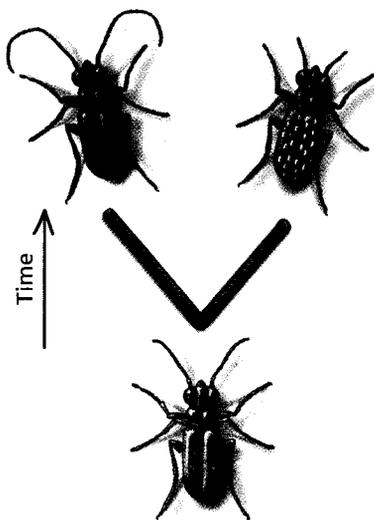


Figure 11.10 How different are two species? There is no true minimum or maximum amount of divergence that must occur before populations become reproductively isolated. (a) These two species of dragonfly look alike but cannot interbreed. (b) Dog breeds provide a dramatic example of how the evolution of large physical differences does not always result in reproductive incompatibility.

(a) Gradualism



(b) Punctualism

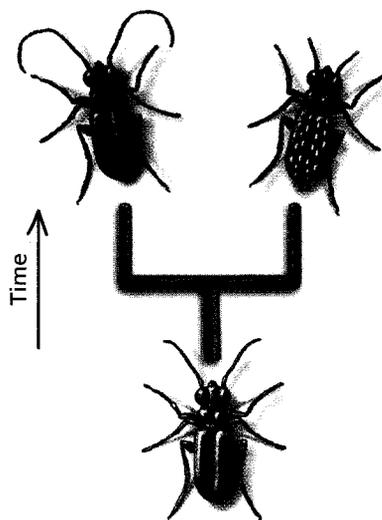
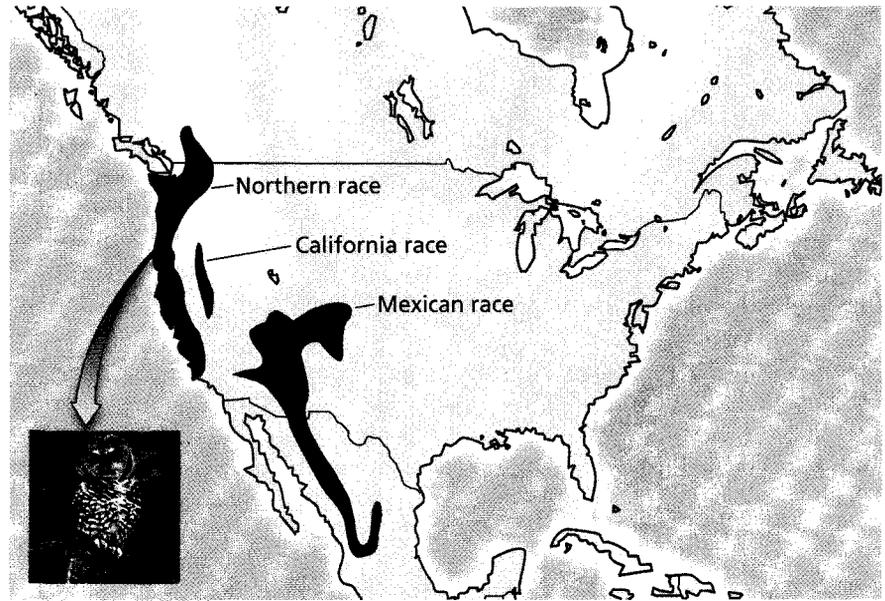


Figure 11.11 Punctuated equilibrium. The pattern of evolutionary change in groups of species may be (a) smooth—representing a constant level of small changes, or (b) more punctuated—with hundreds of thousands of years of seeming stasis followed unpredictably by rapid, large changes occurring within a few thousand years. Paleontologists Stephen Jay Gould and Niles Eldredge argued that evidence from the fossil record indicated that the second pattern—punctuated equilibrium—was predominant. Debate over the “tempo” of evolutionary change continues.

Figure 11.12 Genealogical species. The northern spotted owl belongs to the same biological species as the Mexican and California spotted owl, but its geographic isolation has resulted in the development of a unique gene pool in this population.



This definition of biological race is actually very similar to another commonly used species definition called the genealogical species concept.

According to the **genealogical species concept**, a species is defined as “the smallest group of reproductively compatible organisms containing all of the known descendants of a single common ancestor.” More so than the biological species concept, the genealogical species concept emphasizes unique evolutionary lineages; thus it vastly increases the number of different species that can be identified. For example, the spotted owl, *Strix occidentalis*, is currently described under the biological species concept as a single species with three distinct populations—called northern, California, and Mexican (Figure 11.12). The northern population is the iconic endangered owl of old-growth forests in the northwestern United States. This population is physically isolated from the California and Mexican populations. As a result, its gene pool is separate, and any trait that evolved in the northern spotted owl population is found only within that population. Although spotted owls from Mexico can produce living, fertile offspring with northern spotted owls from Oregon and thus belong to the same biological species, according to the genealogical species concept the northern spotted owl should be identified as a unique genealogical species because it is a unique lineage, representing all the descendants of the first spotted owls to colonize the Pacific Northwest. And while the California and Mexican populations of the spotted owl are not endangered, much effort has been expended to prevent the extinction of the northern population lineage and its unique gene pool.

The advantages of the genealogical species concept are that species are more easily delineated. If the gene pool of a population is consistently different from other related populations, then according to the genealogical species concept, that population represents a different species even if the populations are reproductively compatible. The genealogical species concept can apply to all groups of living species whether they reproduce sexually or not. Its disadvantage is that it can be difficult to apply in practice—different populations of the same biological species have to be studied carefully in order to determine if their gene pools differ.

Indigo’s question about whether race matters, at least biologically, can now be restated as: Do the racial groups on the census form represent populations of the human species whose gene pools were isolated until relatively recently? In other words, should we consider human races to be different genealogical species? To answer this question, we must first understand how these racial categories came to be identified in American society.

11.3 Humans and the Race Concept

Until the height of the European colonial period in the seventeenth and eighteenth centuries, few cultures distinguished between broad groups of humans based on shared physical characteristics. People primarily identified themselves and others as belonging to particular cultural groups with different customs, diets, and languages. As northern Europeans began to contact people from other parts of the world, being able to set these people “apart” made the process of colonization and subjugation less morally questionable. Thus, when Linnaeus classified all humans as a species, he was careful to distinguish definitive varieties (what we would now call races) of humans. Linnaeus recognized five races of *Homo sapiens*. Not only did Linnaeus describe physical characteristics, he ascribed particular behaviors and aptitudes to each race; reflecting the widespread biases of the scientists of his day, he set the European race as the superior form (Figure 11.13). The classification shown in Figure 11.13 is one of dozens of examples of how scientists’ work has been used to legitimize cultural practices—in this case, hundreds of years of injustice based on physical differences among people was supported by a scientific classification that seemed to make “natural” the poverty and oppression experienced by nonwhite groups.

Numerous scientists since Linnaeus have also proposed hypotheses about the number of races that the human species can be divided into. The most common number is 6: white, black, Pacific Islander, Asian, Australian Aborigine, and Native American; although, some scientists have described as many as 26 different races of the human species. The physical characteristics used to identify these races are typically skin color; hair texture; and eye, skull, and nose shape.

To answer Indigo’s question about the biological meaning of race, we must determine if the physical characteristics that Linnaeus and other scientists used to delineate their hypothesized human races developed because these groups evolved independently (or mostly independently) of each other. We can test this hypothesis by looking at the fossil record for evidence of isolation during human evolution and by looking at the gene pools of these proposed races for the vestiges of that isolation.

1. HOMO.

Sapiens. Diurnal; varying by education and situation.

2. Four-footed, mute, hairy.

Wild Man.

3. Copper-coloured, choleric, erect.

American.

Hair black, straight, thick; nostrils wide, face harsh; beard scanty; obstinate, content free. Paints himself with fine red lines. Regulated by customs.

4. Fair, sanguine, brawny.

European.

Hair yellow, brown, flowing; eyes blue; gentle, acute, inventive. Covered with close vestments. Governed by laws.

5. Sooty, melancholy, rigid.

Asiatic.

Hair black; eyes dark; severe, haughty, covetous. Covered with loose garments. Governed by opinions.

6. Black, phlegmatic, relaxed.

African.

Hair black, frizzled; skin silky; nose flat; lips tumid; crafty, indolent, negligent. Anoints himself with grease. Governed by caprice.

Figure 11.13 Linnaean classification of human variety. Linnaeus published this classification of the varieties of humans in the tenth edition of *Systema Naturae* in 1758. The behavioral characteristics he attributed to each variety reflect a widespread bias among his contemporaries that the European race was superior to other races; this classification was used as justification for the oppression of nonwhite races. Interestingly, one variety of humans recognized by Linnaeus—the *Wild Man* in his classification—is the chimpanzee!

Table 11.1 Comparison of three species concepts.

Species concept	Definition	Pros	Cons
Biological	Species consist of organisms that can interbreed and produce fertile offspring and are reproductively isolated from other species.	Useful in identifying boundaries between populations of similar organisms. Relatively easy to evaluate for sexually reproducing species.	Cannot be applied to organisms that reproduce asexually or to fossil organisms. May not be meaningful when two populations of the same species are separated by large geographical distances.
Genealogical	Species consist of organisms that can interbreed and are all descendants of a common ancestor and represent independent evolutionary lineages.	Most evolutionary meaningful because each species has its own unique evolutionary history. Can be used with asexually reproducing species.	Difficult to apply in practice. Requires detailed knowledge of gene pools of populations within a biological species. Cannot be applied to fossil organisms.
Morphological	Species consist of organisms that share a set of unique physical characteristics that is not found in other groups of organisms.	Easy to use in practice on both living and fossil organisms. Only a few key features are needed for identification.	Does not necessarily reflect evolutionary independence from other groups.

The Morphological Species Concept

The ancestors of humans are known only through the fossil record. We cannot delineate fossil species using the biological species concept. Instead, paleontologists use a more practical definition: A species is defined as a group of individuals that have some reliable physical characteristics distinguishing them from all other species. In other words, individuals in the same species have similar morphology—they look alike in some key feature. The differences among species in these key physical characteristics are assumed to correlate with isolation of gene pools. In the real world, scientists use this **morphological species concept** to distinguish among living organisms since applying the biological and genealogical species concepts can often be nearly impossible in practice. Table 11.1 summarizes the three species concepts.

Natural populations are variable, so a morphological species concept presents a challenge for scientists working with fossil organisms. This challenge is illustrated by the dinosaur, triceratops. In the 1880s, paleontologists working in Wyoming had described at least five different species of triceratops, each different in size or appearance. By the 1990s, scientists were convinced that these five species were actually a single species, *T. horridus*. What had seemed to be differences among species actually reflected variations within *T. horridus* (Figure 11.14). This later analysis was partially based on the close proximity of the original fossils, found in only two Wyoming counties. Paleontologists must use clues about the location, age, and environment of fossils, as well as their morphology, to convincingly group them into different species.

