Unit 3

GENETICS

CHAPTERS

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"... [G]enetics has come to occupy an important position at the center of the sciences of life ... genetics became allied with biochemistry; it revolutionized bacteriology, played a major role in the emergence of the molecular biology of the fifties, resisted the challenge of ecology, took hold of cancer research and is even now reaching out to revolutionize taxonomy and its old rival embryology."

From "Mendel, Mendelism and Genetics" by Robert C. Olby. Online, World Wide Web, July 2 1997. Available http://www.netspace.org/MendelWeb/MWolby.html. Reprinted by permission of the author.

These tiger cub siblings look very similar to one another because they have inherited characteristics from their parents.

This researcher, above, is analyzing fragments of DNA that have been sorted into DNA fingerprints. The fruit fly at right is missing its right eye due to a genetic mutation.

Deoxyribonucleic acid (DNA)

This white-skinned, blue-eyed alligator has a genetic condition called leucism. The fruit fly, right, is often studied in genetics because it multiplies quickly and has only eight chromosomes.

CHAPTER 9

FUNDAMENTALS OF GENETICS

The unique appearance of this white-skinned, blue-eyed alligator is the result of a genetic condition.

FOCUS CONCEPT: ***Reproduction and Inheritance***

As you read, notice how Mendel developed hypotheses to help predict the outcome of different genetic crosses.

BIOLOGY INTERACTIVE TUTOR

Unit 5—*Heredity*
Topics 1–6

SECTION 9-1

MENDEL'S LEGACY

***Genetics** is the field of biology devoted to understanding how characteristics are transmitted from parents to offspring. Genetics was founded with the work of Gregor Johann Mendel, an Austrian monk who experimented with garden peas. This section describes Mendel's experiments and the principles of genetics that resulted from them.*

OBJECTIVES

- Describe the steps involved in Mendel's experiments on garden peas.
- Distinguish between dominant and recessive traits.
- State two laws of heredity that were developed from Mendel's work.
- Explain the difference between an allele and a gene.
- Describe how Mendel's results can be explained by scientific knowledge of genes and chromosomes.

GREGOR MENDEL

In 1842, at the age of 21, Gregor Mendel entered a monastery in Brunn, Austria. His task of tending the garden gave him time to think and to observe the growth of many plants. In 1851 he entered the University of Vienna to study science and mathematics. His mathematics courses included training in the then-new field of statistics. Mendel's knowledge of statistics later proved valuable in his research on **heredity**—the transmission of characteristics from parents to offspring. When Mendel returned to the monastery, he taught in a high school and also kept a garden plot. Although he studied many plants, he is probably remembered most for his experiments with garden peas, *Pisum sativum*.

Mendel's Garden Peas

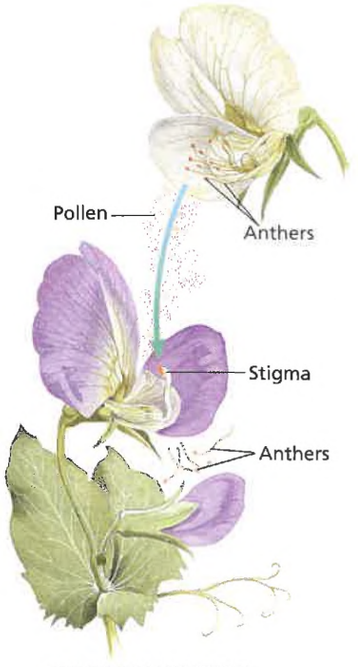
Mendel observed seven characteristics of pea plants. Each characteristic occurred in two contrasting **traits:** *plant height* (long or short stems), *flower position along stem* (axial or terminal), *pod color* (green or yellow), *pod appearance* (inflated or constricted), *seed texture* (smooth or wrinkled), *seed color* (yellow or green), and *flower color* (purple or white). Mendel used his knowledge of statistics to analyze his observations of these seven characteristics.

Mendel collected seeds from his pea plants, carefully recording the characteristics of the plant from which each seed was collected. The next year he planted the seeds. He observed that purple-flowering plants grew from the seeds obtained from purple-flowering plants, but he noticed that some white-flowering plants also grew from the seeds of purple-flowering plants. And when experimenting with the characteristic of plant height, he observed that while some tall plants grew from seeds obtained from tall plants, some short plants also grew from seeds obtained from tall plants. Mendel wanted to find an explanation for such variations.

Word Roots and Origins

heredity

from the Latin *hereditas,* meaning "heirship"



CROSS-POLLINATION

FIGURE 9-1

Mendel controlled the breeding of his pea plants and tracked the inheritance of traits by transferring pollen from the anthers of flowers on one plant to the stigma of flowers on a different plant.

Mendel's Methods

Mendel was able to document the traits of each generation's parents by carefully controlling how the pea plants were pollinated. **Pollination** occurs when pollen grains produced in the male reproductive parts of a flower, called the **anthers,** are transferred to the female reproductive part of a flower, called the **stigma.**

Self-pollination occurs when pollen is transferred from the anthers of a flower to the stigma of either the same flower or a flower on the same plant. **Cross-pollination** involves flowers of two separate plants. Pea plants normally reproduce through self-pollination.

Self-pollination can be interrupted—and cross-pollination performed—by removing the anthers from a flower and manually transferring the anther of a flower on one plant to the stigma of a flower on another plant, as shown in Figure 9-1. By doing this, Mendel was able to protect his flowers from receiving any other pollen that might be transferred by wind or insects, giving him more control over the pollination of his pea plants.

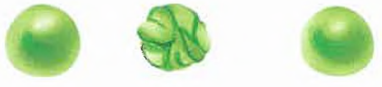
MENDEL'S EXPERIMENTS

Mendel studied each characteristic and its contrasting traits individually. He began by growing plants that were pure for each trait. Plants that are **pure** for a trait always produce offspring with that trait. For example, pea plants pure for the trait of yellow pods self-pollinate to produce offspring with yellow pods. The term **strain** denotes plants that are pure for a specific trait. Mendel produced strains by allowing the plants to self-pollinate for several generations. He eventually obtained 14 strains, one for each of the 14 traits he observed. He called each strain a parental generation, or **P_1 generation.**

Mendel then cross-pollinated these strains by transferring pollen from the anthers of a plant pure for one trait to the stigma of another plant pure for the contrasting trait. For example, if he wanted to cross a plant pure for the trait of yellow pods with one pure for the trait of green pods, he first removed the anthers from the plant that produced green pods. Then he dusted the pollen from a yellow-podded plant onto the stigma of a green-podded plant and allowed the seeds to develop.

When the plants matured, he recorded the number of each type of offspring produced by each P_1 plant. Mendel called the offspring of the P_1 generation the first filial generation, or **F_1 generation.** He then allowed the flowers from the F_1 generation to self-pollinate and collected the seeds. Mendel called the plants in this generation the second filial generation, or **F_2 generation.** Following this process, Mendel performed hundreds of crosses and documented the results of each by counting and recording the observed traits of every cross. Table 9-1 summarizes the results of many of Mendel's crosses.

TABLE 9-1 *Mendel's Crosses and Results*

Characteristic	P cross	F_1 generation	F_2 generation	Actual ratio	Probability ratio
Position of flowers along stem	 axial × terminal	 axial	651 axial 207 terminal	3.14:1	3:1
Height of plant	 tall × short	 tall	787 tall 277 short	2.84:1	3:1
Pod appearance	 inflated × constricted	inflated	882 inflated 299 constricted	2.95:1	3:1
Pod color	 green × yellow	green	428 green 152 yellow	2.82:1	3:1
Seed texture	 smooth × wrinkled	smooth	5,474 smooth 1,850 wrinkled	2.96:1	3:1
Seed color	 yellow × green	yellow	6,022 yellow 2,001 green	3.01:1	3:1
Flower color	 purple × white	purple	705 purple 224 white	3.15:1	3:1

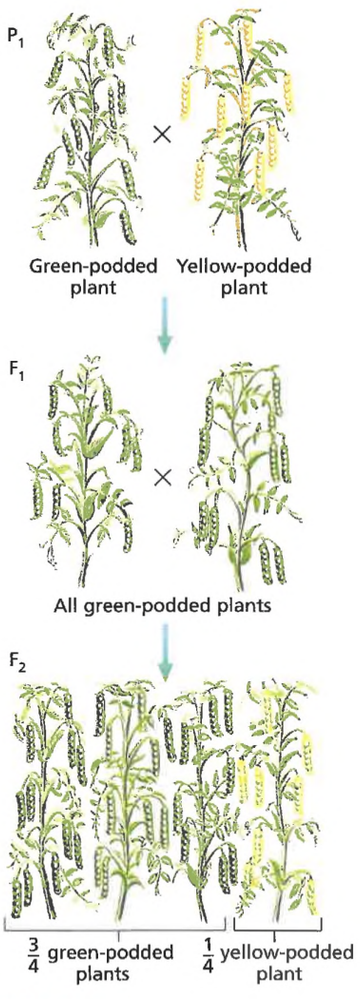


FIGURE 9-2

Pure green-podded pea plants crossed with pure yellow-podded pea plants produce only green-podded plants. Yet when the F_1 generation is permitted to self-pollinate, some yellow-podded plants appear in the F_2 generation.

MENDEL'S RESULTS AND CONCLUSIONS

In one of his experiments, Mendel crossed a plant pure for green pods with one pure for yellow pods, as shown in Figure 9-2. The resulting seeds produced an F_1 generation with only green-podded plants. No yellow pods developed, even though one parent had been pure for yellow pods. Only one of the two traits found in the P_1 generation appeared in the F_1 generation.

Next Mendel allowed the F_1 plants to self-pollinate and planted the resulting seeds. When the F_2 generation plants grew, he observed that about three-fourths of the F_2 plants had green pods and about one-fourth had yellow pods.

Mendel's observations and his careful records led him to hypothesize that something within the pea plants controlled the characteristics he observed. He called these controls *factors*. Mendel hypothesized that each trait was inherited by means of a separate factor. Because the characteristics he studied had two alternative forms, he reasoned that there must be a *pair* of factors controlling each trait.

Recessive and Dominant Traits

Whenever Mendel crossed strains, one of the P_1 traits failed to appear in the F_1 plants. In every case, that trait reappeared in a ratio of about 3:1 in the F_2 generation. This pattern emerged in thousands of crosses and led Mendel to conclude that one factor in a pair may prevent the other from having an effect. Mendel hypothesized that the trait appearing in the F_1 generation was controlled by a **dominant** factor because it masked, or dominated, the other factor for a specific characteristic. The trait that did not appear in the F_1 generation but reappeared in the F_2 generation was thought to be controlled by a **recessive** factor.

Thus, a trait controlled by a recessive factor had no observable effect on an organism's appearance when it was paired with a trait controlled by a dominant factor.

The Law of Segregation

Mendel concluded that the paired factors separate during the formation of reproductive cells. This means that each reproductive cell, or gamete, receives only one factor of each pair. When two gametes combine during fertilization, the offspring have two factors controlling a specific trait. The **law of segregation** states that *a pair of factors is segregated, or separated, during the formation of gametes.*

Word Roots and Origins

recessive

from the Latin *recessus,* meaning "to recede"

The Law of Independent Assortment

Mendel also crossed plants that differed in two characteristics, such as in flower color and seed color. The data from these more-complex crosses showed that traits produced by dominant factors

do not necessarily appear together. A green seed pod produced by a dominant factor could appear in a white-flowering pea plant, as Figure 9-3 shows. Mendel concluded that the factors for different characteristics are not connected. The **law of independent assortment** states that *factors for different characteristics are distributed to gametes independently.*

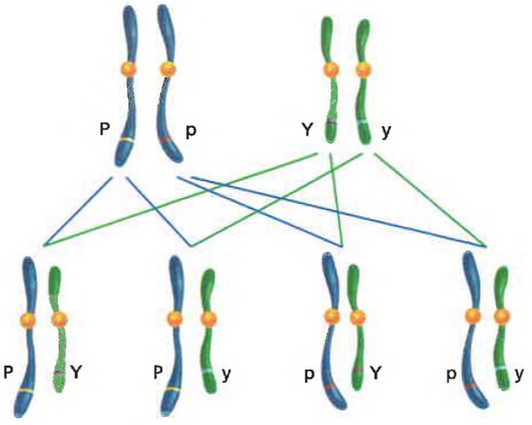


FIGURE 9-3
Independent assortment of these two pairs of homologous chromosomes would give the following allele combinations in gametes. *P* denotes flower color. *Y* denotes seed color.

CHROMOSOMES AND GENES

Most of Mendel's findings agree with what biologists now know about molecular genetics. **Molecular genetics** is the study of the structure and function of chromosomes and genes. Recall from Chapter 8 that a chromosome is a threadlike structure made up of DNA. A gene is the segment of DNA on a chromosome that controls a particular hereditary trait. Because chromosomes occur in pairs, genes also occur in pairs. Each of several alternative forms of a gene is called an **allele.** Mendel's *factors* are now called *alleles.*

Letters are used to represent alleles. Capital letters refer to dominant alleles, and lowercase letters refer to recessive alleles. For example, the dominant allele for the trait of green pod color may be represented by *G,* and the recessive allele for the trait of yellow pod color may be represented by *g.* Whether a letter is capitalized or lowercased is important. The actual letter selected to represent an allele is arbitrary.

Recall from Chapter 8 that during meiosis, gametes receive one chromosome from each homologous pair of chromosomes. This means that when the gametes combine in fertilization the offspring receives one allele for a given trait from each parent.

Mendel's law of independent assortment is supported by the fact that chromosomes segregate independently to gametes during meiosis. Therefore, the law of independent assortment is observed only for genes located on separate chromosomes or located far apart on the same chromosome.

SECTION 9-1 REVIEW

1. List the steps involved in Mendel's experiments on garden peas.
2. Define the terms *dominant* and *recessive.*
3. Differentiate genes from alleles.
4. State in modern terminology the two laws of heredity that resulted from Mendel's work.
5. How might Mendel's conclusions have differed if he had studied two traits determined by alleles carried on the same chromosome?
6. **CRITICAL THINKING** What happens during meiosis that would allow genes located on the same chromosome to separate independently of one another?

Jumping Genes

HISTORICAL PERSPECTIVE

The scientific study of heredity began with the work of Gregor Mendel. The rediscovery of Mendel's work in 1900 is said to mark the birth of the science of genetics. Geneticist Barbara McClintock, born in 1902, devoted her life to this new science. Ironically, certain assumptions about genetics, strongly believed but wrong, prevented early acceptance of McClintock's exciting conclusions.

Early Discoveries

Have you ever looked closely at ornamental corn, also called maize? Today it is planted and marketed for decorative use. In the fall, when the corn ripens, its red, brown, and purple ears are harvested and artistically arranged in centerpieces and door hangings.

In the late 1920s and early 1930s, at Cornell University, geneticists harvested the colorful plant for another purpose. They hoped to trace variations among maize plants to specific genes in an effort to discover how chromosomes carry specific traits to new generations.

As a graduate student at Cornell, Barbara McClintock began work on identifying and labeling the 10 chromosomes of maize. She developed new microscopic techniques and was able to visualize the parts of the maize chromosomes. Scientists were thrilled with her discovery because they could identify the chromosome that carried the gene for a particular trait.

After receiving her doctorate in botany in 1927, McClintock stayed at Cornell. Mostly she worked alone, wanting to observe everything for herself. She once said:

> *No two plants are exactly alike. They're all different, and as a consequence, you have to know that difference.... I don't feel I really know the story if I don't watch the plant all the way along.*

Barbara McClintock

Discovering "Jumping Genes"

McClintock taught for several years at Cornell before taking a position as a research scientist at Cold Spring Harbor Laboratory, a scientific community on Long Island about 40 miles east of New York City. She stayed there for the rest of her life, working in maize genetics. There, during the 1940s and 1950s, she did the research and made the discovery

for which she won the 1983 Nobel Prize in physiology or medicine.

The prevailing opinion among most geneticists in McClintock's time was that genes were lined up on chromosomes in unchanging places, much like beads on a string. McClintock's observations told her otherwise. The changes she saw in corn kernels and chromosomes led her to conclude that some genes, which she called transposons, are able to move to a new place on a chromosome or to a new chromosome entirely. These "jumping genes," she believed, cause differences to appear in a plant's offspring by either activating or inactivating the genes responsible for kernel color. Unlike with genetic recombination, which occurs during meiosis, transposons change the location of genes on chromosomes in the somatic cells of organisms.

McClintock observed two kinds of transposons: dissociators and activators. The dissociators could jump to a new place when signaled by others called activators. The dissociators would then cause changes in nearby genes on the chromosome and in the color of the kernels in maize. McClintock verified her conclusions through repeated experiments.

Ears of maize similar to these demonstrated to McClintock that certain genetic elements transpose.

She Was Right

In the summer of 1951, at Cold Spring Harbor, McClintock presented her discovery at a meeting of scientists from around the world. Her presentation was not well received. McClintock summarized it best when she stated that her discovery went against "the dogma of the constancy of the genome." Although saddened by the lack of interest in her work, she was not discouraged. She knew that she was right and that the evidence would ultimately convince the world that transposons existed.

Why did most geneticists ignore McClintock's conclusions for so long? One reason was that their attention was directed to the work of the new molecular geneticists. Compared with their work, McClintock's seemed traditional, almost old-fashioned. Her fellow scientists were using electron microscopes capable of seeing molecules. Her methods—an ordinary microscope, crossbreeding, and observation—belonged to an earlier era. In working with maize genetics, she was "paddling upstream against the current of scientific opinion."

In the end, McClintock proved to be not behind her time but ahead of it. Biologist Allan Campbell once said of her discoveries, "The time was not ripe."

By the 1970s, the time was ripe. Molecular biologists, using electron microscopes and other technology, saw bits of DNA "jumping around" in bacteria. Transposons are thought to help bacteria better adapt to new environments. For example, transposons probably play a role in spreading genes for antibiotic resistance among bacteria. Scientists later found transposons in eukaryotes other than maize. Today all organisms, including humans, seem to have transposons.

Like McClintock, many geneticists now expect their understanding of transposons to help solve certain mysteries about evolution: how larger organisms developed from single cells and, in general, where new species come from. Transposons may also have medical applications, such as helping scientists discover how white blood cells make antibodies and what causes cells to sometimes multiply wildly, as in cancer.

SECTION

9-2

OBJECTIVES

- Explain how probability is used to predict the results of genetic crosses.
- Use a Punnett square to predict the results of monohybrid and dihybrid genetic crosses.
- Explain how a testcross is used to show the genotype of an individual whose phenotype is dominant.
- Differentiate a monohybrid cross from a dihybrid cross.

GENETIC CROSSES

Today geneticists rely on Mendel's work to predict the likely outcome of genetic crosses. In this section, you will learn how to predict the probable genetic makeup and appearance of offspring resulting from specified crosses.

GENOTYPE AND PHENOTYPE

The genetic makeup of an organism is its **genotype** (JEN-uh-TIEP). The genotype consists of the alleles that the organism inherits from its parents. For example, the genotype of the white-flowering pea plant in Figure 9-4 consists of two recessive alleles for white flower color, represented as *pp*. The genotype of a purple-flowering pea plant may be either *PP* or *Pp*. Either of these two genotypes would result in a pea plant with purple flowers because the *P* allele is dominant.

The appearance of an organism as a result of its genotype is called its **phenotype** (FEE-noh-TIEP). The phenotype of a *PP* or a *Pp* pea plant is purple flowers, whereas the phenotype of a *pp* pea plant is white flowers. Human phenotypes can appear to be altered by behavior. Hair dye, contact lenses of varying colors, and plastic surgery can all change an individual's appearance, but they do not alter the individual's true phenotype or genotype.

FIGURE 9-4

The genotype of the pea plant on the left is *pp*. Its phenotype is white flowers. The phenotype of the pea plant on the right is purple flowers. Its genotype is either *Pp* or *PP*.

When both alleles of a pair are alike, the organism is said to be **homozygous** (HOH-moh-ZIE-guhs) for that characteristic. An organism may be homozygous dominant or homozygous recessive. For example, a pea plant that is homozygous dominant for flower color would have the genotype *PP*. A pea plant that is homozygous recessive for flower color would have the genotype *pp*. When the two alleles in the pair are different, the organism is **heterozygous** (HET-uhr-OH-ZIE-guhs) for that characteristic. A pea plant that is heterozygous for flower color would have the genotype *Pp*.

PROBABILITY

Probability is the likelihood that a specific event will occur. A probability may be expressed as a decimal, a percentage, or a fraction. Probability is determined by the following equation:

$$\text{Probability} = \frac{\text{number of times an event is expected to happen}}{\text{number of opportunities for an event to happen}}$$

For example, in Mendel's experiments the dominant trait of yellow seed color appeared in the F_2 generation 6,022 times. The recessive trait of green seed color appeared 2,001 times. The total number of individuals was 8,023 (6,022 + 2,001). Using the probability equation above, the probability that the dominant trait will appear in a similar cross is

$$\frac{6{,}022}{8{,}023} = 0.75$$

Expressed as a percentage, the probability is 75 percent. Expressed as a fraction, the probability is 3/4.

The probability that the recessive trait will appear in an F_2 generation is

$$\frac{2{,}001}{8{,}023} = 0.25$$

Expressed as a percentage, the probability is 25 percent. Expressed as a fraction, the probability is 1/4. Fractions can also be expressed as ratios. For example, the ratio 1:4 represents the same probability as 1/4. Probability tells us that there are three chances in four that an offspring of two heterozygous individuals will have the dominant trait and one chance in four that it will have the recessive trait.

The results predicted by probability are more likely to occur when there are many trials. For example, many coin tosses should yield a result of heads 50 percent of the time and tails 50 percent of the time. However, if you toss a coin only a few times, you might not get this result. But *each* time a coin is tossed, the probability of landing tails is 50 percent. Only after many, many tries would you be *likely* to get the percentage of heads predicted on the basis of probability, that is, 50 percent heads and 50 percent tails.

Quick Lab

Calculating Probability

Materials paper sack containing 20 jelly beans in an unknown number of color combinations

Procedure

1. Obtain a sack of 20 jelly beans from your teacher. Do not look into the sack. Do not eat the jelly beans. There are three possible colors of jelly beans that can be pulled from the sack. Pull one jelly bean out, and record the color. Return the jelly bean to the sack, and shake the bag to mix them.
2. Repeat step 1 until you have examined 20 jelly beans.
3. Determine the probability of each color of jelly bean that you pulled from the sack. Compare your results with those of the rest of the class.

Analysis Does anyone have the same probabilities as you? Are there some probabilities that are very close to yours? Are there some probabilities that are very different from yours? Based on these observations, determine the number of jelly beans of each color that are in your sack.

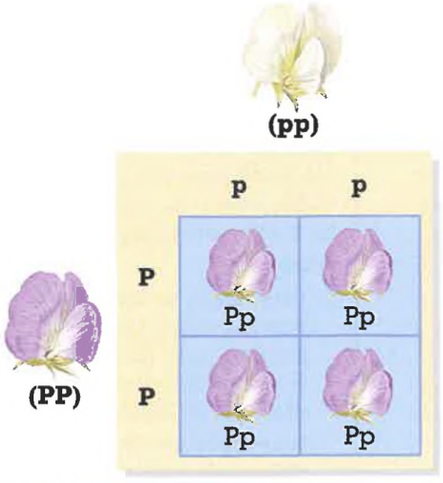


FIGURE 9-5
A pea plant homozygous for purple flowers crossed with a pea plant homozygous for white flowers will produce only purple-flowering offspring. Note that all of the offspring will be heterozygous for flower color.

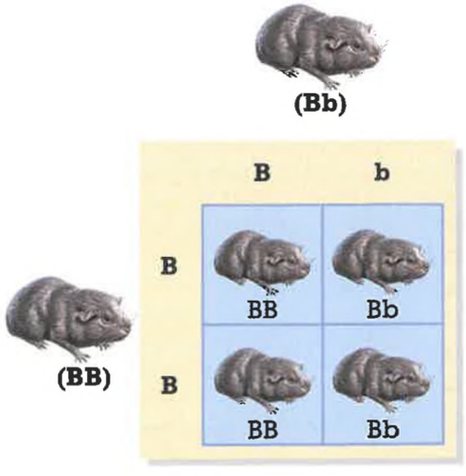
PREDICTING RESULTS OF MONOHYBRID CROSSES

A cross between individuals that involves one pair of contrasting traits is called a **monohybrid** (MAWN-oh-HIE-brid) **cross.** A cross between a pea plant that is pure for producing purple flowers and one that is pure for producing white flowers is an example of a monohybrid cross. Biologists use a diagram called a **Punnett** (PUHN-uht) **square,** like the one shown in Figure 9-5, to aid them in predicting the probability that certain traits will be inherited by offspring. The following examples show how a Punnett square can be used to predict the outcome of different types of crosses.

Example 1: Homozygous × Homozygous

The cross represented in Figure 9-5 is a monohybrid cross between a pea plant homozygous for purple flower color (*PP*) and a pea plant homozygous for white flower color (*pp*). The alleles contributed by the homozygous dominant parent are represented by *P*s on the left side of the Punnett square. The alleles contributed by the homozygous recessive parent are represented by *ps* across the top of the Punnett square. Each box within the Punnett square is filled in with the letters that are above it and beside it outside the square. The combinations of alleles in the four boxes indicate the possible genotypes that can result from the cross. The predicted genotype is *Pp* in every case. Thus, there is a 100 percent probability that the offspring will have the genotype *Pp* and thus the phenotype purple flower color.

FIGURE 9-6
Crossing a guinea pig homozygous for black coat color with one heterozygous for black coat color produces all black-coated offspring. Note that half of the offspring are predicted to be homozygous for coat color.



Example 2: Homozygous × Heterozygous

Figure 9-6 shows a cross between a guinea pig that is homozygous dominant for the trait of black coat color (*BB*) and a guinea pig that is heterozygous for this trait (*Bb*). The letter *b* stands for the recessive allele. Genotype *bb* results in a brown coat. Notice that there are two possible genotypes that can result from this cross, *BB* or *Bb*. The probability of an offspring with the genotype *BB* is 2/4, or 50 percent. The probability of an offspring with the genotype *Bb* is also 2/4, or 50 percent. In other words, you could expect about 50 percent of the offspring resulting from this cross to be homozygous dominant for the black coat and about 50 percent to be heterozygous dominant for a black coat. The probable phenotype is black coat color in every case; thus, 4/4, or 100 percent, of the offspring are expected to have a black coat. What if the homozygous guinea pig had been homozygous recessive for coat color? In this case, the homozygote would have the genotype *bb*. Crossing a *bb* guinea pig with a *Bb* guinea pig is likely to produce about 50 percent *Bb* offspring and about 50 percent *bb* offspring.

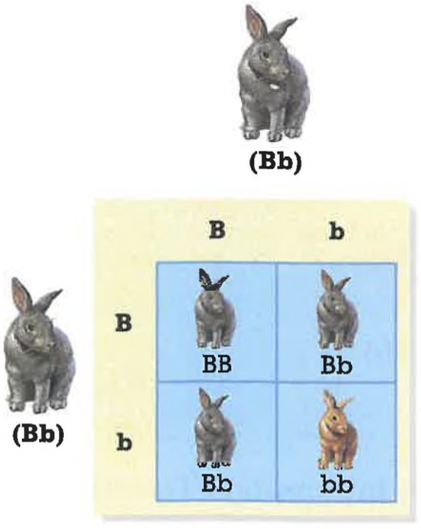


FIGURE 9-7
Crossing two rabbits that are both heterozygous for black coat color tends to produce 50 percent heterozygous black individuals, 25 percent homozygous black individuals, and 25 percent homozygous brown individuals.

Example 3: Heterozygous × Heterozygous

In rabbits, the allele for black coat color (*B*) is dominant over the allele for brown coat color (*b*). The Punnett square in Figure 9-7 shows the predicted results of crossing two rabbits that are both heterozygous (*Bb*) for coat color. As you can see, 1/4 (25 percent) of the offspring are predicted to have the genotype *BB*, 1/2 (50 percent) are predicted to have the genotype *Bb*, and 1/4 (25 percent) are predicted to have the genotype *bb*. Thus, 3/4 (75 percent) of the offspring resulting from this cross are predicted to have a black coat. One-fourth (25 percent) of the offspring are predicted to have a brown coat.

The ratio of the genotypes that appear in offspring is called the **genotypic ratio.** The probable genotypic ratio of the monohybrid cross represented in Figure 9-7 is 1 *BB*:2 *Bb*:1 *bb*. The ratio of the offsprings' phenotypes is called the **phenotypic ratio.** The probable phenotypic ratio of the cross represented in Figure 9-7 is 3 black:1 brown.

Example 4: Testcross

Recall that in guinea pigs, both *BB* and *Bb* result in a black coat. How might you determine whether a black guinea pig is homozygous (*BB*) or heterozygous (*Bb*)? You could perform a **testcross,** in which an individual of unknown genotype is crossed with a homozygous recessive individual. A testcross can determine the genotype of any individual whose phenotype is dominant. You can see from Figure 9-8 that if the unknown genotype is homozygous black, all offspring will be black. If the individual with the unknown genotype is heterozygous black, about half of the offspring will be black. In reality, if the cross produced one brown offspring in a litter of eight, the genotype of the black-coated parent is likely to be heterozygous.

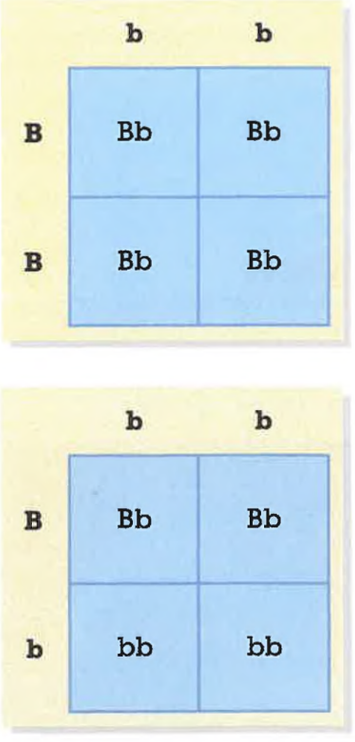
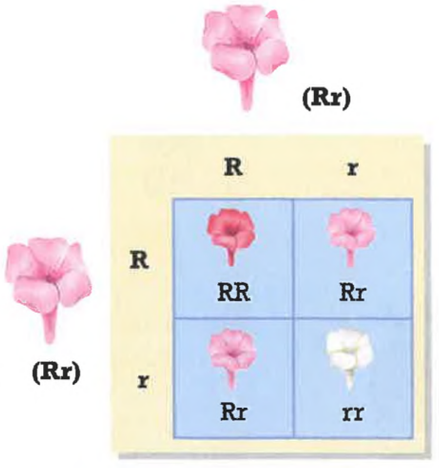


FIGURE 9-8
If a black guinea pig is crossed with a brown guinea pig and even one of the offspring is brown, chances are that the black guinea pig is heterozygous for coat color.

FIGURE 9-9

When red-flowering four o'clocks are crossed with white-flowering four o'clocks, all of the F_1 offspring produce pink flowers, an intermediate between the two phenotypes. When the F_1 generation is interbred, red-flowering, pink-flowering, and white-flowering plants are produced because the trait for red flower color has incomplete dominance over the trait for white flower color.



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Example 5: Incomplete Dominance

Recall that in Mendel's pea-plant crosses, one allele was completely dominant over another, a relationship called **complete dominance.** In complete dominance, heterozygous plants and dominant homozygous plants are indistinguishable in phenotype. For example, both pea plants *PP* and *Pp* for flower color have purple flowers.

Sometimes, however, the F_1 offspring will have a phenotype in between that of the parents, a relationship called **incomplete dominance.** Incomplete dominance occurs when two or more alleles influence the phenotype, resulting in a phenotype intermediate between the dominant trait and the recessive trait. In four o'clocks, for example, both the allele for red flowers (*R*) and the allele for white flowers (*r*) influence the phenotype. Neither allele is completely dominant over the other allele. When four o'clocks self-pollinate, red-flowering plants produce only red-flowering offspring, and white-flowering plants produce only white-flowering offspring. However, when red four o'clocks are crossed with white four o'clocks, the F_1 offspring all have *pink* flowers. One hundred percent of the offspring of this cross have the (*Rr*) genotype, which results in a pink phenotype.

What would be the result of crossing two pink-flowering (*Rr*) four o'clocks? As the Punnett square in Figure 9-9 shows, the probable genotypic ratio is 1 *RR*:2 *Rr*:1 *rr*. Given that neither the allele for red flowers (*R*) nor the allele for white flowers (*r*) is completely dominant, the probable phenotypic ratio is 1 red:2 pink:1 white.

FIGURE 9-10

The roan coat of this horse consists of both white hairs and red hairs. Both phenotypes are expressed in individuals heterozygous for coat color when the traits are codominant.

Example 6: Codominance

Codominance occurs when both alleles for a gene are expressed in a heterozygous offspring. In codominance, neither allele is dominant or recessive, nor do the alleles blend in the phenotype. For example, the genes for both white coat color and red coat color are expressed in the horse shown in Figure 9-10. The capital letter *R* is used to indicate red coat color, and *R'* is used to indicate white coat color. Thus, the *RR'* symbol would represent the coat color of the roan horse in Figure 9-10.

PREDICTING RESULTS OF DIHYBRID CROSSES

A **dihybrid** (die-HIE-brid) **cross** is a cross between individuals that involves two pairs of contrasting traits. Predicting the results of a dihybrid cross is more complicated than predicting the results of a monohybrid cross because there are more possible combinations of alleles to work out. For example, to predict the results of a cross involving both seed texture and seed color, you have to consider how the four alleles from each parent can combine.

Homozygous × Homozygous

Suppose that you want to predict the results of a cross between a pea plant that is homozygous for round, yellow seeds and one that is homozygous for wrinkled, green seeds. In pea plants, the allele for round seeds (*R*) is dominant over the allele for wrinkled seeds (*r*), and the allele for yellow seeds (*Y*) is dominant over the allele for green seeds (*y*).

As Figure 9-11 shows, the Punnett square used to predict the results of a cross between a parent of the genotype *RRYY* and a parent of the genotype *rryy* will contain 16 boxes. The independently sorted alleles from one parent—*RY, RY, RY,* and *RY*—are listed along the left side of the Punnett square. The independently sorted alleles from the other parent—*ry, ry, ry,* and *ry*—are listed along the top of the Punnett square. Each box is filled with the letters that are above it and to the left of it outside the square. Notice that the genotype of all the offspring of this cross will be heterozygous for both traits, *RrYy;* therefore, the phenotype of all the offspring will have round, yellow seeds.

rryy

RRYY

	ry	ry	ry	ry
RY	RrYy	RrYy	RrYy	RrYy
RY	RrYy	RrYy	RrYy	RrYy
RY	RrYy	RrYy	RrYy	RrYy
RY	RrYy	RrYy	RrYy	RrYy

FIGURE 9-11

This Punnett square shows a dihybrid cross between a pea plant that is homozygous recessive for wrinkled, green seeds *(rryy)* and a pea plant that is homozygous dominant for smooth, yellow seeds *(RRYY)*.

