Adv Biology: DNA and RNA Study Guide

- Chapter 12
- Vocabulary -Notes
- What experiments led up to the discovery of DNA being the hereditary material?
    - The discovery that DNA is the genetic code involved many experiments.
        - Experiments by Griffith, Avery, Hershey and Chase, Watson and Crick.
    - Proteins thought to be genetic material before discovery.
- Know what the following scientists did: Griffith, Avery, Hershey and Chase, Watson and Crick, and Rosalind Franklin

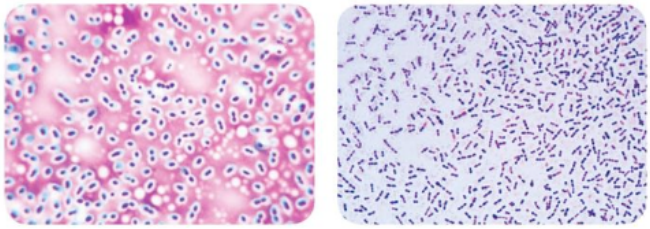

Figure 12.1 The smooth (S) strain of *S. pneumoniae* can cause pneumonia, though the rough (R) strain is not disease causing. The strains can be identified by the appearance of the colonies.

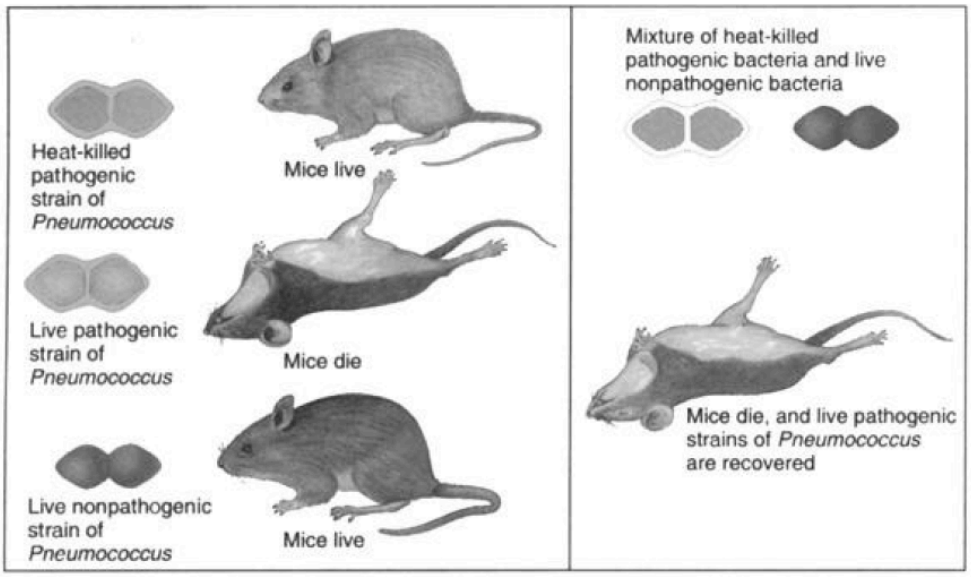

Figure 6.1
Griffith's discovery of the "transforming principle."

Figure 12.6 Rosalind Franklin's Photo 51 and X-ray diffraction data helped Watson and Crick solve the structure of DNA. When analyzed and measured carefully, the pattern shows the characteristics of helix structure.

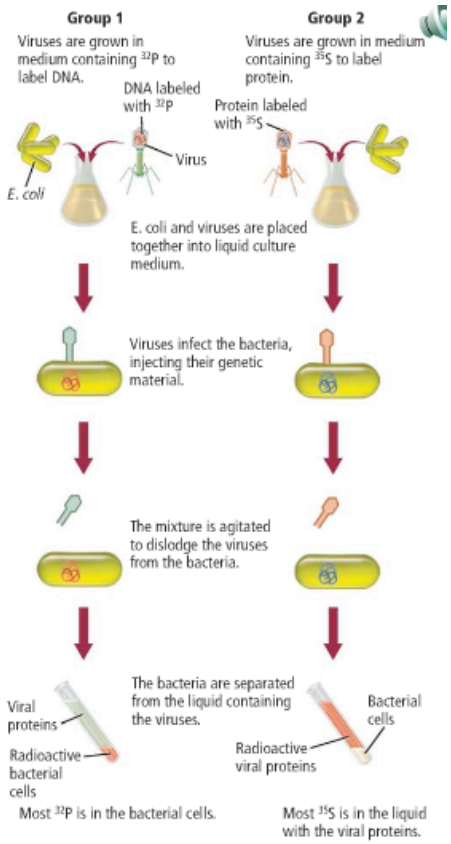

Figure 12.3 Hershey and Chase used radioactive labeling

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Interactive Table To explore more about Hershey and Chase, visit biologygmh.com.