One advantage of the fossil record, however, is that it provides a view of the change in species over time. As described in Chapter 9, the hominin fossil record (the fossil record of humans and their extinct ancestors) consists of a sequence of specimens that are clearly similar to each other but show a pattern of change over time, and are interpreted as making up an evolutionary lineage. The



Figure 11.14 How many species of triceratops? Scientists in the early part of the twentieth century identified several different triceratops species by using the morphological species concept. Scientists who later reexamined the fossil evidence concluded that these several species represent different ages and sexes within a single species.

morphological differences between hominin species are clear, meaning that reconstructing the movement of human ancestors out of Africa is relatively straightforward.

Modern Humans: A History

The immediate predecessor of *Homo sapiens* was *Homo erectus*, a species that first appeared in east Africa about 1.8 million years ago and spread to Asia and Europe over the next 1.65 million years. Fossils identified as early *H. sapiens* appear in Africa in rocks that are approximately 250,000 years old. The fossil record shows that these early humans rapidly replaced *H. erectus* populations in the Eastern Hemisphere.

There is considerable debate among paleontologists about whether *H. sapiens* evolved just once, in Africa (this is called the out-of-Africa hypothesis), or throughout the range of *H. erectus* (known as the multiregional hypothesis). Even if *H. sapiens* evolved in Africa and then migrated to Europe and Asia, it is unclear whether populations of early humans hybridized with *H. erectus* in different areas of the globe (the hybridization and assimilation hypothesis). Because this scientific question is still unresolved, it is difficult to know when the ancestral population of modern humans split into regional populations; it could have been anytime from 150,000 to 1.8 million years ago (Figure 11.15).

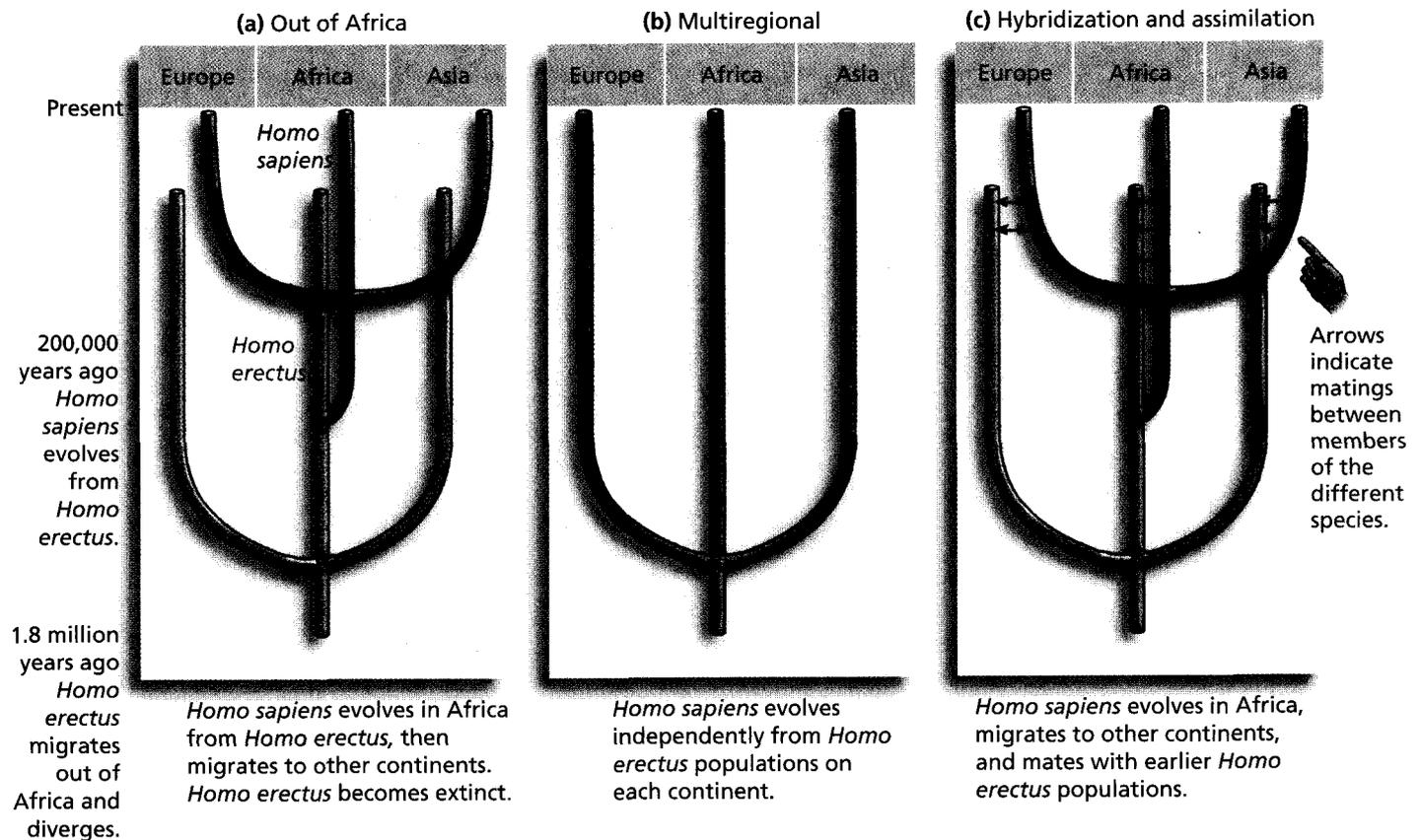


Figure 11.15 Three models of modern human origins. (a) The out-of-Africa hypothesis indicates that modern humans arose in Africa and replaced populations of *Homo erectus* that had moved around the globe. (b) The multiregional evolution hypothesis suggests that *H. sapiens* evolved from *H. erectus* multiple times throughout its range. (c) Hybridization and assimilation is an intermediate hypothesis stating that *H. sapiens* evolved in Africa and replaced *H. erectus* populations but that there was some hybridization among local forms of *H. erectus* and incoming *H. sapiens*.

Most paleontologists favor the out-of-Africa hypothesis—that all modern human populations descended from African ancestors within the last few hundred thousand years. This hypothesis is supported by the close genetic similarity among people from very different geographic regions. Humans have much less genetic diversity (measured by the number of different alleles that have been identified for any gene) than any other great ape, which indicates that they are a young species that has had little time to accumulate many different gene variants. The out-of-Africa hypothesis is also supported by evidence that human populations in Africa are more genetically diverse than other human populations around the world. Again, because the amount of genetic diversity within a population or species is a measure of its age, this observation indicates that African populations are the oldest human populations. On balance, the out-of-Africa hypothesis has the strongest support; although with the evidence accumulated to date, none of the other hypotheses can be completely rejected.

If the out-of-Africa hypothesis is correct, the physical differences we see among human populations must have arisen in the last 150,000 to 200,000 years, or in about 10,000 human generations. In evolutionary terms, this is not much time. The recent shared ancestry of human groups does not support the hypothesis that the commonly defined human races are very different from each other.

Genetic Evidence of Divergence

While the fossil evidence discussed thus far indicates that members of the human species have not had much time to diverge and thus are not likely to be very different from each other, Indigo's question about the meaning of race is still relevant. After all, even if two races differ from one another only slightly, if the difference is consistent, then perhaps it is fair to say that people are biologically more similar to members of their own race than to people of a different race.

If a population represents a biological race, there will be a record in its gene pool of its isolation from other groups. Recall that when populations are isolated from each other, little gene flow occurs between them. If an allele appears in one population, it cannot spread to another, and evolutionary changes that occur in one population do not necessarily occur in others. Chapter 9 described the genetic nature of evolutionary change—when a trait becomes more common in a population due to evolution, it is because the allele for that trait has become more common. Evolution results in a change in **allele frequency** in a population, that is, in the percentage of copies of any given gene that are a particular allele. For example, in a population of 50 people, imagine that two individuals carry 1 copy of the allele that codes for blood type B, and the remainder carry 2 copies of the allele that codes for blood type O. Since every person carries 2 copies of each gene, there are actually 100 copies of the blood-type gene in the population of 50 people. Because two of these copies are allele B, the frequency of the B allele is 2 out of 100, or 2%, in this population. An evolutionary change in this population would be seen as an increase or decrease in the frequency of the B allele in the next generation.

Because evolution leaves a genetic record, we can make two predictions to test a hypothesis of whether biological races exist within a species. If a race has been isolated from other populations of the species for many generations, it should have these two traits:

1. Some unique alleles
2. Differences in allele frequency for some genes relative to other races

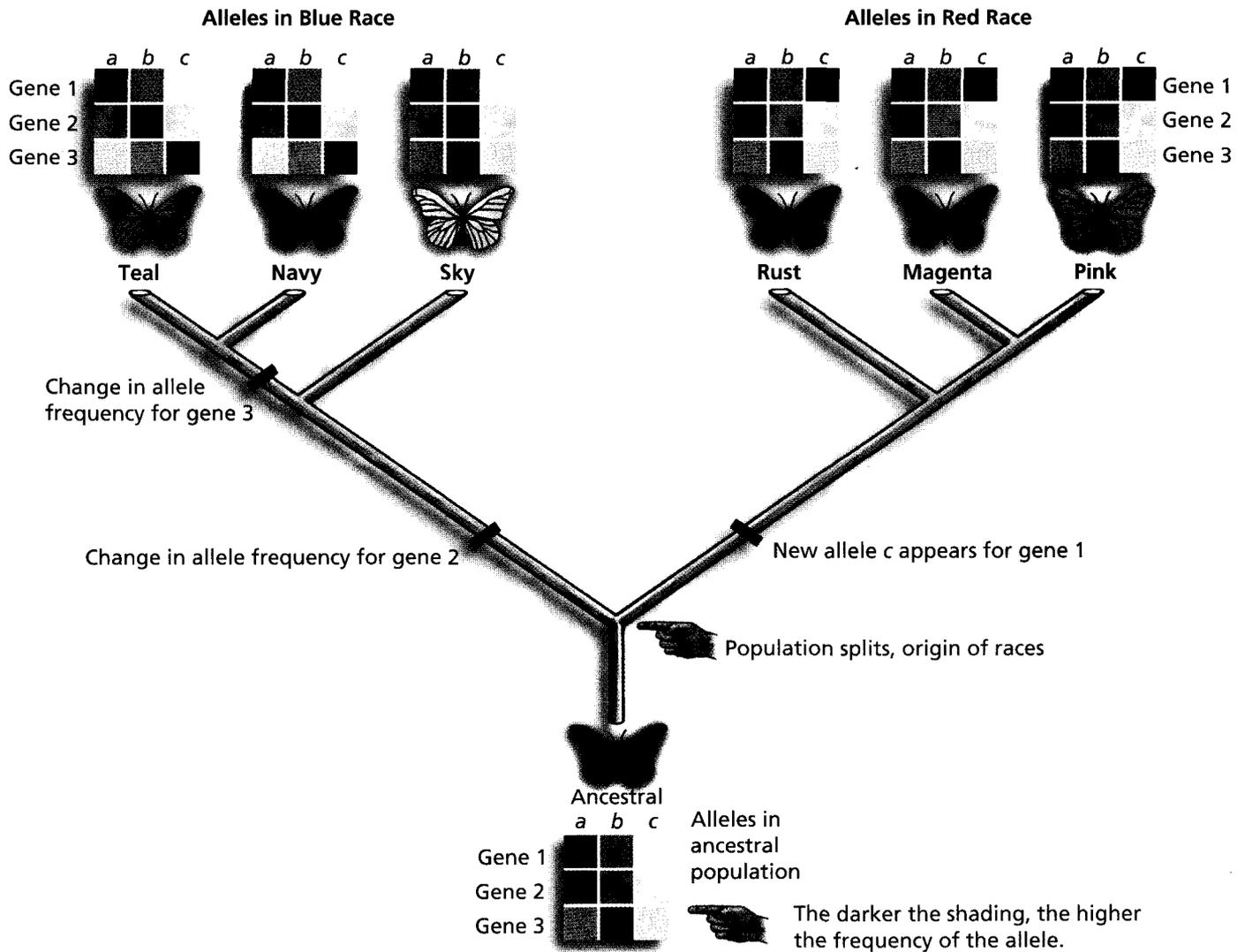


Figure 11.16 Genetic evidence of isolation between races. New alleles that appear in one population will not spread to the other populations because gene flow is restricted; thus, each race should have unique alleles. The frequency of alleles for various genes will also be more similar among populations within a race than between races.

The tree diagram in Figure 11.16 illustrates these predictions of the hypothesis of biological races. In the figure, butterfly populations colored teal, navy, and sky are all part of the same race (“blues”), and populations colored rust, magenta, and pink are part of a separate race (“reds”). The grid at the bottom of the tree illustrates the frequency of alleles for three genes in the ancestral butterfly population. For instance, there are two alleles for gene 1—one that is very common (allele *a*) and thus high in frequency, and one that is rare (allele *b*) and low in frequency. The two races described at the top of the tree originated when the ancestral population split, and the two resulting populations became isolated from each other. Notice the following patterns:

- **A race-specific allele.** Not long after the divergence between the blue and red races, mutation causes a new allele for gene 1 (that is, allele *c*) to arise but only in the red race. Because the two races are isolated, this allele does not spread to the gene pool of the blue race—there is no allele *c* for gene 1 in any of the blue populations. Additionally, because

the populations colored rust, magenta, and pink diverge *after* this allele appears in reds, all of these populations contain individuals that carry allele *c* for gene 1.

- **Similar allele frequencies in populations within races.** Also not long after the divergence between reds and blues, natural selection results in a change in the allele frequency of gene 2. Perhaps the environment inhabited by blues favors individuals that carry allele *b*—this results in these individuals having more offspring than do the individuals that carry only allele *a*. Thus allele *b* becomes more common in the blue race. This evolutionary change occurred before the divergence of the populations colored teal, navy, and sky. Therefore, all of these blue race populations have a similar pattern of allele frequency for this gene, but the pattern differs from that in the populations that make up the red race.

As a result of the evolutionary independence of the blue race and the red race, if you compare the allele frequency grids of all the populations, you will notice that populations colored teal, navy, and sky are similar (although not identical) to each other, and populations colored rust, magenta, and pink are similar to each other. However, the allele frequencies for the genes in the teal population are distinctly different from those in the rust, magenta, and pink populations.

Observing a pattern of unique allele frequencies in different populations of the same species is one piece of supporting evidence showing that the populations have been isolated from each other. For example, scientists have observed that certain alleles are more common in apple-eating populations of apple maggot flies than in the hawthorn-eating populations. This observation has led researchers to conclude that these populations of flies are genetically isolated from each other and should be considered different races.

Human Races Are Not Biological Groups

Recall the six major human races described by many authors: white, black, Pacific Islander, Asian, Australian Aborigine, and Native American. Do these groups show the predicted pattern of race-specific alleles and unique patterns of allele frequency? In a word, no.

No Race-Specific Alleles Have Been Identified. Let us first examine whether any alleles that are unique to a race have been identified. Sickle-cell anemia is a condition we discussed in Chapter 6, and one that has long been thought to be a “black” disease. This illness occurs in individuals who carry 2 copies of the sickle-cell allele, resulting in red blood cells that deform into a sickle shape under certain conditions. The consequences of these sickling attacks include heart, kidney, lung, and brain damage. Many individuals with sickle-cell anemia do not live past childhood.

Nearly 10% of African Americans and 20% of Africans carry 1 copy of the sickle-cell allele. However, if we examine the distribution of the sickle-cell allele more closely, we see that the pattern is not quite so simple. Just as we can divide the human species into populations that share similarity in skin color and eye shape (the typical races), we can divide these races into smaller populations that live in a defined geographic area and share cultural and language similarities. When we do this, we find that not all populations classified as black have a high frequency of the sickle-cell allele. In fact, in populations from southern and north-central Africa, which are traditionally classified by race as black, this allele is very rare or absent. Among populations that are classified as white or Asian, there are some in which the sickle-cell allele is relatively common, such as among white populations in the Middle East and

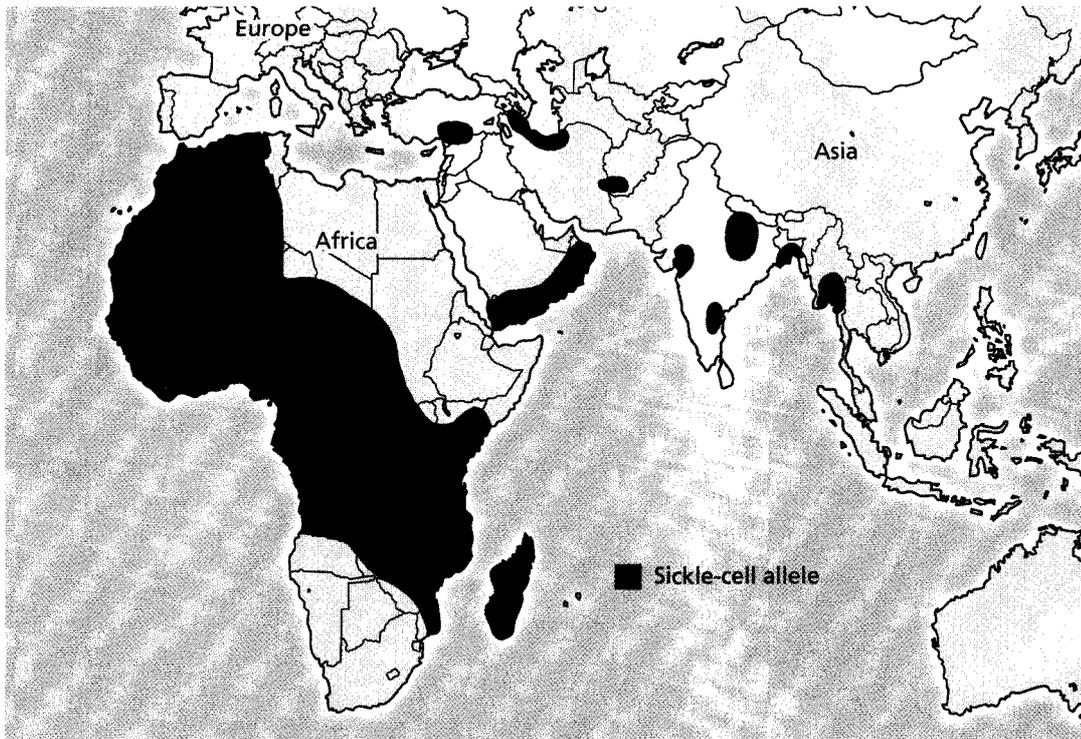


Figure 11.17 The sickle-cell allele: Not a “black gene.” The map illustrates where the sickle-cell allele is found in human populations. Note that it is not found in all African populations but is found in some European and Asian populations.

Asian populations in northeast India (Figure 11.17). Thus, the sickle-cell allele is not a characteristic of all black populations nor is it unique to a supposed “black race.”

Similarly, cystic fibrosis, a disease that results in respiratory and digestive problems and early death, was often thought of as a disease of the “white race.” Cystic fibrosis occurs in individuals who carry 2 copies of the cystic fibrosis allele. As with sickle-cell anemia, it has become clear that the allele that causes cystic fibrosis is not found in all white populations and is found, in low frequency, in some black and Asian populations. Thus, the cystic fibrosis allele is not a characteristic of all white populations, nor is it unique to a supposed “white race.”

These examples of the sickle-cell allele and cystic fibrosis allele demonstrate the typical pattern of gene distribution. Scientists have not identified a single allele that is found in all (or even most) populations of a commonly described race and that is not found in other races. The hypothesis that human races represent mostly independent evolutionary groups is not supported by these observations.

Populations Classified in the Same Race Do Not Have Similar Allele Frequencies. What about the second prediction of the hypothesis that human racial groups are biologically independent—that we should observe unique patterns of allele frequency within these different races? Until the advent of modern techniques allowing scientists to isolate genes and the proteins they produce, there was no way of directly measuring the frequency of alleles for most of the genes in a population. However, scientists could evaluate the racial categories already in place and assume that their average physical differences reflected genetic differences among them. Thus populations with dark skin were assumed to have a high frequency of “dark skin” alleles, while populations with light skin were assumed to have a low frequency of these alleles. Similar assumptions were made about a range of physical differences—eye shape, skull shape, and hair type all clearly have a genetic basis, and all clearly differ among racial categories. These observations appear to support the

hypothesis that different races have unique allele frequencies. However, physical characteristics such as skin color, eye shape, and hair type are each influenced by several different genes, each with a number of different alleles. Because skin color is affected by numerous genes, each of them affecting the amount and distribution of skin pigment, two human populations with fair skin could have completely different gene pools with respect to skin color.

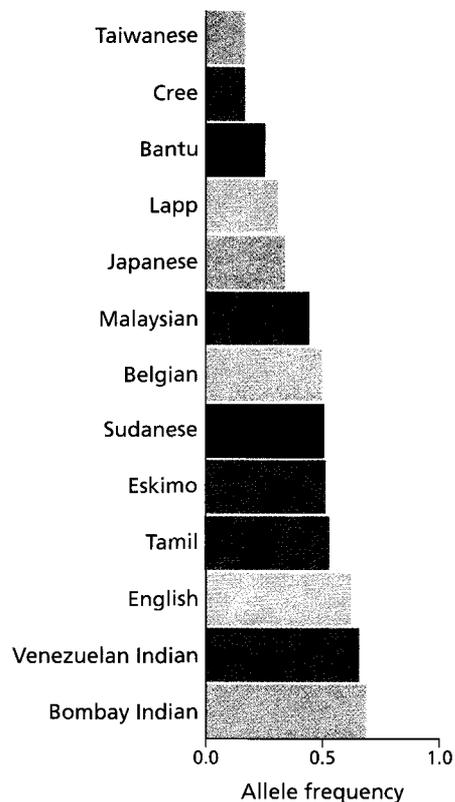
If the physical characteristics that describe races illustrate biological relationships, then the allele frequency for *many different* genes should also be more similar among populations within a race than between populations of different races. In the last half-century, scientists have been able to directly measure the allele frequency of different genes in a variety of human populations. Essay 11.1 on page 304 describes how we can calculate allele frequency from the frequency of genotypes.