Quick Lab

Determining Genotypes

Materials pencil and paper

Procedure The ability to roll the tongue upward from the sides is a dominant, inherited trait. In one family, both parents and three children are all tongue rollers, while one child is not. Determine the genotype and phenotype of each parent.

Analysis Are the parents homozygous or heterozygous? Are the children homozygous or heterozygous?

Heterozygous × Heterozygous

To determine the results of crossing two pea plants heterozygous for round, yellow seeds, the procedure is the same. As Figure 9-12 shows, the offspring of this dihybrid cross are likely to have nine different genotypes. These nine genotypes will result in pea plants with the following four phenotypes:

- 9/16 with round, yellow seeds (genotypes *RRYY, RRYy, RrYY,* and *RrYy*)
- 3/16 with round, green seeds (genotypes *RRyy* and *Rryy*)
- 3/16 with wrinkled, yellow seeds (genotypes *rrYY* and *rrYy*)
- 1/16 with wrinkled, green seeds (genotype *rryy*)

FIGURE 9-12

A dihybrid cross of two individuals heterozygous for both traits is likely to result in nine different genotypes and four different phenotypes.

RrYy

RrYy

	RY	Ry	rY	ry
RY	RRYY	RRYy	RrYY	RrYy
Ry	RRYy	RRyy	RrYy	Rryy
rY	RrYY	RrYy	rrYY	rrYy
ry	RrYy	Rryy	rrYy	rryy

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SECTION 9-2 REVIEW

1. Explain how you might go about determining the genotype of a purple-flowering pea plant.
2. What is the equation used to determine probability? In what ways can probability be expressed?
3. If you were to cross pink-flowering four o'clocks with white-flowering four o'clocks, what results would you expect? Provide a Punnett square to support your answer.
4. Explain how you would use a Punnett square to predict the probable outcome of a monohybrid cross.
5. Explain the difference between a monohybrid cross and a dihybrid cross. Give an example of each.
6. **CRITICAL THINKING** The offspring of two short-tailed cats have a 25 percent chance of having no tail, a 25 percent chance of having a long tail, and a 50 percent chance of having a short tail. Based on this information, what can you hypothesize about the genotypes of the parents?

CHAPTER 9 REVIEW

SUMMARY/VOCABULARY

9-1

- The study of how characteristics are transmitted from parents to offspring is called genetics.
- Self-pollination, in which pollen is transferred from the anthers of a flower to either the stigma of the same flower or the stigma of another flower on the same plant, normally occurs in pea plants. Cross-pollination occurs when pollen is transferred between flowers of two different plants.
- Mendel concluded that inherited characteristics are controlled by factors that occur in pairs. In his experiments on pea plants, one factor in a pair masked the other. The trait that masked the other was called the dominant trait. The trait that was masked was called a recessive trait.
- We now know that the factors that Mendel studied are alleles, or alternative forms of a gene.
- The law of segregation states that a pair of factors is segregated, or separated, during the formation of gametes. The law of independent assortment is observed only for genes that are located on separate chromosomes or far apart on the same chromosome.
- The law of independent assortment states that factors for different characteristics are distributed to gametes independently. You know this to be true from your study of meiosis: during prophase I of meiosis, homologous chromosomes randomly migrate to opposite sides of the dividing cell.

Vocabulary

allele (169)
anther (166)
cross-pollination (166)
dominant (168)
F_1 generation (166)
F_2 generation (166)
genetics (165)
heredity (165)
law of independent assortment (169)
law of segregation (168)
molecular genetics (169)
P_1 generation (166)
pollination (166)
pure (166)
recessive (168)
self-pollination (166)
stigma (166)
strain (166)
trait (165)

9-2

- The genotype is the genetic makeup of an organism. An organism's phenotype is its appearance as a result of its genotype.
- Probability is the likelihood that a specific event will occur. A probability may be expressed as a decimal, a percentage, or a fraction.
- A Punnett square can be used to predict the outcome of genetic crosses.
- A cross between individuals involving one pair of contrasting traits is a monohybrid cross.
- A testcross, in which an individual of unknown genotype is crossed with a homozygous recessive individual, can be used to determine the genotype of an individual whose phenotype is dominant.
- Complete dominance occurs when heterozygous individuals and dominant homozygous individuals are indistinguishable in phenotype.
- Incomplete dominance occurs when two or more alleles influence the phenotype, resulting in a phenotype intermediate between the dominant trait and the recessive trait.
- Codominance occurs when both alleles for a gene are expressed in a heterozygous offspring. Neither allele is dominant or recessive, nor do the alleles blend in the phenotype as they do in incomplete dominance.
- A cross between individuals involving two pairs of contrasting traits is called a dihybrid cross.

Vocabulary

codominance (176)
complete dominance (176)
dihybrid cross (177)
genotype (172)
genotypic ratio (175)
heterozygous (173)
homozygous (173)
incomplete dominance (176)
monohybrid cross (174)
phenotype (172)
phenotypic ratio (175)
probability (173)
Punnett square (174)
testcross (175)

REVIEW

Vocabulary

1. State and define the two laws of heredity.
2. Differentiate self-pollination from cross-pollination.
3. What is the difference between a dominant trait and a recessive trait?
4. Differentiate genotype from phenotype.
5. What is the difference between *homozygous* and *heterozygous*?

Multiple Choice

6. A procedure in which an individual of unknown genotype is crossed with a homozygous recessive individual to determine the genotype of the unknown individual is called a (a) monohybrid cross (b) dihybrid cross (c) hybrid cross (d) testcross.
7. A gene is a (a) segment of DNA (b) chromosome (c) segment of RNA (d) protein.
8. An example of a genotype of a heterozygous individual is (a) *pp* (b) *YY* (c) *Zz* (d) none of the above.
9. In a monohybrid cross of two heterozygous parents (*Pp*), one would expect the offspring to be (a) 1 *pp*:3 *PP* (b) 3 *Pp*:1 *pp* (c) 1 *PP*:2 *Pp*:1 *pp* (d) all *Pp*.
10. In a monohybrid cross between a homozygous dominant parent and a homozygous recessive parent, one would predict the offspring to be (a) 3:4 homozygous recessive (b) 2:4 homozygous recessive (c) 1:4 homozygous recessive (d) all heterozygous.
11. In guinea pigs, black fur is dominant. If a black guinea pig is crossed with a white guinea pig and the litter contains a white offspring, the genotype of the black-haired parent is probably (a) homozygous dominant (b) homozygous recessive (c) pure for the trait (d) heterozygous dominant.
12. Segregation of alleles occurs during (a) mitosis (b) meiosis (c) fertilization (d) pollination.
13. In a dihybrid cross between two heterozygous parents, the probability of obtaining an offspring that is homozygous recessive for both traits would be (a) none (b) 9/16 (c) 3/16 (d) 1/16.
14. If two parents with dominant phenotypes produce an offspring with a recessive phenotype, then (a) both parents are heterozygous (b) one parent is heterozygous (c) both parents are homozygous (d) one parent is homozygous.
15. Suppose that you have found a new species of plant. Some of the plants have red flowers and some have yellow flowers. You cross a red-flowering plant with a yellow-flowering plant, and all the offspring have orange flowers. You might assume that the alleles for flower color (a) have complete codominance (b) have incomplete dominance (c) are either dominant or recessive (d) have mutated.

Short Answer

16. Why did Mendel begin his experiments by allowing pea plants to self-pollinate for several generations?
17. Answer the following questions based on the Punnett square shown below:
    a. Does the Punnett square demonstrate a monohybrid cross or a dihybrid cross?
    b. List the genotypes of the parents.
    c. Give the genotypic ratio predicted by the Punnett square for the cross.

	QT	Qt	qT	qt
QT	QQTT	QQTt	QqTT	QqTt
Qt	QQTt	QQtt	QqTt	Qqtt
qT	QqTT	QqTt	qqTT	qqTt
qt	QqTt	Qqtt	qqTt	qqtt

18. **Unit 5—*Heredity***

Write a report summarizing how an understanding of heredity allows animal breeders to develop animals with desirable traits. Find out what kinds of animals are bred for special purposes.

19. Explain the difference between the P generation, F_1 generation, and F_2 generation.
20. When the dominant and recessive traits are known, why is it not necessary to use the term *homozygous* when referring to the genotype of an individual with a recessive phenotype?
21. Explain the difference between a monohybrid cross and a dihybrid cross.
22. How might crossing-over during meiosis affect the segregation of genes on the same chromosome?
23. Relate the events of meiosis to the law of segregation.
24. In pea plants, smooth seed texture is dominant over wrinkled seed texture. A gardener has a pea plant that produces smooth seeds. How can the gardener determine whether the plant is homozygous or heterozygous for the allele that determines seed texture?
25. In rabbits, the allele for black coat color (*B*) is dominant over the allele for brown coat color (*b*). Predict the results of a cross between a rabbit homozygous for black coat color (*BB*) and a rabbit homozygous for brown coat color (*bb*).

CRITICAL THINKING

1. One rule of probability can be expressed as the following: The probability of two independent events occurring simultaneously is the product of the probability of their occurring separately. If, for example, you had a pair of dice and rolled each die one at a time, what would be the probability that you would get two 4s? On the first roll, you would have a 1/6 chance. On the second roll, you would have a 1/6 chance. The probability of obtaining two 4s would be $1/6 \times 1/6 = 1/36$. Suppose you were playing a game with five dice. What is the chance of rolling a 6 on all five dice?
2. A cross between two pea plants with axial flowers and inflated pods gives the following offspring: 20 with axial flowers and inflated pods, 7 with axial flowers and constricted pods, and 5 with terminal flowers and inflated pods. What is the most probable genotype for the two parents? Explain the results and show the Punnett square. How can the explanation be checked?
3. Two black female mice are crossed with the same brown male mouse. Based on the information shown in the table below, answer the following questions:
   a. What are the genotypes of each parent?
   b. Which trait is dominant?
   c. Is the dominance of the trait in (b) completely dominant, incompletely dominant, or codominant? Explain your answer.

Results of Crossing Two Black Female Mice with One Brown Male Mouse

P_1 generation	F_1 generation
female A × male A	9 black, 7 brown
female B × male A	14 black, 0 brown

EXTENSION

1. Read "The Genes of 1998" in *Discover,* January 1999, on page 33. Describe how a mutation on chromosome 8 causes a rare form of baldness. What might be one explanation for why humans no longer have a sharp sense of smell? Explain how a genetic disorder can actually cause a person to display symptoms of psychiatric illness.
2. Toss a penny and a nickel together 32 times, and record the results as they fall: number of times heads comes up for both the penny and the nickel, number of times tails comes up for both the penny and the nickel, number of times the penny is heads and the nickel is tails, and the number of times the penny is tails and the nickel is heads. Explain how this task illustrates independent assortment.

CHAPTER 9 INVESTIGATION

Modeling Monohybrid Crosses

OBJECTIVES

- Predict the genotypic and phenotypic ratios of offspring resulting from the random pairing of gametes.
- Calculate the genotypic ratio and phenotypic ratio among the offspring of a monohybrid cross.

PROCESS SKILLS

- predicting
- organizing
- analyzing data
- calculating

MATERIALS

- lentils
- green peas
- 2 Petri dishes

Background

1. How many traits are involved in a monohybrid cross? How many alleles are involved?
2. What prevents the expression of a recessive allele?
3. When gametes form, what happens to the alleles for each trait?

PART A Simulating a Monohybrid Cross

1. You will model the random pairing of alleles by choosing lentils and peas from Petri dishes. These dried seeds will represent the alleles for seed color. A green pea will represent *G*, the dominant allele for green seeds, and a lentil will represent *g*, the recessive allele for yellow seeds.
2. Each Petri dish will represent a parent. Label one Petri dish "female gametes" and the other Petri dish "male gametes." Place one green pea and one lentil in the Petri dish labeled "female gametes" and place one green pea and one lentil in the Petri dish labeled "male gametes."
3. Each parent contributes one allele to each offspring. Model a cross between these two parents by choosing a random pairing of the dried seeds from the two containers. Do this by simultaneously picking one seed from each container *without looking.* Place the pair of seeds together on the lab table. The pair of seeds represents the genotype of one offspring.
4. Record the genotype of the first offspring in your lab report in a table like Table A shown below.

TABLE A *GAMETE PAIRINGS*

Trial	Offspring genotype	Offspring phenotype
1		
2		
3		
4		
5		
6		
7		
8		
9		
10		

5. Return the seeds to their original dishes and repeat step 3 nine more times. Record the genotype of each offspring in your data table.
6. Based on each offspring's genotype, determine and record each offspring's phenotype. Assume that the allele for green seeds, *G*, is completely dominant over the allele for yellow seeds, *g*.

PART B Calculating Genotypic and Phenotypic Ratios

7. In your lab report, prepare a data table similar to Table B shown below.
8. Determine the genotypic and phenotypic ratios among the offspring. First count and record the number of homozygous dominant, heterozygous, and homozygous recessive individuals you recorded in Table A. Then record the number of offspring that produce green seeds and the number that produce yellow seeds under "Phenotypes" in your data table.
9. Calculate the genotypic ratio for each genotype using the following equation:

$$\text{Genotypic ratio} = \frac{\text{number of offspring with a given genotype}}{\text{total number of offspring}}$$

10. Calculate the phenotypic ratio for each phenotype using the following equation:

$$\text{Phenotypic ratio} = \frac{\text{number of offspring with a given phenotype}}{\text{total number of offspring}}$$

11. Now pool the data for the whole class, and record the data in your lab report in a table like Table C.
12. Compare your class's sample with your small sample of 10. Calculate the genotypic and phenotypic ratios for the class data, and record them in your data table.
13. Construct a Punnett square showing the parents and their offspring in your lab report.
14. Clean up your materials before leaving the lab.

Analysis and Conclusions

1. What trait is being studied in this investigation?
2. What are the genotypes of the parents? Describe the genotypes of both parents using the terms *homozygous* or *heterozygous,* or both.
3. What does each seed in the Petri dish represent?
4. When the seeds were selected and paired, what did the pairs represent?
5. Did tables B and C reflect a classic monohybrid-cross phenotypic ratio of 3:1?
6. When the class data were tabulated, did a classic monohybrid-cross ratio of a phenotype of 3:1 result?
7. If a genotypic ratio of 1:2:1 is observed, what must the genotypes of both parents be?
8. Show what the genotypes of the parents would be if 50 percent of the offspring were green and 50 percent of the offspring were yellow.
9. Construct a Punnett square for the cross of a heterozygous black guinea pig and an unknown guinea pig whose offspring include a recessive white-furred individual. What are the possible genotypes of the unknown parent?

Further Inquiry

Design a model to demonstrate a dihybrid cross of two parents that are heterozygous for two traits. Construct and complete a Punnett square for this cross.

TABLE B *OFFSPRING RATIOS*

Genotypes	Total	Genotypic ratio
Homozygous dominant (*GG*)		
Heterozygous (*Gg*)		____ : ____ : ____
Homozygous recessive (*gg*)		
Phenotypes		**Phenotypic ratio**
Green seeds		____ : ____ : ____
Yellow seeds		

TABLE C *OFFSPRING RATIOS (Entire Class)*

Genotypes	Total	Genotypic ratio
Homozygous dominant (*GG*)		
Heterozygous (*Gg*)		____ : ____ : ____
Homozygous recessive (*gg*)		
Phenotypes		**Phenotypic ratio**
Green seeds		____ : ____ : ____
Yellow seeds		

CHAPTER 10

NUCLEIC ACIDS AND PROTEIN SYNTHESIS

The most common form of DNA found in living organisms has a spiral-staircase shape, as shown in this computer model of the molecule's structure.

FOCUS CONCEPT: ***Cell Structure and Function***

As you read, pay attention to the roles that DNA and RNA play in storing information and making proteins.

BIOLOGY Interactive Tutor

Unit 6—*Gene Expression*
Topics 1–6

DNA

What enables cells to have different forms and to perform different functions? Ultimately the genetic source of this amazing diversity is deoxyribonucleic acid (DNA). The primary function of DNA in organisms is to store and transmit the genetic information that tells cells which proteins to make and when to make them. Proteins in turn form the structural units of cells and help control chemical processes within cells.

SECTION 10-1

OBJECTIVES

- Explain the principal function of DNA.
- Describe the structure of DNA.
- Define the term *complementary base pairing.*
- Explain the role of complementary base pairing in the replication of DNA.
- Summarize the main features of DNA replication.

STRUCTURE OF DNA

Recall from Chapter 3 that the nucleic acid DNA is an organic compound. DNA is made up of repeating subunits called nucleotides. Each DNA molecule consists of two long chains of nucleotides.

A DNA nucleotide has three parts: a sugar molecule called **deoxyribose;** a phosphate group, which consists of a phosphorus, P, atom surrounded by oxygen, O, atoms; and a molecule that is referred to as a **nitrogen-containing base** because it contains a nitrogen, N, atom. The three parts of a DNA nucleotide are illustrated in Figure 10-1. The deoxyribose sugar and the phosphate group are identical in all DNA nucleotides. However, the nitrogen-containing base may be any one of four different kinds.

The four nitrogen-containing bases found in DNA nucleotides are **adenine, guanine, cytosine,** and **thymine.** It is customary to represent nucleotides by the abbreviations for their nitrogen-containing bases. A nucleotide containing adenine is represented by an *A*. Likewise, C = cytosine, G = guanine, and T = thymine.

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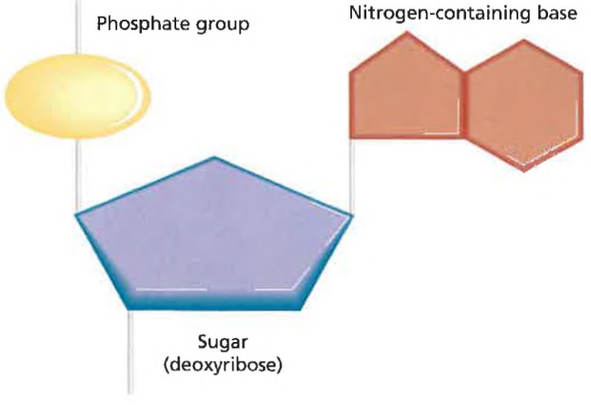


FIGURE 10-1
A DNA molecule is composed of a deoxyribose sugar molecule, a phosphate group, and one of four nitrogen-containing bases.

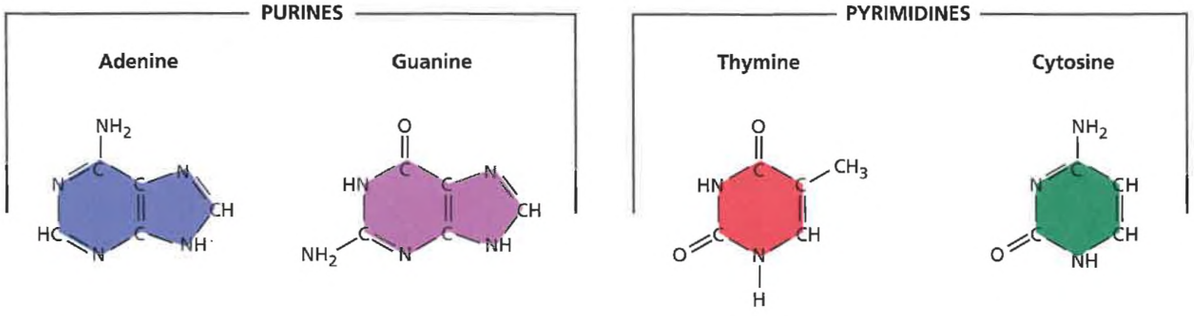


FIGURE 10-2

The four nitrogen-containing bases found in DNA are divided into two groups: purines and pyrimidines. Two-ringed bases are called purines. One-ringed bases are called pyrimidines.

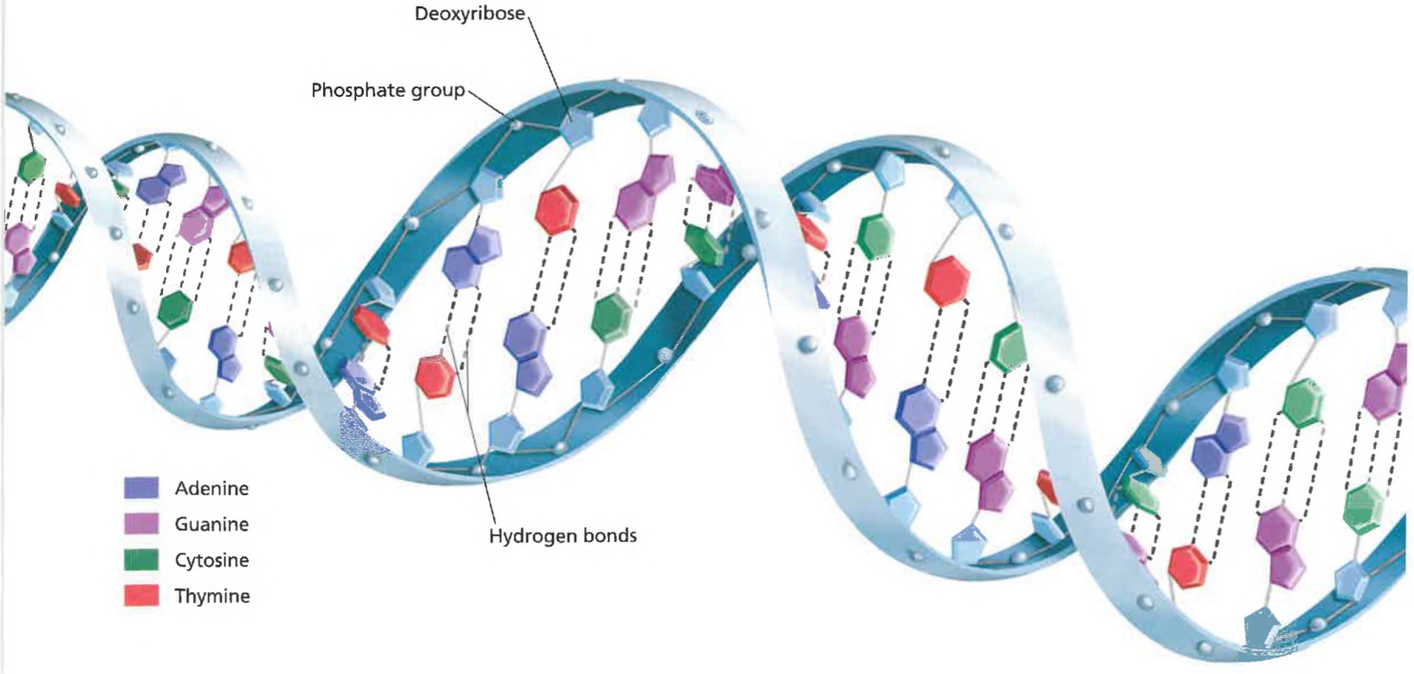
Figure 10-2 shows the structure of these four nucleotides. Notice that adenine and guanine have two rings of carbon, C, and nitrogen, N, atoms. In contrast, cytosine and thymine have only one ring of carbon and nitrogen atoms. Bases that have two rings of carbon and nitrogen atoms, such as adenine and guanine, are called **purines. Pyrimidines** are bases that have one ring of carbon and nitrogen atoms, such as cytosine and thymine.

The Double Helix

In 1953, James Watson and Francis Crick suggested a model for the structure of DNA. The model proposed that DNA is composed of two nucleotide chains that wrap around each other to form a double spiral—similar to a spiral staircase. This shape is called a **double helix.** The double helix structure of DNA is illustrated in Figure 10-3.

FIGURE 10-3

The structure of DNA, which resembles a spiral staircase, is called a double helix.



Watson and Crick relied heavily on scientific evidence reported by other scientists to construct the model. The model was inspired in part by X-ray photographs of DNA crystals, like the one shown in Figure 10-4, that had been studied by Rosalind Franklin and Maurice Wilkins. In addition, the model provided an explanation for how copies of DNA could be made and how genetic information might be stored and used within cells. In 1962, Watson, Crick, and Maurice Wilkins received the Nobel Prize in Medicine for their work on DNA. Rosalind Franklin had died in 1958 and thus was not recognized.

Note in Figure 10-3 that individual nucleotides are connected by covalent bonds between the deoxyribose sugar and phosphate molecules. The alternating deoxyribose sugar and phosphate molecules form a "backbone" to which the nitrogen-containing bases attach. Note also that the nitrogen-containing bases face toward the center of the helix and that they are perpendicular to the sugar-phosphate backbone.

By facing toward the center, the bases on one chain of DNA face the bases on the other chain of DNA, with which they form bonds called hydrogen bonds. The locations of the hydrogen bonds are indicated in Figure 10-3 by dotted lines. The hydrogen bonds help hold the two chains together. Hydrogen bonds are different from the covalent bonds and ionic bonds you read about in Chapter 2. A hydrogen bond is a relatively weak bond that usually forms between molecules. Hydrogen bonds form when two atoms share a hydrogen nucleus—one proton. The hydrogen bonds that form between the bases in DNA form between a hydrogen atom and either an oxygen or a nitrogen atom.

Notice that the base pairs are of uniform length because in each case one base is a double-ringed purine and the other is a single-ringed pyrimidine. The form of DNA that is most commonly found in living organisms has a right-hand twist, with each full turn consisting of ten base pairs.

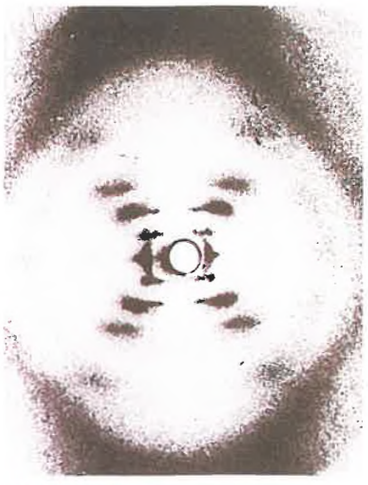


FIGURE 10-4

Rosalind Franklin's X-ray photographs of DNA indicated that DNA is a helix with a sugar-phosphate backbone on the outside and that the helix consists of more than one chain of nucleotides.

Complementary Base Pairing

As Figure 10-3 shows, cytosine pairs with guanine, and adenine pairs with thymine. The DNA nucleotides normally pair in these combinations. These pairs of bases are called **complementary base pairs.** Two rules—called **base-pairing rules**—describe the pairing behavior of the bases. These rules simply state that cytosine bonds with guanine and adenine bonds with thymine.

Complementary base pairs are connected to each other by hydrogen bonds. Note that cytosine and guanine form three hydrogen bonds and adenine and thymine form two hydrogen bonds. As Figure 10-3 shows, the nucleotide sequence in one nucleotide chain of the DNA molecule is an exact complement of the nucleotide sequence in the other chain.

The complementary nucleotide chains in the DNA model led to suggestions of how DNA might copy itself. The ability of DNA to make exact copies of itself is important because, in most cases, cells that divide must pass exact copies of their DNA to offspring cells.

REPLICATION OF DNA

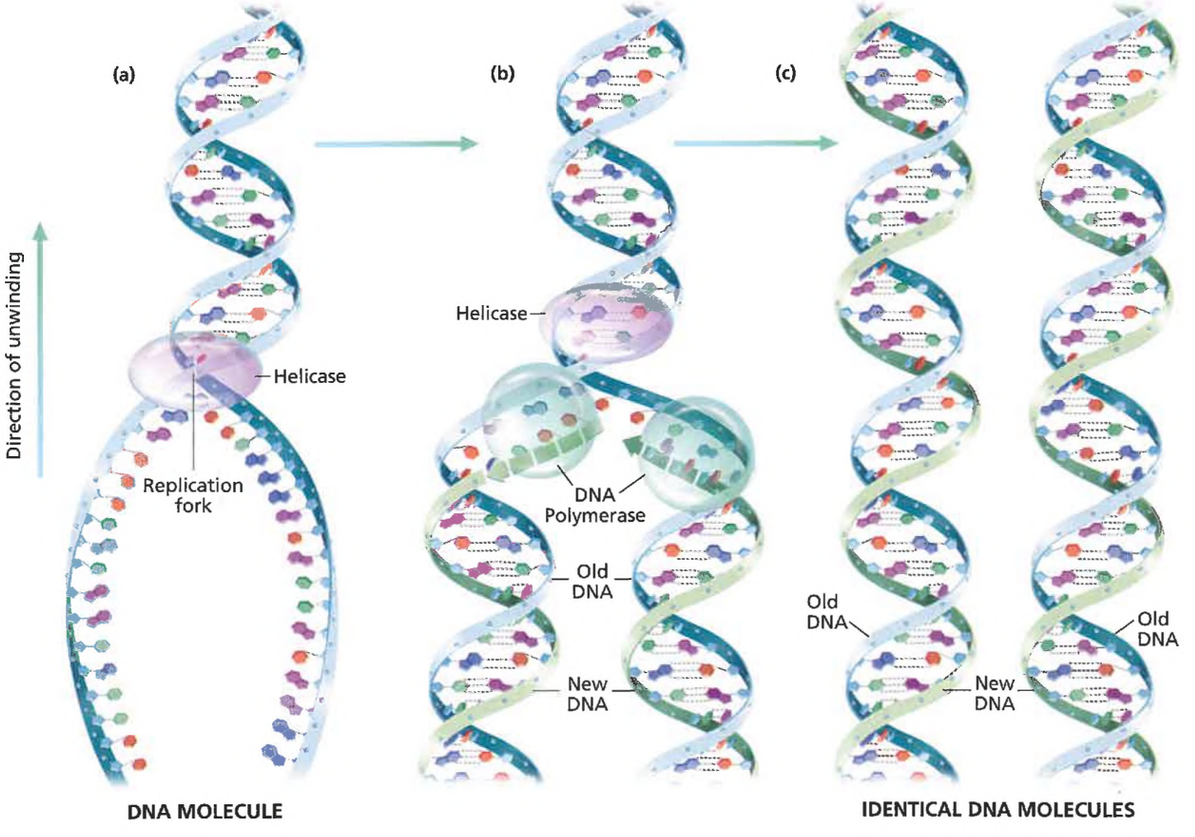
The process of copying DNA in a cell is called **replication.** During replication, the two nucleotide chains separate by unwinding, and each chain serves as a template for a new nucleotide chain.

DNA replication is illustrated in Figure 10-5. The first step is the separation of the two nucleotide chains. The point at which the two chains separate is called the **replication fork.** The chains are separated by enzymes called **helicases.** As the helicase enzymes move along the DNA molecule, they break hydrogen bonds between the complementary bases, and the chains separate.

As Figure 10-5 shows, enzymes called **DNA polymerases** bind to the separated chains of DNA. As DNA polymerases move along the separated chains, new chains of DNA are assembled using nucleotides in the surrounding medium that are complementary to the existing DNA chains. Nucleotides are joined to the new chains by covalent bonds between deoxyribose sugars and phosphate groups. They are joined to the original nucleotide chain by hydrogen bonds.

FIGURE 10-5

(a) During DNA replication, helicase enzymes separate DNA's two chains of nucleotides. (b) DNA polymerases bind to the separated chains of nucleotides. One nucleotide at a time, the enzyme constructs a new complementary chain of nucleotides. (c) At the end of replication, there are two identical copies of the original DNA molecule. Each DNA molecule is made of one chain of nucleotides from the original DNA molecule and one new chain of nucleotides.



The complementary nature of the two chains of DNA is the foundation for accurate DNA replication. Suppose that the sequence of nucleotides in one chain of the original DNA molecule is A-T-T-C-C-G. DNA polymerases would produce a new nucleotide chain with the sequence of T-A-A-G-G-C.

DNA replication does not begin at one end of the molecule and proceed to the other. Rather, DNA polymerases begin replication simultaneously at many points along the separated nucleotide chains. Replication occurring simultaneously at different sites permits faster DNA replication. For example, replication is initiated simultaneously at about 6,000 sites in fruit fly DNA.

When replication is completed, two new exact copies of the original DNA molecule are produced and the cell is ready to undergo cell division. Each new DNA molecule consists of one new nucleotide chain joined by hydrogen bonds to a nucleotide chain from the original DNA molecule.

Accuracy and Repair

The process of DNA replication occurs with a high degree of accuracy—about one error in every 10,000 paired nucleotides. However, a change in the nucleotide sequence at even one location, called a **mutation,** may have serious effects in new cells. A combination of DNA proofreading and repair processes helps keep the error rate to one error per 1 billion nucleotides.

The number of errors and mutations in DNA replication is reduced as enzymes proofread DNA and repair errors. Most repair enzymes detect errors in the complementary base-paired structure of DNA. If noncomplementary bases are paired, the abnormal DNA structure can be recognized and repaired by specific enzymes.

Although DNA replication and proofreading prevent many replication errors, some errors do occur. In addition, DNA can be damaged by a variety of agents, including chemicals and ultraviolet radiation from the sun. Because cells are continuously proofreading and repairing their DNA, the number of mutations is reduced.

Eco Connection

DNA Repair Enzymes in Frogs

Around the world, frog and toad populations are in decline. Research on two declining species inhabiting the Oregon Cascade Range—Cascade frogs and western toads—suggests that these species' DNA repair enzymes are unable to keep up with mutations caused by increased exposure to ultraviolet radiation. Laboratory experiments showed that the DNA repair enzymes of Pacific tree frogs, whose populations do not appear to be decreasing, were better able to repair mutations than those of Cascade frogs and western toads.

SECTION 10-1 REVIEW

1. What are the main functions of DNA?
2. Identify the types and locations of covalent bonds and hydrogen bonds in a DNA molecule.
3. List the base-pairing rules.
4. What roles do enzymes play in DNA replication?
5. How would the deoxyribose sugar-phosphate backbone of nucleotide chains look if purines paired only with purines and pyrimidines paired only with pyrimidines?
6. **CRITICAL THINKING** A DNA molecule (labeled as A) replicates to produce two new DNA molecules (labeled as B). Both of the B DNA molecules then replicate to form four new DNA molecules (labeled as C). Are any nucleotide chains from A present in the C DNA molecules? Explain your answer. If you believe the answer is yes, how many of the A DNA nucleotide chains are present in the C DNA molecules?

SECTION

10-2

OBJECTIVES

- Explain the primary functions of RNA.
- Compare the structure of RNA with that of DNA.
- Describe the structure and function of each type of RNA.
- Summarize the process of transcription.

RNA

Recall that the nucleotides in DNA molecules are grouped into genes that contain the information needed to make specific proteins. In eukaryotes, the genes directing protein production are in the nucleus, and the enzymes and amino-acid building blocks for protein production are in the cytosol. The nucleic acid called ribonucleic acid (RNA) is responsible for the movement of genetic information from the DNA in the nucleus to the site of protein synthesis in the cytosol.

