DNA has a spiral staircase shape, as shown in this model. DNA contains the instructions for making the proteins necessary for life.
From his studies with pea plants, Mendel concluded that hereditary factors determine many of an organism’s traits. But what were these hereditary factors? How did these molecules store hereditary information? Scientists believed that if they could answer these questions, they could understand how cells pass on characteristics to their descendants. The answers to these questions began to emerge during an epidemic of pneumonia in London in the 1920s.

**GRIFFITH’S EXPERIMENTS**

In 1928, British medical officer Frederick Griffith was studying a bacterium called Streptococcus pneumoniae (abbreviated S. pneumoniae). Some types, or strains, of this bacterium can cause the lung disease pneumonia in mammals. Griffith was trying to develop a vaccine against a disease-causing, or virulent (VIR-yoo-luhnt) strain of the bacterium.

As shown in Figure 10-1, each virulent bacterium is surrounded by a capsule made of polysaccharides that protects it from a body’s defense systems. The bacteria in a virulent strain grow as smooth-edged colonies when grown in a Petri dish and are called the S strain. In contrast, a second strain of S. pneumoniae does not cause pneumonia and lacks a capsule. The second strain is called the R strain because it grows into rough colonies. The R strain is also shown in Figure 10-1.

![Colonies of the harmful (S) strain](image1)

![Colonies of the harmless (R) strain](image2)

**FIGURE 10-1**

Griffith studied S. pneumoniae bacteria. The S strain can cause pneumonia. The R strain does not cause pneumonia.
Griffith used the two strains of *S. pneumoniae* bacteria in a series of four experiments, shown in Figure 10-2. These experiments provide insight about the nature of the hereditary material. In Experiments 1 and 2, Griffith injected either live *R* or live *S* cells into mice. He found that only *S* cells killed the mice. In Experiment 3, he injected heat-killed *S* bacteria into mice and found that the mice survived. In his fourth experiment, he injected mice with both heat-killed *S* cells and live *R* cells. He found that the mice died.

Griffith concluded from his four experiments that heat-killed virulent bacterial cells release a hereditary factor that transfers the disease-causing ability to the live harmless cells. This type of transfer of genetic material from one cell to another cell or from one organism to another organism is called **transformation**.

** borough"},"data_root":null}
In 1952, two American researchers, Martha Chase and Alfred Hershey, set out to test whether DNA or protein was the hereditary material viruses transfer when viruses enter a bacterium. Viruses that infect bacteria are called bacteriophages, or just phages. As shown in Figure 10-3 in step 1, Hershey and Chase used radioactive isotopes to label the protein and DNA in the phage. They used radioactive sulfur ($^{35}\text{S}$) to label protein and radioactive phosphorus ($^{32}\text{P}$) to label DNA. Then, they allowed protein-labeled and DNA-labeled phage to separately infect Escherichia coli (abbreviated E. coli) bacteria. In step 2, they removed the phage coats from the cells in a blender. They then used a centrifuge in step 3 to separate the phage from the E. coli. They found that all of the viral DNA and little of the protein had entered E. coli cells. They concluded that DNA is the hereditary molecule in viruses.

**HERSHEY-CHASE EXPERIMENT**

1. How did Griffith’s experiments show that a hereditary factor was involved in bacterial transformation?
2. Describe how the contributions of Avery and his colleagues revealed that DNA is responsible for transformation in bacteria.
3. How did the Hershey and Chase experiment produce evidence that DNA, and not protein, is the hereditary material in viruses?

**SECTION 1 REVIEW**

**CRITICAL THINKING**

4. **Analyzing Methods** Why did heat kill Griffith’s S bacteria?
5. **Analyzing Results** What were the essential differences between the methods and results of Griffith and Avery’s experiments?
6. **Applying Information** What might Hershey and Chase have concluded if they had found both $^{32}\text{P}$ and $^{35}\text{S}$ in the bacterial cells?
CHAPTER 10

DNA STRUCTURE

By the early 1950s, most biologists accepted DNA as the hereditary material. However, they still lacked an understanding of DNA’s structure or how this molecule could replicate, store, and transmit hereditary information and direct cell function. These mysteries would soon begin to unravel at Cambridge University in England.

DNA DOUBLE HELIX

In the 1950s, a young American biologist, James Watson, teamed up with British graduate student Francis Crick at Cambridge University in England to try to determine the structure of DNA. By 1953, they had put together a model for the structure of DNA as shown in Figure 10-4. They proposed that DNA is made of two chains that wrap around each other in the shape of a double helix, a shape similar to a winding spiral staircase. Their final model was correct and was remarkable because it explained how DNA could replicate.

Watson and Crick relied on other scientists’ work to develop their DNA model. Part of that work was X-ray diffraction photographs of DNA crystals, such as the one shown in Figure 10-5. The photographs and crystals were produced by researchers Rosalind Franklin, shown in Figure 10-5, and Maurice Wilkins, at King’s College in London.