Table 12.1 Summary of Hershey-Chase Results

Group 1 (Viruses labeled with ^{32}P)		Group 2 (Viruses labeled with ^{35}S)	
Infected Bacteria	**Liquid with Viruses**	**Infected Bacteria**	**Liquid with Viruses**
• Labeled viral DNA (^{32}P) found in the bacteria • Viral replication occurred • New viruses contained ^{32}P	• No labeled DNA • No viral replication	• No labeled viral proteins (^{35}S) • Viral replication occurred • New viruses did not have a label	• Labeled proteins found • No viral replication

Figure 12.5 Chargaff's data showed that though base composition varies from species to species, within a species C = G and A = T.

Chargaff's Data

	Base Composition (Mole Percent)			
Organism	A	T	G	C
Escherichia coli	26.0	23.9	24.9	25.2
Yeast	31.3	32.9	18.7	17.1
Herring	27.8	27.5	22.2	22.6
Rat	28.6	28.4	21.4	21.5
Human	30.9	29.4	19.9	19.8

- **Know the scientists and what they did to determine that DNA was the heredity molecule and the scientists that discovered the structure of DNA.**

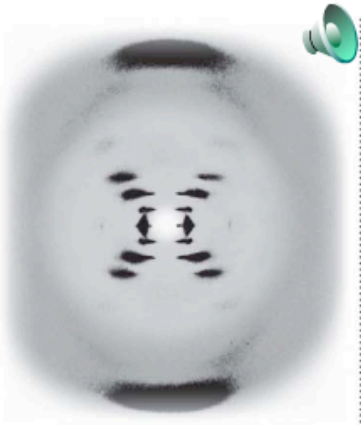


Figure 12.6 Rosalind Franklin's Photo 51 and X-ray diffraction data helped Watson and Crick solve the structure of DNA. When analyzed and measured carefully, the pattern shows the characteristics of helix structure.

X-ray diffraction Wilkins was working at King's College in London, England, with a technique called X-ray diffraction, a technique that involved aiming X rays at the DNA molecule. In 1951, Franklin joined the staff at King's College. There she took the now famous Photo 51 and collected data eventually used by Watson and Crick. Photo 51, shown in **Figure 12.6,** indicated that DNA was a **double helix,** or twisted ladder shape, formed by two strands of nucleotides twisted around each other. The specific structure of the DNA double helix was determined later by Watson and Crick when they used Franklin's data and other mathematical data. DNA is the genetic material of all organisms, composed of two complementary, precisely paired strands of nucleotides wound in a double helix.

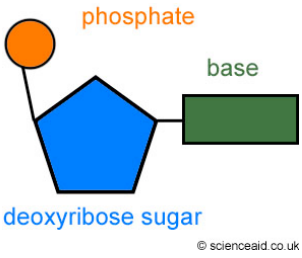
Watson and Crick Watson and Crick were working at Cambridge University in Cambridge, England, when they saw Franklin's X-ray diffraction picture. Using Chargaff's data and Franklin's data, Watson and Crick measured the width of the helix and the spacing of the bases. Together, they built a model of the double helix that conformed to the others' research. The model they built is shown in **Figure 12.7.** Some important features of their proposed molecule include the following:

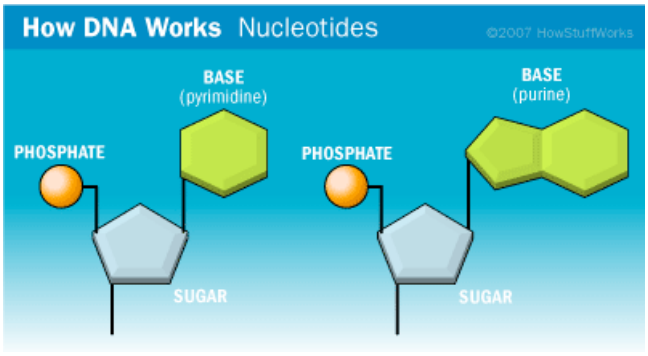
1. two outside strands consist of alternating deoxyribose and phosphate
2. cytosine and guanine bases pair to each other by three hydrogen bonds
3. thymine and adenine bases pair to each other by two hydrogen bonds

DNA structure DNA often is compared to a twisted ladder, with the rails of the ladder represented by the alternating deoxyribose and phosphate. The pairs of bases (cytosine–guanine or thymine–adenine) form the steps, or rungs, of the ladder. A purine base always binds to a pyrimidine base, ensuring a consistent distance between the two rails of the ladder. This proposed bonding of the bases also explains Chargaff's data, which suggested that the number of purine bases equaled the number of pyrimidine bases in a sample of DNA. Remember, cytosine and thymine are pyrimidine bases, adenine and guanine are purines, and C = G and A = T. Therefore, C + T = G + A, or purine bases equal pyrimidine bases. Complementary base pairing is used to describe the precise pairing of purine and pyrimidine bases between strands of nucleic acids. It is the characteristic of DNA replication through which the parent strand can determine the sequence of a new strand.

Figure 12.7 Using Chargaff's and Franklin's data, Watson and Crick solved the puzzle of the structure of DNA.

- Bacteriophage – used in Griffith's experiment
- Nucleotides: the different kinds for DNA and RNA
    - **There are 4 different kinds of nucleotides – the only difference is the type of nitrogenous base: thymine, adenine, cytosine, and guanine. In RNA there is Uracil instead of thymine.**
- What are the base-pairing rules?
    - DNA
        - Adenine pairs with Thymine
        - Guanine pairs with Cytosine
    - RNA – no Thymine, but Uracil
        - Adenine pairs with Uracil
        - Guanine pairs with Cytosine
- Hydrogen bonding: double and triple bonds
    - Adenine pairs with Thymine forming a **double hydrogen bond**
    - Cytosine pairs with Guanine forming a **triple hydrogen bond**
    - What is the structure of DNA?





    - DNA – 3 parts
        - Phosphate group
        - Sugar (dexoyribose)
        - Nitrogenous bases (A,T, G, and C)
- How does the structure of DNA enable it to reproduce itself accurately?
    - Each strand acts as a template for building a new identical strand of DNA with the help of many enzymes.
- Semi-conservative – only half of the original DNA molecule is conserved in each new strand. In DNA replication there are two identical copies (strands) of DNA, Each new molecule consists of a new and original strand.
- **How does replication occur? What are the steps?**
    - Main Idea – DNA replicated by making a strand that is complementary to each original strand.

Semiconservative Replication

When Watson and Crick presented their model of DNA to the science community, they also suggested a possible method of replication—semiconservative replication. During **semiconservative replication,** parental strands of DNA separate, serve as templates, and produce DNA molecules that have one strand of parental DNA and one strand of new DNA. Recall from Chapters 9 and 10 that DNA replication occurs during interphase of mitosis and meiosis. An overview of semiconservative replication is in **Figure 12.10.** The process of semiconservative replication occurs in three main stages: unwinding, base pairing, and joining.

Unwinding DNA helicase, an enzyme, is responsible for unwinding and unzipping the double helix. When the double helix is unzipped, the hydrogen bonds between the bases are broken, leaving single strands of DNA. Then, proteins called single-stranded binding proteins associate with the DNA to keep the strands separate during replication. As the helix unwinds, another enzyme, RNA primase, adds a short segment of RNA, called an RNA primer, on each DNA strand.