STRUCTURE OF RNA

Like DNA, RNA is a nucleic acid made up of repeating nucleotides. However, as Figure 10-6 shows, RNA differs from DNA in its structure. The sugar molecule of every RNA nucleotide is **ribose,** whereas DNA nucleotides contain deoxyribose sugar. The name *ribonucleic acid* is derived from the name of its sugar, just as the name *deoxyribonucleic acid* is derived from the name of its sugar.

A second difference between RNA and DNA nucleotides is that thymine is rarely a part of RNA molecules. **Uracil,** a nitrogen-containing pyrimidine base, usually replaces thymine in RNA. As a result, uracil—not thymine—pairs with adenine in RNA.

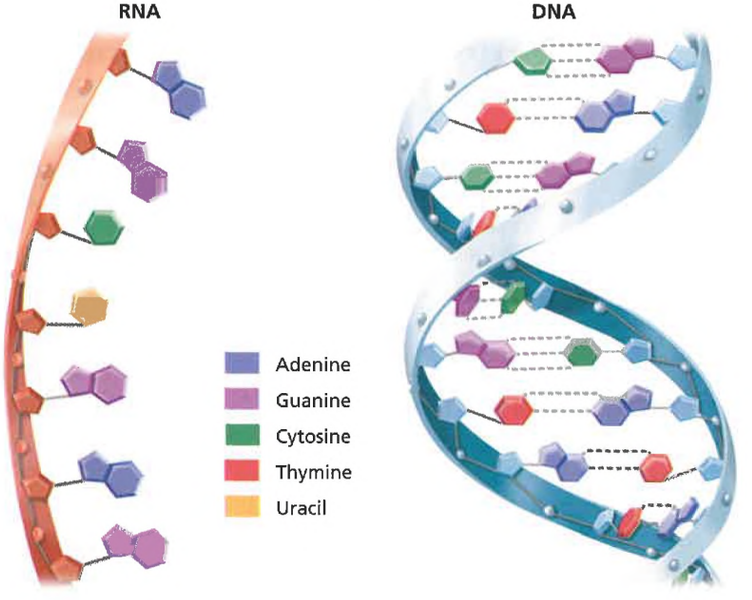


FIGURE 10-6

Like DNA, RNA is a nucleic acid made up of repeating nucleotides. Some forms of RNA involved in protein synthesis are made up of a single chain of nucleotides. Notice also that the nucleotide uracil is found in RNA in place of the DNA nucleotide thymine.

Types of RNA

RNA exists in three different types. Each type of RNA has a different function. The three types of RNA and their common abbreviations are as follows:

Messenger RNA (mRNA) consists of RNA nucleotides in the form of a single uncoiled chain. mRNA carries genetic information from the DNA in the nucleus to the cytosol of a eukaryotic cell.

Transfer RNA (tRNA) consists of a single chain of about 80 RNA nucleotides folded into a hairpin shape that binds to specific amino acids. There are about 45 varieties of tRNA.

Ribosomal RNA (rRNA) is the most abundant form of RNA. rRNA consists of RNA nucleotides in a globular form. Joined by proteins, rRNA makes up the ribosomes where proteins are made.

Quick Lab

Comparing and Contrasting RNA Types

Materials paper and pencil

Procedure Create a chart that compares and contrasts the different forms of RNA. Include descriptions of each form's structure and function.

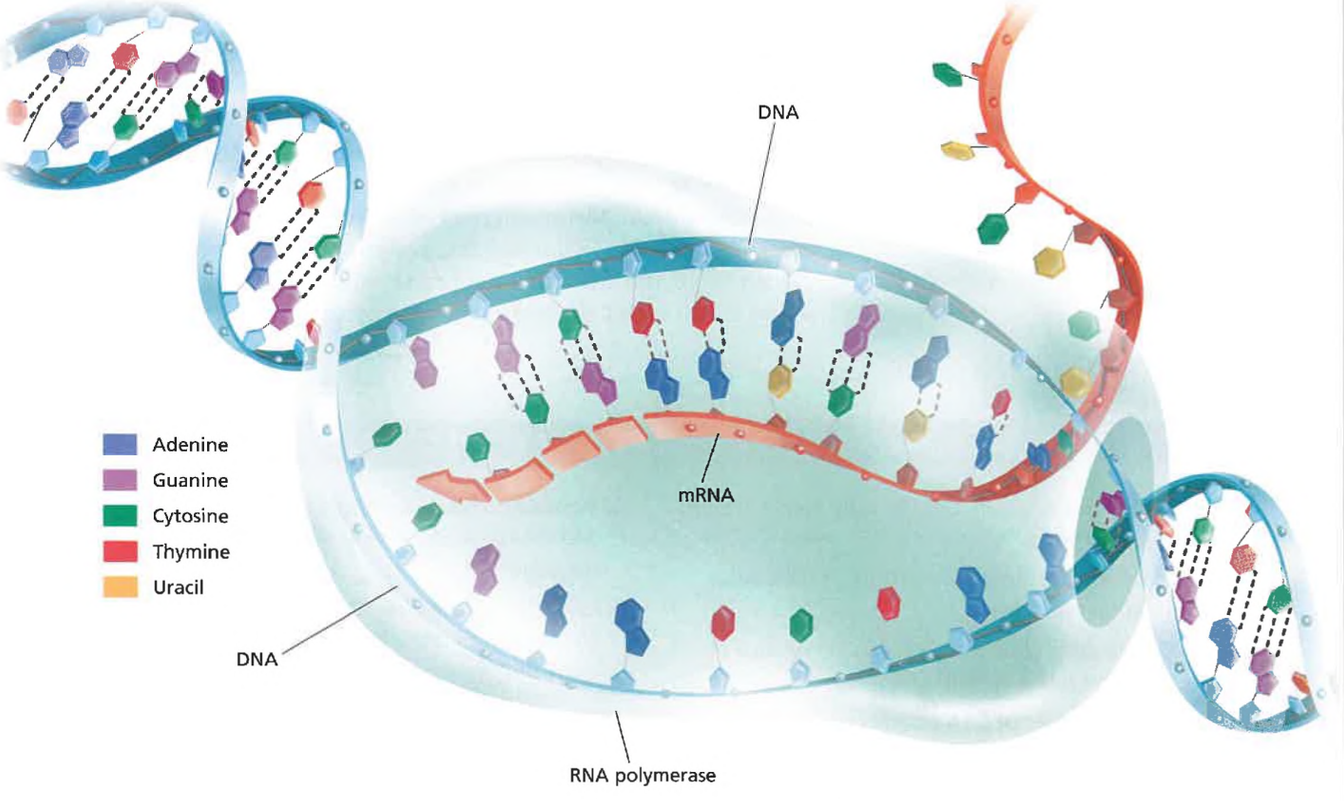
Analysis Which types of RNA are alike structurally? What might happen if one type of RNA was missing?

TRANSCRIPTION

One function of RNA is to carry genetic information from DNA in the nucleus to the cytosol, where it can be used to produce proteins. The process by which genetic information is copied from DNA to RNA is called **transcription.** The process of transcription is shown in Figure 10-7.

FIGURE 10-7

During transcription, RNA polymerase binds to the promoter of a specific gene. Then a complementary copy of that gene's DNA base sequence is made using RNA nucleotides, thus forming the mRNA strand.



Word Roots and Origins

transcription

from the Latin *scribere,* meaning "to write," and *trans,* meaning "across"

Steps of Transcription

RNA polymerase, the primary transcription enzyme, synthesizes RNA copies of specific sequences of DNA. RNA polymerase initiates RNA transcription by binding to specific regions of DNA called **promoters.** The promoter marks the beginning of the DNA chain that will be transcribed. In eukaryotes, promoters mark the beginning of a single gene, but in prokaryotes a promoter may mark the beginning of several functionally related genes. When RNA polymerase binds to a promoter, the DNA molecule in that region separates. Only one of the separated DNA chains, called the template, is used for transcription.

RNA polymerase attaches to the first DNA nucleotide of the template chain. Then it begins adding complementary RNA nucleotides to the newly forming RNA molecule. In Figure 10-7, notice that complementary base pairing determines the nucleotide sequence of the RNA chain in transcription, just as it does in DNA replication. The base-pairing rules are identical to those in DNA replication, except that uracil pairs with adenine.

Transcription continues one nucleotide at a time until the RNA polymerase reaches a DNA region called the **termination signal.** The termination signal is a specific sequence of nucleotides that marks the end of a gene in eukaryotes and may mark the end of several functionally related genes in prokaryotes. At the termination signal, RNA polymerase releases both the DNA molecule and the newly formed RNA molecule. All three types of RNA molecules are transcribed in this process.

Products of Transcription

The products of transcription, called transcripts, are the different types of RNA molecules, including mRNA, tRNA, and rRNA. Although the instructions for making a protein are copied from DNA into mRNA, all three types of RNA are involved in the synthesis of proteins. Following transcription, mRNA moves through the pores of the nuclear membrane into the cytosol of the cell, where it will direct the synthesis of proteins.

SECTION 10-2 REVIEW

1. Define transcription. List the main steps involved in this process.
2. In what ways does the structure of RNA differ from that of DNA?
3. Describe the structure and function of each of the three types of RNA.
4. List three roles of RNA polymerase in transcription.
5. What basic principle ensures that the transcribed RNA molecule is carrying the right genetic message?
6. **CRITICAL THINKING** Does it matter which of the separated DNA chains is used for transcription? Discuss your answer.

PROTEIN SYNTHESIS

Now that you know how RNA is transcribed from DNA, you are ready to learn how the three types of RNA work together to produce proteins. The production of proteins is also called ***protein synthesis.*** *The amount and kind of proteins that are produced in a cell determine the structure and function of the cell. In this way, proteins carry out the genetic instructions encoded in an organism's DNA.*

SECTION 10-3

OBJECTIVES

- Describe the genetic code.
- Distinguish between a codon and an anticodon, and state where each is found.
- Explain the roles of the start codon and stop codons.
- Summarize the process of translation.

PROTEIN STRUCTURE AND COMPOSITION

Like DNA and RNA, proteins are polymers. Proteins are made up of one or more polypeptides, each of which consists of a specific sequence of amino acids linked together by peptide bonds. Recall from Chapter 3 that there are 20 different amino acids that make up proteins. The polypeptides that make up one protein may consist of hundreds or thousands of the 20 different amino acids arranged in a particular sequence. The sequence of the amino acids determines how the polypeptides will twist and fold into the three-dimensional structure of the protein. The function of a protein depends on its ability to bind with other molecules within a cell; that is, the function depends on the protein's three-dimensional structure, which is determined by its amino-acid sequence.

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THE GENETIC CODE

During protein synthesis, the sequence of nucleotides in an mRNA transcript is translated into a sequence of amino acids. A correlation between a nucleotide sequence and an amino-acid sequence—called the **genetic code**—is used by most organisms to translate mRNA transcripts into proteins.

The genetic information necessary for making proteins is encoded in series of three mRNA nucleotides. Each combination of three mRNA nucleotides is called a **codon.** Each codon codes for a specific amino acid. Table 10-1 on the next page lists the 64 codons and the amino acids and instructions they code for in almost all organisms. The near-universality of the genetic code supports the idea that all organisms are evolutionarily related.

Word Roots and Origins

synthesis

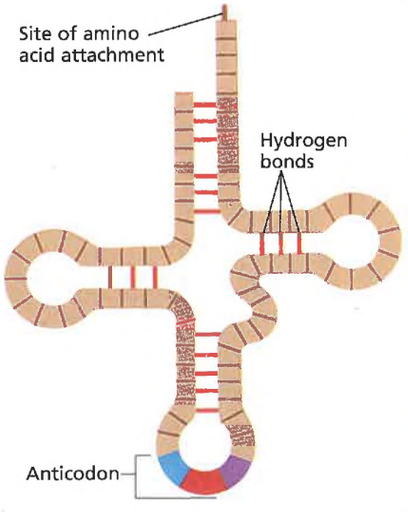
from the Greek *tithenai,* meaning "to put," and *syn,* meaning "together"

TABLE 10-1 Codons in mRNA

First base	Second base U	Second base C	Second base A	Second base G	Third base
U	UUU Phenylalanine	UCU Serine	UAU Tyrosine	UGU Cysteine	U
	UUC Phenylalanine	UCC Serine	UAC Tyrosine	UGC Cysteine	C
	UUA Leucine	UCA Serine	UAA Stop	UGA Stop	A
	UUG Leucine	UCG Serine	UAG Stop	UGG Tryptophan	G
C	CUU Leucine	CCU Proline	CAU Histidine	CGU Arginine	U
	CUC Leucine	CCC Proline	CAC Histidine	CGC Arginine	C
	CUA Leucine	CCA Proline	CAA Glutamine	CGA Arginine	A
	CUG Leucine	CCG Proline	CAG Glutamine	CGG Arginine	G
A	AUU Isolecine	ACU Threonine	AAU Asparagine	AGU Serine	U
	AUC Isolecine	ACC Threonine	AAC Asparagine	AGC Serine	C
	AUA Isolecine	ACA Threonine	AAA Lysine	AGA Arginine	A
	AUG Start	ACG Threonine	AAG Lysine	AGG Arginine	G
G	GUU Valine	GCU Alanine	GAU Aspartic acid	GGU Glycine	U
	GUC Valine	GCC Alanine	GAC Aspartic acid	GGC Glycine	C
	GUA Valine	GCA Alanine	GAA Glutamic acid	GGA Glycine	A
	GUG Valine	GCG Alanine	GAG Glutamic acid	GGG Glycine	G

Notice that several codons code for each amino acid listed in Table 10-1. Codons often differ from one another by the nucleotide in the third position. A few codons do not code for amino acids at all. Instead, these codons signal for translation of an mRNA to start or stop. The **start codon** (AUG), which also codes for the amino acid methionine, engages a ribosome to start translating an mRNA molecule. **Stop codons** (UAA, UAG, UGA) cause the ribosome to stop translating an mRNA.

FIGURE 10-8
Each tRNA transports a specific amino acid to the ribosomes during translation.



TRANSLATION

The process of assembling polypeptides from information encoded in mRNA is called **translation.** The process of translation begins when mRNA leaves the nucleus through pores in the nuclear membrane. The mRNA then migrates to a ribosome in the cytosol, the site of protein synthesis.

tRNA and Anticodons

Amino acids floating freely in the cytosol are transported to the ribosomes by tRNA molecules. Notice in Figure 10-8 that a tRNA

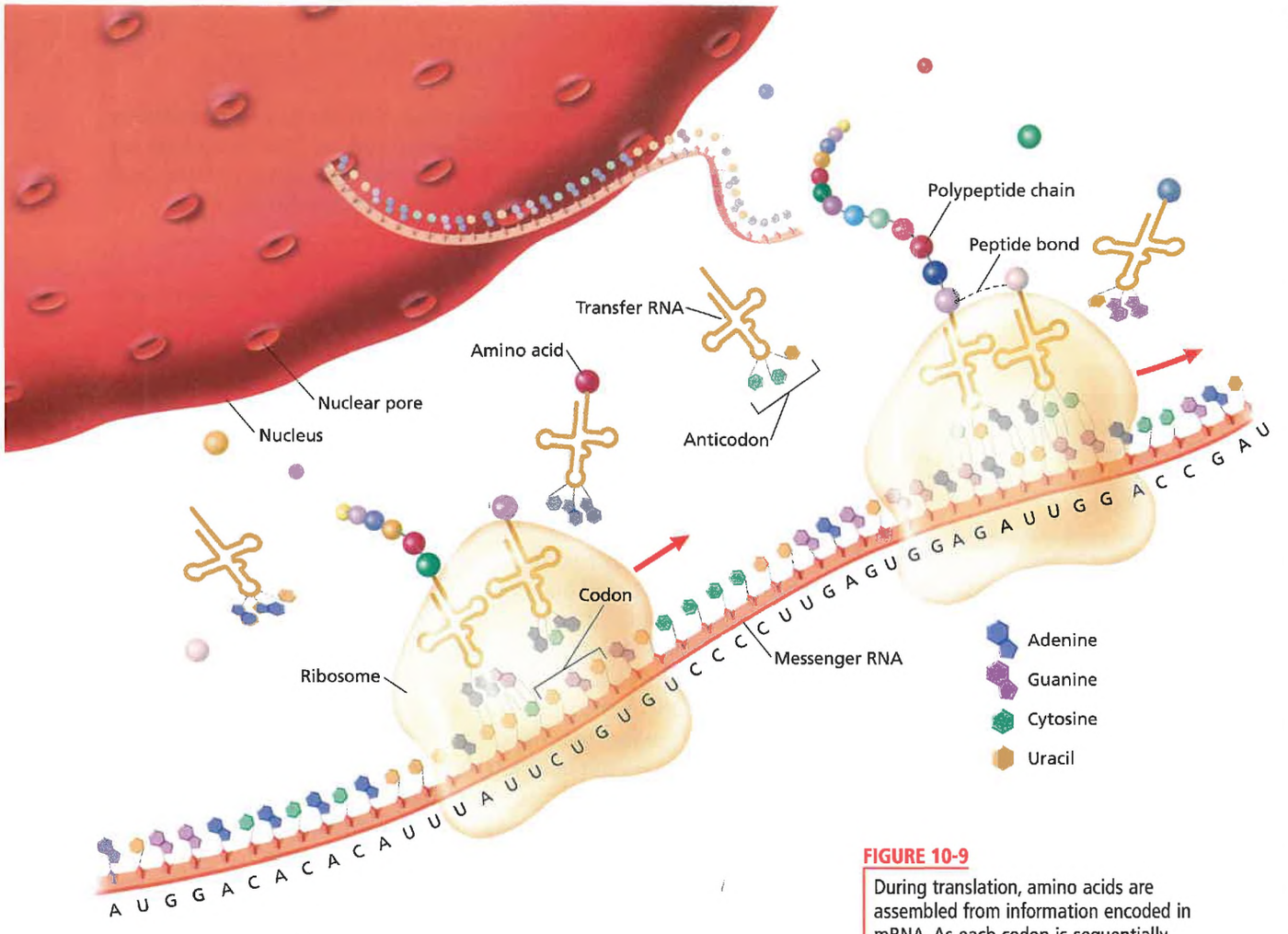


FIGURE 10-9

During translation, amino acids are assembled from information encoded in mRNA. As each codon is sequentially paired with its anticodon, tRNA adds a specific amino acid to the growing polypeptide chain.

molecule has a region that bonds to a specific amino acid. Notice also that the loop opposite the site of amino-acid attachment bears a sequence of three nucleotides called an **anticodon.** The tRNA anticodon is complementary to and pairs with its corresponding mRNA codon.

Notice in Figure 10-9 that the same base-pairing rules followed during transcription are followed during translation. For example, a tRNA with an anticodon sequence of AAA would bind to the mRNA codon sequence of UUU and would be specific for the amino acid phenylalanine. Thus, the pairing of an anticodon with a codon ensures that the amino acids are added to the growing polypeptide in the order prescribed by the mRNA transcript.

Ribosomes

Ribosomes are composed of rRNA and proteins and are usually both free in the cytosol and attached to the endoplasmic reticulum. Ribosomes that are free in the cytosol, as shown in Figure 10-9, produce proteins that will be used within the cell. Membrane proteins and proteins that will be exported for use outside the cell are produced by ribosomes attached to the endoplasmic reticulum.

Quick Lab

Modeling Protein Assembly

Materials colored paper clips (blue = adenine, green = guanine, pink = cytosine, yellow = uracil)

Procedure

1. Make the following mRNA sequence by linking the appropriate colored paper clips to represent the following bases: AUG GAC ACA CAU UUA UUC UGA.
2. Make a second chain of paper clips that represents the tRNA anticodons for the mRNA protein sequence shown in step 1. Use the appropriate color of paper clip for the complementary base.

Analysis How is the tRNA base sequence similar to the original DNA? What is the final product of translation?

Ribosomes have three binding sites that are key to translation. One binding site holds an mRNA transcript so that its codons are accessible to rRNA molecules. The other two binding sites hold tRNAs whose anticodons pair with the mRNA codons.

Protein Assembly

The assembly of a polypeptide begins when a ribosome attaches to the start codon (AUG) on an mRNA transcript. Find the start codon on the mRNA transcript shown in Figure 10-9. The start codon pairs with the anticodon UAC on a tRNA. Because the tRNA that bears the UAC anticodon also carries the amino acid methionine, the first amino acid in every polypeptide is initially methionine. However, this first amino acid may be removed later; thus, all polypeptides do not actually begin with methionine.

As a ribosome moves along an mRNA transcript, each mRNA codon is sequentially paired with its tRNA anticodon, as Figure 10-9 shows. The pairing of an anticodon with a codon causes the specified amino acid to attach to the previously translated amino acid with a covalent bond called a peptide bond. In this way, amino acids are joined to a growing polypeptide chain in the order specified by an mRNA transcript. As each amino acid is added to the polypeptide chain, the ribosome moves three nucleotides—one codon—ahead on the mRNA transcript, where the next amino acid will be translated. Eventually, the ribosome reaches a stop codon, bringing translation to an end. At this point the mRNA is released from the ribosome and the polypeptide is complete.

As you can see in Figure 10-9, several ribosomes may simultaneously translate the same mRNA transcript. A new ribosome begins translating an mRNA transcript almost as soon as the preceding ribosome has moved out of the way. These ribosomes are often spaced as close as 80 nucleotides apart on an mRNA.

The polypeptide chain represents the protein's primary structure. As the polypeptide folds and associates with other polypeptides that make up the protein, it assumes the functional structure of the completed protein.

SECTION 10-3 REVIEW

1. Compare transcription with translation.
2. Distinguish a codon from an anticodon, and explain the significance of each.
3. How does the structure of tRNA relate to its function in translation?
4. Using the information in Table 10-1, list the amino acids that are coded for by the codons AGU, GGG, CCU, and GUG.
5. Explain the significance of the start codon and the stop codons. Do all polypeptides begin with the amino acid coded for by the start codon?
6. **CRITICAL THINKING** What would translation of the mRNA transcript UAACAAGGAGCAUCC produce?

CHAPTER 10 REVIEW

SUMMARY/VOCABULARY

10-1

- DNA stores the information that tells cells which proteins to make and when to make them.
- DNA is made up of two chains of nucleotides.
- A DNA nucleotide is composed of a deoxyribose sugar molecule, a phosphate group, and a nitrogen-containing base. The four nitrogen-containing bases found in DNA nucleotides are adenine (A), guanine (G), cytosine (C), and thymine (T).
- Adenine and guanine are called purines. Cytosine and thymine are pyrimidines.
- Cytosine pairs with guanine, and adenine pairs with thymine. Complementary base pairs are connected to each other by hydrogen bonds.
- Before a cell divides, it copies its DNA by a process called replication. Replication results in two exact copies of the cell's DNA.
- Replication begins with the separation of the DNA chains by helicase enzymes. Then as DNA polymerases move along the separated chains, new chains of DNA are assembled using nucleotides in the surrounding medium.

Vocabulary

adenine (185)
base-pairing rule (187)
complementary base pair (187)
cytosine (185)
deoxyribose (185)
DNA polymerase (188)
double helix (186)
guanine (185)
helicase (188)
mutation (189)
nitrogen-containing base (185)
purine (186)
pyrimidine (186)
replication (188)
replication fork (188)
thymine (185)

10-2

- Nucleotides in DNA are grouped into genes, which contain the information required for the production of specific proteins.
- Three forms of RNA are involved in protein synthesis: mRNA, tRNA, and rRNA.
- mRNA carries genetic information from the DNA in the nucleus to the cytosol of a eukaryotic cell. The process of copying genetic information from DNA to mRNA is called transcription.
- tRNA binds to specific amino acids, helping to form polypeptide chains.
- rRNA makes up the ribosomes where proteins are made.

Vocabulary

messenger RNA (mRNA) (191)
promoter (192)
ribose (190)
ribosomal RNA (rRNA) (191)
RNA polymerase (192)
termination signal (192)
transcription (191)
transfer RNA (tRNA) (191)
uracil (190)

10-3

- The production of proteins is also called protein synthesis.
- The genetic code shown in Table 10-1 is used by most organisms to translate mRNA transcripts into proteins.
- The genetic information necessary for making proteins is encoded in mRNA codons. Each codon codes for a specific amino acid.
- The process of assembling polypeptides from information encoded in mRNA is called translation. During translation, tRNA anticodons pair with corresponding mRNA codons, and amino acids are joined together to form a polypeptide.
- As a polypeptide folds and associates with other polypeptides, it assumes the functional structure of a completed protein.

Vocabulary

anticodon (195)
codon (193)
genetic code (193)
protein synthesis (193)
start codon (194)
stop codon (194)
translation (194)

REVIEW

Vocabulary

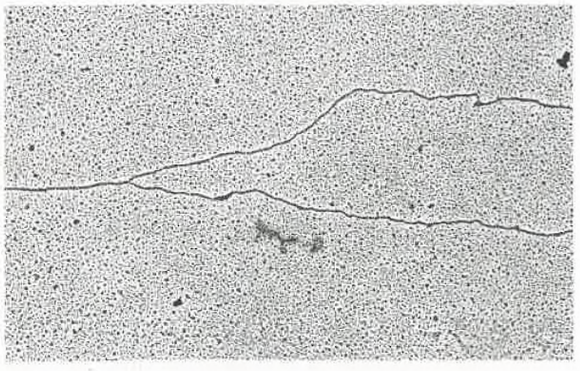
1. Distinguish between a ribosome and ribosomal RNA.
2. Describe the difference between a termination signal and a stop codon.
3. Distinguish between mRNA, tRNA, and rRNA.
4. Describe the difference between a purine and a pyrimidine.
5. Define the term *protein synthesis.*

Multiple Choice Questions

6. DNA
   (a) encodes the information needed for making proteins within the cell
   (b) directs RNA to make lipids that are needed by the cell
   (c) directs RNA to produce glucose
   (d) produces carbohydrates.
7. The physical structure of the genetic code is DNA's sequence of (a) sugars (b) nucleotides (c) phosphates (d) hydrogen bonds.
8. Covalent bonds are found (a) between purines and pyrimidines (b) between nucleotide chains (c) in the sugar-phosphate backbones (d) between RNA and DNA molecules.
9. Complementary base pairing is important for (a) DNA replication (b) RNA transcription (c) RNA translation (d) all of the above.
10. Unlike DNA, RNA
    (a) is a polymer made up of nucleotides
    (b) contains the nitrogen-containing base thymine
    (c) contains the sugar ribose
    (d) does not contain the nitrogen-containing base uracil.
11. Codons are (a) sequences of proteins (b) a site on a tRNA (c) three-nucleotide sequences of mRNA (d) sequences of polypeptides.
12. The pattern of base pairing in DNA can be summarized as follows:
    (a) purines pair with purines
    (b) any purine can pair with any pyrimidine
    (c) adenine pairs with guanine
    (d) adenine pairs with thymine, and cytosine pairs with guanine.
13. The formation of peptide bonds occurs (a) in the nucleus (b) between amino acids (c) during DNA proofreading (d) during transcription.
14. Transcription occurs (a) at ribosomes in both prokaryotes and eukaryotes (b) in the cytosol of eukaryotes (c) in the nucleus of eukaryotes (d) as the last step of protein synthesis.
15. Transporting amino acids to ribosomes for assembly into needed proteins is the function of (a) DNA (b) mRNA (c) rRNA (d) tRNA.

Short Answer

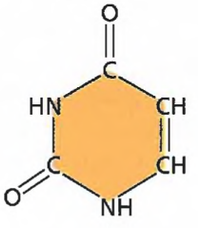
16. What are some ways that the structure of a DNA molecule is related to its function?
17. Is there an advantage to multiple sites of DNA replication? Explain your answer.
18. Would hydrogen bonds or covalent bonds be more important for the identification of mismatches during DNA replication? Explain your answer.
19. What functions are carried out by those few codons that do not code for amino acids?
20. What is the role of ribosomes in protein synthesis?
21. What is the evolutionary significance of a near-universal genetic code?
22. The photograph below shows the DNA of a mammalian cell. What process is the DNA undergoing? What is the structure shown called? Explain your answer.



23. **Unit 6—*Gene Expression***
    Write a report summarizing how antibiotics inhibit protein synthesis in bacteria. How do some antibiotics interfere with translation?

CRITICAL THINKING

1. Use Table 10-1 to find the codons that code for the amino acid alanine. How many codons code for alanine? How do they differ from one another? What significance might the differences have?
2. Refer again to Table 10-1. Using the table, determine the sequence of amino acids that is specified by the following list of codons: AUG UCU AAC AAA CAG GCU UAA.
3. A segment of DNA has the following sequence: AACTACGGTCTCAGCACTCCC. Write the mRNA transcript of this sequence of DNA. Next, write the tRNA anticodons that would pair with the mRNA transcript. Using Table 10-1, write the names of the amino acids coded for by the mRNA transcript.
4. What would happen to the translation process if one nucleotide were not transcribed correctly? Present a minimum of three possibilities.
5. How is a system composed of three bases per codon better suited to code for 20 amino acids than a system composed of two bases per codon?
6. Genetic engineering involves inserting segments of DNA taken from one organism into the DNA of another organism. What would be the likely result of an experiment in which a scientist replaces a faulty stop codon in the DNA of mouse cells with the codon UAG taken from the DNA of a frog, a pine tree, or a clam? What do the results of this experiment suggest about the evolutionary ancestry of these organisms?
7. The diagram below shows a model of the chemical structure of uracil. Compare this diagram with Figure 10-2. How does the chemical structure of uracil differ from the chemical structure of thymine? How is it possible for both thymine and uracil to bond with adenine? (You may wish to look again at the patterns of hydrogen bonding illustrated in Figure 10-3 to help you answer this question.)



URACIL

EXTENSION

1. Prepare a report on the contributions of one of the following scientists to the discovery of the structure of DNA: Erwin Chargaff, Francis Crick, Rosalind Franklin, Linus Pauling, James Watson, or Maurice Wilkins. The book *The Double Helix,* by James Watson, provides information about Watson and Crick's discovery. *The Eight Days of Creation,* by Horace Freeland, provides information about the work of all of these scientists on DNA.
2. Read "Genetics: Repairing the Genome's Spelling Mistakes" in *Science,* July 16, 1999, on page 316. What new gene-therapy technique is being used to correct genetic disorders in rats? What is the goal of this research if it is found to be safe?
3. Read "Gene Cloned for Stretchiest Spider Silk" in *Science News,* February 21, 1998, on page 119. Describe the protein structure that contributes to the extreme elasticity of spider silk.

CHAPTER 10 INVESTIGATION

Modeling Replication and Transcription of DNA

OBJECTIVES

- Construct and analyze a model of DNA.
- Simulate the process of replication using a model.
- Simulate the process of transcription using a model.

PROCESS SKILLS

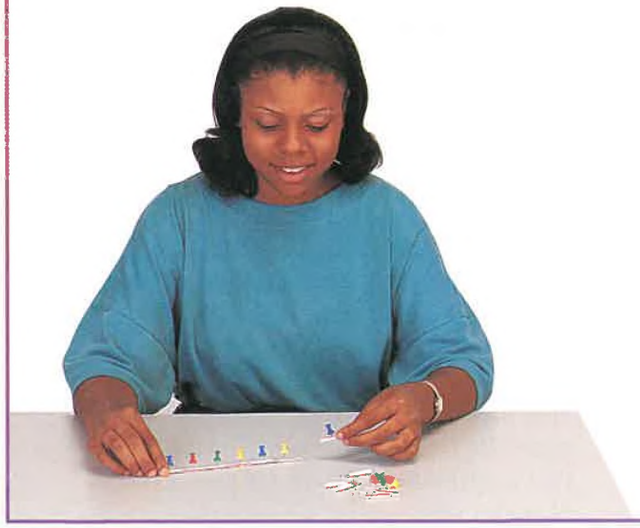
- demonstrating
- identifying
- manipulating a model

MATERIALS

- plastic soda straws, cut into 3 cm sections (54)
- metric ruler
- scissors
- permanent marker
- 54 pushpins (12 red, 12 blue, 12 yellow, 12 green, and 6 white)
- 54 paper clips

Background

1. Describe the structure of DNA.
2. State the base-pairing rules.
3. List the steps involved in the copying of DNA before cell division.

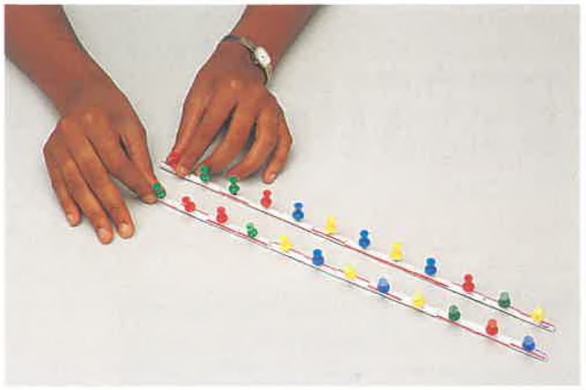


4. What is mRNA, and what is its function in protein synthesis?
5. Describe the process of transcription.

PART A Making a Model of DNA

1. CAUTION **Always cut in a direction away from your face and body.** Cut the soda straws into 3 cm pieces to make 54 segments.
2. Insert a pushpin midway along the length of each straw segment as shown in the figure below. Push a paper clip into one end of each straw segment until it touches the pin.

3. Keeping the pins in a straight line, insert the paper clip from a blue-pushpin segment into the open end of a red-pushpin segment. Add additional straw segments to the red-segment end in the following order: green, yellow, blue, yellow, blue, yellow, green, red, red, and green. Use the permanent marker to label the blue-segment end "top." This chain of segments is one-half of your first model.
4. Assign nucleotides to the corresponding pushpin colors as follows: red = adenine, blue = guanine, yellow = cytosine, and green = thymine.
5. Construct the other half of your first model beginning with a yellow segment across from the blue pushpin at the top of your first model. Keep the pins in a straight line. Link segments together according to the base-pairing rules.



6. When you have completed your model of one DNA segment, make a sketch of the model in your lab report. Use colored pencils or pens to designate the pushpin colors. Include a key that indicates which nucleotide each color represents in your sketch.

PART B Modeling DNA Replication

7. Place the chains parallel to each other on the table with the "top" blue pin of the first chain facing the "top" yellow pin of the second chain.
8. Demonstrate replication by simulating a replication fork at the top pair of pins. Add the remaining straw segments to complete a new DNA model. Be sure to follow the base-pairing rules.
9. Sketch the process of DNA replication in your lab report. Label the replication fork, the segments of original DNA, and the segments of new DNA in your sketch.

PART C Modeling Transcription

10. Place the chains of one of the DNA models parallel to each other on the table. Take the other DNA model apart so that you can use the segments to construct a model of mRNA.
11. Assign the uracil nucleotide to the white pushpins. Using the available pushpins, construct a model of an mRNA transcript of the DNA segment. Begin by separating the two chains of DNA and pairing the mRNA nucleotides with the left strand of DNA as you transcribe from the top of the segment to the bottom of the segment.
12. In your lab report, sketch the mRNA model that you transcribed from the DNA segment.
13. Refer to Table 10-1 on page 194 to determine the sequence of amino acids you transcribed.
14. Clean up your materials before leaving the lab.