In 1962, Watson, Crick, and Wilkins received the Nobel Prize in Medicine for their work on DNA. Rosalind Franklin died in 1958 and so could not be named in the award. However, an important genetics institute in Cambridge now bears her name, and her contribution is recognized around the world.
DNA is a nucleic acid made of two long chains (also called strands) of repeating subunits called nucleotides (NOO-klee-oh-TIED). Each nucleotide consists of three parts: a five-carbon sugar, a phosphate group, and a nitrogenous base. The three parts of a DNA nucleotide are illustrated in Figure 10-6. The five-carbon sugar in a DNA nucleotide is called deoxyribose (dee-AHK5-ee-RIE-bohs). The phosphate group consists of a phosphorus (P) atom bonded to four oxygen (O) atoms. The nitrogenous (nie-TRAHJ-uh-nuhs) base contains nitrogen (N) atoms and carbon (C) atoms and is a base (accepts hydrogen ions).

**Bonds Hold DNA Together**

The DNA double helix is similar to a spiral staircase, as Figure 10-6 shows. The alternating sugar and phosphate molecules form the side “handrails” of the staircase. Nucleotides along each strand are connected by covalent bonds between the sugar of one nucleotide and the phosphate group of the next nucleotide. Each full turn of the DNA helix has 10 nucleotide pairs.

The nitrogenous bases (called “bases” for short) face toward the center of the DNA molecule. The bases on one strand of DNA face—and form bonds called hydrogen bonds with—the bases on the other strand. Nitrogenous bases are bonded in pairs between the two strands by two or three hydrogen bonds. The base pairs form the “steps” of the staircase. The base pairs are of uniform width because, in each pair one base has a two-ring structure and the other base has a single-ring structure.

In Figure 10-6, dashed lines indicate the locations of the hydrogen bonds. Hydrogen bonds between the bases help hold the two chains of the DNA double helix together.
Each nucleotide in a DNA molecule is made of a deoxyribose sugar, a phosphate group, and one of the four nitrogenous bases shown above: thymine, cytosine, adenine, or guanine.

Nitrogenous Bases

The sugar and phosphate group are identical in all DNA nucleotides. However, the nitrogenous base may be any one of four different kinds—thymine (THIE-MIEN), cytosine (SIET-oh-SEEEN), adenine (AD-uh-NEEN), or guanine (GWAH-NEEN). The nitrogenous bases and their chemical structures, called rings, are shown above in Figure 10-7. The nitrogenous bases are often represented by the first letter of their name—T (thymine), C (cytosine), A (adenine), and G (guanine).

Nitrogenous bases that have a double ring of carbon and nitrogen atoms, such as adenine and guanine, are called purines (PYUR-EENZ). Nitrogenous bases that have a single ring of carbon and nitrogen atoms, such as cytosine and thymine, are called pyrimidines (pi-RIM-uh-DENZ).

COMPLEMENTARY BASES

In 1949, American biochemist Erwin Chargaff observed that the percentage of adenine equals the percentage of thymine, and the percentage of cytosine equals that of guanine in the DNA of a variety of organisms. This observation was key to understanding the structure of DNA because it meant bases pair by base-pairing rules—in DNA, cytosine on one strand pairs with guanine on the opposite strand, and adenine pairs with thymine, as shown in Figure 10-8. These pairs of bases are called complementary base pairs. Notice that each complementary base pair contains one double-ringed purine and one single-ringed pyrimidine.

Because of the base-pairing rules, the order of the nitrogenous bases on the nucleotides in one chain of the DNA molecule is complementary to the order of bases on the opposite chain. For example, if a DNA chain has the sequence ATTC, then the other chain must have the complementary sequence TAAG. The order of nitrogenous bases on a chain of DNA is called its base sequence.

Complementary base pairing is important in DNA structure and function for two reasons. First, the hydrogen bonds between the base pairs help hold the two strands of a DNA molecule together. Second, the complementary nature of DNA helps explain how DNA replicates before a cell divides. One strand of a DNA molecule can serve as a template for making a new complementary strand.
DNA Models

The structure of DNA is often simplified when it is drawn or modeled. For example, the DNA double helix is often illustrated as a straight ladder, as shown at the bottom of Figure 10-8. The sugar-phosphate “handrails” are drawn as a straight line so that the base-pair “steps” between the DNA strands are easier to see. Notice that simplifying the DNA structure highlights the complementary base pairs in each of the DNA nucleotides. In some cases the structure of DNA is simplified even more by just writing the first letter of each of the nitrogenous bases in the DNA nucleotides. For example, the DNA in Figure 10-8b would be represented by

\[
\begin{align*}
A & C C T G T G A G A C \\
T & G G A C A C T C T G
\end{align*}
\]

FIGURE 10-8

The DNA double helix resembles a spiral staircase (a), but it is often shown as a straight ladder (b) to more easily show the base pairs.

SECTION 2 REVIEW

1. What piece of information did Franklin and Wilkins have that helped Watson and Crick determine the double helix structure of DNA?
2. Name the three parts of a nucleotide.
3. Summarize the locations of covalent bonds and hydrogen bonds in a DNA molecule.
4. Describe why the two strands of the double helix are considered to be complementary.
5. State the base-pairing rules in DNA.
6. How do the base-pairing rules relate to the structure of DNA?