Let us examine a few examples of data collected on allele frequencies for various genes in different human populations. Figure 11.18a shows the frequency of the allele that interferes with an individual's ability to taste the chemical phenylthiocarbamide (PTC) in several populations. People who carry 2 copies of this recessive allele cannot detect PTC, which tastes bitter to people who carry 1 or no copies of the allele.

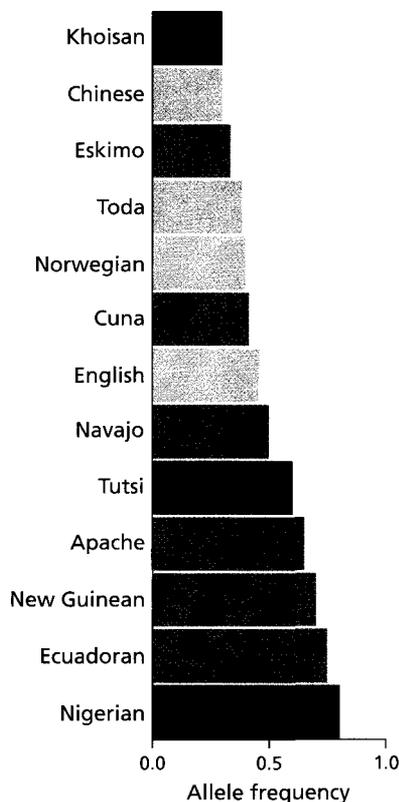
Figure 11.18b lists the frequency of one allele for the gene *haptoglobin 1* in a number of different human populations. Haptoglobin 1 is a protein that helps scavenge the blood protein hemoglobin from old, dying red blood cells.

Figure 11.18c illustrates variation among human populations in the frequency of a repeating DNA sequence on chromosome 8. Repeating

(a) Frequency of the allele that inhibits the ability to taste PTC



(b) Frequency of haptoglobin 1 allele



(c) Frequency of allele 4 of D8s384 sequence, chromosome 8

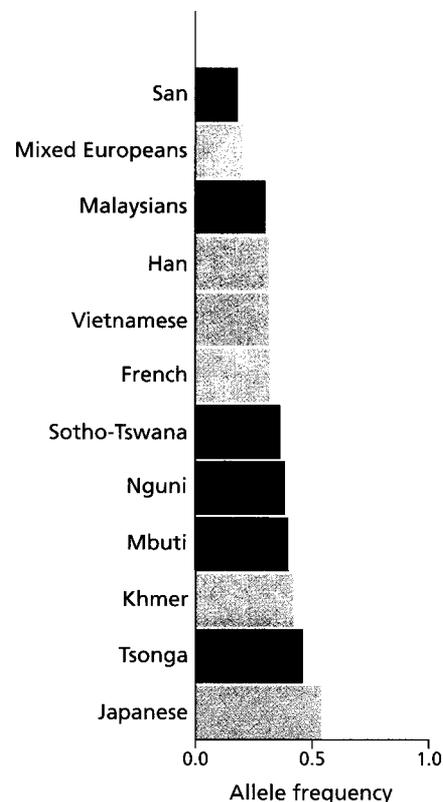


Figure 11.18 Do human races show genetic evidence of isolation? The bars on each of these histograms illustrate the frequency of the described allele in many different human populations. Bars with the same color represent populations within the same commonly defined race. These histograms illustrate that populations within these "races" are not necessarily more similar to each other than they are to populations in different races.

sequences are common in the human genome, and differences among individuals in the number of repeats create the unique signatures called DNA fingerprints (described in Chapter 8). The frequency of one pattern of repeating sequence in a segment of chromosome 8, called allele 4 of the D8s384 sequence, is illustrated for a number of populations.

Notice that the human populations in each part of Figure 11.18 are listed by increasing frequency of the allele in the population. If the hypothesis that human racial groups have a biological basis is correct, then populations from the same racial group should be clustered together on each bar graph. The color coding of each population group in each of the graphs corresponds to the racial category in which they are typically placed. To help us evaluate the hypothesis, we are using stereotypical colors for the races—pale brown for white, dark brown for black, yellow for Asian, red for Native American, and medium brown for Pacific Islanders.

What we see in the three graphs is that allele frequencies for these genes are *not* more similar within racial groups than between racial groups. In fact, in two of the three graphs, the populations with the highest and lowest allele frequencies belong to the same race—for these genes, there is more variability *within* a race than there are average differences *among* races. Scientists have observed this same pattern for every gene they have studied in the human population. These observations do not match the prediction made by the hypothesis that morphological similarity among populations reflects an underlying close genetic relationship. Both the fossil evidence and genetic evidence indicate that the six commonly listed human racial groups do *not* represent biological races.

Human Races Have Never Been Truly Isolated

The genetic analysis that caused scientists to reject the hypothesis that human populations within the same races are very similar to each other, and consistently different from other races, has shown that the exact opposite is true. The evidence that human populations have been “mixing” since modern humans first evolved is contained within the gene pool of human populations.

For instance, the frequency of the B blood group decreases from east to west across Europe (Figure 11.19). The I^B allele that codes for this blood type apparently evolved in Asia, and the pattern of blood group distribution seen in Figure 11.19 corresponds to the movement of Asians into Europe beginning

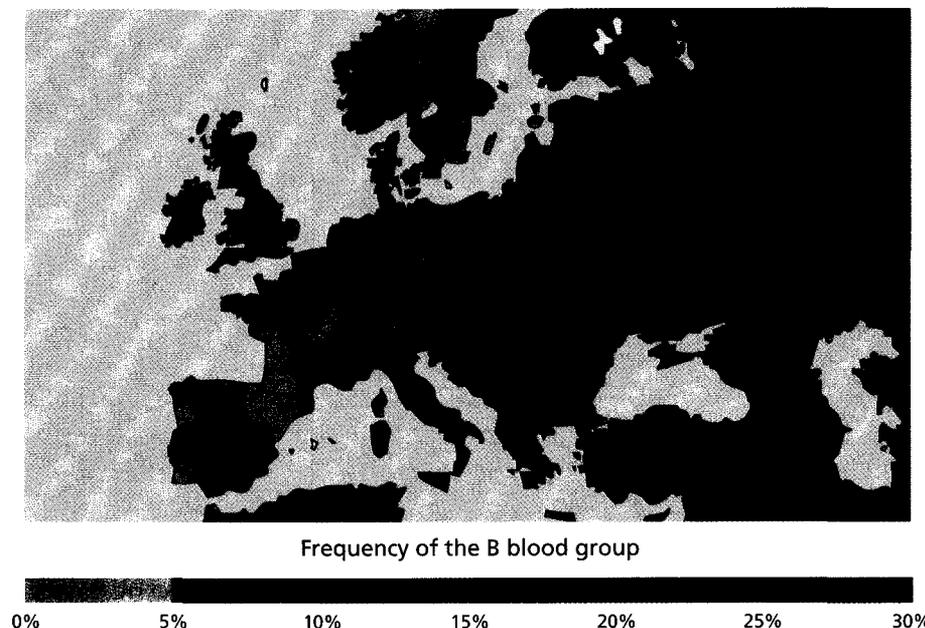


Figure 11.19 The map of blood types indicates mixing between populations. The frequency of the type B blood group in Europe declines from east to west across the continent. This pattern reflects the movement of alleles from Asian populations into European populations over the past 2000 years.

Essay 11.1 The Hardy-Weinberg Theorem

Reginald Punnett, who developed the Punnett square, was a scientist at Cambridge University during the early 1900s. Punnett is considered to be one of the fathers of modern genetics. His verification of Mendel's work helped establish Cambridge University as a center of genetic research. Among Punnett's accomplishments was his dissemination of Mendel's work to a wide and somewhat skeptical scientific audience.

One of these skeptics was George Udny Yule, a statistician at University College, London. Yule argued that inheritance could not work by Mendelian principles—as an example, he used the dominant trait of brachydactyly (having extra fingers). Since this allele is dominant over the five-fingered condition, Yule asserted that we would expect it to eventually become more common. He based this assertion on the observation that a cross between heterozygotes results in three-fourths of the offspring expressing the dominant trait and one-fourth expressing the recessive trait; thus, you should get three brachydactyls for every five-fingered person.

Punnett intuitively knew that Yule's assertion was false, but he did not have the mathematical background to prove his intuition. For help, he turned to another Cambridge scientist named Godfrey Hardy. Hardy was a renowned "pure mathematician" whose teaching revolutionized mathematics education. Legend has it that Hardy wrote the mathematical proof on his shirt cuff during a dinner party, and he felt that it was so simple it fell below his standards of publication. He did eventually publish it as a letter to the editor in the journal *Science* at nearly the same time as Wilhelm Weinberg's identical proof was published in a German journal. Hardy's letter was his only contribution to the field of biology; in his autobiography, *A Mathematician's Apology*, it receives no mention.

The Hardy-Weinberg theorem states that allele frequencies will remain stable in populations that are large in size, randomly mating, and experiencing no migration or natural selection. Subsequent geneticists used this theorem as a baseline for predicting how allele frequencies would change if any of the theorem's assumptions were violated. In other words, the Hardy-Weinberg theorem enables scientists to quantify the effect of evolutionary change on allele frequencies. Today, the Hardy-Weinberg theorem forms the basis of the modern science of population genetics.

In the simplest case, the Hardy-Weinberg theorem (which we abbreviate to Hardy-Weinberg) describes the relationship between allele frequency and genotype frequency for a gene with 2 alleles in a stable population. Hardy-Weinberg labels the frequency of these two alleles, p and q .

Imagine that we know the frequency of alleles for a particular gene in a population; let us say that 70% of the alleles in the population are dominant (A), and 30% are recessive (a). Thus, $p = 0.7$ and $q = 0.3$. Each gamete produced by members of the population carries 1 copy of

the gene. Therefore, 70% of the gametes produced by this entire population will carry the dominant allele, and 30% will carry the recessive allele. The frequency of gametes produced of each type is equal to the frequency of alleles of each type (Figure E11.1a).