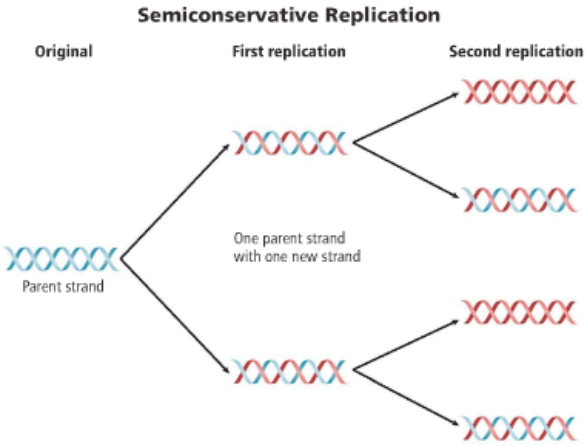


Figure 12.10 In semiconservative replication, the parental DNA separates and serves as templates to produce two daughter DNA, which then can separate to produce four DNA.

Base pairing The enzyme **DNA polymerase** catalyzes the addition of appropriate nucleotides to the new DNA strand. The nucleotides are added to the 3' end of the new strand, as illustrated in **Figure 12.11.** DNA polymerase continues adding new DNA nucleotides to the chain by adding to the 3' end of the new DNA strand. Recall that each base binds only to its complement—A binds to T and C binds to G. In this way, the templates allow identical copies of the original double-stranded DNA to be produced.

Notice in **Figure 12.11** that the two strands are made in a slightly different manner. One strand is called the leading strand and is elongated as the DNA unwinds. This strand is built continuously by the addition of nucleotides to the 3' end.

The other strand of DNA, called the lagging strand, elongates away from the replication fork. It is synthesized discontinuously into small segments, called **Okazaki fragments,** by the DNA polymerase in the 3' to 5' direction. These fragments are later connected by the enzyme DNA ligase. Each Okazaki fragment is about 100–200 nucleotides long in eukaryotes. Because one strand is synthesized continuously and the other is synthesized discontinuously, DNA replication is said to be semidiscontinuous as well as semiconservative.

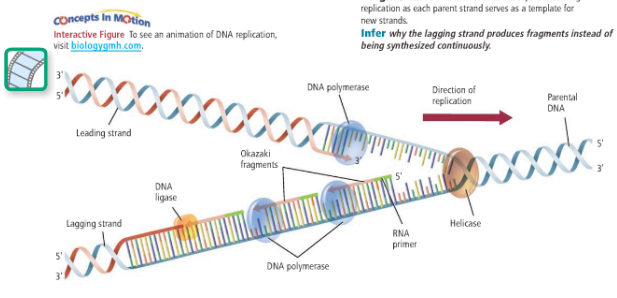


Figure 12.11 The DNA strands are separated during replication as each parent strand serves as a template for new strands.
Infer *why the lagging strand produces fragments instead of being synthesized continuously.*

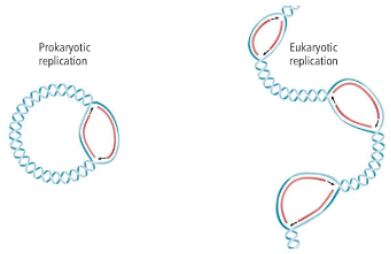


Figure 12.12 Eukaryotes have many origins of replication. Bacteria have one origin of replication, with the DNA replicating in both directions when it unzips.

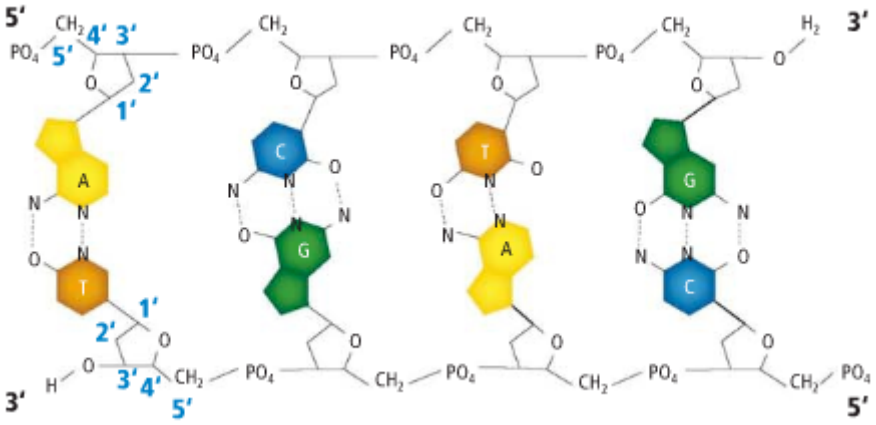
Joining Even though the leading strand is synthesized continuously, in eukaryotic DNA replication there often are many areas along the chromosome where replication begins. When the DNA polymerase comes to an RNA primer on the DNA, it removes the primer and fills in the place with DNA nucleotides. When the RNA primer has been replaced, DNA ligase links the two sections.