CRITICAL THINKING

7. Making Predictions If 2.2 picograms of DNA could be extracted from a certain number of human muscle cells, about how many picograms of DNA could be extracted from the same number of human gamete cells?
8. Applying Information Use the base-pairing rules to determine the base sequence that is complementary to the sequence C-G-A-T-T-G.
9. Making Calculations A plant’s DNA has nucleotides that are 20 percent thymine. What percentage of guanine would be present?
Watson and Crick’s discovery of the double helix structure of DNA caused great excitement in the scientific community. Scientists realized that this model could explain simply and elegantly how DNA can replicate exactly each time a cell divides, a key feature of hereditary material.

**HOW DNA REPLICATION OCCURS**

DNA replication is the process by which DNA is copied in a cell before a cell divides by mitosis, meiosis, or binary fission. During DNA replication, the two nucleotide strands of the original double helix separate along the strands. Because the two strands are complementary, each strand serves as a template to make a new complementary strand. After replication, the two identical double-stranded DNA molecules separate and move to the new cells formed during cell division, as shown in Figure 10-9.

**Steps of DNA Replication**

The process of DNA replication is shown in Figure 10-10. In step 1, enzymes called helicases separate the DNA strands. Helicases move along the DNA molecule, breaking the hydrogen bonds between the complementary nitrogenous bases. This action allows the two DNA strands of the double helix to separate from each other. The Y-shaped region that results when the two strands separate is called a replication fork.

During step 2, enzymes called DNA polymerases add complementary nucleotides, found floating freely inside the nucleus, to each of the original strands. As the nucleotides on the newly forming strand are added, covalent bonds form between the adjacent nucleotides. Covalent bonds form between the deoxyribose sugar of one nucleotide and the phosphate group of the next nucleotide on the growing strand. Hydrogen bonds form between the complementary nitrogenous bases on the original and new strands.

By step 3, DNA polymerases finish replicating the DNA and fall off. The result is two separate and identical DNA molecules that are ready to move to new cells in cell division.

In each new DNA double helix, one strand is from the original molecule, and one strand is new. This type of replication is called semi-conservative replication because each of the new DNA molecules has kept (or conserved) one of the two (or semi) original DNA strands.
**Action at the Replication Fork**

DNA synthesis occurs in different directions on each strand, as shown by the arrows near the replication fork in step 2 of Figure 10-10. As the replication fork moves along the original DNA, synthesis of one strand follows the movement of the replication fork. Synthesis on the other strand, however, moves in the opposite direction, away from the replication fork, which leaves gaps in the newly synthesized strand. The gaps are later joined together by an enzyme called DNA ligase.

**Prokaryotic and Eukaryotic Replication**

In prokaryotic cells, which have one circular chromosome, replication begins at one place along the chromosome. Two replication forks are formed and proceed in opposite directions, like two zippers opening in opposing directions. Replication continues along each fork until they meet and the entire molecule is copied.

In eukaryotic cells, each chromosome is long, but not circular. At the rate that DNA polymerase adds nucleotides (about 50 nucleotides per second in eukaryotic cells), it would take 53 days to replicate the largest human chromosome. Instead, replication begins at many points or origins along the DNA. As with prokaryotes, at each origin, two replication forks move in opposite directions. For example, in a fruit fly chromosome, replication begins simultaneously at about 3,500 sites in a DNA molecule. Only simultaneous replication along chromosomes could allow rapid enough copying of the organism’s entire DNA.
**DNA ERRORS IN REPLICATION**

DNA replication usually occurs with great accuracy. Only about one error occurs for every billion paired nucleotides added. That’s the equivalent of typing this book 1,000 times and making only one typing error. What accounts for this accuracy? DNA polymerases have repair functions that “proofread” DNA in the same way a friend might check a term paper for spelling errors. For example, if an adenine pairs with a cytosine instead of a thymine, DNA polymerase can repair the error by removing the mispaired cytosine and replacing it with a thymine.

When mistakes in DNA replication do occur, the base sequence of the newly formed DNA differs from the base sequence of the original DNA. A change in the nucleotide sequence of a DNA molecule is called a mutation. Mutations can have serious effects on the function of an important gene and disrupt an important cell function.

Some errors escape repair. In addition, chemicals and ultraviolet radiation from the sun can damage DNA. Some mutations can lead to cancer, such as the one shown in Figure 10-11. Thus, an effective mechanism for the repair of damaged DNA is very important to the survival of an organism.

**DNA Replication and Cancer**

DNA replication is an elegant process in which genetic information is passed from cell to cell for thousands of generations. It also explains how mutations can arise and lead to altered cells and organisms. Sometimes, the changes allow individuals to survive and reproduce better, so these variations increase in the population over many generations. Sometimes, mutations that are not repaired can cause diseases such as cancer. For example, mutations that affect genes that control how a cell divides can lead to an abnormal mass of cells called a tumor. Studying DNA replication is one promising avenue to understanding and treating various types of human cancers.

**SECTION 3 REVIEW**

1. Describe what happens at a DNA replication fork during replication.
2. Describe the role of helicases and DNA polymerases during DNA replication.
3. State why DNA replication is a semi-conservative process.
4. Compare the number of replication forks in prokaryotic and eukaryotic DNA during replication.
5. How are replication errors corrected?