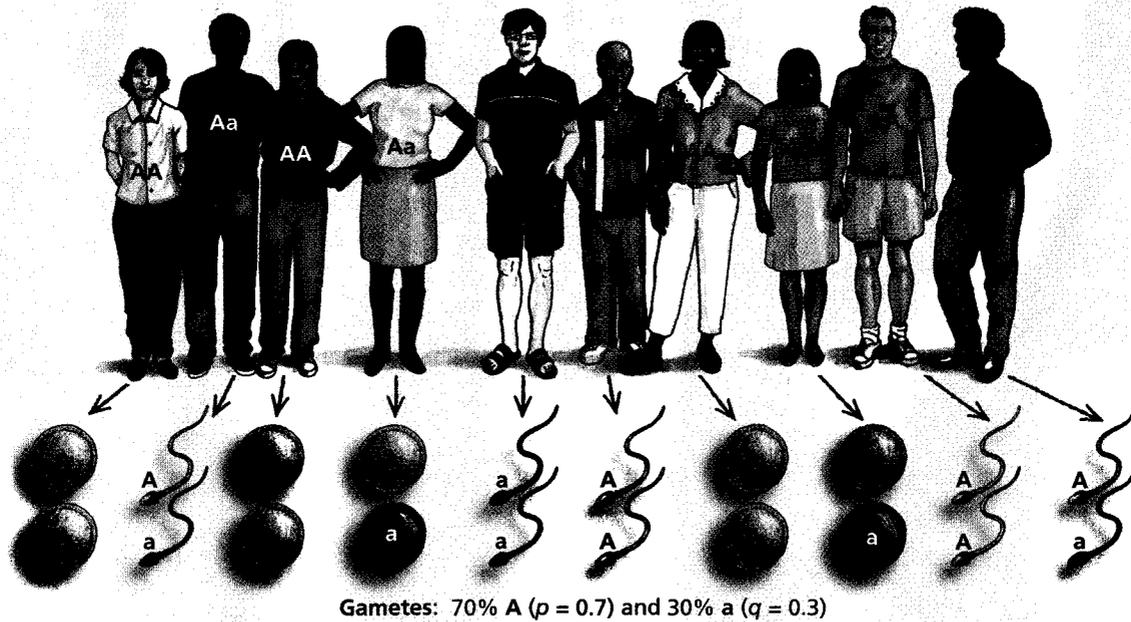
For the purposes of Hardy-Weinberg, we assume that every member of the population has an equal chance of mating with any member of the opposite sex. In other words, there is no relationship between the alleles that an individual carries for the gene and the alleles of her or his partner. The fertilizations that occur in this situation are analogous to the result of a lottery drawing. In this analogy, we can imagine individuals in a population each contributing an equal number of gametes to a "bucket." Fertilizations result when one gamete drawn from the sperm bucket fuses with another drawn from the egg bucket. Since the frequency of gametes carrying the dominant allele in the bucket is equal to the frequency of the dominant allele in the population, the chance of drawing an egg that carries the dominant allele is 70%.

In Figure E11.1b, a modified Punnett square illustrates the relationship between allele frequency in a population and genotype frequency in a stable population. On the horizontal axis of the square, we place the two types of gametes that can be produced by females in the population (A and a), while on the vertical axis we place the two types of gametes that can be produced by males. In addition, on each axis is an indication of the frequency of these types of egg and sperm in the population: 0.7 for A eggs and A sperm, 0.3 for a eggs and a sperm. Used like the typical Punnett square in Chapter 6, the grid of the square also shows the frequency of each genotype in this population. The frequency of the AA genotype in the next generation will be equal to the frequency of A sperm being drawn (0.7) times the frequency that A eggs will be drawn (0.7), or 0.49. This calculation can be repeated for each genotype. The frequency of the AA genotype is $p \times p (= p^2)$, the aa genotype $q \times q (= q^2)$, and the Aa genotype $p \times q \times 2 (= 2pq)$, because an Aa offspring can be produced by an A sperm and an a egg, or an a sperm and an A egg. Yule was proven wrong: The dominant-recessive relationship among alleles does not determine the frequency of genotypes in a population. Hardy and Weinberg mathematically proved that the frequency of genotypes in one generation of a population depends on the frequency of genotypes in the previous generation of the same population. The dominant trait of brachydactyly is rare in human populations because the allele for the trait is very low in frequency—in the absence of any factor that will cause finger number in the population to evolve, it should remain rare.

Scientists rarely have information about allele frequency; however, they often have information about genotype frequency. When scientists know the frequency

(a)

Parental generation: 70% A ($p = 0.7$) and 30% a ($q = 0.3$)



(b)

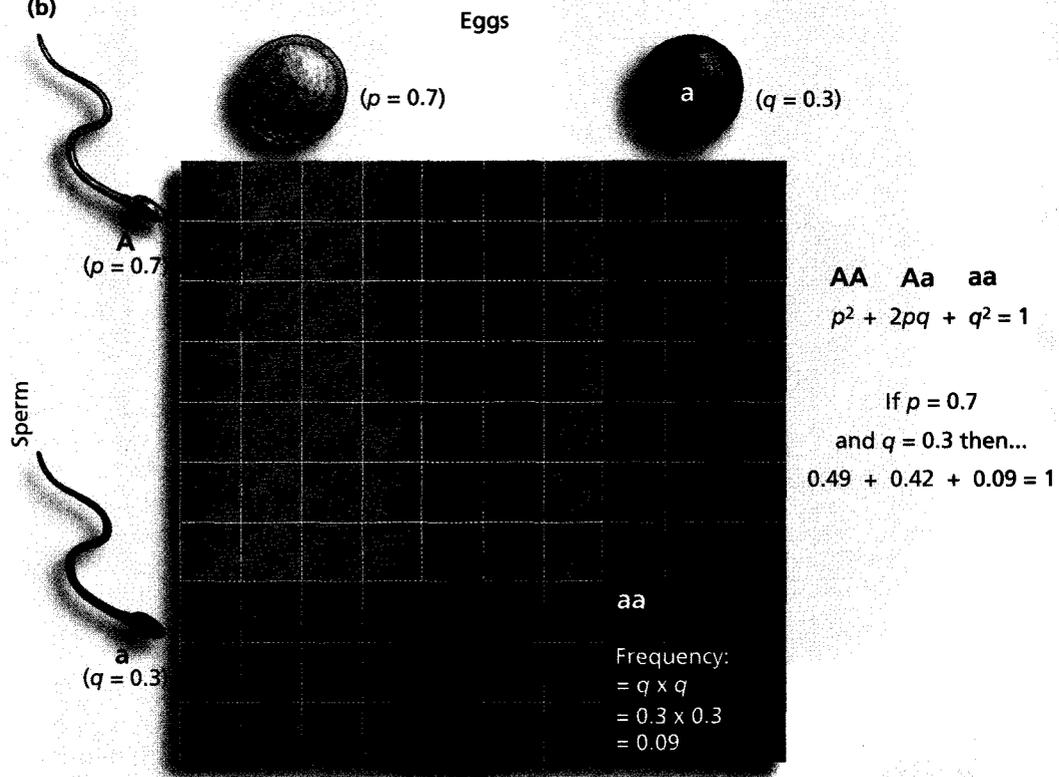


Figure E11.1 The relationship between allele frequency and gamete frequency. (a) The frequency of any allele in a population of adults is equal to the frequency of that allele in gametes produced by that population. (b) Knowing the allele frequency of gametes allows us to predict the frequency of various genotypes in the next generation. In the absence of any process causing evolutionary change, allele frequency should remain constant from one generation to the next.

of a phenotype produced by a recessive allele, they know the frequency of that genotype. They can then use Hardy-Weinberg to calculate the allele frequency in a population. For instance, if the frequency of individuals with

sickle-cell anemia is 1 in 100 births (0.01), we know that q^2 —the frequency of homozygous recessive individuals in the population—is equal to 0.01. Therefore, q is simply the square root of this number, or 0.1.

about 2000 years ago. As the Asian immigrants mixed with the European residents, their alleles became a part of the European gene pool. Populations that encountered a large number of Asian immigrants (that is, those closest to Asia) experienced a large change in their gene pools, while populations that were more distant from Asia encountered a more “diluted” immigrant gene pool made up of the offspring between the Asian immigrants and their European neighbors. Other genetic analyses have led to similar maps—for example, one indicates that populations that practiced agriculture arose in the Middle East, migrated throughout Europe and Asia, and interbred with resident populations about 10,000 years ago.

These data indicate that there are no clear boundaries within the human gene pool. Interbreeding of human populations over hundreds of generations has prevented the isolation required for the formation of distinct biological races.

11.4 Why Human Groups Differ

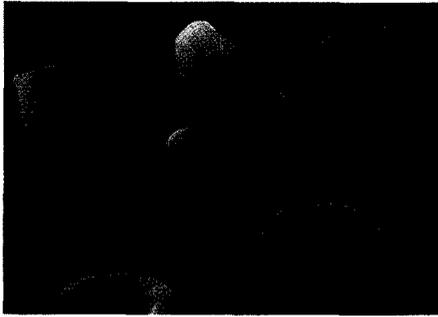
As you learned in the previous section, human races such as those indicated on Indigo’s census form do not represent mostly evolutionarily independent groups; that is, they are not true biological races. However, as is clear to Indigo and to all of us, human populations do differ from each other in many traits. In this section, we explore what is known about why populations share certain superficial traits and differ in others.

Natural Selection

Recall the distribution of the sickle-cell allele in human populations as shown in Figure 11.17 (page 301). It is found in some populations of at least three of the typically described races. The frequency of the sickle-cell allele in these populations is much higher than scientists would predict if its only effect was to cause a life-threatening disease when it is homozygous; that is, when an individual carries 2 copies of the allele. If causing disease was this allele’s only effect, then most individuals who carry 1 copy of it would have lower fitness (or, fewer surviving offspring) than would individuals who have no copies, because at least some of the carriers’ offspring would have sickle-cell disease. Natural selection, the process described in Chapter 10 that results in a higher frequency of alleles that increase fitness and a lower frequency of alleles that decrease fitness, therefore should cause the sickle-cell allele to become rare in a population. The reason that the sickle-cell allele is common in certain populations has to do with the advantage it provides to heterozygotes—individuals who carry 1 copy of the sickle-cell allele—in particular environments.

The sickle-cell allele has the highest frequencies in populations that are at high risk for malaria. Malaria is caused by a parasitic, single-celled organism that spends part of its life cycle feeding on red blood cells, eventually killing the cells. Because their red blood cells are depleted, people with severe malaria suffer from anemia, which may result in death. When individuals carry a single copy of the sickle-cell allele, their blood cells deform when infected by a malaria parasite. These deformed cells quickly die, reducing the parasite’s ability to reproduce and infect more red blood cells and therefore reducing a carrier’s risk of anemia.

The sickle-cell allele reduces the likelihood of severe malaria, so natural selection has caused it to increase in frequency in susceptible populations. The protection that the sickle-cell allele provides to heterozygote carriers is demonstrated by the overlap between the distribution of malaria and the distribution of sickle-cell anemia (Figure 11.20). The sickle-cell anemia allele is an adaptation, a feature that increases fitness, within populations in malaria-prone areas. The allele for sickle-cell disease is not associated with a particular racial category; instead, it is associated with populations that live in particular environments.