Comparing DNA Replication in Eukaryotes and Prokaryotes

Eukaryotic DNA unwinds in multiple areas as DNA is replicated. Each individual area of a chromosome replicates as a section, which can vary in length from 10,000 to one million base pairs. As a result, multiple areas of replication are occurring along the large eukaryotic chromosome at the same time. Multiple replication origins look like bubbles in the DNA strand, as shown in **Figure 12.12.**

In prokaryotes, the circular DNA strand is opened at one origin of replication, as shown in **Figure 12.12.** Notice in the figure that DNA replication occurs in two directions, just as it does in eukaryotes. Recall from Chapter 7 that prokaryotic DNA typically is shorter than eukaryotic DNA and remains in the cytoplasm—not packaged in a nucleus.

- Helicase and ligase
    - Helicase – unwinds the DNA Double Helix and breaks the hydrogen bonds between each nitrogenous base this splitting the molecule into two. The splitting region is called the replication fork (origin of replication). Since DNA is so big, multiple origins of replication (helicase) are formed to speed up replication.
    - Ligase – an enzyme that bonds or glues segments (Okazaki fragments) together
- Okazaki fragments – In DNA replication, one strand, the leading strand, is made continuosly, the other is built in fragments called Okazaki fragments, which are bonded by ligase.
- DNA orientation (5′ and 3′) – **DNA polymerase always moves along the original DNA in the 3′ to 5′ direction.**



- **DNA replication**

Figure 12.11 The DNA strands are separated during replication as each parent strand serves as a template for new strands.
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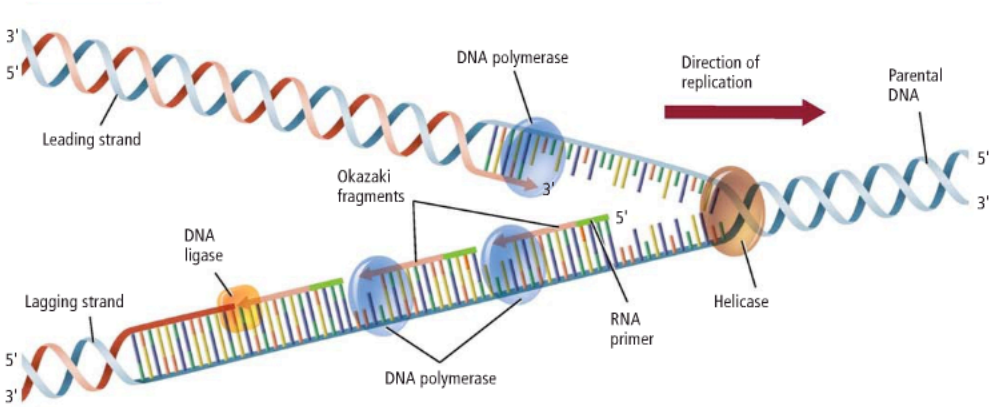


- DNA polymerase – In DNA replication, 2 enzymes of DNA polymerase attatch to each strand and move along the molecule, base by base, adding the appropriate nitrogenous bases each time (A w/T and C w/ G).
- **Prokaryotic replication** -
- RNA polymerase – transcription requires this enzyme, which is similar to DNA polymerase. During transcription, RNA polymerase binds to DNA and separates the DNA strands. RNA polymerase then uses one strand of DNA as a template from which nucleotides are assembled into a strand of RNA.
- Central Dogma