Analysis and Conclusions

1. How many nucleotides did the original DNA model contain?
2. Write the base-pair order for the DNA molecule you created, using the following code: red = adenine, blue = guanine, yellow = cytosine, and green = thymine.
3. What is the name given to the point where replication starts on a DNA molecule?
4. How does the replicated model of DNA compare to the original model of DNA?
5. What would the complementary bases be if one side of a DNA molecule had the bases adenine, cytosine, cytosine, thymine, thymine, and adenine?
6. Speculate about what would happen if the nucleotide pairs in the replicated model were not in the same sequence as the original model.
7. Write the mRNA transcription of the DNA sequence presented below.

   CTG TTC ATA ATT

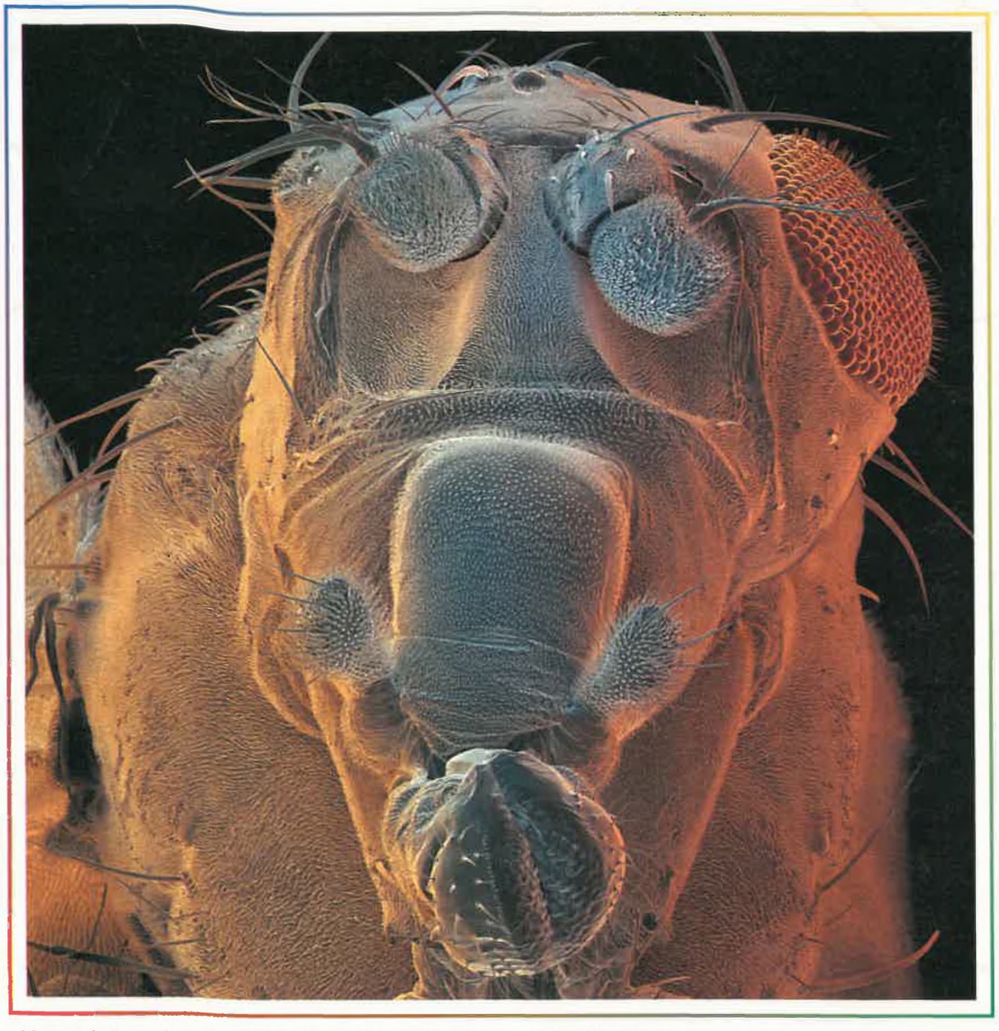
   Next, write the tRNA anticodons that would pair with the mRNA transcription. Finally, write the amino acids coded for by the mRNA transcription using Table 10-1.
8. If you transcribed the "wrong" side of the DNA molecule, what would the result be? How might this affect the proteins that the organism produced?
9. What are the advantages of having DNA remain in the nucleus of eukaryotic cells?

Further Inquiry

Design models for some of the other molecules that are involved in protein synthesis. Use these models along with the DNA model you constructed in this investigation to demonstrate the steps of protein synthesis.

CHAPTER 11

GENE EXPRESSION



This fruit fly has only one eye due to a mutation in a gene that regulates development.

FOCUS CONCEPT: ***Cell Structure and Function***

As you read this chapter, note how gene structure enables prokaryotic and eukaryotic cells to control how and when proteins are produced.

Unit 6—*Gene Expression*
Topics 1–6

SECTION 11-1

CONTROL OF GENE EXPRESSION

Cells use information in genes to build hundreds of different proteins, each with a unique function. But not all proteins are required by the cell at any one time. By regulating gene expression, cells are able to control when each protein is made.

OBJECTIVES

- Define the term *gene expression.*
- Describe the regulation of the *lac* operon in prokaryotes.
- Distinguish between introns and exons.
- Describe the role of enhancers in the control of gene expression.

ROLE OF GENE EXPRESSION

Gene expression is the activation of a gene that results in the formation of a protein. A gene is said to be "expressed," or turned "on," when transcription occurs. But cells do not always need to produce all of the proteins for which their genes contain instructions. Recall from Chapter 3 that proteins have many different functions. Some proteins play a structural role. Others are enzymes that act as catalysts in chemical reactions. Mechanisms to control gene expression have evolved to ensure that each protein is produced only when it is needed.

The complete genetic material contained in an individual is called the **genome** (JEE-nohm). By regulating gene expression, cells are able to control which portion of the genome will be expressed and when. Gene expression occurs in two steps, transcription and translation. Gene expression begins when the enzyme RNA polymerase transcribes the DNA nucleotide sequence of a gene into a specific mRNA. During translation, this mRNA then migrates to a ribosome, where it is translated into a specific protein.

Word Roots and Origins

genome

from the words *gene* and *chromosome*

GENE EXPRESSION IN PROKARYOTES

Scientists first studied gene expression in prokaryotes. Much of our initial knowledge of gene expression comes from the work of French scientists Francois Jacob (1920–) and Jacques Monod (1910–1976). Jacob and Monod discovered how genes control the metabolism of the sugar lactose in *Escherichia coli,* a bacterium that lives in the human intestine.

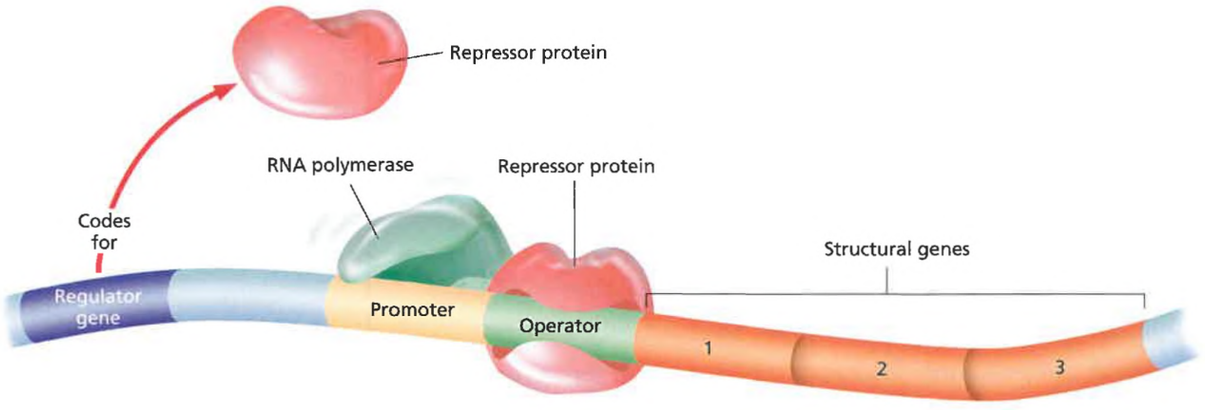


FIGURE 11-1

In the *lac* operon of *E. coli,* three structural genes code for the enzymes needed to utilize lactose. When lactose is absent, a repressor protein attaches to the operator. The presence of the repressor protein prevents RNA polymerase from binding to the structural genes, blocking transcription.

Found naturally in cow's milk, lactose is a disaccharide that is composed of the monosaccharides glucose and galactose. When you drink cow's milk, the presence of lactose stimulates *E. coli* to produce three enzymes. These three enzymes control metabolism of lactose and are adjacent on the chromosome. The production of these enzymes is controlled by three regulatory elements found within the DNA of *E. coli*. These three regulatory elements are as follows:

- **Structural genes** Genes that code for particular polypeptides are called ***structural genes.*** The structural genes studied by Jacob and Monod coded for the enzymes that allow *E. coli* to break down and utilize lactose.
- **Promoter** As you learned in Chapter 10, a promoter is a DNA segment that recognizes the enzyme RNA polymerase and thus promotes transcription.
- **Operator** An **operator** is a DNA segment that serves as a binding site for an inhibitory protein that blocks transcription and prevents protein synthesis from occurring.

The structural genes, the promoter, and the operator collectively form an operon. An **operon** (AHP-uhr-AHN) is a series of genes that code for specific products and the regulatory elements that control these genes. Researchers have found that the clustered arrangement of genes that forms an operon is a pattern that occurs commonly among bacteria. Jacob and Monod named the operon they studied the ***lac* operon** because its structural genes coded for the enzymes that regulate lactose metabolism. The *lac* operon includes the entire segment of DNA required to produce the enzymes involved in lactose metabolism.

In their work with the *lac* operon, Jacob and Monod found that the genes for the enzymes for lactose utilization were expressed *only* when lactose was present. How were the bacteria able to shut off these genes when lactose was absent? Their research showed that gene expression in the *lac* operon exhibits two forms: repression and activation.

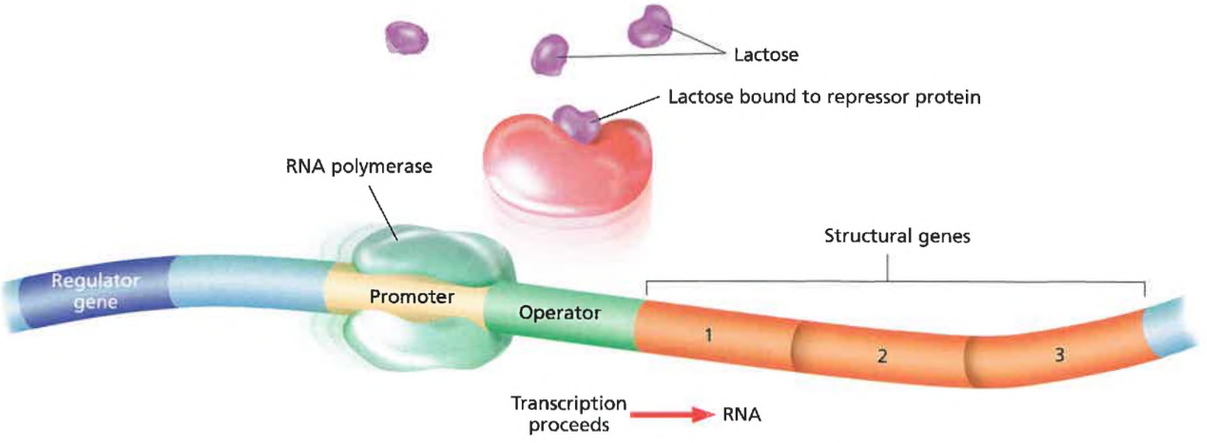


FIGURE 11-2

When lactose is present, it acts as an inducer by binding to the repressor protein and removing it. The removal of the repressor protein allows the transcription of the three structural genes to proceed, producing mRNA.

Repression

In the absence of lactose, a protein called a repressor attaches to the operator. A **repressor protein** is a protein that inhibits a specific gene from being expressed. The attachment of the repressor protein to the operator prohibits RNA polymerase from binding to the structural genes and thus stops transcription from occurring. The blockage of transcription by the action of a repressor protein is called **repression.** Transcription of the structural genes is ultimately controlled by a **regulator gene,** which codes for the production of the repressor protein. The events of repression are summarized in Figure 11-1.

Activation

When lactose is present in the *E. coli* cell, it temporarily binds to the repressor protein on the operator and removes it. The removal of the repressor protein allows RNA polymerase to transcribe the structural genes of the *lac* operon. Since all three structural genes are turned on, all three enzymes required for lactose metabolism are produced. Because it activates, or induces, transcription, lactose acts as an inducer. An **inducer** is a molecule that initiates gene expression. The initiation of transcription by the removal of a repressor protein is called **activation.** Figure 11-2 shows the events that take place when lactose is present in the *E. coli* cell.

The *lac* operon illustrates in simple terms the great advantage of regulating gene expression. Cells of *E. coli* are able to shift between repression and activation, depending on whether lactose is present. Because lactose acts as an inducer, the *lac* operon is transcribed only in the presence of lactose. As a result, lactose induces its own metabolism. When the level of lactose drops, the repressor protein again binds to the operator, shutting off the *lac* operon. The three enzymes used in lactose metabolism are therefore not produced when lactose is not present. By controlling gene expression, *E. coli* conserves resources and produces only those proteins that are needed.

GENE EXPRESSION IN EUKARYOTES

Eukaryotes are vastly different from prokaryotes. Their genomes are much larger than those of prokaryotes. In addition, the DNA of eukaryotic cells is located in several individual chromosomes instead of in the single circular chromosome that occurs in prokaryotes. Finally, most eukaryotes are multicellular organisms made of specialized cells. Although each cell type contains a complete set of the organism's genes, only some of these genes are expressed at a given time. Different cell types produce different proteins. Not surprisingly, the control of gene expression in eukaryotes is far more complex than it is in prokaryotes. Although operons are common in prokaryotes, they have not been found in eukaryotes.

Structure of a Eukaryotic Gene

Much of the control of gene expression in eukaryotes occurs at the level of the individual chromosome. In eukaryotes, gene expression is partly related to the coiling and uncoiling of DNA within each chromosome. Recall from Chapter 8 that eukaryotic DNA is organized as fibers of chromatin wrapped around small specialized proteins called histones. Prior to mitosis or meiosis, the DNA and histones coil tightly, forming the structures we recognize as chromosomes. After mitosis or meiosis, certain regions of the DNA coils relax, thus making transcription possible. This uncoiled form, known as **euchromatin** (yoo-KROH-muh-tin), is the site of active transcription of DNA into RNA. However, some portions of the chromatin remain permanently coiled so that their genes can never be transcribed. Thus, the degree to which DNA is uncoiled indicates the degree of gene expression. Figure 11-3 shows transcription as it occurs in a cell.

FIGURE 11-3

Multiple copies of mRNA are made as transcription occurs at several points along this DNA molecule. (11,055×)

As in the prokaryotes, the promoter is the binding site of RNA polymerase. In the eukaryotic gene, there are two kinds of segments beyond the promoter: introns and exons. **Introns** are the sections of a structural gene that do not code for amino acids and therefore are not translated into proteins. **Exons** are the sections of a structural gene that, when expressed, are translated into proteins.

The benefits of the intron-exon pattern of gene organization are not yet fully understood. However, scientists have noted that the pattern of actively coding portions of DNA interspersed among other noncoding portions of DNA may provide many options for producing different proteins. Perhaps the intron-exon pattern could facilitate the exchange of exons among homologous chromosomes during crossing-over in meiosis. This would result in new combinations of genes, enabling organisms to modify protein structures by replacing one exon with another. If this is the case, the intron-exon pattern of gene organization could serve as an additional source of the genetic diversity that is essential for evolution.

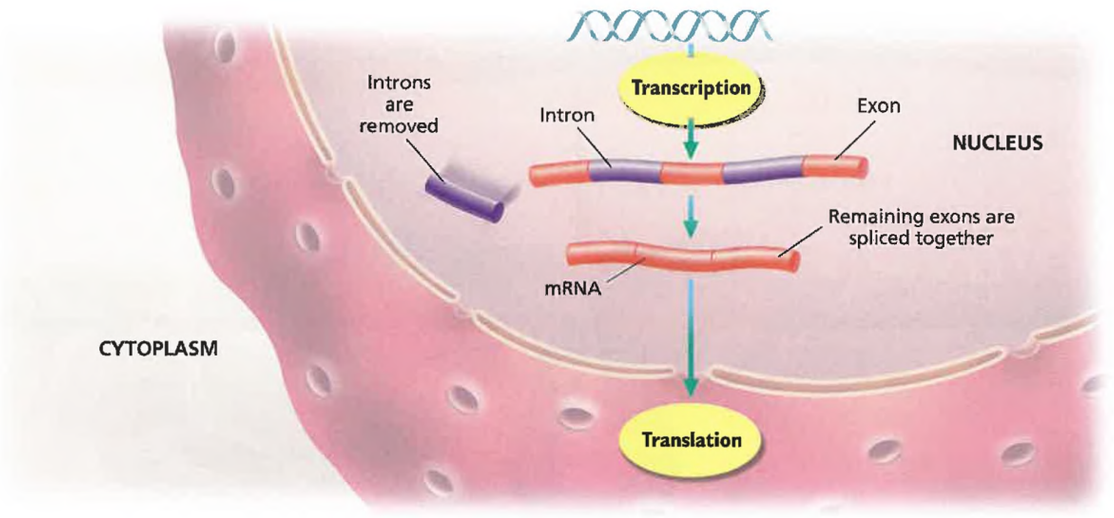


FIGURE 11-4
Both introns and exons are transcribed to form pre-mRNA. Enzymes cut out the introns and join the remaining exons together, forming mRNA.

Control After Transcription

In prokaryotes, transcription and translation occur within the cytoplasm. In eukaryotes, however, transcription occurs in the nucleus, and then mRNA passes through the nuclear envelope and into the cytoplasm, where translation occurs. The physical separation of transcription and translation by the nuclear envelope gives eukaryotes more opportunities to regulate gene expression.

Unlike prokaryotes, eukaryotes can control gene expression by modifying RNA after transcription. When transcription occurs, both introns and exons are transcribed. The result is a large molecule known as pre-mRNA. **Pre-mRNA** is a form of messenger RNA (mRNA) that contains both introns and exons. A molecule of mRNA is formed when introns are removed from pre-mRNA and the remaining exons are spliced (joined) to one another, as shown in Figure 11-4. This occurs when an enzyme splits the pre-mRNA at each end of an intron and joins the exons. The end result is an mRNA containing the exons. The mRNA strand leaves the nucleus and enters the cytoplasm to begin the manufacture of a protein on the ribosomes. When needed, the nucleotides in the removed introns can be used again during the transcription of additional pre-mRNA. Similar RNA splicing occurs following the transcription of transfer RNA and ribosomal RNA.

The removal of introns and splicing of an mRNA molecule has also been found to occur in another way. In the early 1980s, Thomas Cech and his co-workers at the University of Colorado discovered that RNA molecules can act as biological catalysts. The work of Cech and others showed that RNA itself can act as a catalyst to splice introns out of mRNA molecules as they form in the nucleus. Until Cech's discovery, it was thought that all enzymes were proteins.

Quick Lab

Modeling After-Transcription Control

Materials felt-tip markers, paper, scissors, tape

Procedure

1. Write a sentence that contains only three-letter words and makes sense.
2. Hide the words in random places in a long sequence of letters. This sequence should contain random letters and other three-letter words that make no sense in the sentence you are hiding. Print the sequence of letters all the same size, equally spaced, and with no breaks between them.
3. Trade papers with another team. Use scissors to cut out the "introns." Find the message, and reassemble it with tape.

Analysis What represents pre-mRNA in this activity? What represents mRNA?

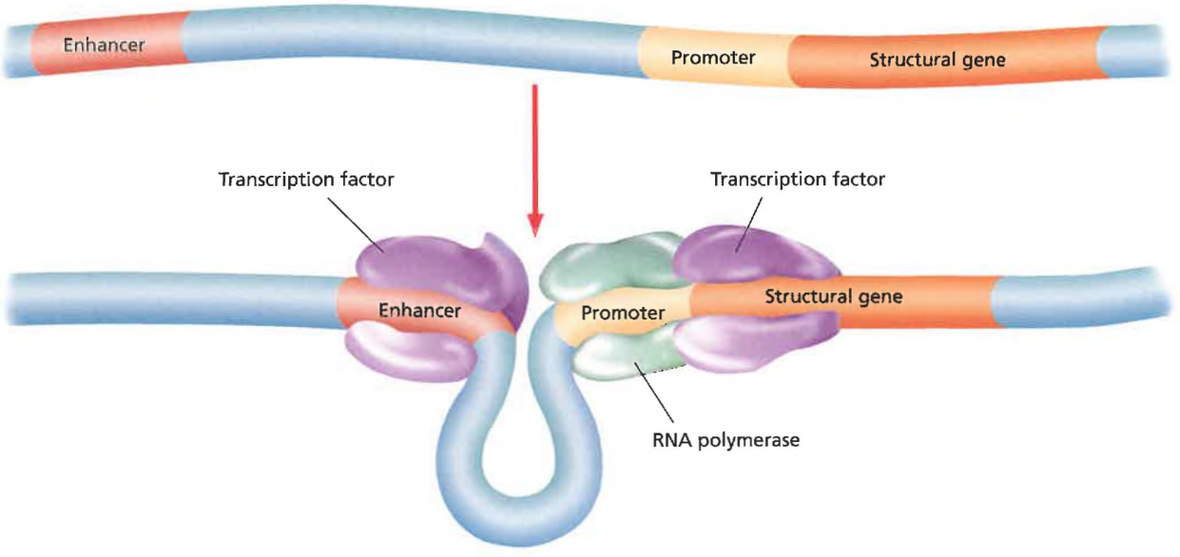


FIGURE 11-5

Many enhancers are located far away from the genes they activate. Transcription factors facilitate transcription by binding to the enhancer and to the RNA polymerase. Bending of the DNA strand brings the enhancer close to the RNA polymerase and the transcription factors associated with it, enabling transcription to begin.

Enhancer Control

Eukaryotic genes on a DNA strand also have noncoding control sequences that facilitate transcription. Such a noncoding control sequence in a eukaryotic gene is called an **enhancer.** An enhancer must be activated for its associated gene to be expressed. Additional proteins, called **transcription factors,** bind to enhancers and RNA polymerase and regulate transcription. Figure 11-5 shows how an enhancer can facilitate transcription, even when it is far away from the gene that it affects.

Activation of enhancers has been studied in the expression of the gene controlling the production of estrogen, a female sex hormone. When estrogen is present in the cell, it binds to a receptor protein in the cytoplasm. The resulting estrogen-receptor protein complex then travels through the pores of the nuclear envelope, entering the nucleus. Once inside the nucleus, the estrogen-receptor protein complex attaches to the enhancer. This activates the enhancer, enabling transcription of specific genes and the synthesis of specific protein molecules to occur.

SECTION 11-1 REVIEW

1. How is it beneficial for organisms to be able to control gene expression?
2. What is the *lac* operon?
3. How does lactose affect the functioning of the *lac* operon?
4. Describe how the intron-exon pattern of gene organization can serve as a source of genetic diversity.
5. Distinguish between mRNA and pre-mRNA.
6. **CRITICAL THINKING** What region of a prokaryotic gene is analogous to the enhancer region of a eukaryotic gene?

GENE EXPRESSION AND DEVELOPMENT

In Section 11-1 you learned how genes are turned on and off in prokaryotes and eukaryotes. Eukaryotes are far more complex than prokaryotes, and most eukaryotes are multicellular. The control of gene expression plays an important role in the growth of eukaryotes as different cells become specialized to perform different tasks.

SECTION 11-2

OBJECTIVES

- Recognize the relationship between gene expression and morphogenesis.
- Describe the influence of homeotic genes on *Drosophila* development.
- Summarize the role of the homeobox in eukaryotic development.
- List the key characteristics of cancer cells.
- Compare and contrast the roles of oncogenes and tumor-suppression genes.

CELL DIFFERENTIATION

All multicellular sexually reproducing organisms begin life as a fertilized egg, or zygote. Although every cell in the developing zygote contains the same genes, only a fraction of the genes are expressed. Certain genes are turned on and off as various proteins are needed at different times during the organism's life. For example, as eukaryotes grow, cells become specialized to perform different tasks. Muscle cells specialize in movement, while liver cells specialize in making enzymes that break down fat. The development of cells having specialized function is called **cell differentiation** (DIF-uhr-EN-shee-AY-shun). As organisms grow and develop, organs and tissues develop to produce a characteristic form. This development of form in an organism is called **morphogenesis** (MOR-foh-JEN-uh-sis).

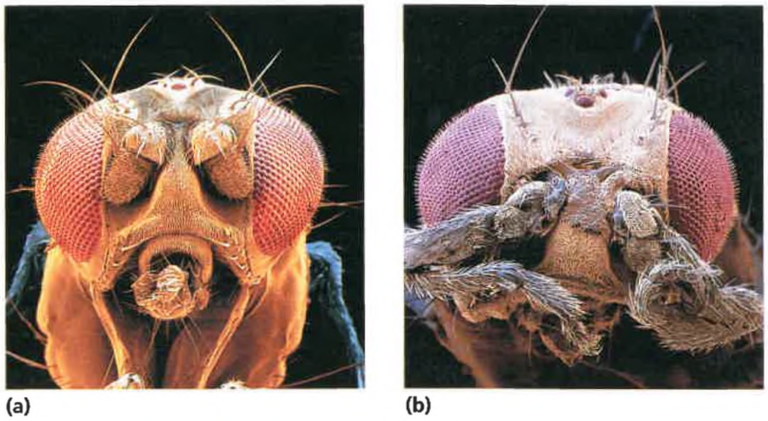
Homeotic Genes

Homeotic (HOH-mee-AHT-ik) **genes** are regulatory genes that determine where certain anatomical structures, such as appendages, will develop in an organism during morphogenesis. Homeotic genes seem to be master genes of development that determine the overall body organization of multicellular organisms. One of the best-known examples of homeotic genes is found in *Drosophila,* the fruit fly. Each homeotic gene of *Drosophila* shares a common DNA sequence of approximately 180 nucleotide pairs. This specific DNA sequence within a homeotic gene regulates patterns of development and is called the **homeobox.** As the *Drosophila* embryo becomes an elongated larva, specific homeoboxes control the morphogenesis of specific regions in the larva. Each of these homeoboxes will also control a specific part of the adult *Drosophila.* As Figure 11-6 shows, a mutation in a homeotic gene can have devastating consequences.

Word Roots and Origins

homeobox

from the Greek *homoio,* meaning "the same"



(a) (b)

FIGURE 11-6
(a) The fruit fly shown here is normal. (b) This fruit fly has legs growing out of its head due to a homeotic mutation.

When a homeotic gene is translated, regulatory proteins are formed. It is thought that these proteins regulate development by switching groups of developmental genes on or off. Switching these genes on or off increases or decreases the rates of cell division in various areas of the developing organism. The resultant variation in growth rates in specific areas of the organism produces specific patterns of structural development.

The same or very similar homeobox sequences have been found in homeotic genes of many eukaryotic organisms. It is thought that all organisms may have similar homeoboxes that code for their anatomy. Figure 11-7 shows examples of homologous homeotic genes in *Drosophila* and mice.

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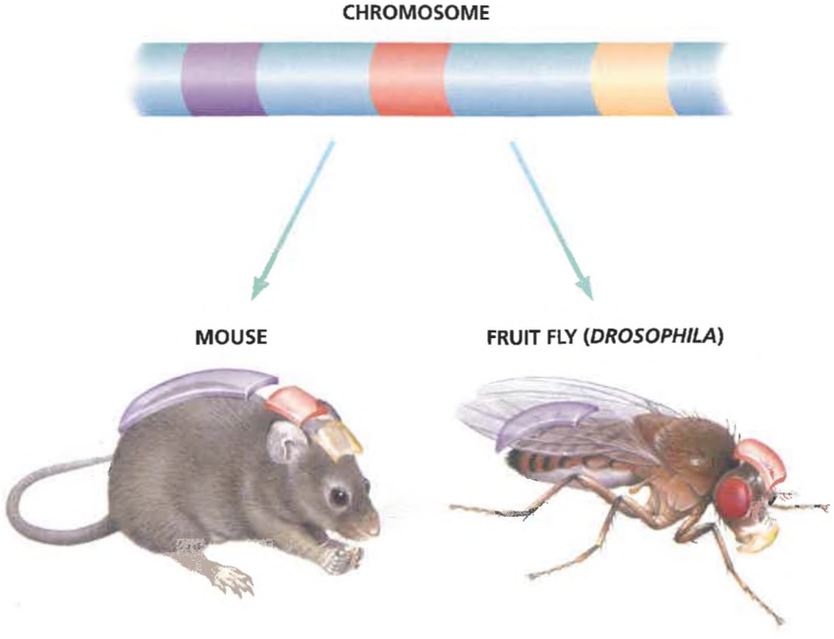


FIGURE 11-7
In many eukaryotes, homeobox sequences govern the development of similar body regions. The gene sequence shown on this chromosome is found in both *Drosophila* and mice. A different color is used to represent each homeobox and the corresponding body region that it controls.

CANCER

A **tumor** is an abnormal proliferation of cells that results from uncontrolled, abnormal cell division. The cells of a **benign** (bi-NIEN) **tumor** remain within a mass. Benign tumors generally pose no threat to life unless they are allowed to grow until they compress vital organs. Examples of benign tumors are the fibroid cysts that occur in a woman's breasts or uterus. Warts are also benign tumors. Most benign tumors can be removed by surgery.

In a **malignant tumor,** the uncontrolled dividing cells invade and destroy healthy tissues elsewhere in the body. Malignant tumors are more commonly known as **cancer. Metastasis** (muh-TAS-tuh-sis) is the spread of cancer cells beyond their original site. When metastasis occurs, the cancer cells break away from the malignant tumor and travel to other parts of the body, where they invade healthy tissue and begin forming new tumors.

Word Roots and Origins

benign

from the Latin *benignus,* meaning "good"

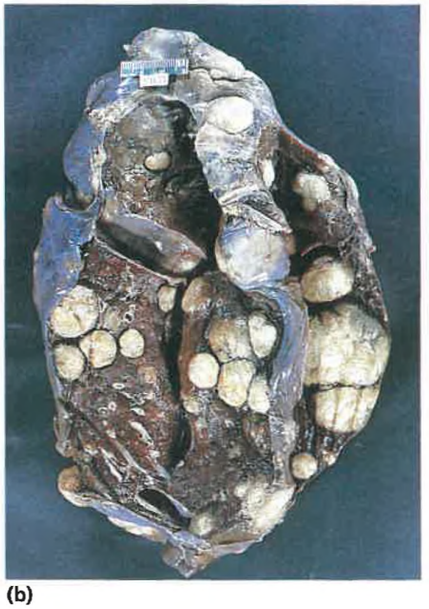
Kinds of Cancer

Malignant tumors can be categorized according to the types of tissues they affect. **Carcinomas** (KAR-si-NOH-muhs) grow in the skin and the tissues that line the organs of the body. Lung cancer, shown in Figure 11-8, and breast cancer are examples of carcinomas. **Sarcomas** (sahr-KOH-muhs) grow in bone and muscle tissue. **Lymphomas** (lim-FOH-muhs) are solid tumors that grow in the tissues that form blood cells. Tumors in blood-forming tissues may cause **leukemia** (loo-KEE-mee-uh), the uncontrolled production of white blood cells. Usually it takes several years for cancer to develop. However, when a vital organ, such as the liver or pancreas, is involved, the symptoms caused by organ dysfunction due to cancer may develop more rapidly.

FIGURE 11-8

(a) Tobacco smoke contains more than 15 known carcinogens. (b) The cancers in this diseased lung are examples of carcinomas. One-third of the cancer deaths in the United States are due to lung cancer. Lung cancer is one of the deadliest forms of cancer; 93 percent of lung cancer patients die within five years after diagnosis. More than 90 percent of lung cancer patients are smokers.

(a)



(b)

Eco Connection

Secondhand Tobacco Smoke

In 1992, the Environmental Protection Agency (EPA) declared secondhand tobacco smoke, also called environmental tobacco smoke, to be a human carcinogen. According to the EPA standards, secondhand smoke contains more than 4,000 chemical compounds, including four known human carcinogens and several other probable human carcinogens. In fact, the air in an enclosed room of smokers could contain up to six times the air pollution of a busy highway. Thousands of nonsmokers die of lung cancer each year as a result of breathing secondhand tobacco smoke. There is no safe level of tobacco smoke.

As more is learned about the contents and effects of tobacco smoke, regulations to protect people from secondhand smoke are being enacted across the United States. In fact, smoking indoors is now prohibited in many public places.

FIGURE 11-9

The hazardous-chemical workers shown in this photograph are removing asbestos from a refinery. Because it is heat resistant and flexible, asbestos has been used to insulate buildings. When inhaled in large amounts over long periods of time, asbestos particles have been shown to cause lung cancer.

Cancer and the Cell Cycle

In normal cells, the frequency of cell division is governed by several factors. A cell must receive adequate nutrition before it can divide. Also, a cell must be attached to other cells, to a membrane, or to fibers between cells in order to divide. (Not all cells, of course, are destined to divide. Recall that cells of certain tissues, such as nervous tissue, cease dividing once they are formed.) Normal cells will stop dividing when they become too crowded, usually after 20 to 50 cell divisions. Cancer cells, however, continue to divide even when they are very densely packed, seemingly ignoring the normal cellular message to stop dividing. They also continue dividing after they are no longer attached to other cells, a trait that facilitates the spread of cancer cells throughout the body.

Causes of Cancer

What triggers the uncontrolled cell division that characterizes cancer? In normal cells, cell division is governed primarily by genes that regulate cell growth and division. Such genes code for **growth factors,** regulatory proteins that ensure that the events of cell division occur in the proper sequence and at the correct rate. Mutations that alter the expression of genes coding for growth factor proteins can lead to cancer. Such mutations can occur spontaneously but are more likely to occur as a result of the organism's exposure to carcinogens. A **carcinogen** (kahr-SIN-oh-jen) is any substance that increases the risk of cancer. Well-known carcinogens include tobacco, asbestos, and ionizing radiation, such as X rays or ultraviolet light from the sun. For example, cigarette tobacco has been found to be the cause of 90 percent of all lung cancers. Most carcinogens are **mutagens** (MYUT-uh-jens), agents that cause mutations to occur within a cell. Figure 11-9 shows hazardous-chemical workers removing the carcinogen asbestos from a refinery.