**CRITICAL THINKING**

6. Analyzing Concepts Why are there two DNA polymerases at one replication fork?
7. Drawing Conclusions Why are DNA repair enzymes important to an organism’s survival?
8. Evaluating Information Is a mutation that occurs during the formation of an egg cell or sperm cell more significant than a mutation that occurs in a body cell? Explain.
DNA REPAIR AND SKIN CANCER

Sometimes, the errors that occur during DNA replication are not fixed by DNA repair enzymes. These unrepaired errors can lead to mutations. Cancer can occur if the mutations happen within genes that control cell growth and cell division. Scientists hope that by studying DNA replication and DNA repair, they can develop treatments or even cure various types of cancers.

Ultraviolet Light and Skin Cancer

Ultraviolet light, the most energetic part of sunlight, is the main cause of mutations that trigger skin cancer. Skin cancer is the most common type of cancer in the United States. Each year, about 1 million Americans get skin cancer.

When UV light reaches the DNA inside a skin cell, thymine bases that are next to each other on the same strand of DNA can become linked by a covalent bond, as shown in the figure below. Linked thymine pairs are called thymine dimers. Thymine dimers are usually detected by enzymes moving along the DNA strand because the dimers cause a kink in the DNA, as shown in the figure below. Dimers that are not repaired during DNA replication can cause mutations in genes that control cell division. The mutation can trigger a skin cell to become cancerous.

DNA Repair Enzymes and Skin Cancer Treatments

Some organisms do not get skin cancer. One reason is that these organisms have a DNA repair enzyme called photolyase (FOH-toh-LIE-AYS). Photolyase is activated by light and can repair thymine dimers caused by UV radiation. Human skin cells can correct UV-induced dimers by a complex process known as excision repair that involves other enzymes. But photolyase uses a more direct and effective mechanism for DNA repair than excision repair. Scientists have already developed a sunscreen containing photolyase to repair the UV-induced DNA damage that occurs when a person is sunburned.

Some researchers want to try to use gene therapy to insert the gene for photolyase in people that are at high risk for skin cancer. Gene therapy is a technique in which a defective gene is replaced with a normal version of the gene. Ongoing studies of DNA repair enzymes may help develop gene therapy and other types of cancer treatments in humans.

REVIEW

1. How can errors during DNA replication lead to cancer?
2. How does the DNA repair enzyme photolyase prevent skin cancer?
3. Supporting Reasoned Opinions
Would you buy a sunscreen that contains photolyase? Why or why not?

Unrepaired DNA damage can prevent accurate copying of the DNA and can lead to mutations. One example of DNA damage is covalent cross-linking between two thymine bases, which is called a thymine dimer.
Protein Synthesis

Characteristics such as hair color are largely determined by genetic factors. But how does inheriting a particular form of a gene result in the appearance of a specific hair color? The structure of DNA helps explain how genes function in making proteins that determine traits in organisms.

Flow of Genetic Information

A gene is a segment of DNA that is located on a chromosome and that codes for a hereditary character. For example, a gene determines a person’s hair color. The gene directs the making of the protein called melanin (a pigment) in hair follicle cells through an intermediate—the nucleic acid called ribonucleic acid, or RNA.

Figure 10-12 summarizes the flow of genetic information in a eukaryotic cell. During transcription, DNA acts as a template for the synthesis of RNA. In translation, RNA directs the assembly of proteins. Forming proteins based on information in DNA and carried out by RNA is called protein synthesis, or gene expression. This central concept can be symbolized as DNA → RNA → protein. Proteins do important work in cells, such as protecting the body against infections and carrying oxygen in red blood cells.
DNA, RNA, AND PROTEIN SYNTHESIS

The structure of RNA is different from the structure of DNA. Each of the three major types of RNA—mRNA, tRNA, and rRNA—play a different role during protein synthesis.

RNA STRUCTURE AND FUNCTION

Like DNA, RNA is a nucleic acid made up of nucleotides. However, as shown in Figure 10-13, the structure of RNA differs from that of DNA in four basic ways. First, RNA contains the sugar ribose, not the sugar deoxyribose found in DNA. Second, RNA contains the nitrogenous base uracil instead of the nitrogenous base thymine found in DNA. Third, RNA is usually single stranded rather than double stranded like DNA. However, within a single-stranded RNA molecule, some regions fold to form short double-stranded sections. In the double-stranded regions, guanine forms base pairs with cytosine, and uracil forms base pairs with adenine. Fourth, RNA is usually much shorter in length than DNA (about the length of one gene). On the other hand, DNA is usually long, containing hundreds or thousands of genes.

Types of RNA

Cells have three major types of RNA, as shown in Figure 10-14. Each type of RNA plays a different role in protein synthesis. The first type of RNA is messenger RNA (mRNA), a single-stranded RNA molecule that carries the instructions from a gene to make a protein. In eukaryotic cells, mRNA carries the genetic “message” from DNA in the nucleus to the ribosomes in the cytosol. The second type of RNA is ribosomal RNA (rRNA), which is part of the structure of ribosomes. Ribosomes are organelles in the cell where protein synthesis occurs. Ribosomes are made of rRNAs and many proteins. Figure 10-14 shows a model of a ribosome. The third type of RNA is transfer RNA (tRNA), which transfers amino acids to the ribosome to make a protein. Although the entire tRNA is made of nucleotides linked together, only three are emphasized in Figure 10-14.
TRANSCRIPTION

Transcription is the process by which the genetic instructions in a specific gene are transcribed or “rewritten” into an RNA molecule. Transcription takes place in the nucleus of eukaryotic cells and in the DNA-containing region in the cytoplasm of prokaryotic cells.