(a) Malaria parasite, *Plasmodium falciparum*

(b) Malaria sickle-cell overlap

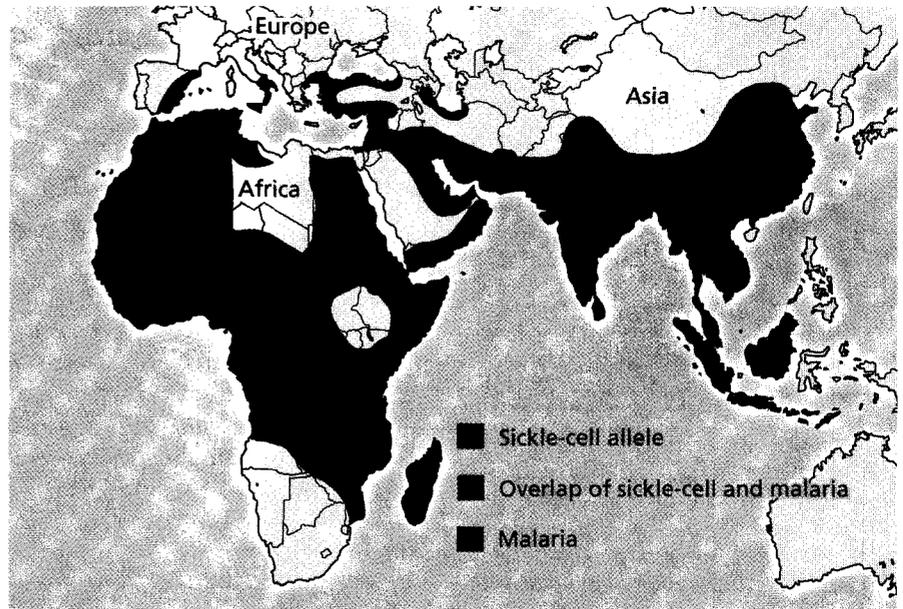


Figure 11.20 The sickle-cell allele is common in malarial environments. (a) Malaria is caused by a microscopic infectious organism, *Plasmodium falciparum* (colored yellow in photo), that is transmitted from person to person by mosquitoes. (b) This map shows the distributions of the sickle-cell allele and malaria in human populations. The overlap is one piece of evidence that the sickle-cell allele is in high frequency in certain populations because it provides protection from malaria.

Another physical trait that has been affected by natural selection is nose form. In some populations, most individuals have broad, flattened noses; in others, most people have long, narrow noses. The pattern of nose shape in populations generally correlates to climate factors—populations in dry climates tend to have narrower noses than do populations in moist climates. Long, narrow noses appear to increase the fitness of individuals in dry environments, serving to increase the water content of inhaled air before it reaches the lungs. A narrower nose has a greater internal surface area, exposing inhaled air to more moisture. For instance, among tropical Africans, people living at drier high altitudes have much narrower noses than do those living in humid rain-forest areas (Figure 11.21). Interestingly, our preconception puts these two populations of

(a) Ethiopian with a narrow nose



(b) Bantu with a broad nose

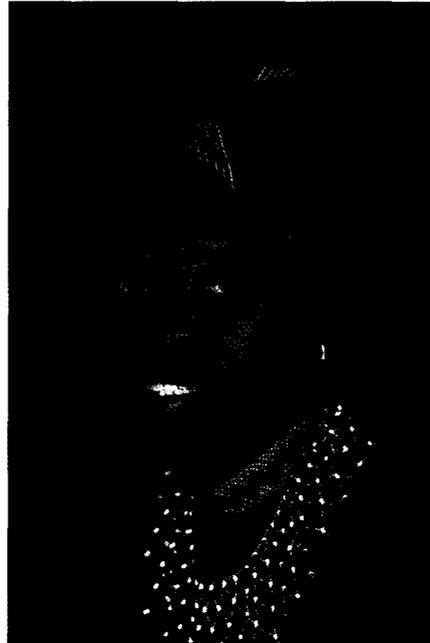


Figure 11.21 Nose shape is affected by natural selection. (a) Long, narrow noses are more common among populations in cold, dry environments. (b) Broad, flattened noses are more common in warm, wet environments.

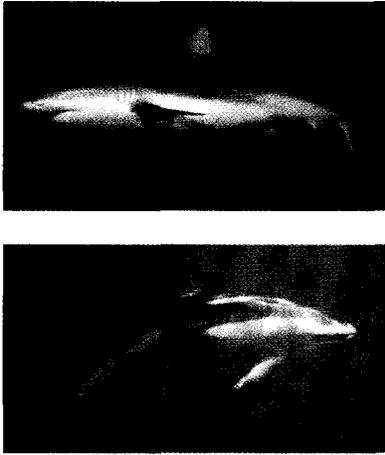


Figure 11.22 Convergence. The similarity in shape between sharks (above) and dolphins (below) results from similar adaptations to life as an oceanic predator of fish. However, sharks are more closely related to stingrays, and dolphins are more closely related to land mammals.

Africans in the same race and explains differences in their nose shape as a result of natural selection, but we place white and black populations into different races and explain their skin color differences as evidence of long isolation from each other. However, like nose shape, skin color is a trait that is strongly influenced by natural selection.

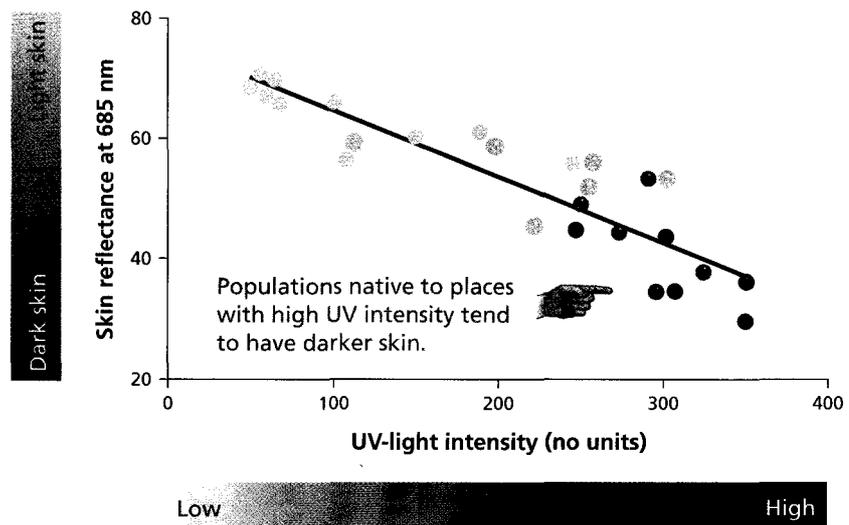
Convergent Evolution

Traits that are shared by populations because they share similar environmental conditions rather than sharing ancestry are termed *convergent*. For example, the similarity in shape between white-sided dolphins and reef sharks is a result of convergence; we know by their anatomy and reproductive characteristics that sharks are most closely related to other fish, and dolphins to other mammals (Figure 11.22). The pattern of skin color in human populations around the globe also appears to be the result of **convergent evolution**. When scientists compare the average skin color in a native human population to the level of ultraviolet (UV) light to which that population is exposed, they see a nearly perfect correlation—the lower the UV light level, the lighter the skin (Figure 11.23).

UV light is light energy in a range that is not visible to the human eye. Among its many effects, this high-energy light interferes with the body's ability to maintain adequate levels of the vitamin folate. Folate is required for proper development in babies and for adequate sperm production in males. Men with low folate levels have low fertility, and women with low folate levels are more likely to have children with severe birth defects. Therefore, individuals who maintain adequate folate levels have higher fitness than individuals who do not. Darker-skinned individuals absorb less UV light and thus have higher folate levels in high-UV environments than light-skinned individuals do. In other words, in environments where UV light levels are high, dark skin is favored by natural selection—it is an adaptation in these environments.

Human populations in low-UV environments face a different challenge. Absorption of UV light is essential for the synthesis of vitamin D. Vitamin D is crucial for the proper development of bones. Women are especially harmed by low vitamin D levels—inadequate development of the pelvic bones can make safely giving birth impossible. There is no risk of not making enough vitamin D when UV light levels are high, regardless of skin color. However, in areas where levels of UV light are low, individuals with lighter skin are able to maximize their absorption of what light is available and thus have higher levels of vitamin D. In these environments, light skin has been favored by natural selection

Figure 11.23 There is a strong correlation between skin color and exposure to UV light. The average reflectance of skin in various human populations is correlated to the average UV radiation that these populations experience. Reflectance is an indication of color—higher reflectance indicates lighter skin. The color of the dots on the graph specifies the racial category of each population.



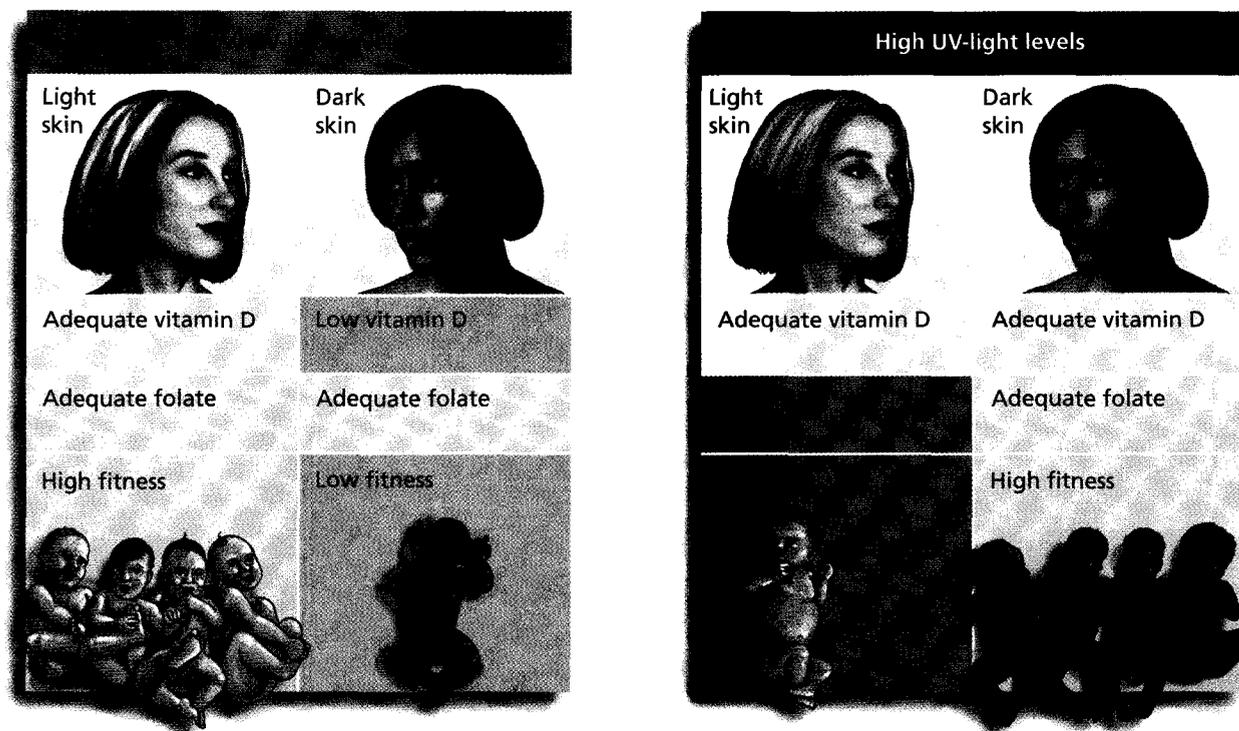


Figure 11.24 The relationship between UV light levels, folate, vitamin D, and skin color. Populations in regions where UV light levels are high experience selection for darker, UV-resistant skin. Populations in regions where UV light levels are low experience selection for lighter, UV-transparent skin.