Whether a person actually develops cancer seems to depend on many factors. Some families exhibit higher-than-average rates of certain cancers, leading researchers to suspect a genetic predisposition to these types of cancer. With regard to cancers caused by mutagens, the number of exposures to the carcinogen and the amount of carcinogen in each exposure are significant factors. Mutations in gametes (egg or sperm cells) are especially important because these mutations are passed along to offspring.

Usually, more than one mutation is needed to produce a cancer cell. Perhaps this helps to explain why the cancer risk increases with the number of exposures to carcinogens and with the age of the individual. The longer an individual lives, the more mutations he or she will accumulate. Heightened awareness of the causes of cancer, combined with improved detection and treatment of the disease, has resulted in a decline in the number of deaths caused by cancer. In the United States, the cancer death rate fell by about 3 percent between the years 1991 and 1995, according to the National Cancer Institute.

Research Notes

The War on Cancer

Cancer, the leading cause of death in the United States, is a genetic disease caused by mutations in the genes that control cell division. Two kinds of genes that control cell division are proto-oncogenes and tumor-suppressor genes. Proto-oncogenes stimulate cell division, while tumor-suppressor genes inhibit cell division.

Under normal circumstances, these genes work together, enabling the body to replace and repair cells. However, a mutation in either a proto-oncogene or a tumor-suppressor gene can cause a cell to begin dividing uncontrollably. Such a cell may quickly become 2 cells, then 4, then 8, then 16, eventually forming a malignant tumor. The malignant tumor invades healthy tissues, often by spreading into the lymph tissues and blood vessels, which can transport cancer cells to distant sites in the body. A malignant tumor that is not destroyed quickly may become established in vital organs and interfere with their functions.

This woman joins other researchers around the world in the search for new cancer treatments.

One strategy for combating cancer is to stop the cell cycle of cancer cells so that they do not continue to divide. Most anticancer drugs interfere with the process of cell division at some step in the cell cycle. Anticancer drugs known as topoisomerase-1 inhibitors prevent the uncoiling of DNA that is necessary for replication. Another class of drugs works by damaging the cell's DNA so that it cannot be copied. Enzymes that monitor DNA replication will activate a series of steps that cause the cell to self-destruct if the DNA is too damaged for enzyme repair. However, these traditional anticancer drugs prevent cell division in all dividing cells, not just in cancer cells; thus, they damage healthy tissues too. A new class of anticancer drugs called farnesyltransferase inhibitors have been shown to target tumor cells but not normal cells.

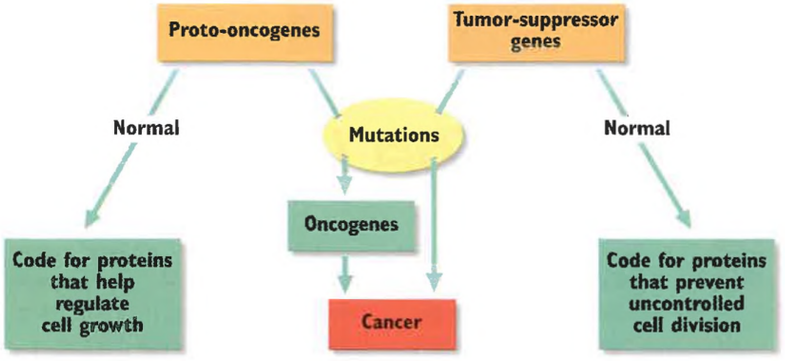
Treating cancer cells based on their genetic makeup may also be helpful. For example, many cancer cells lack both normal copies of the tumor-suppressor gene p53. Cancer cells that have normal p53 genes tend to be very sensitive to chemotherapy, while those with mutant p53 genes often do not respond to chemotherapy treatment. Using a computer database that contains information about 350,000 potential anticancer compounds, oncologists have identified 112 possible compounds that may be effective against cancers associated with mutant p53 genes.

Simply keeping existing tumors under control is another way that cancer can be treated effectively. Malignant tumors typically stimulate their own growth by constructing a nourishing supply of blood vessels—a process called angiogenesis. Scientists know of more than 20 compounds that prevent angiogenesis. Currently, several of these compounds are being tested on human patients. Perhaps these compounds will be useful in slowing down or even stopping the growth of small clusters of cancer cells that are missed by other cancer treatments.

Combinations of several cancer therapies seem to be the best approach to fighting the war against cancer for now. By combining therapies, physicians may be able to eliminate tiny clusters of cancer cells that could rebound and kill patients. For example, combining chemotherapy and radiation has been shown to improve the condition of patients with advanced cancer of the nose and throat. Three years after treatment, 65 percent of patients who received both therapies were still alive, compared with a 24 percent survival rate among patients who received only radiation. In the coming years, cancer is likely to be considered a serious chronic disease. Like the chronic diseases diabetes and hypertension, perhaps cancers will be controlled with treatment for many years.

FIGURE 11-10

Mutations in proto-oncogenes or tumor-suppressor genes can destroy normal gene functioning, possibly resulting in cancer. A mutation in a proto-oncogene can cause it to become an oncogene, a gene that triggers cancer.



Oncogenes

An **oncogene** (AHN-koh-jeen) is a gene that causes cancer or other uncontrolled cell proliferation. Oncogenes begin as normal genes called **proto-oncogenes** that control a cell's growth and differentiation. Normally, proto-oncogenes code for proteins that regulate the rate of the cell cycle by controlling cell growth, cell division, and the ability of cells to adhere to one another. A mutation in a proto-oncogene may cause it to produce more protein or a protein that seems to be unusually active in triggering cell division. The rate of the cell cycle then increases, and cancer occurs as a result.

Other human genes suppress tumor formation. **Tumor-suppressor genes** code for proteins that prevent the uncontrolled rate of cell division. When tumor-suppressor genes mutate, the proteins for which they code are either defectively expressed or not expressed at all, causing a predisposition to cancer. Figure 11-10 summarizes the actions of oncogenes and tumor-suppressor genes.

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Viruses and Cancer

Certain viruses can cause cancer in plants and animals. Many viral genes are actually oncogenes. Viruses can also stimulate uncontrolled growth in host cells by causing mutations in proto-oncogenes or tumor-suppressor genes, thus accelerating the rate of cell division in the host cell. Or they may activate the cell's own oncogenes. Viruses have been found to cause various kinds of leukemia.

SECTION 11-2 REVIEW

1. How can morphogenesis be affected by the control of gene expression?
2. What is the role of homeotic genes in *Drosophila*?
3. What does the presence of the homeobox among eukaryotes suggest about evolution?
4. List three ways in which cancer cells differ from normal cells.
5. Describe how mutations in proto-oncogenes or tumor-suppressor genes could cause cancer.
6. **CRITICAL THINKING** Why might X rays be more dangerous to an ovary or a testis than to muscle tissue?

CHAPTER 11 REVIEW

SUMMARY/VOCABULARY

11-1

- Gene expression is the activation of a gene that results in the formation of a protein. Only a fraction of any cell's genes are expressed at any one time.
- Structural genes code for a particular product. Regulatory elements (a promoter and an operator) regulate the transcription of structural genes. In prokaryotes, the structural genes, the promoter, and the operator collectively form an operon.
- A promoter is the segment of DNA that recognizes the enzyme RNA polymerase and thus promotes transcription. An operator is the segment of DNA that can block transcription and thus prevent protein synthesis from occurring.
- In the bacterium *E. coli,* the *lac* operon codes for the three enzymes required for lactose metabolism.
- A repressor protein can inhibit a specific gene from being expressed. The blockage of transcription by the action of a repressor protein is called repression. A regulator gene controls the expression of a particular gene by coding for a repressor protein.
- An inducer is a molecule that initiates gene expression. In *E. coli,* lactose serves as an inducer.
- Eukaryotes do not have operons. The genomes of eukaryotes are larger and more complex than those of prokaryotes.
- Eukaryotic genes are organized into noncoding sections called introns and coding sections called exons.
- An enhancer must be activated for a eukaryotic gene to be expressed. Transcription factors initiate transcription by binding to enhancers and RNA polymerases.

Vocabulary

activation (205)
enhancer (208)
euchromatin (206)
exon (206)
gene expression (203)
genome (203)
inducer (205)
intron (206)
lac operon (204)
operator (204)
operon (204)
pre-mRNA (207)
regulator gene (205)
repression (205)
repressor protein (205)
structural gene (204)
transcription factor (208)

11-2

- The development of specialized cells is called cell differentiation. The development of form in an organism is called morphogenesis. Both cell differentiation and morphogenesis are governed by gene expression.
- Homeotic genes are regulatory genes that determine where anatomical structures will be placed during development. Within each homeotic gene, a specific DNA sequence known as the homeobox regulates patterns of development. The homeoboxes of many eukaryotic organisms appear to be very similar.
- Cancer is the uncontrolled growth of abnormal cells. Cancerous cells may form a tumor. Tumors may be benign or malignant.
- A carcinogen is any substance that increases the risk of cancer. Mutagens are substances that cause mutations.
- Mutations of proto-oncogenes or tumor-suppressor genes may lead to cancer.
- Some viruses can cause cancer.

Vocabulary

benign tumor (211)
cancer (211)
carcinogen (212)
carcinoma (211)
cell differentiation (209)
growth factor (212)
homeobox (209)
homeotic gene (209)
leukemia (211)
lymphoma (211)
malignant tumor (211)
metastasis (211)
morphogenesis (209)
mutagen (212)
oncogene (214)
proto-oncogene (214)
sarcoma (211)
tumor (211)
tumor-suppressor gene (214)

REVIEW

Vocabulary

Explain the difference between the terms in each of the following sets:

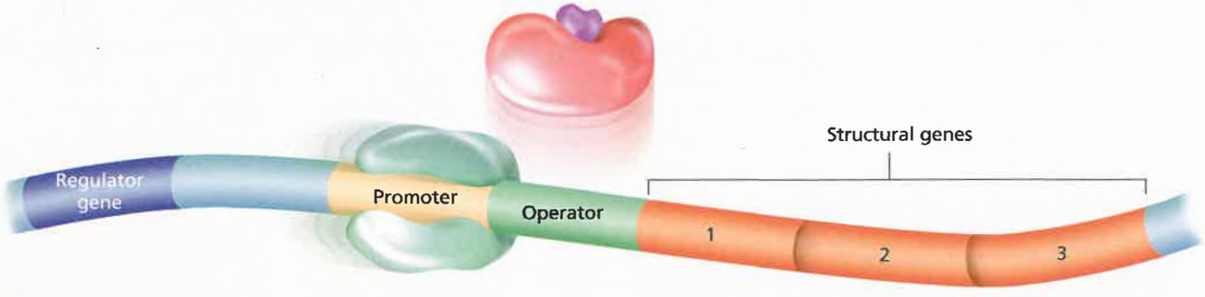
1. operator, promoter
2. gene, genome
3. intron, exon
4. gene, homeotic gene
5. carcinogen, mutagen, oncogene

Multiple Choice

6. A repressor protein is coded for by a(n) (a) structural gene (b) regulator gene (c) promoter (d) enhancer.
7. Active DNA transcription in eukaryotes occurs within (a) an operon (b) an operator (c) an intron (d) euchromatin.
8. When present in an *E. coli* cell, lactose (a) binds with a repressor (b) stops transcription from occurring (c) binds with mRNA (d) acts as a regulator.
9. In eukaryotes, introns and exons are interspersed regions of a(n) (a) protein (b) DNA molecule (c) RNA molecule (d) transcription factor.
10. Enhancers (a) initiate transcription (b) join amino acids (c) unwind DNA (d) transport proteins into the nucleus.
11. The control of gene expression enables organisms to (a) reproduce more quickly (b) remove mutations from their DNA (c) produce proteins only when needed (d) form new combinations of genes.
12. Unlike eukaryotes, prokaryotes (a) have introns and exons (b) lack nuclei (c) have chromosomes of RNA (d) have enhancer sequences.
13. In eukaryotic cells, pre-mRNA contains (a) introns only (b) exons only (c) neither introns nor exons (d) both introns and exons.
14. A malignant tumor found in bone or muscle tissue is an example of (a) a sarcoma (b) leukemia (c) a carcinoma (d) a lymphoma.
15. The transformation of a normal gene into an oncogene may result in (a) a loss of cell division (b) the release of new viruses (c) cancer (d) the transcription of introns.

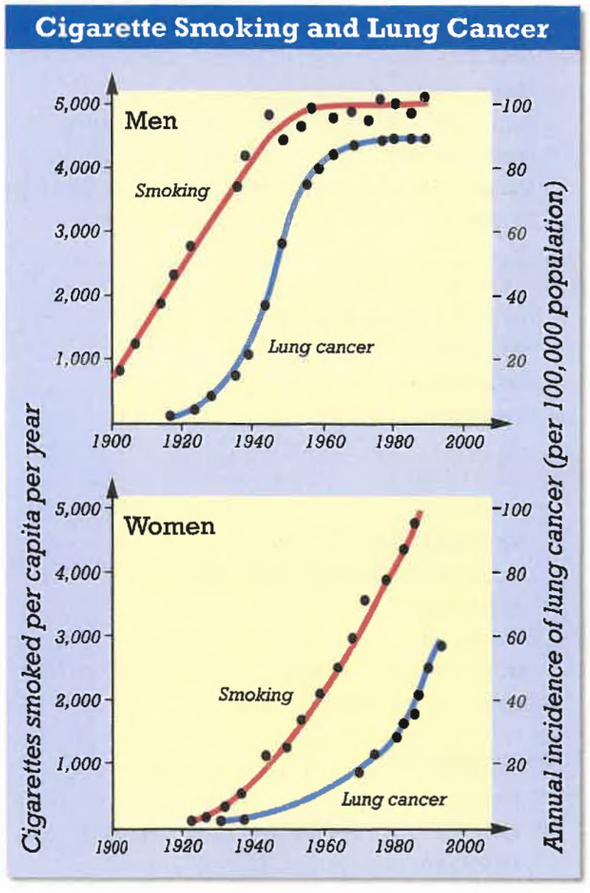
Short Answer

16. In which organism did Jacob and Monod study the *lac* operon? Where is this organism commonly found?
17. What causes the *lac* operon to shut off? Why can this mechanism be considered a feedback mechanism?
18. How does *E. coli* benefit by making enzymes to utilize lactose only when lactose is in the cellular environment?
19. Describe the events that take place after estrogen binds to a receptor protein in the cytoplasm.
20. How does cell differentiation differ from morphogenesis?
21. What happens when a malignant tumor undergoes metastasis?
22. Name three commonly known carcinogens.
23. What does it mean for a person to be "genetically predisposed" to cancer?
24. What does the study of homeoboxes suggest regarding the evolutionary relationships among eukaryotes?
25. Study the diagram of the *lac* operon shown below.
    a. Describe the role of the following elements shown in the diagram: promoter, operator, structural genes.
    b. What does it mean to say that a gene is turned "on"?
    c. Are the structural genes turned "on" in the diagram of the *lac* operon shown below?



CRITICAL THINKING

1. A molecular biologist isolates mRNA from the brain and liver of a mouse and finds that the two types of mRNA are different. Can these results be correct, or has the biologist made an error? Explain your answer.
2. Kwashiorkor is a disease in children caused by a diet high in carbohydrates but lacking in complete protein. When children with kwashiorkor are suddenly put on a diet rich in protein, they may become very ill with ammonia poisoning, and some even die. The high level of ammonia in their blood is due to the inadequate metabolism of protein. What does this tell you about the enzymes that metabolize protein?
3. Mutations may occur in gametes or in body cells. In which cell type is a mutation likely to be a source of genetic variation for evolution? Why?
4. *Drosophila* feed on fermenting fruit, which often contains a large amount of alcohol. If *Drosophila* are fed a diet that has a high alcohol content, there is an increase in the amount of dehydrogenase, an enzyme that metabolizes alcohol, in the digestive tract. What does this increase tell you about the enzyme?
5. The graphs at right show the number of cigarettes smoked per capita per year since 1900 and the annual incidence of lung cancer among men and women. What is the relationship between the number of cigarettes smoked and the incidence of lung cancer? Why do you think the incidence of lung cancer among women has increased sharply in the last 30 years while the incidence of lung cancer among men has remained relatively stable during this period?



EXTENSION

1. Using your library, research forms of human cancer associated with viruses, such as leukemia (human T lymphotrophic virus), liver cancer (hepatitis B virus), Burkitt's lymphoma (Epstein-Barr virus), and cervical cancer (human Papillomavirus). Write a report on the symptoms, possible treatments, and prognoses of patients with these forms of cancer.
2. Construct a chart in which you compare and contrast the qualities in bacteria and fruit flies that make them ideal experimental tools for the scientist. Make sure to include similarities as well as differences between the two species.
3. Read "Got Cancer Killers?" in *Discover,* June 1999, on page 68. Write a short report about the potential cancer cure being researched at Lund University, in Sweden. Explain how the cancer-killing protein alpha-lactalbumin protects nursing infants. Describe the next step toward making a treatment available to cancer victims.

CHAPTER 11 INVESTIGATION

Modeling Gene Expression in the *Lac* Operon

OBJECTIVES

- Make a model of the *lac* operon.
- Demonstrate the mechanisms that regulate gene expression in the *lac* operon of *Escherichia coli*.
- Simulate the transcription of the structural genes in the *lac* operon.

PROCESS SKILLS

- comparing and contrasting
- identifying
- demonstrating
- manipulating a model

MATERIALS

- pipe cleaner
- large colored beads, 6
- colored modeling clay in three colors
- labeling tape
- marking pen
- pencil
- paper

Background

1. Define *gene*.
2. What is the role of RNA polymerase in protein synthesis?
3. Where does protein synthesis occur? What is the function of mRNA in protein synthesis?
4. What is the role of ribosomes during protein synthesis?
5. What are the roles of the operator, promoter, and structural genes within the *lac* operon?
6. How does the presence or absence of lactose affect the *lac* operon?
7. What is a regulator gene?

PART A Making a Model of the *Lac* Operon

1. In this investigation, you will use the materials provided to make a model of a *lac* operon. Allow the pipe cleaner to represent the portion of DNA that constitutes the *lac* operon.
2. Thread the pipe cleaner through three beads of similar size, shape, and color. These three beads represent the structural genes of the *lac* operon.
3. Add one bead to represent the operator portion of the *lac* operon. Also add beads to represent the promoter and the regulatory gene, respectively.
4. Using labeling tape and a marking pen, label each of the beads you have placed on the pipe cleaner. This represents a model of the *lac* operon.
5. Compare the sequence of the labeled beads on the pipe cleaner with the sequence of segments in the diagram of the *lac* operon in Figure 11-1. When your model of the *lac* operon correctly reflects the parts of the *lac* operon in the figure, proceed to Part B.

PART B The *Lac* Operon When It Is Turned Off

6. Choose one color of modeling clay to represent the enzyme RNA polymerase and choose another color to represent the repressor molecule. Use the modeling clay to mold an RNA polymerase molecule and a repressor molecule.
7. Using the molecules you made out of clay in step 6, modify your model of the *lac* operon so that it shows the *lac* operon when it is turned off.
8. In your lab report, draw your model of the *lac* operon when it is turned off. Label all parts of your drawing. How does the presence of the repressor molecule prevent transcription of the structural genes?

PART C The *Lac* Operon When It Is Turned On

9. Choose a third color of modeling clay to represent the inducer molecule. Use the modeling clay to form an inducer molecule.
10. Using the inducer molecule you made out of clay, modify your model of the *lac* operon so that it shows the *lac* operon when it is turned on.
11. Simulate the activation of the *lac* operon and the transcription of the structural genes.
12. In your lab report, prepare a diagram of your model that shows the expression of the structural genes in the *lac* operon. Include ribosomes and mRNA in your diagram. Label all parts of your diagram.
13. The graphic organizer below shows the sequence of steps that occurs after lactose enters *E. coli* cells. Copy this graphic organizer in your lab report. Complete the graphic organizer by describing what takes place during step 2 and step 3. Explain how the end product affects the events shown in the graphic organizer.
14. Clean up your materials before leaving the lab.

Analysis and Conclusions

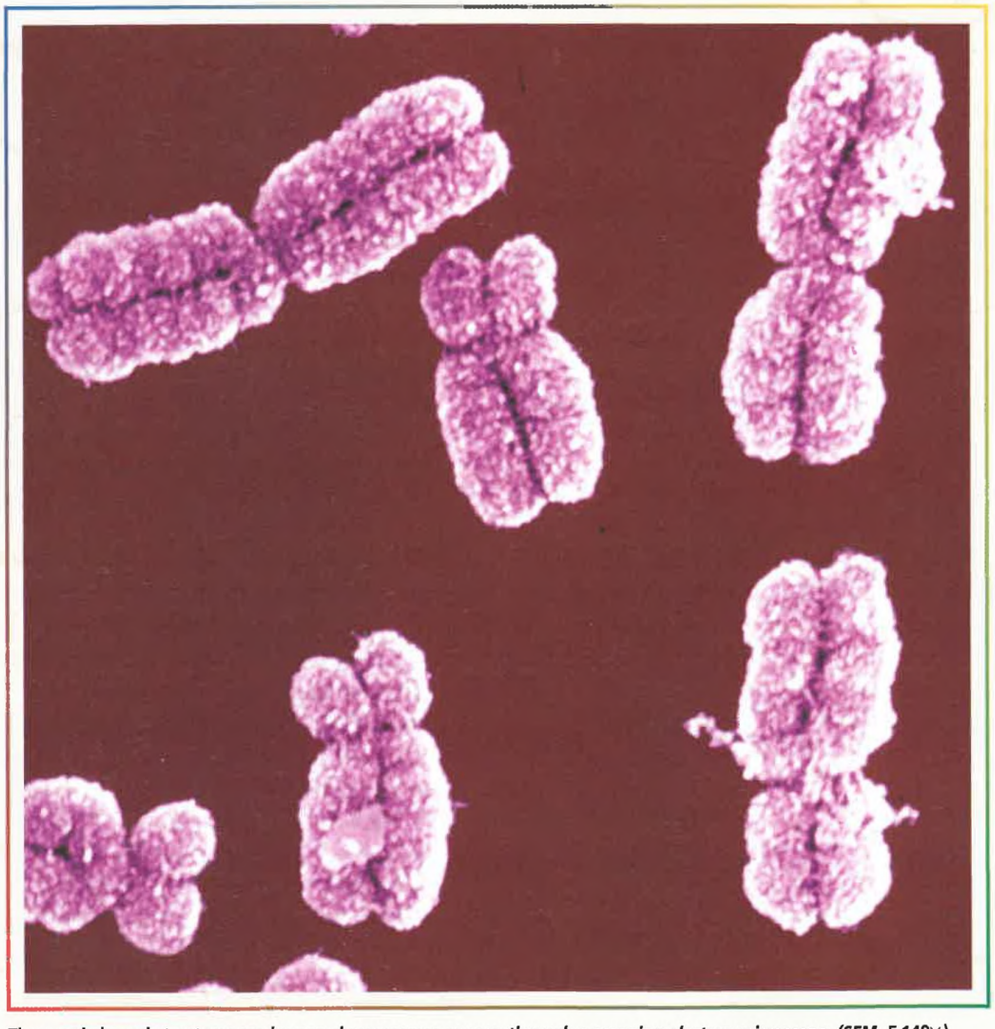
1. Compare the processes of repression and activation.
2. What substance serves as an inducer in the *lac* operon?
3. How might a mutation in the regulator gene affect the *lac* operon?
4. Look at the diagram you made in step 12. Refer to your diagram, and predict what will happen when the inducer is no longer present.
5. How would the loss of the promoter site from the operon affect the production of the enzymes needed to utilize lactose?
6. In homes and apartments, a consistent temperature is maintained by means of a thermostat, which regulates when heating (or air conditioning) is turned on or off. In what way does the *lac* operon function like a thermostat?
7. Biological processes often take place in a series of sequential steps called a biochemical pathway. Many biochemical pathways are controlled by feedback inhibition. In feedback inhibition, a pathway's end product affects an earlier step in the pathway and causes the pathway to stop. Explain why the *lac* operon in *E. coli* is considered an example of feedback inhibition.

Further Inquiry

1. Use classroom or library references to find additional examples of feedback inhibition in biology. Describe why models of feedback inhibition are sometimes called feedback loops.
2. The products of the *lac* operon are produced when lactose is present. In this way, the presence of a specific molecule stimulates transcription of the structural genes. In contrast, some operons are repressed when a specific molecule is present. Use classroom or library references to find out how the *trp* operon functions in *E. coli.* Then compare activation and repression in the *trp* operon with activation and repression in the *lac* operon.

CHAPTER 12

INHERITANCE PATTERNS AND HUMAN GENETICS



These rod-shaped structures are human chromosomes as seen through a scanning electron microscope. (SEM, 5,148×)

FOCUS CONCEPT: ***Reproduction and Inheritance***

As you read this chapter, note how Mendel's theories of inheritance (Chapter 9) and our knowledge of chromosome structure and protein synthesis (Chapters 10 and 11) have helped shape the study of genetics.

BIOLOGY INTERACTIVE TUTOR

Unit 6—*Gene Expression*
Topics 1–6

CHROMOSOMES AND INHERITANCE

You have learned how DNA in chromosomes contains instructions for protein synthesis and how chromosomes are transmitted from one generation to the next. In this chapter you will learn how biologists use their knowledge of DNA and chromosome behavior to study how traits are inherited and expressed.

SECTION 12-1

OBJECTIVES

- Explain the role of sex chromosomes in sex determination.
- Describe how sex linkage affects the inheritance of traits.
- Explain the effect of crossing-over on the inheritance of genes in linkage groups.
- Summarize the procedure involved in constructing a chromosome map.
- Distinguish between chromosome mutations and gene mutations.

SEX DETERMINATION

In the early 1900s, geneticist Thomas Hunt Morgan, of Columbia University, began breeding experiments with *Drosophila,* the fruit fly. *Drosophila* has four pairs of homologous chromosomes. Morgan observed that one chromosome pair was different in males than it was in females. In females, the two chromosomes in the pair were identical. In males, however, while one chromosome looked like those of the corresponding female pair, the other chromosome was shorter and hook-shaped. Morgan called the chromosome that appeared to be the same in males and females the X chromosome. He called the shorter, hook-shaped chromosome the Y chromosome. Morgan correctly hypothesized that the X and Y chromosomes are sex chromosomes. Recall from Chapter 8 that sex chromosomes determine an individual's sex. All of the other chromosomes, those not involved in sex determination, are called autosomes.

Like other chromosomes, the sex chromosomes form pairs and segregate into separate cells during meiosis I. As a result, the gametes that form during meiosis II each have *either* an X chromosome or a Y chromosome. In mammals and most insects, males have one X chromosome and one Y chromosome, which are symbolized XY, and females have two X chromosomes, which are symbolized XX. Gametes produced by males can contain either an X chromosome or a Y chromosome, whereas gametes produced by females contain only an X chromosome.

In humans and fruit flies, an egg that is fertilized by a sperm with an X chromosome will be a female zygote (XX), and an egg that is fertilized by a sperm with a Y chromosome will be a male zygote (XY). As shown in Figure 12-1, this system of sex determination means that 50 percent of the offspring of any mating will be male and 50 percent will be female.

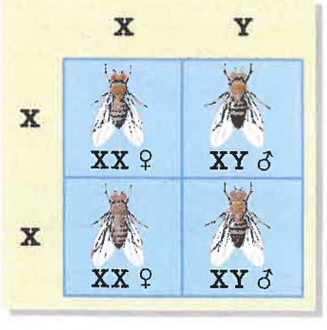


FIGURE 12-1
As this Punnett square shows, approximately half of all *Drosophila* offspring are likely to be female (♀), and half are likely to be male (♂).

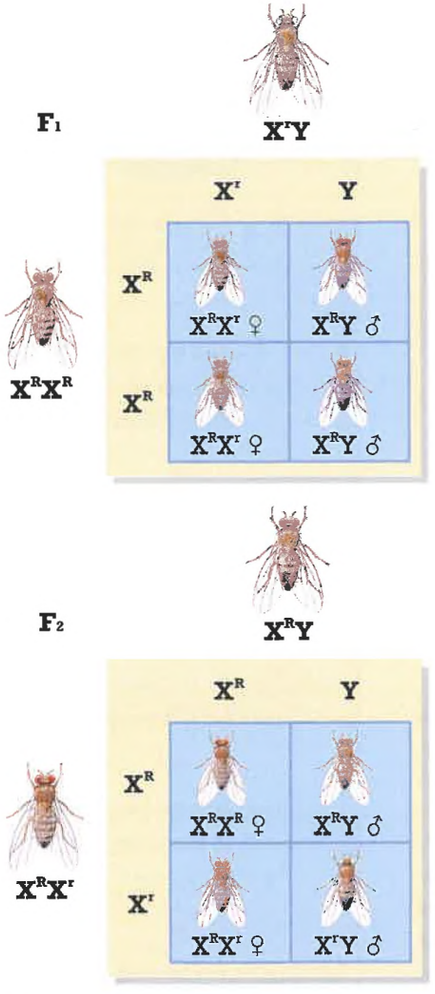


FIGURE 12-2

Eye color is an X-linked trait in fruit flies. Alleles for eye color are carried on the X chromosome—*R* for red and *r* for white.

Sex Linkage

The discovery of the different sizes and shapes of the X and Y chromosomes led Morgan to hypothesize that more genes could be carried by the X chromosome than by the smaller Y chromosome. Genes found on the X chromosome are said to be **X-linked genes.** Genes found on the Y chromosome are **Y-linked genes.** The presence of a gene on a sex chromosome is called **sex linkage.**

Morgan's *Drosophila* experiments confirmed the existence of X-linked traits. Although most fruit flies have red eyes, a few males have white eyes. When Morgan crossed a white-eyed male with a red-eyed female, the results of the cross followed Mendel's predictions: the F_1 generation all had red eyes. Morgan next crossed members of the F_1 generation. The F_2 generation that resulted exhibited the expected ratio of three red-eyed flies to one white-eyed fly. However, all of the white-eyed flies were male.

Why were there no white-eyed females? Morgan hypothesized that the gene for eye color is carried on the X chromosome. Figure 12-2 shows his reasoning. Assume that the X chromosome carries the gene for eye color, either X^R (red eyes) or X^r (white eyes). If an X^RX^R female (red-eyed) is crossed with an X^rY male (white-eyed), all of the F_1 females will be X^RX^r (red-eyed) and all of the F_1 males will be X^RY (red-eyed). Note that the Y chromosome does not carry a gene for eye color. In the F_2 generation, half the females will be X^RX^R, and the other half will be X^RX^r; therefore, all of the females will be red-eyed. Half of the F_2 males will be X^RY (red-eyed), but the other half will be X^rY (white-eyed). Morgan correctly concluded that eye color in *Drosophila* is an X-linked trait.

LINKAGE GROUPS

Because there are thousands more genes than there are chromosomes, each chromosome carries many genes. The genes located on one chromosome form a **linkage group.** Two or more genes that are found on the same chromosome are thus said to be linked. Because they are on the same chromosome, linked genes tend to be inherited together.

Morgan demonstrated the existence of linkage groups in his work with *Drosophila.* In *Drosophila* the allele *G* for gray body is dominant to the allele *g* for black body. The allele *L* for long wings is dominant to the allele *l* for short wings. Morgan crossed homozygous gray, long-winged (*GGLL*) flies with homozygous black, short-winged (*ggll*) flies to produce an F_1 generation of heterozygous gray, long-winged (*GgLl*) flies. Then he crossed members of this F_1 generation with one another (*GgLl* × *GgLl*) to produce an F_2 generation. Morgan knew that if the alleles for body color and wing length were on

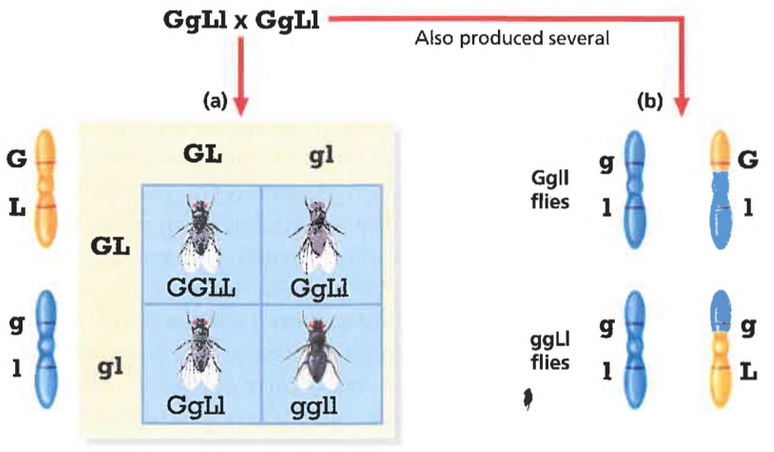


FIGURE 12-3

(a) Because the genes for body color and wing length are linked, the cross *GgLl* × *GgLl* produces a 3:1 phenotypic ratio. (b) Crossing-over produces gametes with new combinations of alleles, leading to unexpected phenotypes among the offspring.

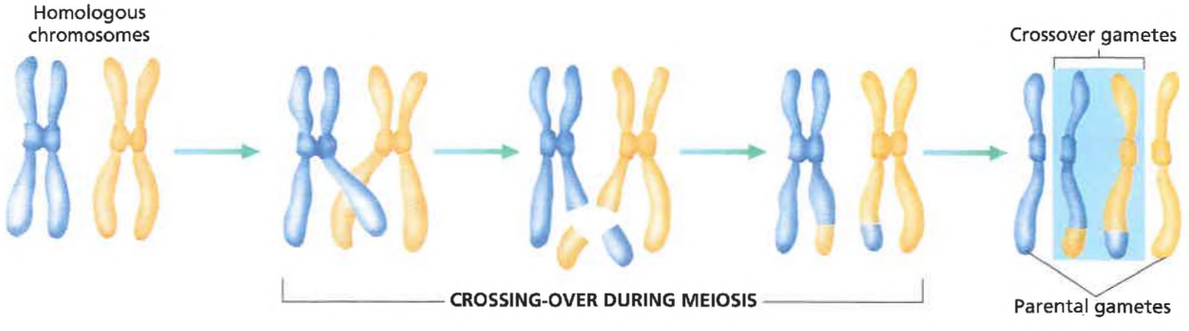
different chromosomes, they should assort independently and produce an F_2 generation with a phenotypic ratio of 9:3:3:1. Morgan predicted that if the alleles were on the same chromosome, however, an F_2 generation with a phenotypic ratio of 3 gray, long-winged flies: 1 black, short-winged fly would result. The results of the cross closely approximated this 3:1 ratio. Morgan hypothesized that the genes for body color and wing length are linked, as shown in Figure 12-3a.