Steps of Transcription

Transcription occurs in three steps, as shown in Figure 10-15. In step 1, RNA polymerase, an enzyme that catalyzes the formation of RNA on a DNA template, binds to a promoter. A promoter is a specific nucleotide sequence of DNA where RNA polymerase binds and initiates transcription. After RNA polymerase binds to the promoter, the DNA strands unwind and separate.

In step 2, RNA polymerase adds free RNA nucleotides that are complementary to the nucleotides on one of the DNA strands. The resulting chain is an RNA molecule. As in DNA replication, complementary base pairing determines the nucleotide sequence in the newly made RNA. For example, if the bases on the DNA strand was ATCGAC, the bases on the RNA strand would be UAGCUG. Unlike DNA replication, transcription uses only a specific region (a gene) on one of the two DNA strands to serve as the template. As RNA polymerase moves past, the separated DNA strands rewind.

During step 3, RNA polymerase reaches a termination signal, a specific sequence of nucleotides that marks the end of a gene. Upon reaching this “stop” signal, RNA polymerase releases both the DNA and the newly formed RNA. The RNA made during transcription can be one of many types including mRNA, tRNA, or rRNA. The newly made RNA can now perform its job in the cell, and the RNA polymerase can transcribe another gene.

**FIGURE 10-15**

During transcription, the enzyme RNA polymerase “reads” one of the chains, the template strand. RNA polymerase adds and then joins complementary RNA nucleotides, resulting in an RNA strand.
THE GENETIC CODE

During the next process of gene expression, amino acids are assembled based on instructions encoded in the sequence of nucleotides in the mRNA. The genetic code is the term for the rules that relate how a sequence of nitrogenous bases in nucleotides corresponds to a particular amino acid. In the genetic code, three adjacent nucleotides (“letters”) in mRNA specify an amino acid (“word”) in a polypeptide. Each three-nucleotide sequence in mRNA that encodes an amino acid or signifies a start or stop signal is called a codon.

Table 10-1 lists the 64 mRNA codons and the amino acids they encode in most organisms. For example, the codon GCU specifies the amino acid alanine in the genetic code. The genetic code is nearly universal to all life on Earth and supports the idea that all organisms share an ancient common ancestor.

Some amino acids are encoded by two, three, or more different codons, as shown in Table 10-1. These codons often differ from one another by only one nucleotide. No codon encodes more than one amino acid. One special codon, AUG, acts as a start codon. A start codon is a specific sequence of nucleotides in mRNA that indicates where translation should begin. The start codon encodes the amino acid methionine. Certain sequences of nucleotides in mRNA (UAA, UAG, or UGA), called stop codons, do not code for amino acids, but instead signal for translation to end.

### TABLE 10-1 Codons in mRNA

<table>
<thead>
<tr>
<th>First base</th>
<th>Second base</th>
<th>Third base</th>
</tr>
</thead>
<tbody>
<tr>
<td>U</td>
<td>U</td>
<td>U</td>
</tr>
<tr>
<td>UUU</td>
<td>Phenylalanine</td>
<td></td>
</tr>
<tr>
<td>UUC</td>
<td>Serine</td>
<td></td>
</tr>
<tr>
<td>UUA</td>
<td>Leucine</td>
<td></td>
</tr>
<tr>
<td>UUG</td>
<td></td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>CC</td>
<td>G</td>
</tr>
<tr>
<td>CUU</td>
<td>Leucine</td>
<td></td>
</tr>
<tr>
<td>CUC</td>
<td>Proline</td>
<td></td>
</tr>
<tr>
<td>CUA</td>
<td>CCA</td>
<td></td>
</tr>
<tr>
<td>CUG</td>
<td>CCG</td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>AC</td>
<td>U</td>
</tr>
<tr>
<td>AUU</td>
<td>Isolecine</td>
<td></td>
</tr>
<tr>
<td>AUC</td>
<td>Threonine</td>
<td></td>
</tr>
<tr>
<td>AUA</td>
<td>ACA</td>
<td></td>
</tr>
<tr>
<td>AUG</td>
<td>ACG</td>
<td></td>
</tr>
<tr>
<td>G</td>
<td>GC</td>
<td>U</td>
</tr>
<tr>
<td>GUU</td>
<td>Alanine</td>
<td></td>
</tr>
<tr>
<td>GUC</td>
<td>GCA</td>
<td></td>
</tr>
<tr>
<td>GUA</td>
<td>GCC</td>
<td></td>
</tr>
<tr>
<td>GUG</td>
<td>GCG</td>
<td></td>
</tr>
</tbody>
</table>

Copyright © by Holt, Rinehart and Winston. All rights reserved.
Although the instructions for making a protein are copied from DNA to mRNA, all three major types of RNA are involved in translation—the making of a protein.