(Figure 11.24). An exception to this pattern is for populations living in low-UV environments but have high levels of vitamin D in their diet; in this case, being able to make vitamin D is less important, and skin color may be darker.

Because UV light has important effects on human physiology, it has served as a mechanism for natural selection for skin color in human populations. Where UV light levels are high, dark skin is an adaptation, and populations become dark-skinned. Where UV light levels are low, light skin is usually an adaptation, and populations evolve to become light-skinned. The pattern of skin color in human populations is a result of the convergence of different populations in similar environments, not evidence of separate races of humans. Natural selection has caused differences among human populations, but it has also resulted in some populations superficially appearing more similar to some other human populations. Convergence in skin color and other physical characteristics has contributed to the commonly held hypothesis that people with similar skin color are more alike than people with different skin colors. As we saw in the previous section, there is no evidence to support this hypothesis. In fact, populations that appear to be similar could be quite different from each other, simply by chance.

Genetic Drift

As we have seen, differences among populations may arise through the effect of natural selection in various environments. However, differences may also arise through chance processes. A change in allele frequency that occurs due to chance is called **genetic drift**. Human populations tend to travel and colonize new areas, and so we seem to be especially prone to evolution via genetic drift.

Founder Effect. A common cause of genetic drift occurs when a small sample of a larger population establishes a new population. The gene pool of this sample is rarely an exact model of the source population's gene pool. The difference between a subset of a population and the population as a whole is called sampling

error. As discussed in Chapter 1, sampling error is more severe for smaller subsets of a population, such as those that typically found new settlements. This type of sampling error is often referred to as the **founder effect** (Figure 11.25a).

Genetic diseases that are at unusually high levels in certain populations often result from the founder effect. For example, the Amish of Pennsylvania are descended from a population of 200 German founders established approximately 200 years ago. Ellis-van Creveld syndrome, a recessive disease that causes dwarfism (among other effects), is 5000 times more common in the Pennsylvania Amish population than in other German American populations. This difference is a result of a single founder in that original population who carried this very rare recessive allele. Since the Pennsylvania Amish usually marry others within their small religious community, this allele has stayed at a high level—1 in 8

(a) **Founder effect:** A small sample of a large population establishes a new population.



Frequency of red allele is low in original population.



Several of the travelers happen to carry the red allele.



Frequency of red allele much higher in new population.

(b) **Population bottleneck:** A dramatic but short-lived reduction occurs in population size.



Frequency of red allele is low in original population.



Many survivors of tidal wave happen to carry red allele.



Frequency of red allele much higher in new population.

(c) **Chance events in small populations:** The carrier of a rare allele does not reproduce.



Frequency of red allele is low in original population.



The only lizard with red allele happens to fall victim to an eagle and dies.



Red allele is lost.

Figure 11.25 The effects of genetic drift. A population may contain a different set of alleles because (a) its founders were not representative of the original population; (b) a short-lived drop in population size caused a change in allele frequency in one of the populations; (c) one population is so small that low-frequency alleles are lost by chance.

Pennsylvania Amish are carriers of the Ellis-van Creveld allele, compared to less than 1 in 100 non-Amish German Americans.

Plants with animal-dispersed seeds appear to be especially prone to the founder effect. For example, cocklebur, a widespread weed that produces hitchhiker fruit (Figure 11.26), consists of populations that are quite variable in form. The variation among populations appears to have been caused by the subset of burrs that were carried from an ancestral location to new colonies.

Population Bottleneck. Genetic drift may also occur as the result of a **population bottleneck**, a dramatic but short-lived reduction in population size followed by a rapid increase in population (Figure 11.25b). Bottlenecks often occur as a result of natural disasters. As with the founder effect, the new population differs from the original because the gene pool of the survivors is not an exact model of the source population's gene pool.

A sixteenth-century bottleneck on the island of Puka Puka in the South Pacific resulted in a human population that is clearly different from other Pacific island populations: The 17 survivors of a tsunami on Puka Puka were all relatively petite, and their modern descendants are significantly shorter in stature compared to populations found on other islands. Bottlenecks are experienced by non-human populations as well; the genetic similarity among individuals in a large population of Galápagos tortoises on the island of Isabela seems to suggest that most of these animals were wiped out during a volcanic eruption about 88,000 years ago and that the current population descended from a tiny group of survivors. Many less common breeds of dogs, cats, and other pet animals are constantly at risk of experiencing a severe genetic bottleneck, especially if their popularity declines for a period of time.

Genetic Drift in Small Populations. Even without a population bottleneck, allele frequencies may change in a population due to chance events. When an allele is low in frequency within a small population, only a few individuals carry a copy of it. If one of these individuals fails to reproduce, or passes on only the more common allele to surviving offspring, the frequency of the rare allele may drop in the next generation (Figure 11.25c). When the population is very small, there is a relatively high probability that a rare allele will fail to be passed on to the next generation because of chance events. If the population is small enough, even relatively high-frequency alleles may be lost after a few generations by this process.

A human population that illustrates the effects of genetic drift in small populations is the Hutterites, a religious sect with communities in South Dakota and Canada. Modern Hutterite populations trace their ancestry back to 442 people who migrated from Russia to North America between 1874 and 1877. Hutterites tend to marry other members of their sect, and so the gene pool of this population is small and isolated from other populations. Genetic drift in this population over the last century has resulted in a near absence of type B blood among the Hutterites, as compared to a frequency of 15% to 30% in other European migrants in North America. Genetic drift in populations that remain small for many generations can lead to a rapid loss of alleles, which may be very harmful to a population. While this problem is uncommon in humans, the effects of genetic drift on small populations of endangered species can lead to extinction, which will be explored in Chapter 14.

Humans are a highly mobile species, and we have been founding new populations for millennia. Most early human populations were also probably quite small. These factors make human populations especially susceptible to the founder effect, population bottlenecks, and genetic drift, and have contributed to the differences among modern human groups. However, in addition to natural selection and random genetic change, humans' highly social nature and extensive culture have contributed to superficial differences in the physical appearance of various human populations.

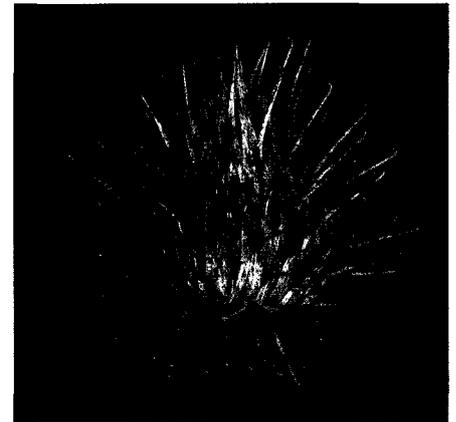
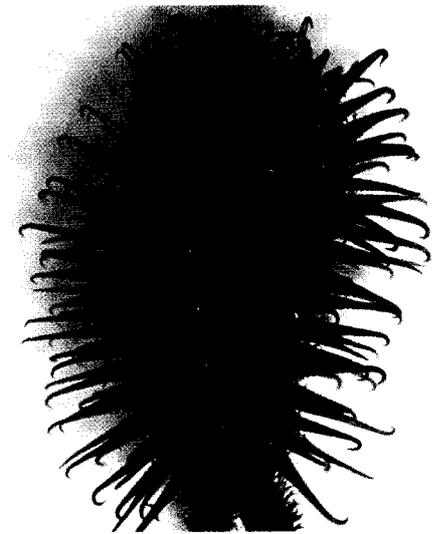
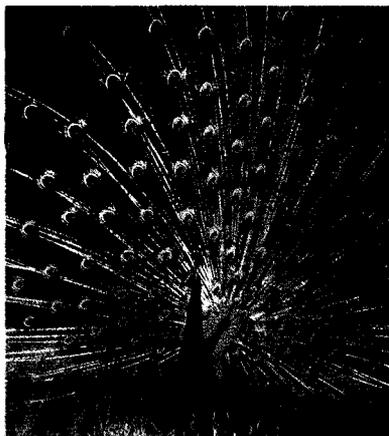


Figure 11.26 An example of the founder effect in plants. Cocklebur disperses by hooking the spikes on its fruits to the fur (or sock) of a passing animal. When these burrs are removed at a distant location, the plant can found a new population that is a genetic subset of the parent population. As a result, the founder effect is very common in cockleburs and may contribute to the large morphological differences in fruit size and shape among cocklebur populations.

(a) Peacock



(b) Lion



(c) Blue morpho butterfly

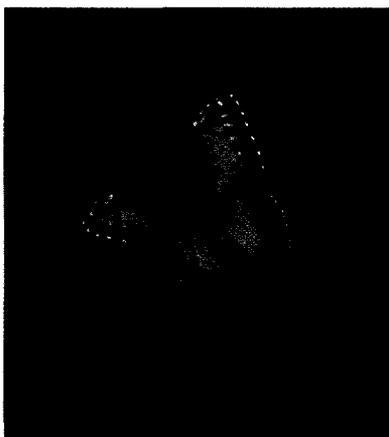


Figure 11.27 The effects of sexual selection. Sexual selection is responsible for many unique and fantastic characteristics of organisms from (a) the peacock's tail to (b) the male lion's mane to (c) the bright colors of butterflies.

Sexual Selection

Men and women within a population may have preferences for particular physical features in their mates. These preferences can cause populations to differ in appearance. When a trait influences the likelihood of mating, that trait is under the influence of a form of natural selection called **sexual selection**. Darwin hypothesized sexual selection in 1871 as an explanation for many of the differences between males and females within a species. For instance, the enormous tail on a male peacock results from female peahens that choose mates with showier tails. Because large tails require so much energy to display, and males with these tails are more conspicuous to their predators, peacocks with the largest tails must be both physically strong and smart in order to survive. Peahens can use the size of the tail, therefore, as a measure of the "quality" of the male. Tail length does appear to be a good measure of overall fitness in peacocks. Research has demonstrated that the offspring of well-endowed males are more likely to survive to adulthood than are the offspring of males with scanty tails. When a peahen chooses a male with a large tail, she is ensuring that her offspring will receive high-quality genes. The same phenomenon seems to account for the differences between males and females in many species (Figure 11.27). In humans, there is some evidence that the difference in overall body size between men and women is a result of sexual selection—namely, a widespread female preference for larger males—perhaps again because size may be an indication of overall fitness. In these cases, female choice for particular mates has led to the evolution of the population.