Unexpectedly, the cross also produced several gray, short-winged (*Ggll*) flies and several black, long-winged flies (*ggLl*). If the genes for body color and wing length were indeed on the same chromosome, how could they be separated? Morgan realized that these results could have occurred only if the alleles had somehow changed or become rearranged. Mutations could have caused the changes, but mutations usually only occur in one individual out of tens of thousands. The alleles must therefore have become rearranged. Morgan inferred that this rearrangement had taken place through crossing-over. Recall from Chapter 8 that crossing-over is the exchange of pieces of DNA between homologous chromosomes. Figure 12-3b shows how crossing-over accounts for the unexpected phenotypes in the F_2 generation of Morgan's experiment.

Crossing-over does not create new genes or delete old ones. Instead, it changes the locations of genes among the chromosomes that carry them, thus producing new gene combinations, as shown in Figure 12-4.

FIGURE 12-4

When traits do not appear according to the expected ratio in offspring, crossing-over may have occurred. Parental gametes contain alleles on the same chromosome that have been inherited together. Crossover gametes contain new combinations of alleles that are not found in the parental gametes.



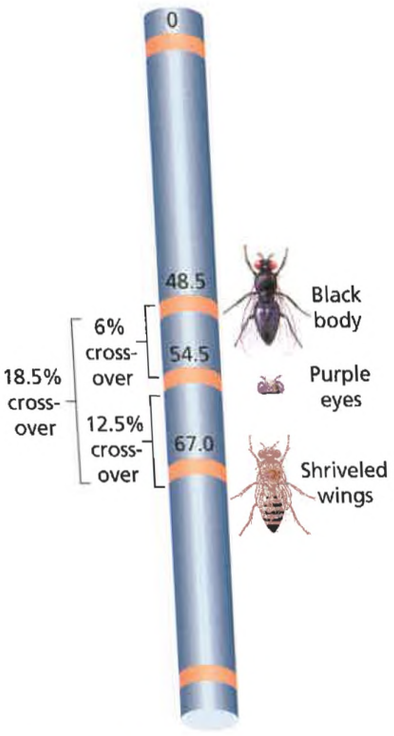


FIGURE 12-5

The genes for black body and purple eyes are separated by crossing-over 6 percent of the time, while the genes for purple eyes and shriveled wings are separated by crossing-over 12.5 percent of the time. The genes for black body and shriveled wings are separated by crossing-over 18.5 percent of the time.

CHROMOSOME MAPPING

The likelihood that crossing-over will result in the separation of two genes depends on the genes' distance from each other on the chromosome. The farther apart two genes are, the likelier they are to be separated by crossovers. The results of crossing-over appear in the offspring as new combinations of traits. The greater the percentage of offspring that show the new combination of traits, the farther apart the two genes are located on a chromosome.

Scientists can conduct breeding experiments to determine how frequently genes for particular traits are separated from one another among the offspring. This information can be used to prepare chromosome maps. A **chromosome map** is a diagram that shows the linear sequence of genes on a chromosome. Alfred H. Sturtevant, one of Morgan's students, used crossing-over data to construct a chromosome map of *Drosophila*.

To construct his chromosome map, Sturtevant compared the frequency of crossing-over for several genes. The percentage of crossing-over between the genes for two traits is proportional to the distance between them on a chromosome. For example, two genes that are separated by crossing-over 1 percent of the time are considered to be one **map unit** apart. Figure 12-5 illustrates how crossover percentages can be used to determine the positions of the genes for black body, purple eyes, and shriveled wings in *Drosophila*.

In recent years, new techniques of gene mapping have been developed. These techniques have helped to map the chromosomes of many species, even those with many chromosomes and tens of thousands of genes.

MUTATION

As you learned in Chapter 10, a change in the DNA of an organism is called a mutation. Mutations can involve an entire chromosome or a single DNA nucleotide, and they may take place in any cell. **Germ-cell mutations** occur in an organism's germ cells (gametes). Germ-cell mutations do not affect the organism itself, but they may be passed on to offspring if the affected gamete is fertilized. **Somatic** (soh-MAT-ik) **mutations** take place in an organism's body cells and can therefore affect the organism. Certain types of human skin cancer and leukemia result from somatic mutations. Somatic mutations are not passed on to offspring.

Lethal mutations cause death, often before birth. However, some mutations result in phenotypes that are beneficial. Organisms with beneficial mutations have a better chance of reproducing and therefore have an evolutionary advantage. Such mutations provide the variation upon which natural selection acts.

Word Roots and Origins

somatic

from the Greek *sōmatikos*, meaning "body"

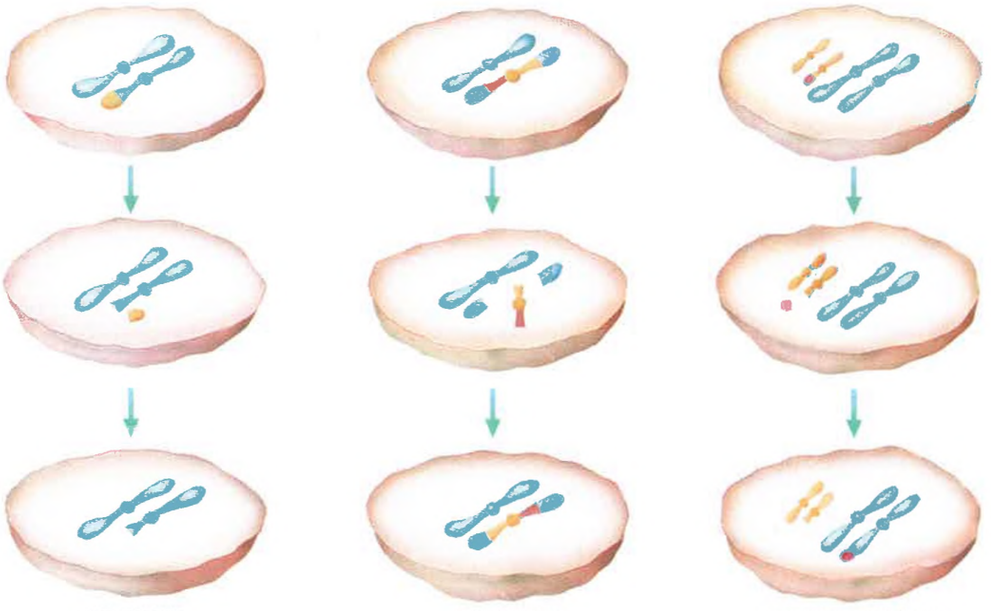


FIGURE 12-6

In many chromosome mutations, a piece of chromosome breaks off. The piece may be lost or may reattach in a reversed position. In translocations, a broken piece attaches to a nonhomologous chromosome.

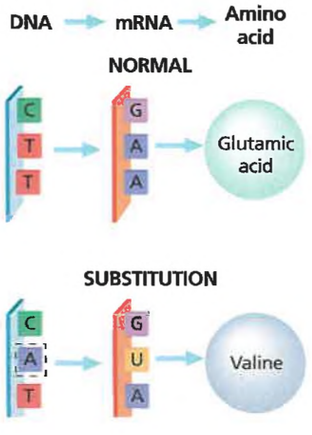
Chromosome Mutations

Chromosome mutations are either changes in the structure of a chromosome or the loss of an entire chromosome. A **deletion** is the loss of a piece of a chromosome due to chromosomal breakage. As a consequence, all of the information carried by the missing piece may be lost. An **inversion** is a chromosome mutation in which a chromosomal segment breaks off and then reattaches in reverse orientation to the same chromosome. A chromosome mutation in which a chromosome piece breaks off and reattaches to another, nonhomologous chromosome is a **translocation.** Figure 12-6 shows these mutations.

Some types of chromosomal mutations alter the number of chromosomes found in the cell. **Nondisjunction** (NON-dis-JUHNK-shuhn) is the failure of a chromosome to separate from its homologue during meiosis. When nondisjunction occurs, one gamete receives an extra copy of a chromosome and the other gamete lacks the chromosome entirely. Human disorders resulting from nondisjunction are discussed in Section 12-2.

FIGURE 12-7

In a substitution, one nucleotide replaces another, forming a new codon that may signal the insertion of the wrong amino acid.



Gene Mutations

Gene mutation may involve large segments of DNA or a single nucleotide within a codon. As you will recall from Chapter 10, a codon consists of three nucleotides that cause a specific amino acid to be inserted into a polypeptide during protein synthesis. The substitution, addition, or removal of a single nucleotide is called a **point mutation.**

In point mutations called **substitutions,** one nucleotide in a codon is replaced with a different nucleotide, resulting in a new codon. An example of a substitution mutation is shown in Figure 12-7. If the new codon codes for the same amino acid as the original codon, the

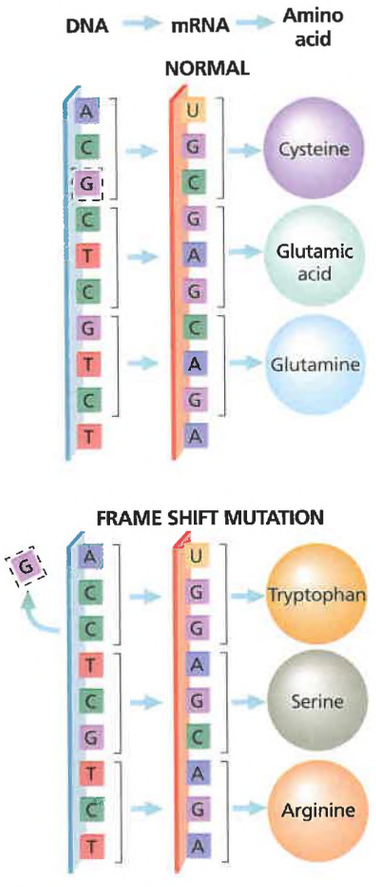


FIGURE 12-8

Deleting a nucleotide causes all subsequent codons to be incorrectly read, resulting in a frame shift mutation. Adding a nucleotide will have the same effect.

substitution will have no effect. However, if the new codon is a "stop" codon or if it codes for a different amino acid, the resulting protein will be affected.

The genetic disorder **sickle cell anemia** (also called sickle cell disease) is caused by a point mutation that substitutes adenine for thymine in a single DNA codon, as shown in Figure 12-7. This substitution results in a defective form of the protein hemoglobin. Hemoglobin is found within red blood cells, where it binds with oxygen and transports it throughout the body. The red blood cells of people with two copies of the mutant allele for sickle cell anemia have a distorted, sickle shape, causing anemia (loss of red blood cells) and circulatory problems. Because of this, children with sickle cell anemia may suffer damage to the brain, heart, lungs, and many other organs and tissues. The sickle cell allele is especially widespread among African Americans. In the United States, approximately 1 out every 500 African Americans has sickle cell anemia.

Individuals who are heterozygous for the sickle cell allele make both normal and altered forms of hemoglobin and are generally healthy. In the United States, approximately 1 out of 10 African Americans is heterozygous for the sickle-cell allele and is therefore a carrier for sickle cell anemia. A simple blood test can reveal the presence of the allele.

Two forms of point mutations are nucleotide insertions and nucleotide deletions. In nucleotide deletion mutations, one or more nucleotides in a gene are lost. In insertion mutations, one or more nucleotides are added to a gene. Deletion and insertion mutations tend to have more serious effects than substitution mutations. Because each codon consists of a group of three sequential nucleotides, the addition or deletion of a single nucleotide causes the remaining codons to be incorrectly grouped, resulting in a **frame shift mutation,** as shown in Figure 12-8. In fact, frame shift mutations occur anytime the number of nucleotides inserted or deleted is not a multiple of three. Figure 12-8 shows a frame shift mutation that results from the deletion of one nucleotide. Thus, a frame shift mutation occurring near the beginning of a gene will prevent a number of codons from coding for the proper amino acids.

SECTION 12-1 REVIEW

1. How does the inheritance of sex chromosomes result in approximately equal numbers of males and females among the offspring of fruit flies?
2. Offer an explanation for why Morgan did not find white-eyed female *Drosophila* in the F_2 generation when he crossed white-eyed males with red-eyed females.
3. How does crossing-over show that genes are found on chromosomes?
4. How can crossing-over between two alleles be used to map their locations on chromosomes?
5. What are point mutations?
6. **CRITICAL THINKING** Biologists have observed that chromosome mutations often occur during nuclear division. Why do you think this is so? Explain your answer.

SECTION 12-2

HUMAN GENETICS

Biologists have studied many different organisms in their search to discover the fundamental principles of genetics. These fundamental principles also apply to humans. Much of what we have discovered about the inheritance of traits has been learned in the study of human genetics.

OBJECTIVES

- Show how pedigree analysis can be used to illustrate the inheritance of traits.
- Explain the inheritance of ABO blood groups.
- Give examples of traits or disorders transmitted by autosomal dominant, autosomal recessive, polygenic, and X-linked recessive inheritance.
- Compare sex-linked traits with sex-influenced traits.
- Explain how nondisjunction can cause human genetic disorders.

STUDYING HUMAN INHERITANCE

Patterns of inheritance are significantly more complicated to study among humans than among *Drosophila.* Humans have up to 20 times as many genes as *Drosophila,* and our 23 pairs of chromosomes are made up of about 100,000 genes. Geneticists have often focused on studying disease-causing genes because such genes are easily traced from one generation to the next and because they are of great concern to the human population.

Pedigree Analysis

Biologists discover how traits are inherited by studying phenotypes among members of the same species from one generation to the next. In particular, they often study members of the same family. In such studies, geneticists often prepare a **pedigree,** a family record that shows how a trait is inherited over several generations. Figure 12-9 shows a pedigree illustrating a trait that is inherited as

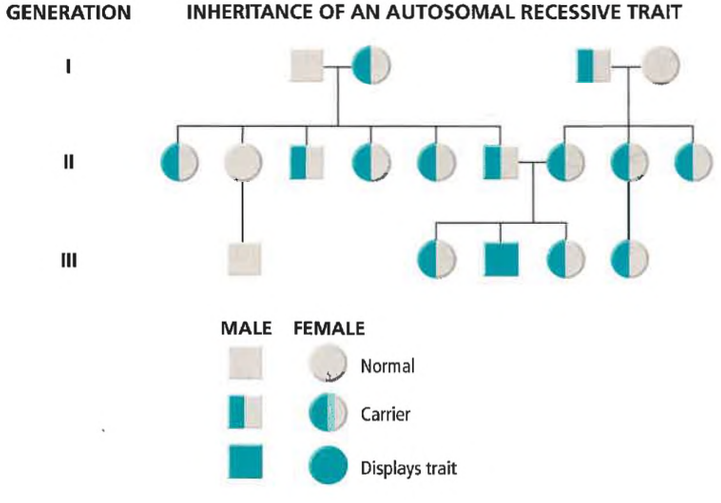


FIGURE 12-9
This pedigree shows the inheritance of an autosomal recessive trait. Pedigrees are particularly important if the trait is a genetic disorder and family members wish to know if they are carriers or if their children will have the disorder.

a recessive autosomal trait. When analyzing pedigrees, biologists find that certain phenotypes are usually repeated in predictable patterns from one generation to the next. These patterns are called **patterns of inheritance.** Individuals who have one copy of a recessive autosomal allele are called **carriers.** Carriers usually do not express the recessive allele, but they can pass it along to their offspring.

GENETIC TRAITS AND DISORDERS

Genes controlling human traits exhibit several patterns of inheritance. Some of these genes have been subjects of intense scientific interest because they cause genetic disorders. **Genetic disorders** are diseases or debilitating conditions that have a genetic basis. Table 12-1 lists several patterns of inheritance and examples of traits or disorders for each.

TABLE 12-1
Patterns of Inheritance for Several Human Traits

Single Allele (Dominant)
Huntington's disease (HD)
Achondroplasia (dwarfism)
Cataracts
Polydactyly (extra fingers or toes)
Single Allele (Recessive)
Albinism
Cystic fibrosis
Phenylketonuria (PKU)
Hereditary deafness
X-Linked
Colorblindness
Hemophilia
Muscular dystrophy
Icthyosis simplex (scaly skin)
Polygenic
Skin, hair, and eye color
Foot size
Nose length
Height
Multiple Alleles
ABO blood groups

Traits Controlled by a Single Allele

Single-allele traits are controlled by a single allele of a gene. Geneticists have discovered that more than 200 human traits are governed by a single dominant allele. **Huntington's disease (HD)** is caused by a dominant allele located on an autosome and is therefore said to show an autosomal-dominant pattern of inheritance. The first symptoms of HD—mild forgetfulness and irritability—appear in victims in their thirties or forties. In time, HD causes loss of muscle control, uncontrollable physical spasms, severe mental illness, and eventually death. Unfortunately, most people who have the HD allele do not know they have the disease until after they have had children. Thus, the disease is unknowingly passed on from one generation to the next.

Recently, however, scientists have discovered a genetic marker for the HD allele. A **genetic marker** is a short section of DNA that is known to have a close association with a particular gene located nearby. Thus, the presence of a genetic marker in a DNA sample is a strong indicator that a particular allele (in this case, the allele for HD) is also present. People who have the genetic marker for the HD allele have a 96 percent chance of developing HD. By conducting a test on sample cells, geneticists are now able to inform a person of the presence of the marker before he or she becomes a parent.

More than 250 other single-allele traits are controlled by homozygous recessive alleles. Cystic fibrosis (CF) and sickle cell anemia are examples of single-allele recessive traits. Single-allele recessive traits are fully expressed only when the individual has two copies of the recessive allele and is thus homozygous recessive. Because cystic fibrosis and sickle cell anemia are caused by recessive alleles located on autosomes, they are said to show an autosomal-recessive pattern of inheritance.

Traits Controlled by Multiple Alleles

Multiple-allele traits are controlled by three or more alleles of the same gene that code for a single trait. In humans, the ABO blood groups are controlled by the three alleles I^A, I^B, and i. Each individual's ABO blood group genotype consists of two of these alleles, which determine his or her ABO blood type. The alleles I^A and I^B are codominant (both are expressed when together), and both are dominant to the i allele. Table 12-2 shows the possible ABO blood group genotypes and the ABO blood types they produce.

TABLE 12-2
ABO Blood Types

Genotype	Blood type
I^AI^A	A
I^Ai	A
I^BI^B	B
I^Bi	B
I^AI^B	AB
ii	O

Polygenic Traits

Although some human traits are governed by a single gene, most human characteristics are controlled by several genes. A trait that is controlled by two or more genes is called a **polygenic** (PAHL-ee-JEHN-ik) **trait.** Skin color, for example, is influenced by the additive effects of three to six genes. Each gene results in a certain amount of a brownish black pigment called melanin. The more melanin produced, the darker the skin; the less melanin produced, the lighter the skin. Eye color is also a polygenic trait. Light-blue eyes have very little melanin. Very dark brown eyes have a great deal of melanin. Polygenic traits show many degrees of variation.

It is important to note that the expression of many traits, particularly those that are governed by many genes, is influenced by the environment. For example, human height is a polygenic trait controlled by an unknown number of genes that play a role in determining the growth of the skeleton. However, height is also influenced by environmental factors, such as nutrition and disease.

X-Linked Traits

Colorblindness is a recessive X-linked disorder in which an individual cannot distinguish between certain colors. Recall that genes for X-linked traits are found only on the X chromosome. Although many forms of colorblindness exist, the most common is the inability to distinguish red from green. About 8 percent of males are colorblind.

Hemophilia (HEE-moh-FIL-ee-uh) is another recessive X-linked disease that occurs almost exclusively in males. This disorder impairs the ability of the blood to clot following a cut, bruise, or other injury. Another recessive X-linked trait in humans is **Duchenne muscular dystrophy** (DIS-troh-fee), a form of muscular dystrophy that weakens and progressively destroys muscle tissue. These and several other important genetic disorders are described in Table 12-3 on the following page.

Not all or even most X-linked traits are diseases. There are hundreds of genes on the X chromosome, but only a few are associated with diseases. The others code for proteins that perform many normally needed functions in the body.

Sex-Influenced Traits

The presence of male or female sex hormones influences the expression of certain human traits, called **sex-influenced traits.** In

Quick Lab

Modeling Linkage

Materials two kinds of candy, toothpicks, pencil, paper

Procedure Use two kinds of candy to represent genes for two traits. Long noses are dominant over short noses. Large ears are dominant over small ears. One color of candy will represent the dominant allele, and a different color candy will represent the recessive allele. Use these materials to determine the outcome of a cross between two individuals, each heterozygous for both traits. Your teacher will tell you if the genes are linked or not linked.

1. Draw a large Punnett square on your paper. Use the appropriate alleles to make gametes for each individual. Then place the allele combinations in each square representing the possible zygotes from that cross.
2. If your team is working with genes that are linked, you must first use toothpicks to link the genes together before you arrange the gametes on your Punnett square.

Analysis What is the offspring's phenotypic ratio when the genes are not linked? What is the phenotypic ratio when the genes are linked? Explain the difference.

TABLE 12-3 *Some Important Genetic Disorders*

Disorder	Symptom	Defect	Pattern of inheritance	Frequency among human births
Huntington's disease	gradual deterioration of brain tissue in middle age; shortened life expectancy	production of an inhibitor of brain cell metabolism	autosomal dominant	1/10,000
Cystic fibrosis	mucus clogs lungs, liver, and pancreas; victims usually don't survive to adulthood	failure of chloride ion transport mechanism	autosomal recessive	1/2,080 (whites)
Sickle cell anemia	impaired blood circulation, organ damage	abnormal hemoglobin molecules	autosomal recessive	1/500 (African Americans)
Tay-Sachs disease	deterioration of central nervous system in infancy; death occurs in early childhood	defective form of enzyme hexosaminidase A	autosomal recessive	1/1,600 (Jews of European descent)
Phenylketonuria	failure of brain to develop in infancy; if untreated, causes death in childhood	defective form of enzyme phenylalanine hydroxylase	autosomal recessive	1/18,000
Hemophilia	failure of blood to clot	defective form of blood-clotting factor	X-linked recessive	1/7,000
Muscular dystrophy	wasting away of muscles; shortened life expectancy	muscle fibers degenerate	X-linked recessive	1/10,000

a sex-influenced trait, males and females have different phenotypes, even when they share the same genotype. For example, pattern baldness is controlled by the allele *B*, which is dominant in males but recessive in females. Both men and women who are homozygous (*BB*) will eventually lose their hair. The allele *B´* codes for the normal, nonbald phenotype. A heterozygous (*BB´*) woman will not lose her hair, but a heterozygous (*BB´*) man will. These differences in gene expression are due to higher levels of the male sex hormone testosterone in men, which interacts with the genotype *BB´* to produce baldness in men. The alleles that code for most sex-influenced traits are located on the autosomes. Therefore, males and females can have the same genotype, but the sex-influenced trait will be expressed in only one sex.

Disorders Due to Nondisjunction

Nondisjunction occurring during meiosis can cause gametes to lack a chromosome or to have an extra chromosome, as shown in Figure 12-10. If nondisjunction occurs during egg formation in humans, one egg will have 22 chromosomes instead of the normal 23 ($1n$) chromosomes. Another egg will have 24 chromosomes. If one of these eggs combines with a normal sperm, the resulting zygote will have either 45 or 47 chromosomes instead of the normal 46 ($2n$) chromosomes. A zygote with 45 chromosomes has only one copy of a particular chromosome, a condition called **monosomy** (MAHN-uh-SOH-mee). A zygote with 47 chromosomes has three copies of a particular chromosome, a condition called **trisomy** (trie-SOH-mee).

Such abnormalities in chromosomal number are often lethal. However, some instances of monosomy or trisomy allow development to proceed. An extra chromosome 21 results in **Down syndrome** (also called **trisomy-21**), which includes mild to severe mental retardation, characteristic facial features, muscle weakness, heart defects, and short stature.

Nondisjunction can also affect the sex chromosomes. Males with an extra X chromosome have Klinefelter's syndrome (XXY). These persons have some feminine characteristics and are sometimes mentally retarded and infertile. Individuals who have a single X chromosome instead of a pair of sex chromosomes have Turner's syndrome (XO, the O meaning that there is only one sex chromosome). People with Turner's syndrome have a female appearance, but they do not mature sexually and they remain infertile. Zygotes that receive only a single Y chromosome do not survive because the X chromosome contains information that is essential for development.

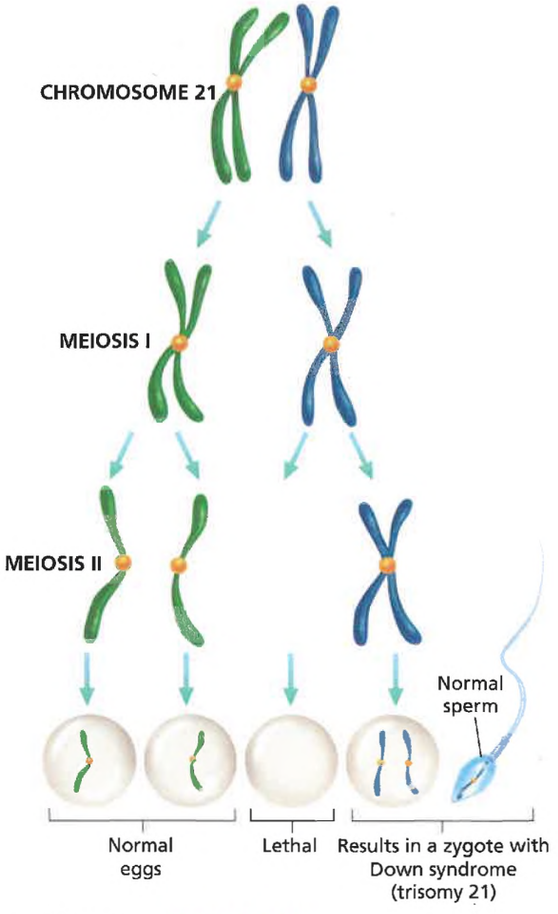


FIGURE 12-10

Nondisjunction can cause abnormalities in chromosome number. Normal gametes have one copy of each chromosome. Down syndrome can result when a gamete (an egg, in the example shown here) containing two copies of chromosome 21 is fertilized by a normal sperm.

DETECTING HUMAN GENETIC DISORDERS

A person with a family history of genetic disorders may wish to undergo **genetic screening** before becoming a parent. Genetic screening is an examination of a person's genetic makeup. It may involve constructing a karyotype, a picture of an individual's chromosomes grouped in pairs and arranged in sequence. Other techniques test an individual's blood for the presence or absence of certain proteins. These procedures can detect potential genetic disorders that might be passed on to children. Couples at risk may wish to undergo **genetic counseling,** a form of medical guidance that informs them about problems that could affect their offspring.

Word Roots and Origins

monosomy

from the Greek *mono,* meaning "one," and *soma,* meaning "body" or "chromosome"

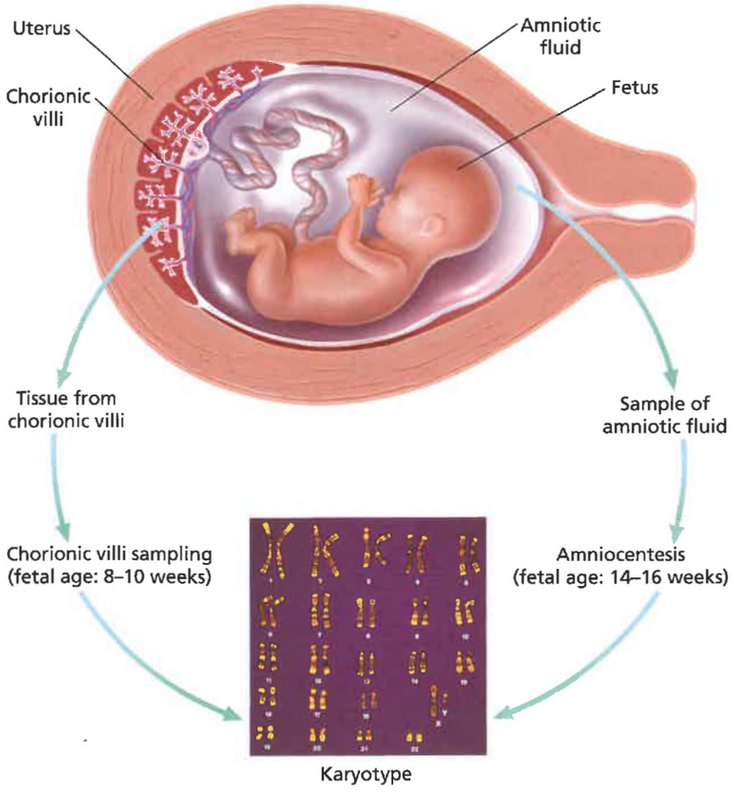


FIGURE 12-11

Fetal cells obtained by amniocentesis or chorionic villi sampling can be used to prepare fetal karyotypes, enabling physicians to diagnose chromosomal abnormalities before a child's birth.

Physicians can also diagnose more than 200 genetic disorders in the fetus using a variety of tools and techniques. Figure 12-11 shows amniocentesis and chorionic villi sampling, two forms of prenatal (before birth) testing that can reveal fetal abnormalities. During **amniocentesis** (AM-nee-OH-sen-TEE-sis) the physician removes a small amount of amniotic fluid from the amnion, the sac that surrounds the fetus, between the fourteenth and sixteenth weeks of pregnancy. Fetal cells and proteins from the fluid then can be analyzed and a karyotype can also be prepared. During **chorionic** (KOR-ee-ON-ik) **villi** (VIL-IE) **sampling** the physician obtains a sample of the chorionic villi, a tissue that grows between the mother's uterus and the placenta, between the eighth and tenth week of pregnancy. The villi have the same genetic makeup as the fetus because they were both coded for by fetal DNA. Tissue samples from the villi can be used to produce a karyotype.

In some cases, genetic screening is performed immediately after birth. In the United States, approximately 1 out of every 10,000 babies is afflicted with **phenylketonuria** (FEN-uhl-KEET-oh-NUHR-ee-uh), or **PKU**, a genetic disorder in which the body cannot metabolize the amino acid phenylalanine. The accumulation of excess phenylalanine causes severe brain damage. PKU can be detected by means of a blood test administered to infants during the first few days of life. The dangers of PKU can be eliminated by placing these infants on a special diet that lacks phenylalanine.

SECTION 12-2 REVIEW

1. A husband and wife are heterozygous for cystic fibrosis. Their son has cystic fibrosis. Their second child, a daughter, does not. Prepare a pedigree for this family.
2. A husband and wife have the ABO blood group genotypes I^AI^B and *ii*. What ABO blood types can their children have?
3. Compare the inheritance of Huntington's disease with the inheritance of sickle cell anemia.
4. Is pattern baldness a sex-linked trait or a sex-influenced trait? Explain your answer.
5. How can nondisjunction change chromosome number?
6. **CRITICAL THINKING** Colorblindness is rare among females. Why? Explain your answer.

CHAPTER 12 REVIEW

SUMMARY/VOCABULARY

12-1

- Sex chromosomes determine the sex of an organism.
- A sex-linked gene is found on one sex chromosome but not on the other. Genes found on the X chromosome are X-linked genes. Genes found on the Y chromosome are Y-linked genes.
- The genes found on one chromosome make up a linkage group. The genes found on a chromosome are said to be linked.
- Linked genes can be separated by crossing-over. The percentage of crossing-over between two genes is directly proportional to the distance between them.
- The frequency of crossing-over between genes can be used to construct a chromosome map.
- Crossing-over creates new combinations of genes and therefore serves as a source of genetic variation.
- Germ-cell mutations occur in gametes and can be passed on to offspring. Somatic mutations occur in body cells and affect only the individual organism.
- Chromosome mutations are changes in the structure of a chromosome or the loss of an entire chromosome. Gene mutations are changes in one or more of the nucleotides in a gene.

Vocabulary

chromosome map (224)
deletion (225)
frame shift mutation (226)
germ-cell mutation (224)
inversion (225)
lethal mutation (224)
linkage group (222)
map unit (224)
nondisjunction (225)
point mutation (225)
sex linkage (222)
sickle cell anemia (226)
somatic mutation (224)
substitution (225)
translocation (225)
X-linked gene (222)
Y-linked gene (222)

12-2

- A pedigree is a family record that shows how a trait is inherited over several generations.
- Single-allele traits are controlled by a single allele of a gene. Multiple-allele traits are controlled by three or more alleles of a gene.
- Polygenic traits are controlled by two or more different genes.
- The genes for X-linked human traits, such as colorblindness, Duchenne muscular dystrophy, and hemophilia, are found on the X chromosome.
- A sex-influenced trait is expressed differently in men than it is in women, even when individuals have the same genotype.
- Nondisjunction during meiosis can cause gametes to have one too few or one too many chromosomes. If such a gamete is fertilized, a genetic disorder such as monosomy ($2n$=45) or trisomy ($2n$=47) can occur.
- Genetic screening examines a person's genetic makeup and can identify people at risk of passing on genetic disorders to their children. Genetic counseling informs these individuals about problems that could affect their prospective offspring.
- A karyotype can be used to reveal chromosomal abnormalities.
- Amniocentesis and chorionic villi sampling enable physicians to test a fetus for the presence of genetic disorders.

Vocabulary

amniocentesis (232)
carrier (228)
chorionic villi sampling (232)
colorblindness (229)
Down syndrome (231)
Duchenne muscular dystrophy (229)
genetic counseling (231)
genetic disorder (228)
genetic marker (228)
genetic screening (231)
hemophilia (229)
Huntington's disease (HD) (228)
monosomy (231)
multiple-allele trait (229)
pattern of inheritance (228)
pedigree (227)
phenylketonuria (PKU) (232)
polygenic trait (229)
sex-influenced trait (229)
single-allele trait (228)
trisomy (231)
trisomy-21 (231)

REVIEW

Vocabulary

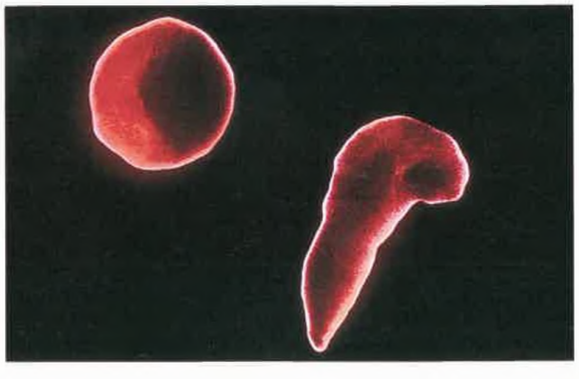
1. Distinguish between germ-cell mutations and somatic mutations.
2. Define the term *nondisjunction.*
3. Distinguish between multiple-allele traits and polygenic traits.
4. Describe the difference between a sex-linked trait and a sex-influenced trait.
5. Distinguish between amniocentesis and chorionic villi sampling.