**Protein Structure**

Every protein is made of one or more polypeptides. Polypeptides are chains of amino acids linked by peptide bonds. There are 20 different amino acids found in the proteins of living things. Each polypeptide chain may consist of hundreds or thousands of the 20 different amino acids, arranged in a sequence specific to each protein. The amino acid sequence determines how the polypeptides will twist and fold into the three-dimensional structure of the protein. The shape of the protein is critical to its function.

**Steps of Translation**

The translation or decoding of the genetic instructions to form a polypeptide involves five main steps, as shown in Figure 10-16. In step 1, two ribosomal subunits, tRNA, and an mRNA join together. Enzymes first attach a specific amino acid to one end of each tRNA according to the genetic code. The other end of each tRNA contains the **anticodon**, three nucleotides on the RNA that are complementary to the sequence of a codon in mRNA.

**FIGURE 10-16**

During translation, amino acids are assembled from information encoded in mRNA. As the mRNA codons move through the ribosome, tRNAs add specific amino acids to the growing polypeptide chain. The process continues until a stop codon is reached and the newly made protein is released.
A tRNA carrying the amino acid methionine at one end and the anticodon UAC at the other end pairs with the start codon AUG on the mRNA. The first amino acid in nearly all polypeptides is methionine, but this amino acid may be removed later.

In step 2, the polypeptide chain is put together. A tRNA carrying the appropriate amino acid pairs its anticodon with the second codon in the mRNA. The ribosome then detaches methionine from the first tRNA, and a peptide bond forms between methionine and the second amino acid. The first tRNA then exits the ribosome. The ribosome then moves a distance of one codon along the mRNA.

During step 3, the polypeptide chain continues to grow as the mRNA moves along the ribosome. A new tRNA moves in, carrying an amino acid for the next mRNA codon. The growing polypeptide chain moves from one tRNA to the amino acid attached to the next tRNA.

The polypeptide grows one amino acid at a time until step 4. At this step, the ribosome reaches the stop codon. The newly made polypeptide falls off.

During step 5, the components of translation come apart. The last tRNA leaves the ribosome, and the ribosome moves away from the mRNA. The translation machinery is now free to translate the same or another mRNA.

### 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 were missing?

### Elongation (continued)

The first tRNA detaches and leaves its amino acid behind. Elongation continues. The polypeptide chain continues to grow.

### Termination

The process ends when a stop codon is reached. A stop codon is one for which there is no tRNA that has a complementary anticodon.

### Disassembly

The ribosome complex falls apart. The newly made polypeptide is released.
Translating Many Ribosomes at Once

Because a new ribosome begins translating mRNA almost as soon as the preceding ribosome has moved aside, several ribosomes may translate the same mRNA transcript at the same time. In fact, prokaryotes lack a nuclear envelope separating their DNA from ribosomes in the cytosol, thus translation can begin on an mRNA even before transcription of the mRNA has finished. In eukaryotes, translation of an mRNA occurs only after transcription is finished.

THE HUMAN GENOME

In the years since Watson and Crick discovered the structure of DNA, biologists have achieved a milestone in applying this knowledge to human biology. The entire gene sequence of the human genome, the complete genetic content, is now known. Biologists have deciphered the order of the 3.2 billion base pairs in the 23 human chromosomes. The human genome is so large that it would take a person almost 10 years to read the total sequence aloud.

The challenge now is to learn what information the DNA sequences actually encode. An important new field called bioinformatics uses computers to compare different DNA sequences. Scientists can program computers to help interpret most DNA sequences and predict where genes lie along the DNA.

To learn where and when human cells use each of the proteins coded for in the approximately 30,000 genes in the human genome will take much more analysis. This information is important because learning which gene sequences control particular biological functions may help diagnose, treat, and prevent genetic disorders, cancer, and infectious diseases in the future.

SECTION 4 REVIEW

1. Summarize the flow of genetic information.
2. List the four ways in which the structure of RNA differs from that of DNA.
3. Describe the structure and function of each of the three types of RNA.
4. Sequence the main steps of transcription.
5. What is the genetic code?
6. Compare the roles of the three different types of RNA during translation.
7. Describe the significance of identifying the entire sequence of the human genome.

CRITICAL THINKING

8. Making Comparisons How does the role of RNA polymerase in transcription differ from that of DNA polymerase in DNA replication?
9. Applying Information What amino acids would translation of the mRNA with the sequence UAACAGGAGCAUCC produce?
10. Analyzing Processes Discuss why it is important which of the two DNA strands serves as a template during transcription.
11. Drawing Conclusions How does the structure of tRNA relate to its function in translation?
Discovery of DNA

- Griffith's experiments showed that hereditary material can pass from one bacterial cell to another. This is called transformation.

- Avery's work showed that DNA is the hereditary material that transfers information between bacterial cells.

- Hershey and Chase confirmed that DNA, and not protein, is the hereditary material.

Vocabulary

- virulent (p. 193)
- transformation (p. 194)
- bacteriophage (p. 195)

DNA Structure

- Watson and Crick created a model of DNA by using Franklin's and Wilkins's DNA diffraction X-rays.

- DNA is made of two nucleotide strands that wrap around each other in the shape of a double helix.

- A DNA nucleotide is made of a deoxyribose sugar, a phosphate group, and one of four nitrogenous bases: adenine (A), guanine (G), cytosine (C), or thymine (T).