Some apparently sexually selected traits seem to have little or no relationship to fitness and reflect simply a "social preference." In our highly social species, this type of sexual selection may be common. For example, some scientists have hypothesized that a trait common in the Khoikhoi people of South Africa evolved because of a male preference. Women in this population store large amounts of fatty tissue in their buttocks and upper thighs, giving them a body shape that is considerably different from other African populations. Men in these populations prefer women with this body shape and appear to have caused selection for this trait in the population, although this pattern of fat storage appears to have little effect on a woman's fitness. Other scientists have suggested that lack of facial and thick body hair in many Native American and Asian populations resulted from selection by both men and women for less hairy mates. Some even hypothesize that many physical features that are unique to particular human populations evolved as a result of these socially derived preferences. While the hypothesis that sexual selection was a key process for creating differences among human populations is intriguing, there is as yet little evidence to support these ideas and no simple way to test them.

Assortative Mating

Some differences between human populations may be reinforced by the ways in which people choose their mates. Individuals usually prefer to marry someone who is like themselves, by a process called **positive assortative mating**. For example, there is a tendency for people to mate assortatively by height—that is, tall women tend to marry tall men—and by skin color. When two populations differ in obvious physical characteristics, the number of matings between them may be small if the traits of one population are considered unattractive to members of the other population. Assortative mating has been observed in other organisms as well; for instance, sea horses choose mates that are similar in size to themselves, and in some species of fruit flies, females will mate only with males who have the same body color. Positive assortative mating tends to maintain and even exaggerate physical differences between populations. In highly social humans, assortative mating may be an important cause of differences between groups.

While human populations may show superficial differences due to natural selection in certain environments—genetic drift, sexual selection, and

assortative mating—many of these differences are literally no more than skin deep. Beneath a veneer of physical differences, humans are basically the same.

11.5 Race in Human Society

The discussion in this chapter may still leave Indigo unsatisfied. Scientific data indicate that the racial categories on her census form are biologically meaningless. Races that were once thought of as unitary groups have been revealed to be hugely diverse collections of populations. Two unrelated individuals of the “black race” are no more likely to be biologically similar than a black person and a white person. Yet everywhere she looks, Indigo sees evidence that the racial categories on her census form matter to people—from the existence of her college’s Black Student Association to the heated discussions in her American Experience class about immigration policies in the United States.

Part of the disparity between what recent science has revealed and what our common experience tells us about the reality of race comes from the fact that racial categories are *socially* meaningful. In the United States, we all learn that skin color, eye shape, and hair type are the primary physical characteristics that denote meaningful differences among groups. These physical characteristics have this significance due to the history of European colonization, slavery, immigration, and Native American oppression. In other words, race is a social construct—a product of history and learned attitudes. The construction of racial groups allowed some “races” to justify unethical and inhumane treatment of other “races.” Thus, human races were described in the seventeenth century primarily to support **racism**, the idea that some groups of people are naturally superior to others. The United States government collects information about race on the census form as part of its effort to measure and ameliorate the lingering effects of historical, state-supported racism, but the Census Bureau acknowledges that the races with which people identify “should not be interpreted as being primarily biological or genetic.”

It may be easier to see that racial categories are socially constructed if you imagine what might have happened if Western history had followed a different path. If the origin of American slaves had been from around the Mediterranean Sea, we might now identify racial groups on the basis of some other physical difference besides skin color—perhaps height, weight, or the presence of thick facial hair. Alternatively, compare the racial groupings in modern North America to those in modern Rwanda, where individuals are identified with different racial groups (Hutu and Tutsi) based on physical stature only. This classification reflects the differential social status attained by the typically taller Tutsi tribe and the typically shorter Hutu tribe under European colonization in the nineteenth century. In the United States, we would classify Hutu and Tutsi together in the same “black race”—an assignment that many members of these two groups would vigorously reject. In every society, children learn from birth which physical differences among people are significant in distinguishing “us” from “them.” Even if a child is never explicitly taught racial categories, the fact that many communities are highly segregated into racial enclaves provides a lesson about which physical characteristics mark someone as “different from me.”

When socially constructed racial categories are considered biologically meaningful, they become traps that are extremely difficult for individuals to escape. The most important insight that has come from studies of human diversity is that grouping human populations on the basis of skin color and eye shape is as arbitrary as grouping them on the basis of height and weight. However, arbitrary groupings are not necessarily bad. We all group ourselves into social categories: Christian or Muslim, baseball or football fan, cat or dog person. Even if the racial categories on the census form were once part of a racist system, when people identify themselves as members of a particular race, they are

acknowledging a shared history with others who also identify themselves as members of that race. This self-identification can be important for realizing individual and group goals of equality and self-determination as well as continuing the fight against the real and serious vestiges of state-supported racism. The biological evidence tells Indigo that she is able to choose her racial category based on her own history and relationships—and that she should feel free to choose “none of the above” if she desires.

CHAPTER REVIEW

Summary

11.1 What Is a Species?

- All humans belong to the same biological species, *Homo sapiens sapiens*. A biological species is defined as a group of individuals that can interbreed and produce fertile offspring. Biological species are reproductively isolated from each other, thus separating the gene pools of species (p. 284).
- Reproductive isolation is maintained by pre-fertilization or post-fertilization factors (pp. 285–286).
- Speciation occurs when populations of a species become isolated from each other. These populations diverge from each other, and reproductive isolation between the populations evolves (pp. 288–292).

Web Tutorial 11.1 The Process of Speciation

11.2 The Race Concept in Biology

- Biological races are populations of a single species that have diverged from each other but have not become reproductively isolated. This definition of race corresponds to the definition of the genealogical species concept (pp. 293–294).

11.3 Humans and the Race Concept

- The fossil record provides evidence that the modern human species is approximately 200,000 years old, which is not much time for major differences between human groups to have evolved (pp. 297–298).
- The genetic evidence for biological races includes alleles that are unique to a particular race; as well as similar allele frequencies for a number of genes among populations within

racies but differences in allele frequencies among populations in different races (pp. 298–300).

- Modern human groups do not show evidence that they have been isolated from each other and formed distinct races (p. 305).
- Genetic evidence indicates that human groups have been mixing for thousands of years (p. 306).

11.4 Why Human Groups Differ

- Similarities among human populations may evolve as a result of natural selection. The sickle-cell allele is more common in populations where malaria incidence is high, and light skin is more common in areas where the UV light level is low; both adaptations are a result of natural selection in these environments (p. 306).
- Human populations may show differences due to genetic drift, which is defined as changes in allele frequency due to chance events such as founder effects or population bottlenecks (pp. 309–311).
- Sexual selection, whereby individuals—typically females—choose mates that display some “attractive” quality, may also be responsible for creating differences among human populations (p. 312).
- Positive assortative mating, in which individuals choose mates who are like themselves, can reinforce differences between human populations (p. 312).

11.5 Race in Human Society

- While race in the human species has no biological meaning, it is an important social construct based on shared history and self-identity (p. 313)

Learning the Basics

1. Describe the three steps of speciation.
2. Can speciation occur when populations are not physically isolated from each other? How?
3. Describe three ways that evolution can occur via genetic drift.
4. Which of the following is an example of a pre-fertilization barrier to reproduction?
 - A. A female mammal is unable to carry a hybrid offspring to term.;
 - B. Hybrid plants produce only sterile pollen.;
 - C. A hybrid between two bird species sings a song that

is not recognized by either species.; **D.** A male fly of one species performs a “wing-waving” display that does not convince a female of another species to mate with him.; **E.** A hybrid embryo is not able to complete development.

5. According to the most accepted scientific hypothesis about the origin of two new species from a single common ancestor, most new species arise when _____.
A. many mutations occur; **B.** populations of the ancestral species are isolated from each other; **C.** there is no natural selection; **D.** a Creator decides that two new species would be preferable to the old one; **E.** the ancestral species decides to evolve
6. For two populations of organisms to be considered separate biological species, they must be _____.
A. reproductively isolated from each other; **B.** unable to produce living offspring; **C.** physically very different from each other; **D.** a and c are correct; **E.** a, b, and c are correct
7. The statement that “human populations classified in the same race appear to be more genetically similar than human populations placed in different races” is _____.
A. true; **B.** false
8. Similarity in skin color among different human populations appears to be primarily the result of _____.
A. natural selection; **B.** convergence; **C.** shared ancestry among these populations; **D.** a and b are correct; **E.** a, b, and c are correct
9. The tendency for individuals to choose mates who are like themselves is called _____.
A. natural selection; **B.** sexual selection; **C.** positive assortative mating; **D.** the founder effect; **E.** random mating
10. When you identify yourself as a member of a particular human group based on shared customs, language, and recent history, you are using the _____.
A. biological definition of race; **B.** social construct definition of race; **C.** psychological definition of race; **D.** incorrect definition of race; **E.** morphological definition of race

Analyzing and Applying the Basics

1. Wolf populations in Alaska are separated by thousands of miles from wolf populations in the northern Great Lakes of the lower 48 states. Wolves in both populations look similar and have similar behaviors. However, the U.S. government has treated these two populations quite differently, listing the Great Lakes populations as endangered until recently but allowing hunting of wolves in Alaska. Some opponents of wolf protection have argued that the “wolf” should not be considered endangered at all in the United States because of the large population in Alaska, while supporters of wolf protection state that the Great Lakes population represents a unique population that deserves special status. Should these two populations be considered different races or species? What information would you need to test your answer?
2. The frequency of phenylketonuria (PKU), which results from the inability to metabolize the amino acid phenylalanine, in Irish populations is 1 in every 7000 births, while the frequency in urban British populations is 1 in 18,000 and only 1 in 36,000 in Scandinavian populations. Give two reasons that this allele, which results in severe mental retardation in homozygous individuals, may be found in different frequencies in these populations. (If you have read Essay 11.1, you should also be able to use Hardy-Weinberg to calculate the frequency of this allele in each population.)
3. Medical researchers have often excluded particular racial groups from their studies to minimize variability among the subjects of their studies. Given the biological understanding of race, does this policy make sense?

Connecting the Science

1. Black people in the United States have higher rates of hypertension (high blood pressure), heart disease, and stroke than do white people. Is this difference likely to be biological? How could you test your hypothesis?
2. The only information that was collected from *every resident* of the United States in the 2000 census was name, place of residence, sex, age, and race. (Note that some residents received a “long form” with many additional questions, but everyone had to answer these five basic questions.) Do you think it is important to collect race data from all citizens? Why or why not? Is there some other piece of information that you think is more useful to the government?