Multiple Choice

6. If a heterozygous red-eyed female *Drosophila* is crossed with a red-eyed male *Drosophila,* (a) half the male offspring will be red-eyed and half will be white-eyed (b) three-fourths of the male offspring will be red-eyed and one-fourth will be white-eyed (c) all the offspring will be red-eyed (d) one-fourth of the male offspring will be red-eyed and three-fourths will be white-eyed.
7. A chromosomal map shows (a) whether a gene is autosomal or recessive (b) the positions of genes along a chromosome (c) the presence of mutant alleles (d) the sex of the individual.
8. The deletion of a single nucleotide results in (a) nondisjunction (b) monosomy (c) a frame shift mutation (d) a translocation.
9. Geneticists can use pedigrees to determine (a) environmental effects on trait expression (b) whether someone could be a carrier for a genetic disorder (c) the frequency of a gene in a population (d) the position of a gene on a chromosome.
10. A geneticist working with *Drosophila* discovers a mutant phenotype that appears only in males who are offspring of males showing the same phenotype. This information suggests that the mutant phenotype is (a) autosomal dominant (b) autosomal recessive (c) X-linked (d) Y-linked.
11. A man and a woman have the same genotype for a particular trait, yet only one of them expresses that trait. This evidence suggests that the trait is (a) sex-linked (b) polygenic (c) sex-influenced (d) multiple-allele.
12. Klinefelter's syndrome is an example of (a) monosomy (b) trisomy (c) a point mutation (d) translocation.
13. A karyotype can reveal (a) chromosomal abnormalities (b) blood type (c) point mutations (d) carriers for recessive traits.
14. Testing for phenylketonuria (PKU) enables physicians to (a) recognize abnormalities in chromosome number (b) prescribe a special diet (c) correct fetal defects before birth (d) determine the sex of a fetus.
15. The greatest amount of phenotypic variation is seen in (a) polygenic traits (b) single-allele traits (c) multiple-allele traits (d) sex-linked traits.

Short Answer

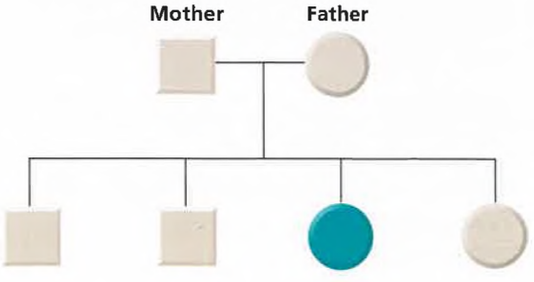
16. What evidence led Morgan to hypothesize that the gene for eye color in *Drosophila* is carried on the X chromosome?
17. Why is hemophilia carried by females but expressed in males and rarely in females?
18. What is a linkage group? How many linkage groups do humans have?
19. How does a chromosome mutation differ from a point mutation?
20. What is the pattern of inheritance of Huntington's disease?
21. What is a genetic marker?
22. List the possible genotypes for a person whose ABO blood group is type A.
23. The photograph below shows red blood cells taken from an individual. Notice that one of the red blood cells is bent, while the other one is normal. Does this person have sickle-cell anemia? What is this person's genotype with respect to sickle cell anemia?



24. Explain how you would distinguish the karyotype of a normal human male from that of a human male with Down syndrome.
25. Describe how the karyotype of an XXY human would differ from that of an XO human.

CRITICAL THINKING

1. In *Drosophila* the genes for body color and wing length are on the same chromosome. Gray body (*G*) is dominant to black body (*g*), and long wings (*L*) are dominant to short wings (*l*). Assume that both dominant alleles are on the same chromosome. Draw a Punnett square representing the cross *GgLl* × *GgLl*. Write the phenotypic and genotypic ratios that would be expected among the offspring, assuming that crossing-over does not occur.
2. Individuals who are heterozygous for sickle cell anemia generally have no symptoms of the disease. However, they should avoid extreme conditions that severely reduce the amount of oxygen available to the body, such as playing vigorous sports at high elevations. Explain why this would be advisable.
3. The karyotypes of some Down syndrome individuals show that they have 46 chromosomes. However, close examination of these karyotypes reveals that three copies of chromosome 21 are indeed present in these individuals. Explain how a translocation can account for this rare form of Down syndrome.
4. A 20-year-old man diagnosed with muscular dystrophy has a sister who is soon to be married. If you were the man, what would you tell your sister?
5. The individual shown in green in the pedigree below is afflicted with a genetic disorder. State the pattern of inheritance for the disorder and whether the disorder is autosomal or sex-linked. Explain your answer.



6. What advice might a genetic counselor give to the unaffected brother and sisters shown in the pedigree in question 5?

EXTENSION

1. Read "Chromosomes Show Plants' Secret Complexity" in *Science News,* December 18, 1999, on page 389. Explain why the mustard plant *Arabidopsis thaliana* is a favorite laboratory plant of geneticists.
2. Read "High Risk Defenses" in *Natural History,* February 1999, on page 40. Explain what Pythagoras meant when he said, "Do not eat broad beans!" Describe how the mutant gene for cystic fibrosis is a protection against typhoid fever.
3. Biologists have long been interested in studying the inheritance of traits in twins, particularly identical twins who have been raised apart. Do library or on-line research, and prepare a report on the study of twins in genetics.
4. Do library or on-line research, and prepare a report on the history of the use of *Drosophila* in genetic studies. Conclude your report with a list of the advantages of using *Drosophila.*

CHAPTER 12

INTERACTIVE EXPLORATION

Meiosis: Down Syndrome

OBJECTIVES

- Compare the events of a normal meiotic division with those resulting in Down syndrome.
- Determine the relationship between parental age and the likelihood that an offspring will have Down syndrome.

MATERIALS

- computer with CD-ROM drive
- CD-ROM *Interactive Explorations in Biology: Cell Biology and Genetics*
- graph paper

Background

This interactive exploration allows you to learn about the cause of Down syndrome, an inherited condition that results in mental retardation, short stature, stubby hands and feet, and a characteristic heavy eyefold. This condition is a consequence of nondisjunction, or the failure of chromosomes to separate normally during meiosis. In this exploration, you will have the opportunity to examine how the age of each parent affects the events of meiosis.

Prelab Preparation

1. Load and start the program "Meiosis: Down Syndrome." You will see an animated diagram like the one below. Click the Navigation button, and then click the Topic Information button. Read the focus questions, and review the concepts of ploidy, meiosis, aneuploidy, and nondisjunction.
2. Now click the word *Help* at the top left of the screen, and select How to Use This Exploration. Listen to the instructions for operating the exploration. Click the Interactive Exploration button on the Navigation Palette to begin the exploration.

FEEDBACK METERS

Incidence of Down Syndrome: *displays the frequency of Down syndrome births for the combination of parents chosen*

VARIABLES

Age of Mother: *allows you to set the mother's age*

Age of Father: *allows you to set the father's age*

Procedure

PART A Normal Meiosis

1. Click the Normal button to observe a simulation of normal meiosis. For simplicity, this animation shows only two pairs of chromosomes.
2. Click the Detail button. Then click the Forward button (the one with the right-facing arrow) to progress through the eight steps of a normal meiotic division. As you view each step, read the caption and study the illustration.
3. Click the Close button.
4. Click the Start button to observe the same meiotic events in continuous motion. How many gametes formed after meiosis was completed?

PART B Nondisjunction

5. Click the Nondisjunction button.
6. Click the Detail button. Then click the Forward button to observe nondisjunction. As you view each step, read the caption and study the illustration. What differences between normal meiosis and nondisjunction do you observe in frame 4?
7. Click the Close button.
8. Click the Start button to observe nondisjunction in continuous motion.

PART C Effect of the Father's Age

Make a table like Table A shown below.

TABLE A *EFFECT OF THE FATHER'S AGE*

Age of father	Incidence of Down syndrome
25	
30	
35	
40	
45	
50	

9. Click and slide the left-hand indicator so that the age of the mother is 25.
10. Click and slide the other indicator so that the age of the father is 25.
11. Click the Plot Point button. In your table, record the probability that these parents will have a child with Down syndrome, shown by the meter labeled "Incidence of Down Syndrome per 1000 Live Births."
12. Repeat steps 10–11 five times, each time increasing the age of the father by five years. Make a graph of the age of the father versus the incidence of Down syndrome. What can you conclude about the effect of the father's age on the likelihood of having a child with Down syndrome?

PART D Effect of the Mother's Age

Make a table like Table B shown below.

TABLE B *EFFECT OF THE MOTHER'S AGE*

Age of mother	Incidence of Down syndrome
25	
30	
35	
40	
45	
50	

13. Click the Reset Graph button.
14. Click and slide the indicator so that the age of the father is 25.
15. Click and slide the indicator so that the age of the mother is 25.
16. Click the Plot Point button. In your table, record the incidence of Down syndrome per 1,000 live births.
17. Repeat steps 15–16 five times, each time increasing the age of the mother by five years. Be sure to record the incidence of Down syndrome for each age. Make a graph of the mother's age versus the incidence of Down syndrome. What can you conclude about the effect of the mother's age on the likelihood of having a child with Down syndrome?

Analysis and Conclusions

1. In step 12, why did you hold the mother's age constant while varying the father's age?
2. In the United States, the age at which women have their first child has been increasing. How might this affect the incidence of Down syndrome?

CHAPTER 13

DNA TECHNOLOGY

The alteration of a gene that controls ripening gives these genetically engineered tomatoes a better taste and a longer shelf life than other commercially grown tomatoes.

FOCUS CONCEPT: ***Reproduction and Inheritance***

As you read, notice the ways that scientists are endowing organisms with traits that they did not inherit naturally by changing the organisms' genes.

BIOLOGY INTERACTIVE TUTOR

Unit 6—*Gene Expression*
Topics 1–6

SECTION 13-1

THE NEW GENETICS

An understanding of the molecular basis of inheritance has led to a new form of applied genetics called genetic engineering. ***Genetic engineering*** *is the application of molecular genetics for practical purposes. Genetic engineering can be used to identify genes for specific traits or to transfer genes for a specific trait from one organism to another organism.*

OBJECTIVES

- Define *genetic engineering.*
- Explain how restriction enzymes can be used to make recombinant DNA.
- Explain how cloning vectors can be used to clone and transfer genes.
- List the steps in a gene-transfer experiment.

MANIPULATING GENES

The technology involved in genetic engineering is called **DNA technology.** DNA technology can be used to cure diseases, to treat genetic disorders, to improve food crops, and to do many other things that may improve the lives of humans. Before you can understand DNA technology, you should understand restriction enzymes and cloning vectors, which genetic engineers use to manipulate genes.

Restriction Enzymes

Recall that a DNA molecule is a long sequence of nucleotides. Genetic engineers use certain bacterial enzymes—called **restriction enzymes**—to cut DNA molecules into more manageable pieces. As Figure 13-1 shows, restriction enzymes recognize

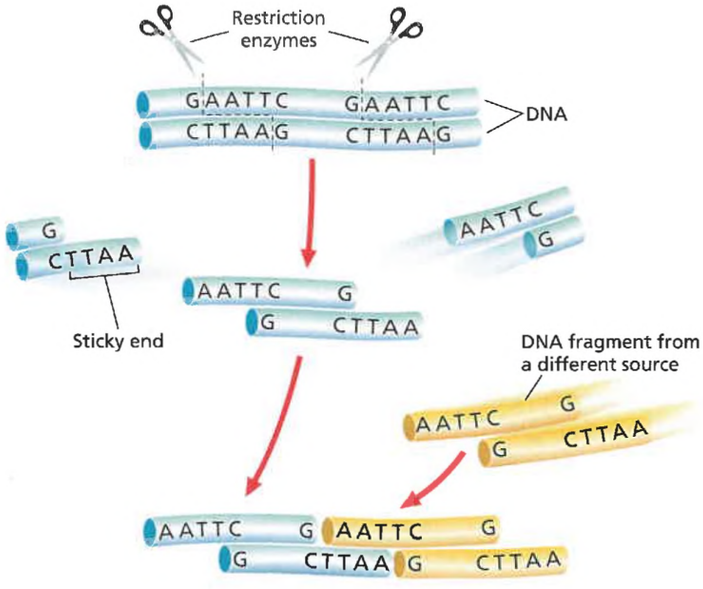


FIGURE 13-1
The restriction enzyme represented by the scissors in this figure recognizes the sequence CTTAAG on each chain of DNA. Then it cuts each chain between the A nucleotide and the G nucleotide, producing DNA fragments with sticky ends.

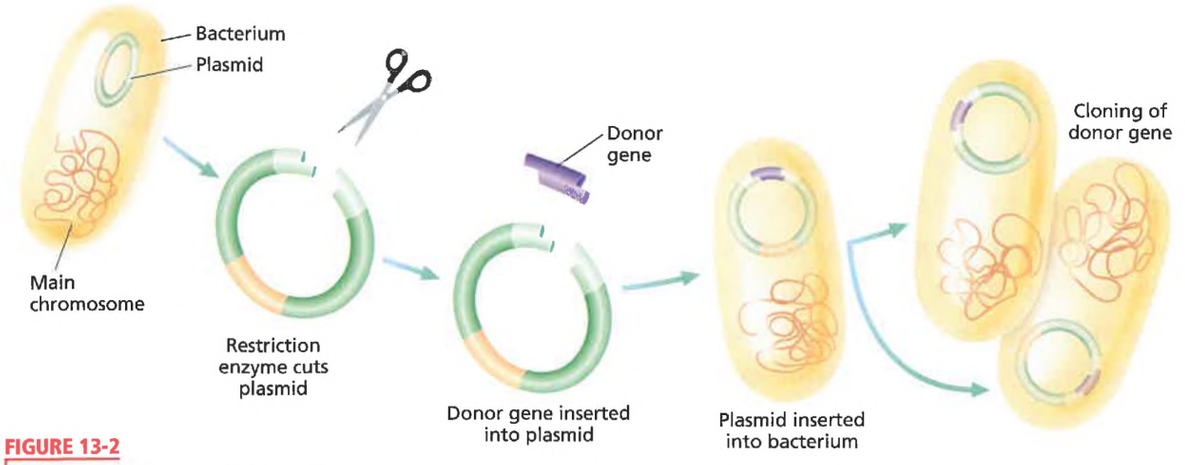
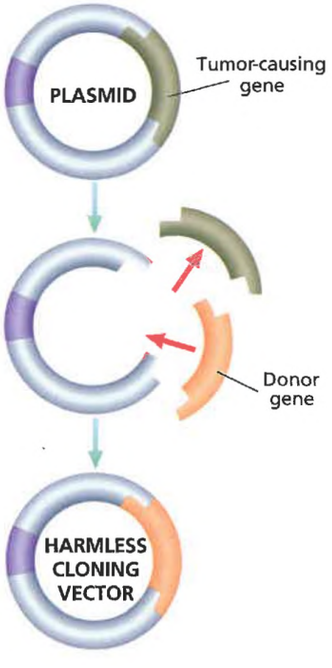


FIGURE 13-2

A donor gene from another organism can be spliced into a plasmid. The plasmid containing the donor gene is then placed inside a bacterium. As the bacterium divides, clones of the donor gene are made.

FIGURE 13-3

The tumor-causing gene in this plasmid can be replaced with a donor gene. When the harmless plasmid containing the donor gene is placed in bacteria, it can be used to transfer new genes into plants.



specific sequences of nucleotides. Then they cut the DNA at a specific site within the sequence.

The restriction enzyme shown in Figure 13-1 recognizes the nucleotide sequence CTTAAG on both chains of DNA. In one chain, the sequence runs from left to right; on the complementary chain, the sequence runs from right to left. The restriction enzyme cuts each chain separately between the G nucleotides and the A nucleotides. In this way, single-chain "tails" of DNA, called **sticky ends,** are created on each DNA segment cut by the restriction enzyme. Sticky ends readily bind to complementary chains of DNA. Thus, pieces of DNA that have been cut with the same restriction enzyme can bind together to form a new sequence of nucleotides.

Cloning Vectors

Restriction enzymes can be used to isolate a specific gene. Once a gene has been isolated, it can be transferred by a cloning vector to an organism. A **cloning vector** is a carrier that is used to clone a gene and transfer it from one organism to another. Many bacteria contain a cloning vector called a plasmid. A **plasmid** is a ring of DNA found in a bacterium in addition to its main chromosome.

To be used as a cloning vector in gene-transfer experiments, a plasmid is isolated from a bacterium, as shown in Figure 13-2. Using restriction enzymes, the plasmid is then cut and a **donor gene**—a specific gene isolated from another organism—is spliced into it. Then the plasmid is returned to the bacterium, where it is replicated as the bacterium divides, making copies of the donor gene. Once many copies of the donor gene have been made, plasmids with the donor gene can be isolated from bacteria. Each plasmid now contains a **gene clone,** an exact copy of a gene. One example of a cloning vector, shown in Figure 13-3, is a plasmid that carries a gene that causes tumors in some plants. This plasmid can be modified to no longer cause tumors by replacing the tumor-causing gene with a donor gene. The modified plasmid can be used to transfer the donor gene into plants by infecting the plants with bacteria that carry the plasmid.

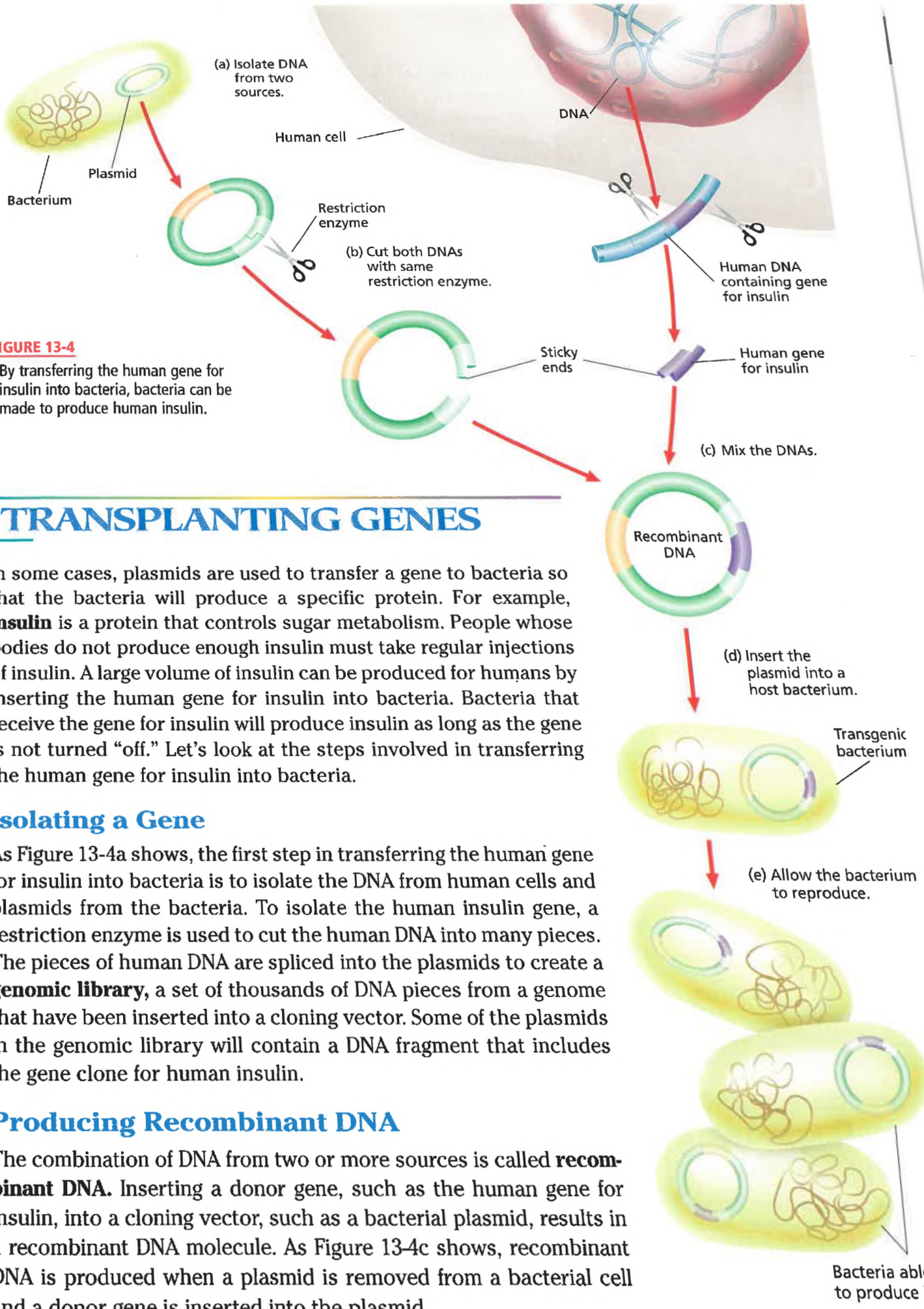


FIGURE 13-4
By transferring the human gene for insulin into bacteria, bacteria can be made to produce human insulin.

TRANSPLANTING GENES

In some cases, plasmids are used to transfer a gene to bacteria so that the bacteria will produce a specific protein. For example, **insulin** is a protein that controls sugar metabolism. People whose bodies do not produce enough insulin must take regular injections of insulin. A large volume of insulin can be produced for humans by inserting the human gene for insulin into bacteria. Bacteria that receive the gene for insulin will produce insulin as long as the gene is not turned "off." Let's look at the steps involved in transferring the human gene for insulin into bacteria.

Isolating a Gene

As Figure 13-4a shows, the first step in transferring the human gene for insulin into bacteria is to isolate the DNA from human cells and plasmids from the bacteria. To isolate the human insulin gene, a restriction enzyme is used to cut the human DNA into many pieces. The pieces of human DNA are spliced into the plasmids to create a **genomic library,** a set of thousands of DNA pieces from a genome that have been inserted into a cloning vector. Some of the plasmids in the genomic library will contain a DNA fragment that includes the gene clone for human insulin.

Producing Recombinant DNA

The combination of DNA from two or more sources is called **recombinant DNA.** Inserting a donor gene, such as the human gene for insulin, into a cloning vector, such as a bacterial plasmid, results in a recombinant DNA molecule. As Figure 13-4c shows, recombinant DNA is produced when a plasmid is removed from a bacterial cell and a donor gene is inserted into the plasmid.

Cloning DNA

The plasmid containing recombinant DNA is inserted into a host bacterium. A host organism receiving recombinant DNA is called a **transgenic organism.** In this case, the transgenic organism is a bacterium containing both bacterial DNA and human DNA.

The transgenic bacterium is placed in a nutrient medium where it can grow and reproduce, as illustrated in Figure 13-4e. Within each bacterium, the plasmid is copied many times, making clones of the gene for insulin. Thousands of bacteria are produced very quickly through cell division, resulting in thousands of bacteria that carry the gene for insulin. The transgenic bacteria can then be used to produce large amounts of insulin.

EXPRESSION OF CLONED GENES

Once a donor gene, such as the human gene for insulin, is transferred to a host cell, it is transcribed and translated as though it were in its own cell. However, not all of the genes in a cell's genome are expressed. Genes are often turned off until the proteins they code for are needed. As you can imagine, it can be difficult to induce host cells to express foreign genes. One way to induce a prokaryotic host cell to express a foreign gene is to also transfer the sequences (promoters) that turn on the foreign gene. In another method, genetic engineers insert a donor gene into prokaryotes beside a gene that is normally produced in large quantities within a cell. That way, the donor gene is expressed along with the host cell's frequently expressed gene.

An obstacle in the expression of eukaryotic genes in prokaryotic hosts is the difference in gene processing. As you know, eukaryotic DNA contains noncoding sequences that are not found in prokaryotic DNA. In order for a prokaryotic cell to receive a functional donor gene, only the coding sequences should be inserted into the host prokaryotic cell. Otherwise, the prokaryotic cell will not remove the noncoding sequences of the gene and the protein will not be produced. Thus, successful gene-transfer experiments require extensive knowledge of the processes required to express genes in different types of cells.

SECTION 13-1 REVIEW

1. Define *genetic engineering.*
2. What role do restriction enzymes play in genetic engineering?
3. How do sticky ends function?
4. Explain the role of cloning vectors in genetic engineering.
5. What steps are used to produce insulin using recombinant DNA and bacteria?
6. **CRITICAL THINKING** List three ways that genetic engineering could be used to improve the lives of humans.

SECTION 13-2

DNA TECHNOLOGY TECHNIQUES

In Section 13-1, you learned about some of the tools and procedures genetic engineers use to manipulate genes and transplant them into other organisms. In this section, you will learn about some of the techniques used to analyze the nucleotide sequence of an individual's DNA.

OBJECTIVES

- Explain what a DNA fingerprint is and how it is prepared.
- Distinguish between the following laboratory techniques: RFLP analysis, gel electrophoresis, and polymerase chain reaction.
- Describe the purpose of the Human Genome Project and the potential uses of the information collected in the project.
- Explain how gene therapy may be used in humans.

DNA FINGERPRINTS

A **DNA fingerprint** is a pattern of bands made up of specific fragments from an individual's DNA. The banding patterns of DNA fragments from two different individuals may be compared to establish whether they are related. The DNA fingerprints of members of two different species can also be compared to determine how closely the species are related. Using DNA fingerprints to compare samples of blood or tissue found at a crime scene with a suspect's blood sample may even help solve a crime. The fragments of DNA in a DNA fingerprint appear as fuzzy bands of stain arranged in columns, like those shown in Figure 13-5.

FIGURE 13-5
If you look carefully at the DNA fingerprints that this researcher is examining, you will see many columns of bands. The pattern of bands in each column can be analyzed to establish whether two individuals are related.

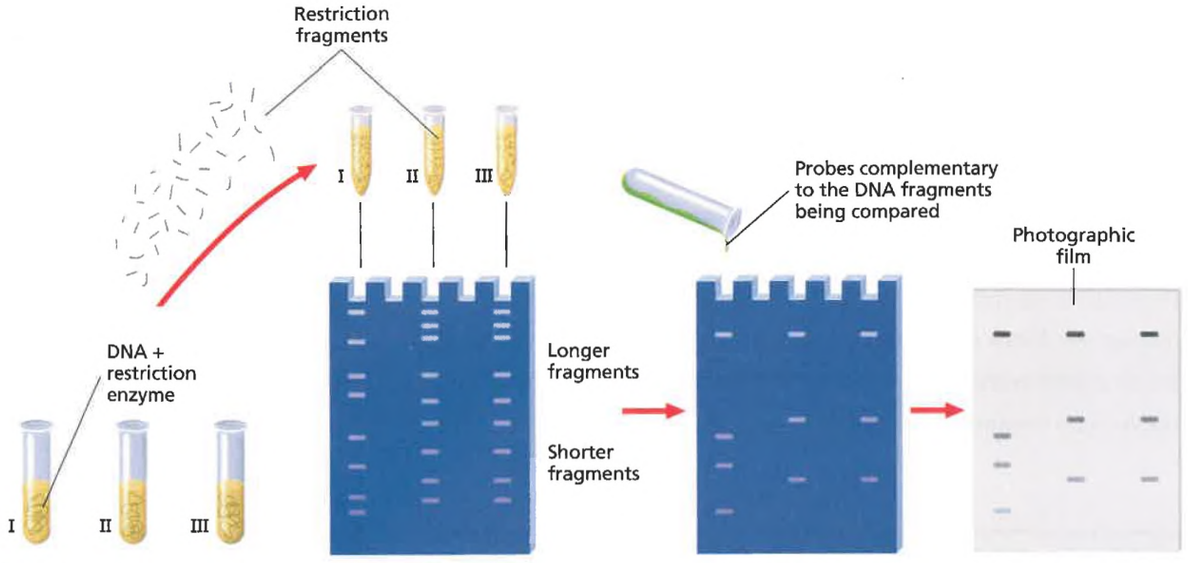


FIGURE 13-6

(a) To make a DNA fingerprint, the DNA sample is first cut into many fragments by restriction enzymes. (b) The DNA fragments are then separated according to their size by gel electrophoresis. (c) Radioactive probes then bind to DNA fragments that have been selected for comparison. (d) Photographic film allows visualization of the radioactive probes that are bound to the DNA fragments, producing a DNA fingerprint.

Making a DNA Fingerprint

The method for preparing a DNA fingerprint is called restriction fragment length polymorphism (RFLP) analysis. **RFLP analysis** involves extracting DNA from a specimen of blood or other tissue and cutting it into fragments using restriction enzymes, as shown in 13-6a. The number of fragments and the length of each fragment vary from person to person.

The fragments of DNA are then separated using a technique called **gel electrophoresis.** Gel electrophoresis separates nucleic acids or proteins, primarily according to their size and charge. To make a DNA fingerprint, samples of the DNA being compared are placed in wells made on the gel, as shown in Figure 13-6b. An electric current is then run through the gel for a given period of time. The DNA fragments, which are negatively charged, migrate toward the positively charged end of the gel, but not all at the same rate. The pores in the gel allow smaller DNA fragments to migrate faster—and thus farther across the gel—than longer fragments, separating the fragments by size.

The final step in preparing a DNA fingerprint is making visible only the bands that are being compared. The DNA fragments that have been separated on the gel are split into single chains and blotted onto filter paper. Then **probes**—radioactive segments of DNA that are complementary to the segments being compared—are added to the filter paper. The probes bind to complementary fragments of DNA in the samples, forming visible bands when they are exposed to photographic film, as shown in Figure 13-6c. The exposed film is developed to reveal a DNA fingerprint. The bands can then be analyzed visually or by a computer.

Word Roots and Origins

electrophoresis

from the Latin *electrocus,* meaning "electricity," and the Greek *phoresis,* meaning "to carry"

Accuracy of DNA Fingerprints

The accuracy of DNA fingerprints depends on how unique the prints are. The complete nucleotide sequence of each individual is certainly unique for each person, except in the case of identical twins, who share identical DNA. However, complete sets of DNA are not compared in DNA fingerprints. The DNA technology in use today deals only with a small portion of a person's DNA. Nevertheless, DNA fingerprints are very accurate because they compare segments of DNA that tend to vary the most from person to person. The segments of DNA that vary the most are noncoding segments where the DNA repeats over and over. These repeated patterns are found throughout the genome.

A repeating pattern might consist of the bases GGAT on one chain, matched by the complementary sequence CCTA on the other chain. DNA fingerprinting typically compares the repeat patterns at five different sites. It is highly unlikely—less than one chance in a million—that all five sites compared in DNA fingerprints will match exactly between two people who are not identical twins. The odds against a match occurring through sheer chance multiply as more sites are compared.

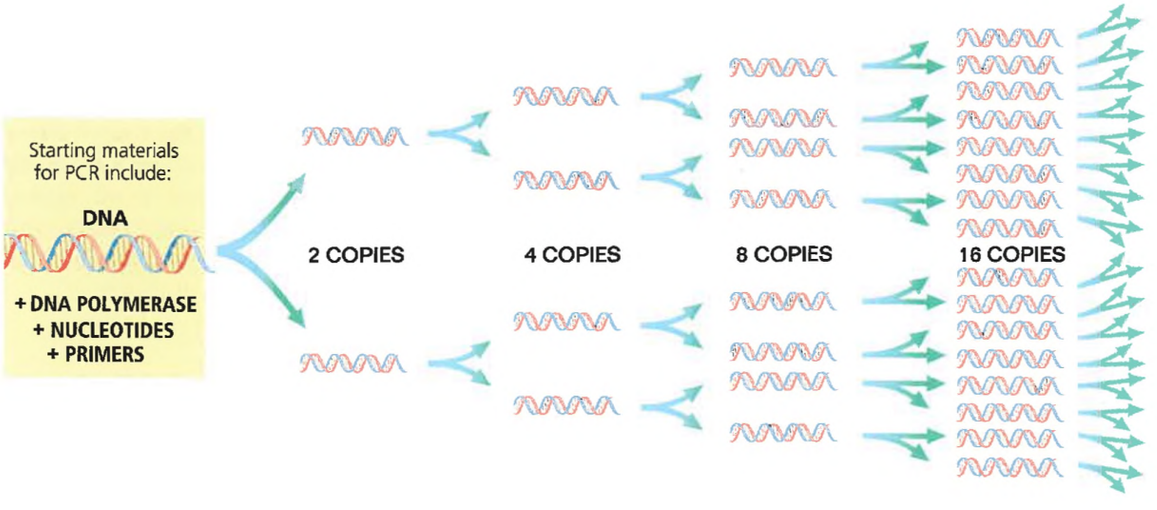
Polymerase Chain Reaction

To make a DNA fingerprint, a certain amount of DNA is needed. If only a very tiny amount of DNA is available, the **polymerase chain reaction (PCR)** can be used to quickly make many copies of selected segments of the available DNA.

Notice in Figure 13-7 that PCR requires a DNA molecule or a fragment of DNA, a supply of the four DNA nucleotides, DNA polymerase (the enzyme involved in DNA replication), and primers. A **primer** is an artificially made single-stranded sequence of DNA required for the initiation of replication. When these ingredients are combined and incubated, the selected regions of DNA quickly

FIGURE 13-7

The polymerase chain reaction (PCR) can be used to multiply selected regions of DNA in a sample. Notice that the number of copies of the selected regions of DNA doubles with each cycle of the reaction.



Quick Lab

Comparing Unique Characteristics

Materials ink pad, paper, pencil, scissors

Procedure

1. Cut four 3 in. squares of plain paper.
2. Draw lines on a full-sized sheet of paper that will divide that sheet into four equal squares.
3. Each team member will press his or her right thumb on the ink pad and then will quickly press the inked thumb in a square on the large sheet of paper and again on one of the small squares of paper.
4. Examine each of the thumbprints, and make a list of characteristics that the prints have in common. Describe how each thumbprint is different from the others. Then shuffle the four individual thumbprints, and try to match each one with its duplicate on the large sheet of paper.

Analysis What characteristics are common to all thumbprints? What characteristics made each thumbprint unique? How do a person's fingerprints relate to his or her DNA fingerprints?

double. Every five minutes, the sample of DNA doubles again, resulting in many copies of the sample in a short amount of time, as shown in Figure 13-7.

The new copies of the DNA sample can then be used to make a DNA fingerprint. PCR can use minuscule amounts of a specimen, as few as 50 white blood cells that might be found in a nearly invisible speck of blood, rather than the 5,000 to 50,000 cells needed for RFLP analysis. PCR is important not only for solving violent crimes but also for diagnosing genetic disorders from a few embryonic cells and for studying ancient fragments of DNA found in minute amounts.

HUMAN GENOME PROJECT

Using DNA technology, scientists all over the world are collaborating on one of the most ambitious research efforts in the history of genetics, the **Human Genome Project.** Two of the goals of the Human Genome Project are to determine the nucleotide sequence of the entire human genome—approximately 3 billion nucleotide pairs, or about 100,000 genes—and to map the location of every gene on each chromosome. In addition, the human genome is being compared with the genomes of other organisms in an effort to provide insight into fundamental questions about how genomes are organized, how gene expression is controlled, how cellular growth and differentiation are under genetic control, and how evolution occurs.

This project began in 1990. In 1996, the project had analyzed 1 percent of the 3 billion nucleotide pairs of DNA in the human genome. By knowing even 1 percent of the sequence, it is possible for scientists to establish the identity of and determine the function of about 16,000 genes. Genome research continues internationally at universities, laboratories, scientific institutions, and private companies.