- Nucleotides along each DNA strand are linked by covalent bonds. Complementary nitrogenous bases are bonded by hydrogen bonds.

- Hydrogen bonding between the complementary base pairs, G-C and A-T, holds the two strands of a DNA molecule together.

Vocabulary

- nucleotide (p. 197)
- deoxyribose (p. 197)
- purine (p. 198)
- pyrimidine (p. 198)
- base-pairing rules (p. 198)
- base sequence (p. 198)

DNA Replication

- DNA replication is the process by which DNA is copied in a cell before a cell divides.

- Replication begins with the separation of the DNA strands by helicases. Then, DNA polymerases form new strands by adding complementary nucleotides to each of the original strands.

- Each new DNA molecule is made of one strand of nucleotides from the original DNA molecule and one new strand.

- Changes in DNA are called mutations. Proofreading and repair prevent many replication errors.

Vocabulary

- DNA replication (p. 200)
- replication fork (p. 200)
- semi-conservative replication (p. 200)
- DNA polymerase (p. 200)
- mutation (p. 202)

Protein Synthesis

- The flow of genetic information can be symbolized as DNA → RNA → protein.

- RNA has the sugar ribose instead of deoxyribose and uracil in place of thymine. RNA is single stranded and is shorter than DNA.

- During transcription, DNA acts as a template for directing the synthesis of RNA.

- The genetic code identifies the specific amino acids coded for by each mRNA codon.

- The RNA called mRNA carries the genetic “message” from the nucleus to the cytosol; rRNA is the major component of ribosomes; tRNA carries specific amino acids, helping to form polypeptides.

Vocabulary

- ribonucleic acid (RNA) (p. 204)
- transcription (p. 204)
- translation (p. 204)
- protein synthesis (p. 204)
- ribose (p. 205)
- messenger RNA (mRNA) (p. 205)
- ribosomal RNA (rRNA) (p. 205)
- transfer RNA (tRNA) (p. 205)
- RNA polymerase (p. 206)
- promoter (p. 206)
- termination signal (p. 206)
- genetic code (p. 207)
- codon (p. 207)
- anticodon (p. 208)
- genome (p. 210)
USING VOCABULARY

1. For each pair of terms, explain how the meanings of the terms differ.
   a. purine and pyrimidine
   b. ribosome and ribosomal RNA
   c. messenger RNA and transfer RNA
   d. termination signal and stop codon
   e. transcription and translation

2. Explain the relationship between codon and gene.

3. Use the following terms in the same sentence: DNA replication, replication fork, helicase, and DNA polymerase.

4. Word Roots and Origins The word transcription is derived from the Latin scribere, which means “to write.” The prefix trans means “across.” Using this information, explain why the term transcription is a good name for the biological process it describes.

UNDERSTANDING KEY CONCEPTS

5. Summarize Griffith’s transformation experiments.

6. Describe how Avery’s experiments led to the understanding of DNA as the molecule of heredity in bacteria.

7. Describe the contributions of Hershey and Chase to the understanding that DNA is the hereditary molecule in viruses.

8. State how Watson and Crick were able to build a structural model of DNA.

9. Identify the components of a nucleotide.

10. Name the bonds that link the nucleotides along a DNA strand.

11. List the rules of complementary base pairing.

12. Summarize the major steps that occur during DNA replication.

13. Name the function of DNA polymerase during DNA replication.

14. State how complementary base pairing is important in the replication of DNA.

15. Differentiate the number of replication forks in prokaryotic and eukaryotic DNA.

16. Describe the importance of repair enzymes for the identification of errors during DNA replication.

17. Outline the flow of genetic information in cells.

18. Compare the structure of RNA to that of DNA.

19. Summarize how RNA is formed from a gene during the process of transcription.

20. Identify the function of the genetic code.

21. Differentiate the functions of the three types of RNA involved in protein synthesis.

22. Sequence the major steps of translation.

23. Discuss the importance of learning about the human genome.

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

25. CONCEPT MAPPING Use the following terms to create a concept map that describes the structure of DNA and how it is copied: nucleotides, phosphate group, deoxyribose, nitrogenous base, double helix, replication, purine, pyrimidine, DNA polymerases, and genes.

CRITICAL THINKING

26. Analyzing Information Why is it unlikely that any particular mutation would have any noticeable effect in a population?

27. Interpreting Graphics A segment of DNA has the following sequence:

   T A C G G T C T C A G C

   Write the mRNA transcript from this sequence of DNA. Next, write the tRNA anticodons that would pair with the mRNA transcript. Use Table 10-1 to write the names of the amino acids coded for by the mRNA transcript.

28. Analyzing Concepts A DNA molecule replicates to produce two new DNA molecules. Both of the two new DNA molecules then replicate to form four more new DNA molecules. Are any nucleotide chains from the original DNA present in the last four new DNA molecules? If so, how many?

29. Analyzing Current Research Scientists have determined essentially all of the 3 billion or so nucleotides that spell out the human genome. This genetic information will revolutionize the diagnosis, prevention, and treatment of many human diseases. Propose why this information is important for research on human disease.