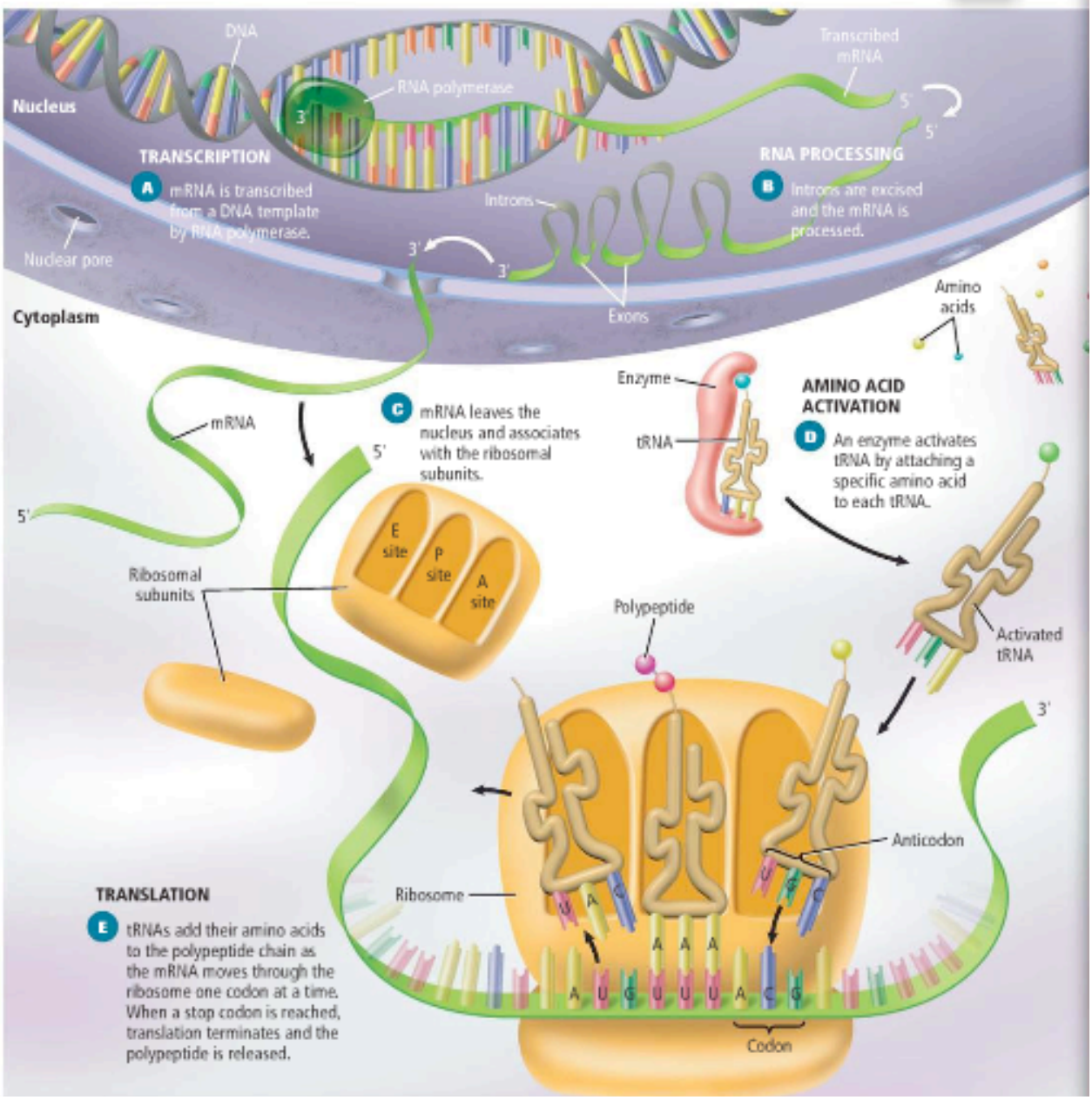
  Transcription Translation
  - DNA ➔ RNA ➔ Protein

  Replication
- Introns and exons
  - Introns – the DNA of eukaryotic cells contain these gene sequences of nucleotides, which **are not involved in the coding for proteins.**
  - Exons – the DNA sequence that **code for proteins**, because they are **expressed in proteins.**
- What are the differences between DNA and RNA?
  1. RNA has ribose, while DNA has Dexoyribose.
  2. RNA has Uracil, while DNA has Thymine.
  3. RNA is a single stranded nucleic acid, while DNA DNA is double stranded.

What are the steps involved in protein synthesis? (See Below)

Visualizing Transcription and Translation

Figure 12.15
Transcription takes place in the nucleus. Translation occurs in the cytoplasm and results in the formation of polypeptides.