It is hoped that the knowledge gained from the Human Genome Project will improve diagnoses, treatments, and even cures for the approximately 4,000 human genetic disorders. Scientists have already discovered specific genes responsible for several genetic disorders, including cystic fibrosis, Duchenne muscular dystrophy, and colon cancer. As many as 5 percent of the babies born in the United States each year are afflicted with a genetic disorder that could one day be treated or prevented using the information provided by the Human Genome Project. Identifying these genes and the defective proteins for which they code may make it possible to design therapies aimed at correcting the gene defects responsible for genetic disorders.

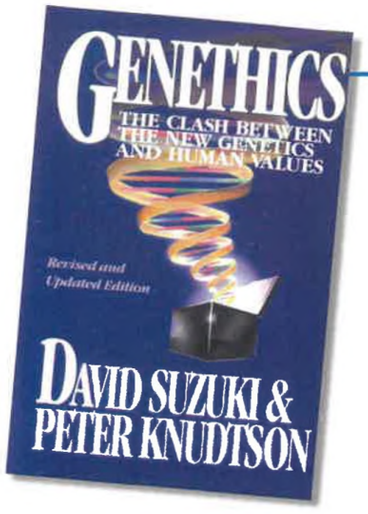
Gene Therapy

Treating a genetic disorder by introducing a gene into a cell or by correcting a gene defect in a cell's genome is called **gene therapy.** In 1990, doctors first began to develop and test gene therapies on

Literature & Life

Recombinant-DNA Technology

This excerpt is from *Genethics: The Clash Between the New Genetics and Human Values,* by David Suzuki and Peter Knudtson.



Already recombinant DNA technology, along with rapid DNA sequencing and other related laboratory techniques, has begun to offer profound new insights into the workings of genes. First, it has helped to establish the virtual universality of both the genetic code and the graceful molecular dances of genes in nature. Second, it has revolutionized the study of genes of multicellular organisms, including humans, that have long been inaccessible. In so doing, it has led to dramatic discoveries concerning the structure and function of genes in complex plants and animals. One such discovery is that their coded instructions for assembling amino acids into proteins—called *exons*—are often interspersed with long intervening segments of DNA—called *introns*—of largely unknown function. Introns are neatly removed from nuclear RNA molecules prior to protein synthesis. A second discovery is that the comparison of DNA sequences in different species can often serve as a faint chronological record of otherwise hidden evolutionary relationships. Third, recombinant DNA technology has already led to the complete chemical characterization of a number of relatively small viral genomes and has initiated that process in more complex species, including our own. Finally, by facilitating the exchange of genetic components between cells of different species, it has exploded the boundaries of comparative genetics. We are now just beginning to grasp the evolutionary ingenuity with which the genes of different species—however interchangeable their codes—are variously packaged, punctuated and controlled.

But the rewards from recombinant DNA technology will be practical as well as intellectual. Genetic engineering holds great promise in agriculture—for modifying the productivity, growth requirements and nutrition of food crops. In medicine, it is opening up new vistas in the design of vaccines, in the diagnosis of disease and in genetic counseling, and even the possibility of new genetic therapies for ancient hereditary diseases. In the biotechnology industry, it already has established its value in the manufacture of antibiotics, hormones and an assortment of other biologically active substances.

For the first time, we find that we can command individual genes to do our bidding. In the future, we will forever be faced with the temptation to harness our knowledge of hereditary processes long before we have resolved the possible long-term consequences of our applications. If history is any guide, we can expect no shortage of ingenious schemes to reap rewards from our genetic engineering skills. But each of us has a responsibility to ensure that equal imagination is devoted to the search for ways to apply this knowledge wisely and to share its fruits with all humankind.

Reading for Meaning

Suzuki and Knudtson point out some general applications for genetic engineering. List possible uses that you think would benefit humankind. What might be advantages and disadvantages of each item on your list?

Read Further

Suzuki and Knudtson's book, *Genethics,* raises concerns about modern technology's amazing techniques for manipulating genes and how those techniques will be used. When and for what purposes do you think we should perform such genetic engineering?

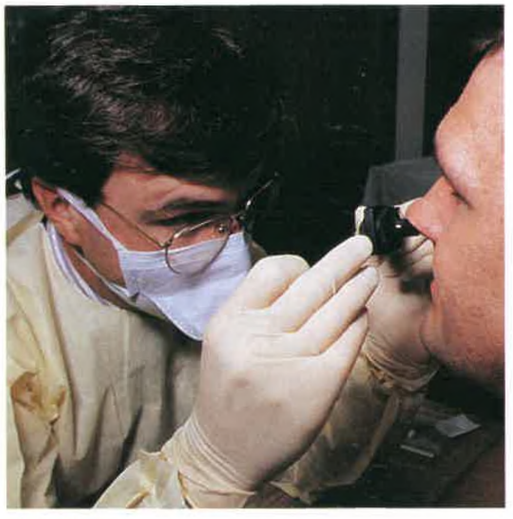


FIGURE 13-8

This patient is receiving gene therapy for cystic fibrosis. Dr. Terrence Flotte (left), of the University of Florida College of Medicine, administers healthy copies of the gene responsible for cystic fibrosis through the patient's nose.

humans. Gene therapy is well suited for treating genetic disorders that result from a deficiency of a single enzyme or protein. As you learned in Chapter 11, the genetic disorder cystic fibrosis is caused by one defective gene, resulting in the malfunction of a single protein. Some success has been reported with nasal sprays that carry a normal cystic fibrosis gene to the cells in the nose and lungs—cells that are particularly affected by a defective cystic fibrosis protein. Figure 13-8 shows the gene-therapy procedure that has been used with some cystic fibrosis patients. The treatment has to be repeated periodically because the cystic fibrosis gene is not inserted on a chromosome but rather in the nucleus of cells; thus, it is not passed on to future generations. Gene-therapy possibilities for hemophilia B, lung cancer, AIDS, ovarian cancer, brain tumors, malignant melanoma, and several other terminal diseases are also under way. Until the obstacles regarding how and where to insert genes safely and directly into eukaryotic chromosomes are overcome, gene therapy may offer only limited and temporary success as a treatment. But researchers hope to overcome these obstacles and to one day provide permanent cures for genetic disorders using gene therapy.

Ethical Issues

The Human Genome Project is producing much information about human susceptibility to disease. However, a genetic susceptibility to a disease does not ensure that the person will get the disease. Nor does such a gene indicate the severity of the disease, should it occur, or how the person would respond to treatment. Many people worry about how personal genetic information will be used. Some think this type of information could be used by insurance companies and employers to discriminate against individuals who are genetically susceptible to a disease. For example, an insurance company may decide to deny insurance to people who are predisposed to diseases that are expensive to treat. The information provided by the Human Genome Project will undoubtedly involve ethical decisions about how society should use the information.

SECTION 13-2 REVIEW

1. Define *DNA fingerprint,* and discuss the accuracy of using DNA fingerprints to establish relatedness.
2. Describe the major steps and techniques involved in preparing a DNA fingerprint.
3. Compare the polymerase chain reaction and DNA replication.
4. Describe the purpose of the Human Genome Project, and name the potential uses of the information collected in the project.
5. What is gene therapy, and how does it differ from traditional treatments for diseases?
6. **CRITICAL THINKING** What genetic disorders not discussed in this chapter might be treated using DNA technology?

SECTION 13-3

PRACTICAL USES OF DNA TECHNOLOGY

The production of insulin by inserting the human gene for insulin into bacteria is one commercial use of DNA technology. DNA technology can also be used to produce prescription drugs and vaccines and to improve food crops.

OBJECTIVES

- Explain how DNA technology can be used to produce medical products.
- Describe some ways that DNA technology can be used to improve crop yields and the food supply.
- Discuss some environmental and ethical issues in genetic engineering.

PRODUCING PHARMACEUTICAL PRODUCTS

Many medicines are proteins. In the past, these proteins were derived from animal tissues or plants. Today, some proteins can be produced far more inexpensively using DNA technology. Insulin is one of the many products now produced through DNA technology. Table 13-1 lists several other pharmaceutical products produced in this way. As in the production of insulin, these pharmaceutical products can be produced in bulk by bacteria. Just as yeast are fermented in large vats in the production of beer, bacteria can be grown in large vats to produce specific proteins.

TABLE 13-1 *Medicines Produced by DNA Technology*

Product	Medical uses
Colony-stimulating factors	used to treat immune-system deficiencies by stimulating the production of white blood cells
Erythropoietin	used to treat anemia by stimulating the production of red blood cells
Growth factors	used to promote the healing of wounds by stimulating growth and differentiation of different types of cells
Human growth hormone	used as a treatment for dwarfism
Interferons	used to treat viral infections and some cancers by preventing the replication of viruses
Interleukins	used to treat a variety of conditions, including HIV infections, cancer, and immune deficiencies, by activating and stimulating different kinds of white blood cells
Tissue plasminogen activator	used to prevent heart attacks and strokes by dissolving blood clots
Atrial peptides	used to treat high blood pressure and kidney failure

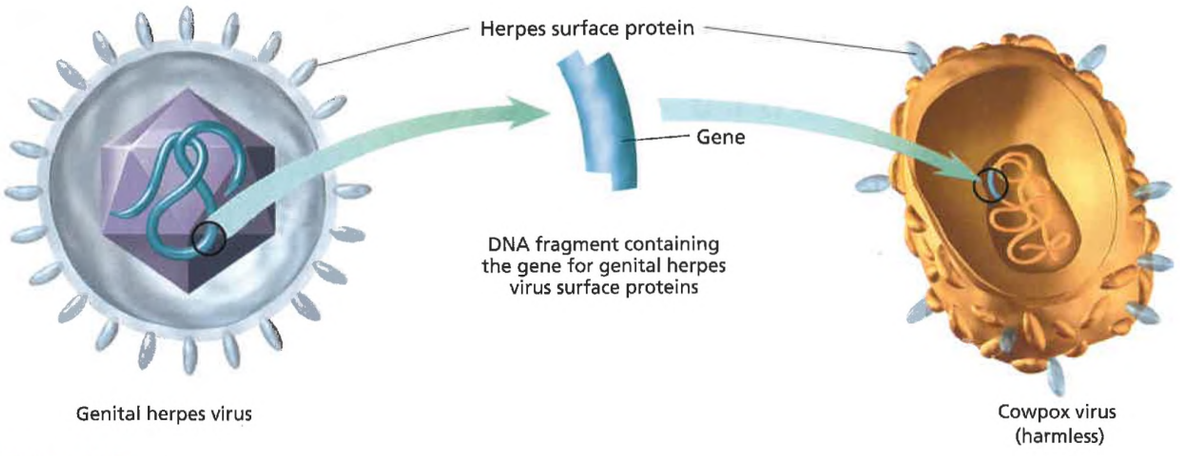


FIGURE 13-9

The gene that codes for the surface proteins of the genital herpes virus can be transferred to a cowpox virus—a virus that is harmless to humans—to produce a vaccine against genital herpes. The cowpox virus then produces the surface proteins characteristic of the genital herpes virus. A person receiving the vaccine will be protected against genital herpes virus infections in the future.

GENETICALLY ENGINEERED VACCINES

Many viral diseases, such as AIDS, smallpox, and polio, cannot be treated effectively by existing drugs. Instead, many viral diseases are combated by prevention, using vaccines. A **vaccine** is a solution that contains a harmless version of a virus or a bacterium. Traditionally, vaccines have been made of disease-causing agents—also called **pathogens**—that have been treated (chemically or physically) so that they can no longer cause disease. Vaccines can also be produced using active pathogens that carry surface proteins that are the same as or very similar to a more-harmful virus. When a person receives a vaccine, his or her body recognizes the pathogen's surface proteins and mobilizes against the pathogen. In the future, if the same pathogen enters the body, the body is prepared to combat it quickly and to prevent or weaken the pathogen's effects.

Usually, a person who receives a vaccine does not become ill. However, on rare occasions a vaccine may cause the disease it is intended to protect people against. DNA technology can be used to produce effective vaccines, which may be safer than some traditionally prepared vaccines. As Figure 13-9 shows, the genes for a disease-causing virus's surface proteins can be inserted into a harmless virus. The transplanted genes cause the harmless virus to produce the surface proteins that alert the body to the presence of the disease-causing virus. DNA technology can also be used to alter the genome of a pathogen so that it no longer causes a disease. The altered pathogens can then be used as a vaccine against unaltered forms of the pathogen.

Word Roots and Origins

pathogen

from the Greek *pathos,* meaning "suffering"

INCREASING AGRICULTURAL YIELDS

DNA technology has been used to develop new strains of plants, which in turn can be used to improve food crop yields. By transferring genes for enzymes that are harmful to hornworms into tomato plants, scientists can make tomato plants toxic to hornworms and effectively protect the plants from these pests, which otherwise could seriously damage them. Figure 13-10 shows a hornworm on a tomato plant that is not toxic to hornworms.

The crop cassava, used to make tapioca pudding and other food products, is highly susceptible to pests and diseases, which often cost farmers up to 80 percent of a cassava crop. Using DNA technology, scientists have made cassava plants resistant to some diseases. In addition, strains of wheat, cotton, and soybeans that are resistant to weed-controlling chemicals—called **herbicides**—have been developed. Such herbicide-resistant crops can be protected from weeds more easily and less expensively than crops that are susceptible to the herbicides.

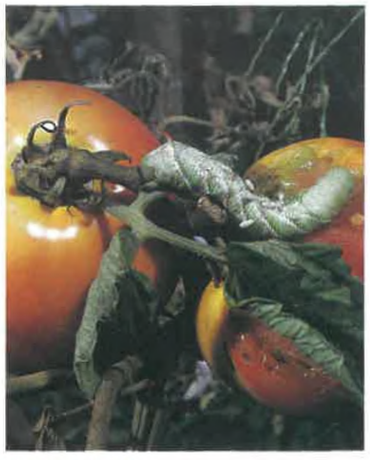


FIGURE 13-10

Tomato hornworms, like the member of *Manduca quinque maculata* shown here, feed on the leaves and fruits of tomatoes and other related plants. A large hornworm is capable of stripping a tomato plant of its foilage.

Crops That Do Not Need Fertilizer

To make proteins and nucleic acids, all plants require the element nitrogen, N. Although nitrogen is the most abundant element found in the atmosphere, it is in a form that plants are unable to use. Some plants, such as soybeans and peanuts, have bacteria living in their roots that convert, or "fix," nitrogen in the atmosphere into forms of nitrogen that plants can use. Other types of plants take up nitrogen directly from the soil.

To help crops grow, farmers apply expensive nitrogen fertilizers to the soil. Currently, researchers are working to isolate and clone genes from nitrogen-fixing bacteria and transplant the genes into plants. It is hoped that transgenic food crops containing genes for nitrogen fixation will be able to grow in nitrogen-poor soil, where crops often are grown only after the soil has been treated with nitrogen fertilizers.

internetconnect

SCILINKS NSTA

TOPIC: Herbicides
GO TO: www.scilinks.org
KEYWORD: HM251

SAFETY AND ENVIRONMENTAL ISSUES

Many people are concerned about procedures of genetic engineering and the safety of genetically engineered products. In the United States, genetic engineering is regulated by the Food and Drug Administration (FDA), the National Institutes of Health Recombinant DNA Advisory Committee, the Department of Agriculture (USDA), and the Environmental Protection Agency (EPA). These organizations set standards for safety procedures and products and require special permits and labels for the sale and use of certain products.

Word Roots and Origins

herbicide

from the Latin *herba,* meaning "plant," and *cida,* meaning "to kill"

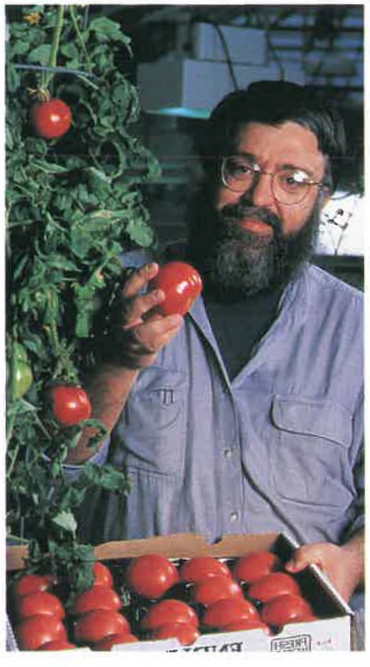
Genetically Engineered Foods

Some people are concerned that foods produced by genetic engineering could contain toxic proteins or substances that cause allergies in people who consume them. One precaution required by the FDA requires manufacturers of genetically engineered foods to provide scientific evidence that allergy-inducing properties have not been transferred to new foods when the new foods contain a gene transplanted from a food known to cause allergic reactions, such as peanuts. In general, however, foods produced by transgenic crops can be sold without special permits or labels if the product is identical to products produced by nontransgenic crops. However, if a genetically engineered food contains a new protein, carbohydrate, or fat, the FDA generally requires additional approval before the product can be introduced to the food supply.

Notice that the genetically-engineered tomatoes in Figure 13-11 look just like other tomatoes. Scientists isolated and cloned the gene that codes for an enzyme necessary for ripening in tomatoes. By changing this one gene in the genetically-engineered tomatoes, they were able to make a tomato that ripens without becoming soft. Typically, supermarket tomatoes are picked before they are ripe because ripe tomatoes are soft and bruise easily.

FIGURE 13-11

Plant physiologist Athanasios Theologis, shown here, genetically engineered tomatoes to ripen without becoming soft. His genetically engineered tomatoes are comparable to greenhouse-grown tomatoes, which taste better than commercially grown tomatoes that are picked while they are still green.



Genetically Engineered Crops

Some people are concerned that genetically engineered crops could spread into the wild and wipe out native plant species. In addition, they worry that transgenic crop plants could transmit their new genes to other species in neighboring areas. Rice and lawn grasses, for example, exchange genes in their pollen with native plants that are related to them. Exchanging these types of genes with wild plant species could cause powerful new "superweeds" that could take over large areas of land because they would have advantages over native plant species. Regulatory agencies sometimes require labels on the packages of transgenic plants to indicate their proper use and the risks of using transgenic plants that may pose hazards to the environment.

SECTION 13-3 REVIEW

1. List two types of medical products that can be produced using DNA technology.
2. What is a vaccine, and what are the benefits of producing vaccines using DNA technology?
3. List three traits for which genes are being transplanted into crop plants.
4. What benefit are plants that contain a nitrogen-fixing gene transplanted from bacteria?
5. Describe two potential safety and environmental problems that could result from genetic engineering.
6. **CRITICAL THINKING** The FDA does not require special labels for genetically engineered food products that are identical to similar products produced by traditional breeding techniques. Do you think that genetically engineered food products should be labeled as such? Why or why not?

CHAPTER 13 REVIEW

SUMMARY/VOCABULARY

13-1

- Genetic engineering brings DNA technology and molecular genetics together for practical purposes.
- Restriction enzymes, which are used to isolate and transfer genes, are specific in the nucleotide sequences they recognize and cut. When a restriction enzyme cuts a piece of DNA, it creates single chains—called sticky ends—on the ends of each piece of DNA.
- Sticky ends bind to complementary sticky ends, forming recombinant DNA molecules out of DNA fragments from two or more organisms.
- Cloning vectors, such as plasmids and viruses, are used to clone and transplant genes from one organism to another one.
- Transgenic organisms contain a donor gene and express it just as they do their own DNA as long as the donor gene is turned on.

Vocabulary

cloning vector (240)
DNA technology (239)
donor gene (240)
gene clone (240)
genetic engineering (239)
genomic library (241)
insulin (241)
plasmid (240)
recombinant DNA (241)
restriction enzyme (239)
sticky end (240)
transgenic organism (242)

13-2

- A DNA fingerprint is a pattern of bands that represent certain fragments from an individual's DNA. These fragments are typically noncoding repeating sequences that vary from person to person.
- DNA fingerprints of individuals can be compared to establish relatedness. Chances are less than one in one million that five sites of DNA fingerprints from two people will match, unless the two people are identical twins. As the number of sites that are compared in a DNA fingerprint increases, so does validity of the DNA fingerprint.
- Gel electrophoresis is a technique used to separate DNA or protein fragments by their length and charge.
- Polymerase chain reaction (PCR) can be used to quickly make additional copies of segments of DNA when the original sample is small. The results of PCR can then be used to make a DNA fingerprint.
- The goal of the Human Genome Project is to determine the nucleotide sequence of the entire human genome and to map the location of all genes. This information might then be used to diagnose, treat, cure, and prevent human genetic disorders.
- Gene therapy refers to treating genetic disorders by correcting a defect in a gene or by providing a normal form of a gene. It is hoped that gene therapy can be used to cure genetic disorders in the future.

Vocabulary

DNA fingerprint (243)
gel electrophoresis (244)
gene therapy (246)
Human Genome Project (246)
polymerase chain reaction (PCR) (245)
primer (245)
probe (244)
RFLP analysis (244)

13-3

- DNA technology is used to produce medical products that are often safer and less expensive than those produced by conventional means.
- DNA technology is used to produce disease-resistant, pest-resistant, and herbicide-resistant crops. Perhaps these crops will improve the quality and quantity of the human food supply.
- Current research involves efforts to isolate genes from nitrogen-fixing bacteria and to transplant them into plants. Such transgenic plants may be able to grow in nitrogen-poor soil without the addition of fertilizers.
- Many safety, environmental, and ethical issues involved in the new DNA technology have not been resolved.

Vocabulary

herbicide (251)
pathogen (250)
vaccine (250)

REVIEW

Vocabulary

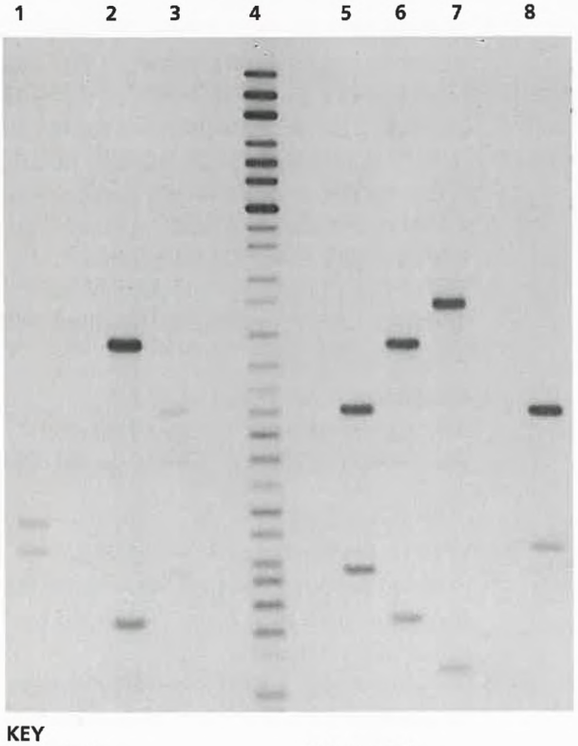
1. Define *recombinant DNA*.
2. Relate restriction enzymes to genomic libraries.
3. Relate a host organism, a donor gene, and a transgenic organism.
4. Distinguish between PCR and RFLP.
5. Distinguish between a primer and a probe.

Multiple Choice

6. A plasmid is (a) a cell (b) a nucleus (c) a bacterium (d) an extra ring of DNA.
7. A molecule containing DNA from two sources is called (a) recombinant DNA (b) RFLP DNA (c) a DNA clone (d) a plasmid.
8. Enzymes that cut DNA molecules in specific locations are called (a) sticky ends (b) restriction enzymes (c) cloning vectors (d) cloning enzymes.
9. Carriers used for transferring DNA from one organism to another are called (a) sticky ends (b) restriction enzymes (c) cloning vectors (d) cloning enzymes.
10. The host organism into which a cloning vector is placed is called a (a) plasmid (b) virus (c) donor (d) transgenic organism.
11. A eukaryotic donor gene is likely to be expressed in a prokaryotic host organism if (a) the donor gene is a promoter gene (b) the donor gene is transferred along with the genes that turn it on (c) the donor gene is placed beside a gene that is not expressed (d) all of these.
12. DNA technology has been used to (a) produce pharmaceutical products (b) produce herbicide-resistant crops (c) treat genetic diseases (d) all of these.
13. Gel electrophoresis is used to (a) separate DNA fragments (b) produce DNA fragments with sticky ends (c) cut DNA into fragments (d) quickly make copies of DNA.
14. PCR is used to (a) separate DNA fragments (b) produce DNA fragments with sticky ends (c) cut DNA into fragments (d) quickly make copies of DNA.
15. Genetic engineering has been used to make plants (a) toxic to insects (b) immune to vaccines (c) able to produce insulin (d) all of these.

Short Answer

16. Explain what happens when a restriction enzyme is used on DNA.
17. How is a DNA fingerprint prepared?
18. List three practical uses of PCR.
19. Explain how gel electrophoresis can be used to separate fragments of DNA.
20. What is a cloning vector?
21. The photograph below shows 8 columns on a gel. Several of these columns contain DNA fingerprints of samples taken from a crime scene, a victim, and four suspects. Indicate which suspect's DNA fingerprint matches the blood found at the crime scene. How likely is it that blood found at the crime scene belongs to the suspect?



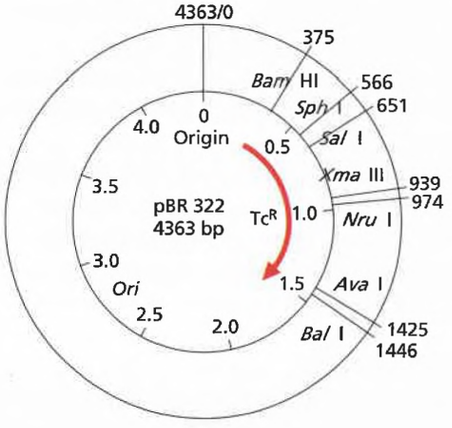
KEY
1 Control
2 Blood
3 Victim
4 Ladder
5 Suspect 1
6 Suspect 2
7 Suspect 3
8 Suspect 4

22. Discuss the accuracy of DNA fingerprints.
23. State two possible benefits of the work being completed by the Human Genome Project.
24. Explain how gene therapy has been used to treat cystic fibrosis. Explain why gene therapy has not been used to cure cystic fibrosis.
25. Describe how genetic engineering can be used to produce vaccines.
26. List two ways that genetic engineering may increase crop yields.

CRITICAL THINKING

1. In the past, breeders developed new plant and animal varieties by selecting an organism with desirable traits, breeding it with another organism with similar traits, and then breeding the offspring so that the desirable traits would be passed on to the strain. Name an advantage and a disadvantage of genetic engineering techniques over traditional breeding techniques.
2. The United States government has stringent regulations requiring researchers to confine genetically engineered organisms to the laboratory. What concerns do you think might have led to the enactment of these regulations?
3. Natural selection is a mechanism of evolution whereby the members of a population who are best adapted to their environment survive and produce offspring. How is natural selection affected by genetic engineering?
4. How might an insect-resistant crop that is the product of genetic engineering affect a population of insects that depends on the crop for food?
5. Why do you think the United States authorized limited gene therapy trials?
6. Examine the restriction map of the bacterial plasmid pBR 322, shown below. This is a commonly used plasmid composed of 4,363 base pairs. The map shows sites at which certain restriction enzymes cut the DNA of the plasmid. For example, the restriction enzyme called *Sph*I cuts the plasmid at base pair 566. Suppose you want to isolate from the plasmid the gene that codes for resistance to the antibiotic tetracycline, which is indicated as Tc^R. What restriction enzymes would you use? How many base pairs make up the Tc^R gene? How might you check to be certain that your procedure was successful?

Restriction Map of pBR 322 DNA



EXTENSION

1. Read "DNA Detectives" in *Popular Science,* August 1999, on page 48. What is an advantage of providing hand-held gene readers to police investigators? What is a disadvantage?
2. Read "Genetic-Code Breaker" in *Discover,* March 2000, on page 22. According to Francis Collins, one of the Human Genome Project's chief researchers, what is the main reason that we should know the sequences of our 46 chromosomes?
3. Read "Who Owns Our Genes?" in *Time,* January 11, 1999, on page 51. Briefly explain the controversy in economics and ethics over the patenting of human genes as they are sequenced by laboratories.

CHAPTER 13 INVESTIGATION

Gel Electrophoresis

OBJECTIVES

- Use restriction enzymes to cut DNA.
- Separate DNA fragments of different sizes.

PROCESS SKILLS

- conducting agarose gel electrophoresis

MATERIALS

- protective clothing
- crushed ice
- ice bucket
- microtube rack
- microtube A—Uncut DNA
- microtube B—*Hind*III
- microtube C—*Bam*HI
- microtube D—*Eco*RI
- microtube E—Unknown
- permanent marker
- 0.5–10 µL micropipetter
- micropipetter tips
- 10× restriction buffer for each restriction enzyme
- 34 µL Lambda virus DNA
- 37°C water bath
- gel-casting tray
- 6-well gel comb
- 65°C hot-water bath
- 0.8% agarose
- hot mitt
- zipper-lock plastic bag
- 10 mL graduated cylinder
- 1× TBE buffer
- freezer
- 5 µL loading dye
- gel chamber and power supply
- WARD'S DNA stain
- staining trays
- distilled water
- metric ruler

Background

1. DNA has a negative charge and flows toward the positive end of a gel during electrophoresis. Small DNA fragments move faster than larger fragments.
2. The distance that each DNA fragment moves is used to calculate the R_f, or relative mobility, of a fragment. The R_f is used to calculate the number of base pairs in the fragment.

PART A Cutting DNA

1. Wear safety goggles, gloves, and a lab apron at all times.
2. Fill an ice bucket with ice. Obtain one each of the following microtubes: A—Uncut DNA, B—*Hind*III, C—*Bam*HI, D—*Eco*RI, and E—Unknown. Microtubes B–D contain 1 µL of the indicated restriction enzyme. Place all microtubes in the ice. *Restriction enzymes MUST be kept on ice until step 6.*
3. With a permanent marker, write the initials for everyone in your group *on the top* of microtubes A–E.
4. CAUTION **If you get a chemical on your skin or clothing, wash it off at the sink while calling to your teacher.** Set a micropipetter to 1 µL, and put a tip on the end of the micropipetter, as shown in (a) below. Using a new tip for each microtube, add 1 µL of the corresponding 10× restriction buffer to each of microtubes B–D. Place the buffer on the side of the tube. *Do not touch the micropipetter tips to the solutions in the microtubes.*

(a) MICROPIPETTER

(b) CASTING TRAY

5. Reset the micropipetter to 8 µL. Using the micropipetter and a new tip for each microtube, add 8 µL of the Lambda virus DNA to the side of each of microtubes B–D. Gently tap each microtube on your lab table until the solutions are thoroughly mixed. *Do not shake the microtubes!* Reset the micropipetter to 10 µL, and add 10 µL of Lambda DNA to microtube A.
6. Place all of the microtubes into a 37°C water bath. After 50–60 minutes, remove the microtubes from the water bath, and immediately put them into a freezer. If the class period ends before 50 minutes has passed, your teacher will give you further directions. While the restriction enzymes are working, go to Part B.

PART B Preparing an Agarose Gel

7. Set up a gel-casting tray, as shown in (b). Place a gel comb in the grooves of the gel-casting tray. Make sure

that the comb does not touch the bottom of the tray. If it does, get another comb from your teacher.

8. Write the names of the members of your group on a paper towel. Carry your tray to the table with the melted agarose, and place your tray on the paper towel.
9. Using a hot mitt, pour melted 0.8% agarose into your gel-casting tray until the agarose reaches a depth of 3 mm. Make sure that the agarose spreads evenly throughout the tray. *Do not move your gel tray before the agarose solidifies.*
10. Let the gel cool (about 20–30 minutes) until the agarose solidifies.
11. While the gel is cooling, write your name, the date, and your class period on a zipper-lock plastic bag. Pour 5 mL of 1× TBE buffer into the bag.
12. When the gel has solidified, carefully remove the gel comb by pulling it straight up. If the comb does not come up easily, pour a little 1× TBE buffer on the comb area. After removing the gel comb, open the plastic bag and carefully slide the gel tray into the bag. *Do not remove the gel from the gel-casting tray.* Store the gel according to your teacher's instructions.

PART C Running a Gel

13. Retrieve your microtubes (A–E) and your gel. If the materials in the microtubes are frozen, hold each tube in your hand until the solutions thaw.
14. Set a micropipetter to 1 µL, and place a tip on the end. Add 1µL of loading dye to each microtube. *Use a new tip for each microtube.* Gently tap each microtube on your lab table to thoroughly mix the solutions. *Do not shake the microtubes.*
15. Remove your gel (still in the gel-casting tray) from the plastic bag, and place it in a gel chamber. Orient the gel so that the wells are closest to the black wire, or anode.
16. Set a micropipetter to 10 µL, and place a new tip on the end. Open microtube A, and remove 10 µL of solution. Carefully place the solution into the well in lane 1, the left-most lane. To do this, place both elbows on the lab table, lean over the gel, and slowly lower the micropipetter tip into the opening of the well before depressing the plunger. *Do not jab the micropipetter tip through the bottom of the well.*
17. *Using a new micropipetter tip for each tube,* repeat step 16 for each of the remaining microtubes. Use lane 2 for microtube B, lane 3 for microtube C, lane 4 for microtube D, and lane 5 for microtube E.
18. Very slowly fill the gel chamber with 1× TBE buffer until the level of the buffer is approximately 1–2 mm above the surface of the gel.
19. CAUTION **Follow all of the manufacturer's precautions regarding the use of this equipment.** Close the gel chamber and connect it to a power supply according to your teacher's instructions.
20. Allow an electric current to flow through the gel. You will see a blue line moving away from the wells. When the blue line is approximately 5 mm from the end of the gel, disconnect the power supply and remove the gel. Store the gel overnight in the plastic bag.

PART D Analyzing a Gel

21. To stain a gel, carefully place the gel (wells up) into a staining tray. Pour WARD'S DNA stain into the staining tray until the gel is completely covered. Cover the staining tray, and label it with your initials. Allow the stain to sit for at least 2 hours. Next, carefully pour the stain into the sink drain, and flush it down the drain with water. *Do not let the stained gel slip out of the staining tray.*
22. To destain a gel, cover the gel with distilled water by pouring water to one side of the gel. Let the gel sit overnight (or at least 8–12 hours). The bands of DNA will appear as purple lines against a light background.
23. Calculate the R_f for each fragment using the following equation:

$$R_f = \frac{\text{distance in mm that DNA fragment migrated}}{\text{distance in mm from well to the dye}}$$

24. Dispose of your materials according to your teacher's directions, and wash your hands before leaving the lab.

Analysis and Conclusions

1. Which two samples appear to have the same pattern of DNA bands?
2. Which restriction enzyme cut the DNA in the unknown sample? Justify your answer.
3. What are some measures that you took to prevent contamination of your DNA samples during this lab?