30. Applying Information List all codons in the genetic code that could be changed into a stop codon by a single nucleotide mutation.
1. For which of the following is DNA responsible?
   A. directing RNA to make lipids
   B. directing RNA to produce glucose
   C. encoding information for making proteins
   D. encoding information for changing the genetic code

2. Where is RNA found?
   F. only in proteins
   G. only in the nucleus
   H. only in the cytoplasm
   J. in the nucleus and cytoplasm

3. What is the basic unit of DNA called?
   A. sugar
   B. nucleotide
   C. phosphate
   D. nucleic acid

4. Which of the following nucleic acids is involved in translation?
   F. DNA only
   G. mRNA only
   H. DNA and mRNA
   J. mRNA and tRNA

5. What is the ratio of purines to pyrimidines for these organisms?
   A. about 1:1
   B. about 1:2
   C. about 1:3
   D. about 1:4

6. Within each organism, which nucleotides are found in similar percentages?
   F. A and T, G and C
   G. A and C, G and T
   H. A and C, G and U
   J. A and G, T and U

**Percentage of Each Nitrogenous Base in Different Organisms**

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>T</th>
<th>G</th>
<th>C</th>
</tr>
</thead>
<tbody>
<tr>
<td>E. coli</td>
<td>24.7</td>
<td>23.6</td>
<td>26.0</td>
<td>25.7</td>
</tr>
<tr>
<td>Human</td>
<td>30.4</td>
<td>30.1</td>
<td>19.6</td>
<td>19.9</td>
</tr>
<tr>
<td>Wheat</td>
<td>27.3</td>
<td>27.1</td>
<td>22.7</td>
<td>22.8</td>
</tr>
</tbody>
</table>

5. What is the ratio of purines to pyrimidines for these organisms?
   A. about 1:1
   B. about 1:2
   C. about 1:3
   D. about 1:4

6. Within each organism, which nucleotides are found in similar percentages?
   F. A and T, G and C
   G. A and C, G and T
   H. A and C, G and U
   J. A and G, T and U

**SHORT RESPONSE**

DNA is made up of two strands of subunits called nucleotides. The two strands are twisted around each other in a double helix shape.

Explain why the structure of a DNA molecule is sometimes described as a zipper.

**EXTENDED RESPONSE**

DNA can be damaged by mistakes made during its replication. The mistakes are called mutations.

Part A Explain eukaryotic DNA replication.

Part B Explain how a mutation during replication can affect a protein that is synthesized.
Modeling DNA Replication and Protein Synthesis

OBJECTIVES
- Construct and analyze a model of DNA.
- Use a model to simulate the process of replication.
- Use a model to simulate the process of protein synthesis.

PROCESS SKILLS
- demonstrating
- identifying
- manipulating a model

MATERIALS
- plastic soda straws of two different colors, 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
- 3 in. × 5 in. note cards
- oval-shaped card

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 are the roles of mRNA, rRNA and tRNA in protein synthesis?

5. Describe the process of transcription and the process of translation.

PART A Making a Model of DNA

1. CAUTION Sharp or pointed objects may cause injury. Handle pushpins carefully. Insert a pushpin midway along the length of each straw segment of one color, as shown in the figure below. Push a paper clip into one end of each straw segment until the clip touches the pin.

2. 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.

3. Assign nucleotides to the corresponding pushpin colors as follows: red = adenine, blue = guanine, yellow = cytosine, and green = thymine.

4. Construct the other half of your first model. Begin 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 in this second strand of DNA according to the base-pairing rules.

5. 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

6. Place the chains parallel to each other on the table. The “top” blue pin of the first chain should face the “top” yellow pin of the second chain.

7. 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.

8. 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 Protein Synthesis

9. Place the chains of one of the DNA models parallel to each other on the table.

10. Repeat step 1, but use the straw segments of the second color.

11. Assign the uracil nucleotide to the white pushpins. Using the available pushpins and the second set of straw segments, 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 207 and the photo at the left. Label the note cards with amino acids that you will need to translate your mRNA model. Use the “ribosome” oval cards to model translation.

14. In your lab report, write the sequence of amino acids that resulted from the translation.

15. Clean up your materials before leaving the lab.

Analysis and Conclusions

1. Write the base-pair order for the DNA molecule you created by using the following code: red = adenine, blue = guanine, yellow = cytosine, and green = thymine.

2. How does the replicated model of DNA compare with the original model of DNA?

3. Predict what would happen if the nucleotide pairs in the replicated model were not in the same sequence as the pairs in the original model.

4. What is the relationship between the anticodon of a tRNA and the amino acid the tRNA carries?

5. Write the mRNA transcript of the DNA sequence presented below.

   CTG TTC ATA ATT

   Next, write the tRNA anticodons that would pair with the mRNA transcript. Use Table 10-1 to write the amino acids coded for by the mRNA transcript.

6. If you transcribed the “wrong” side of the DNA molecule, what would the result be? How might the proteins that the organism produced be affected?

7. What are the advantages of having DNA remain in the nucleus of eukaryotic cells?

Further Inquiry

Design models to represent a eukaryotic and a prokaryotic cell. Use these models along with the models you constructed in this investigation to demonstrate where replication, transcription, and the steps of protein synthesis occur.