- What are the different kinds of mutations?
  - Gene mutations – changes in single genes:
    - Point mutations – changes that involve one or few nucleotides because they occur at a single point in the DNA.

        - Substitutions – one base changed to another bases in the DNA sequences
    - Frameshift mutations – shift the reading frame of the DNA. They can then change every amino acid that follows the point of the muatuon and change the protein that is produced.
        - Insertions – base inserted in the DNA seqence.
        - Deletions - base removed from the DNA seqence.
  - Chromosomal – in whole chromosomes:
    - Translocation – part of chromosome breaks off and attaches to another chromosome.
    - Duplications – produces an extra copy of part of a chromosone.
    - Deletion – loss of a part of a chromosome.
    - Inversion – reverses the direction of part of a chromosome.
- What are the effect of different kinds of mutations on cells and organisms?
  - Substitutions usually affect one amino acid, while insertions and deletions have much more drastic effects b/c
    - They could affect more than one amino acid.
    - Stop codon is still correct in substitution.
    - Maybe the same amino acid might result

Concepts in Motion

Table 12.3 Mutations

Interactive Table To explore more about types of mutations, visit biologygmh.com.

Mutation Type	Analogy Sentence	Example of Associated Disease
Normal	THE BIG FAT CAT ATE THE WET RAT	
Missense (substitution)	THE BIZ FAT CAT ATE THE WET RAT	Achondroplasia: improper development of cartilage on the ends of the long bones of arms and legs resulting in a form of dwarfism
Nonsense (substitution)	THE BIG RAT	Muscular dystrophy: progressive muscle disorder characterized by the progressive weakening of many muscles in the body
Deletion (causing frameshift)	THB IGF ATC ATA TET HEW ETR AT	Cystic fibrosis: characterized by abnormally thick mucus in the lungs, intestines, and pancreas
Insertion (causing frameshift)	THE BIG ZFA TCA TAT ETH EWE TRA	Crohn's disease: chronic inflammation of the intestinal tract, producing frequent diarrhea, abdominal pain, nausea, fever, and weight loss
Duplication	THE BIG FAT FAT CAT ATE THE WET RAT	Charcot-Marie-Tooth disease (type 1A): damage to peripheral nerves leading to weakness and atrophy of muscles in hands and lower legs
Expanding mutation (tandem repeats) Generation 1 Generation 2 Generation 3	 THE BIG FAT CAT ATE THE WET RAT THE BIG FAT CAT CAT CAT ATE THE WET RAT THE BIG FAT CAT CAT CAT CAT CAT CAT ATE THE WET RAT	Huntington's disease: a progressive disease in which brain cells waste away, producing uncontrolled movements, emotional disturbances, and mental deterioration

- Double helix – the structure of DNA, **a twisted ladder shape, formed by two strands of nucleotides twisted around each other.**

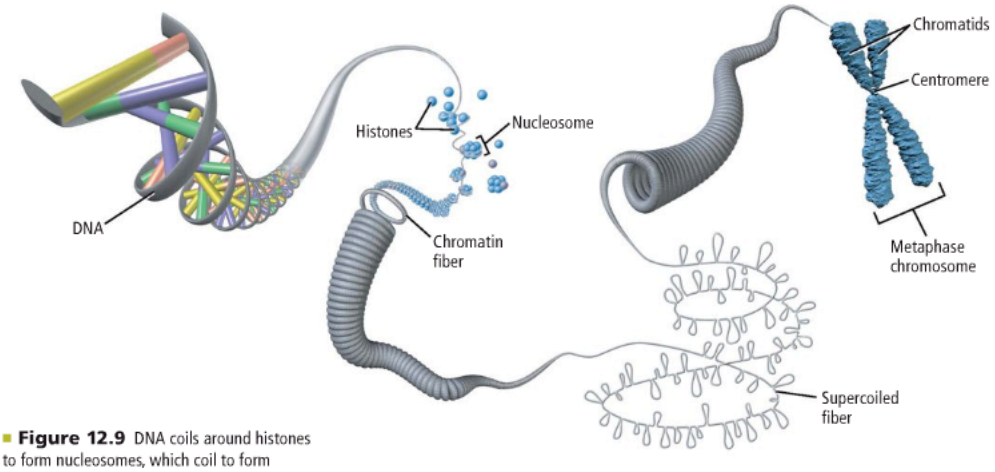


Figure 12.9 DNA coils around histones to form nucleosomes, which coil to form chromatin fibers. The chromatin fibers supercoil to form chromosomes that are visible in the metaphase stage of mitosis.

- Purines and Pyrimidines – **Because a pyrimidine (Single ring) pairs with a purine (double ring), the helix has a uniform width. (T w/ A and C w/ G)**
  - Purine – double ring
  - Pyrimide – sing ring
- Structure of a nucleotide –

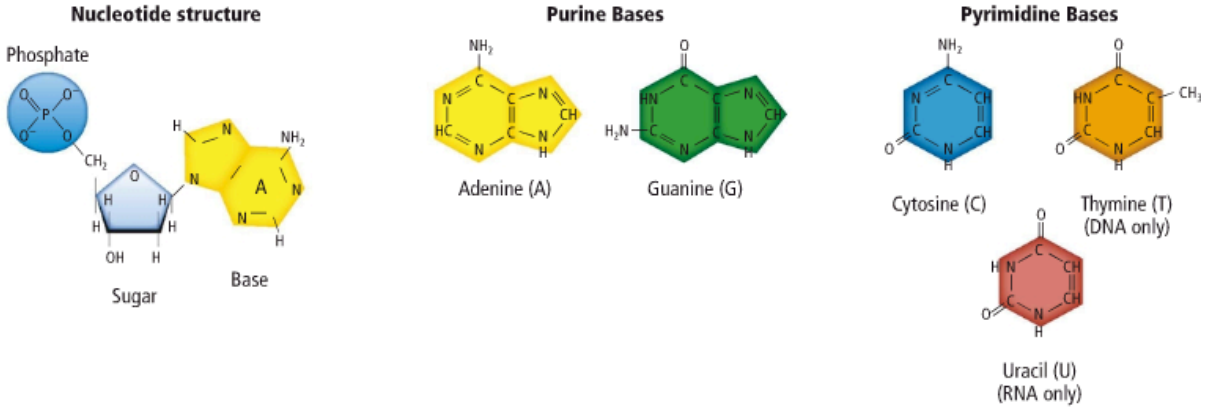


Figure 12.4 Nucleotides are made of a phosphate, sugar, and a base. There are five different bases found in nucleotide subunits that make up DNA and RNA.
Identify *What is the structural difference between purine and pyrimidine bases?*

- RNA:

Table 12.2 Comparison of Three Types of RNA

Concepts In Motion — Interactive Table To explore more about the types of RNA, visit biologygmh.com.

Name	mRNA	rRNA	tRNA
Function	Carries genetic information from DNA in the nucleus to direct protein synthesis in the cytoplasm	Associates with protein to form the ribosome	Transports amino acids to the ribosome
Example			

  - Messenger (mRNA) – contains the instructions for assembling amino acids into proteins. It is the copy of DNA that goes to the ribosome.
  - Ribosomal (rRNA) – makes up ribosomes.
  - Transfer (tRNA) – transfers each amino acid to the ribosomes during the construction of a protein.
- Transcription and translation
  - Transcription – the process by which RNA is made from DNA. It occurs in the nucleus. It requires RNA polymerase. **Example TAC becomes TUG.**
  - Translation – the decoding of an mRNA message into a polypeptide/protein. It takes place in the ribosome. mRNA has to attach to the ribosome which is located in the cytoplasm of the cell. Translation happens when the mRNA molecule attached to the ribosome, as each of the codons is read the proper amino acid is brought to the ribosome by tRNA. **Example AUG: Amino Acid Sequence – Met, tRNA anticodon – UAC.**
- Codons and anticodons
  - Codon – the genetic code is read three letters at a time. Each three-letter combination called a codon. Each codon specifies a single amino acid that is to be added to the polypeptide.
  - Anticodon – tRNA has **three unpaired bases** called anticodons in additon to one amino acid. Anticodons are complementary to one mRNA codon. **Ex. Codon: AUG – Anticodon: UAC**
- Mutagens – substances which cause mutations such as chemicals and radiation mutations.
- DNA → RNA → Protein – **Central Dogma**