5 - Nucleic Acid Structure

In Part 5, we will first learn about the major experiments that established DNA as the genetic material of nearly all organisms (recall that we learned in Part 1 that some viruses use RNA as the genetic material). Then we will learn about the structure of both DNA and RNA.

A. DNA is the Genetic Material

Transformation

The physician Frederick Griffith was interested in developing a vaccine against the bacterium *Streptococcus pneumoniae*, one of the major causes of pneumonia, ear infections, and meningitis in children. Some strains (varieties) of *S. pneumoniae* produce a polysaccharide **capsule** that surrounds the bacterial cell wall. These encapsulated strains of *S. pneumoniae* are more virulent (disease causing) than strains that do not produce a capsule. Further, the encapsulated strains of *S. pneumoniae* form smooth colonies (called type S) on bacterial culture media, those strains without capsules form rough colonies (called type R) on culture media.

In 1928, Griffith showed the following (see **figure 5.1**):

- When smooth (type S) strains of *S. pneumoniae* were injected into mice, the mice died. The smooth strain of *S. pneumoniae* could be cultured from the blood of the dead mouse.
- When rough (type R) strains of *S. pneumoniae* were injected into mice, the mice survived. No bacteria were isolated from the blood of the living mouse.
- When smooth (type S) *S. pneumoniae* were heat-killed to lyse the bacterial cells, and the bacterial extract was then injected into mice, the mice survive. No bacteria were isolated from the blood of the living mouse.
- When live rough (type R) bacteria were mixed with heat-killed smooth (type S) bacteria and injected into mice, the mice died. Note that although neither the rough (type R) bacteria nor the heat-killed smooth (type S) bacteria killed mice on their own, the mixture of the two killed the mice. The living bacteria isolated from the blood of the dead mice were smooth (type S) bacteria.

In this final experiment, Griffith reasoned that some chemical released from the heat-killed smooth (type S) bacteria was internalized by the rough (type R) bacteria. This chemical could change phenotype, converting the rough (type R) bacteria into smooth (type S) bacteria. This change in phenotype is called **transformation**. The transformed bacteria then passed the type S trait to their progeny. As a result, the chemical responsible for transformation (the **transforming principle**) had properties of the genetic material. The transforming principle changed the phenotype of the bacterial cells and is inherited when the bacterial cell divides. Unfortunately, Griffith did not identify the chemical responsible for transformation.

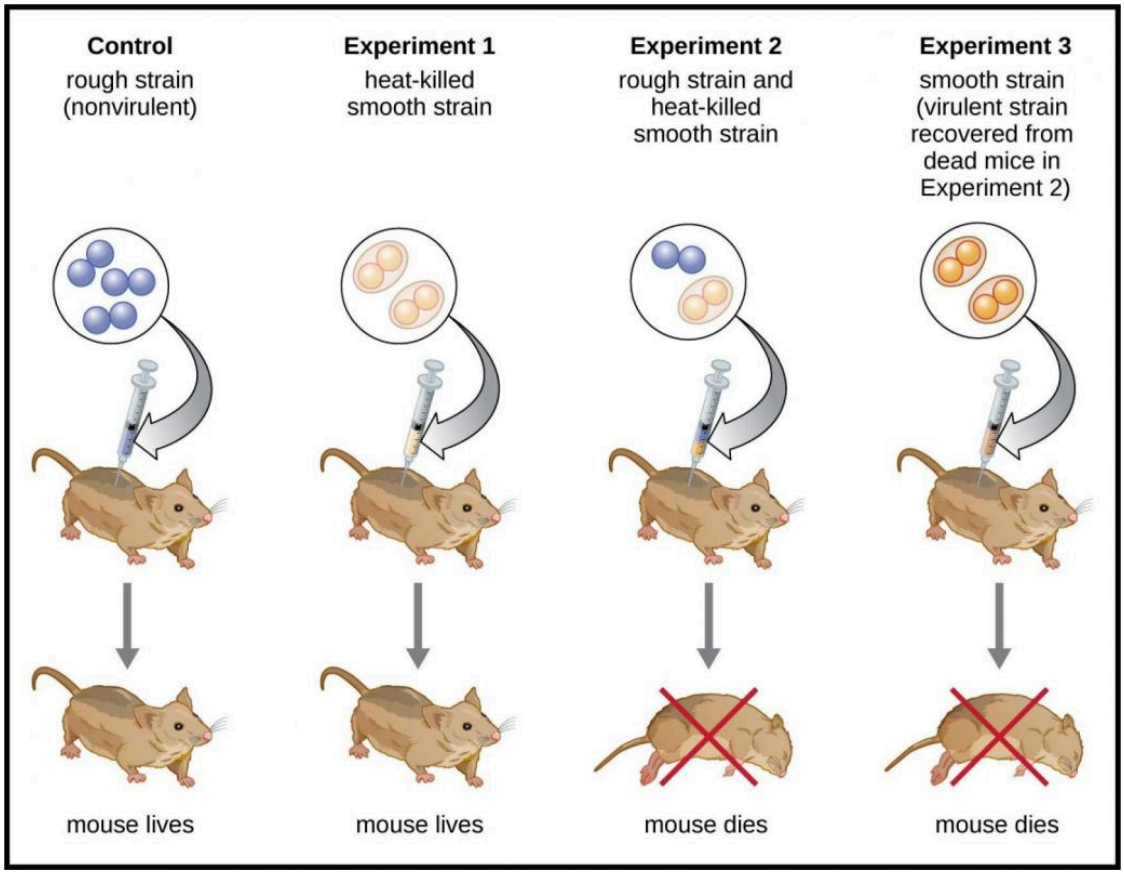


Figure 5.1 ***The Griffith Experiment ---*** *image used from OpenStax (access for free at https://openstax.org/books/biology-2e/pages/1-introduction)*

Key Questions

- Describe the Griffith experiment.
- What is meant by the “transforming principle”?
- When smooth (type S) bacteria were "heat-killed", what major class of molecules was denatured (destroyed)? What major class of molecules was not denatured?

DNA is the Transforming Principle

Oswald Avery, Maclyn McCarty, and Colin MacLeod wanted to identify the chemical responsible for transforming rough (type R) into smooth (type S) bacteria in Griffith's experiment. Avery and his colleagues focused on three candidate chemicals: DNA, RNA, and protein (see **figure 5.2**). Avery, McCarty, and MacLeod performed three experiments:

- In one experiment, rough (type R) bacterial cells were mixed with bacterial extracts from heat-killed smooth (type S) cells in the presence of **ribonuclease (RNase)** to digest RNA. When RNA was eliminated from the bacterial extract from type S cells, the rough bacteria were still transformed into smooth bacteria. Thus, digestion of RNA had no effect on transformation.
- In a second experiment, rough (type R) bacterial cells were mixed with bacterial extracts from heat-killed smooth (type S) cells in the presence of **protease** to digest proteins. When protein was eliminated from the bacterial extract from type S cells, the rough bacteria were still transformed into smooth bacteria. Thus, digestion of protein had no effect on transformation.
- In a final experiment, rough (type R) bacterial cells were mixed with bacterial extracts from heat-killed smooth (type S) cells in the presence of **deoxyribonuclease (DNase)** to digest DNA. Interestingly, the rough bacteria were not transformed into smooth bacteria when DNA was eliminated from the bacterial extract. Thus, the digestion of DNA prevented transformation.

Avery and colleagues concluded from these experiments that DNA (not RNA nor protein) was the chemical responsible for transforming rough bacteria into smooth bacteria in Griffith's experiment. Therefore, DNA is the genetic material of the bacterium *S. pneumoniae*.

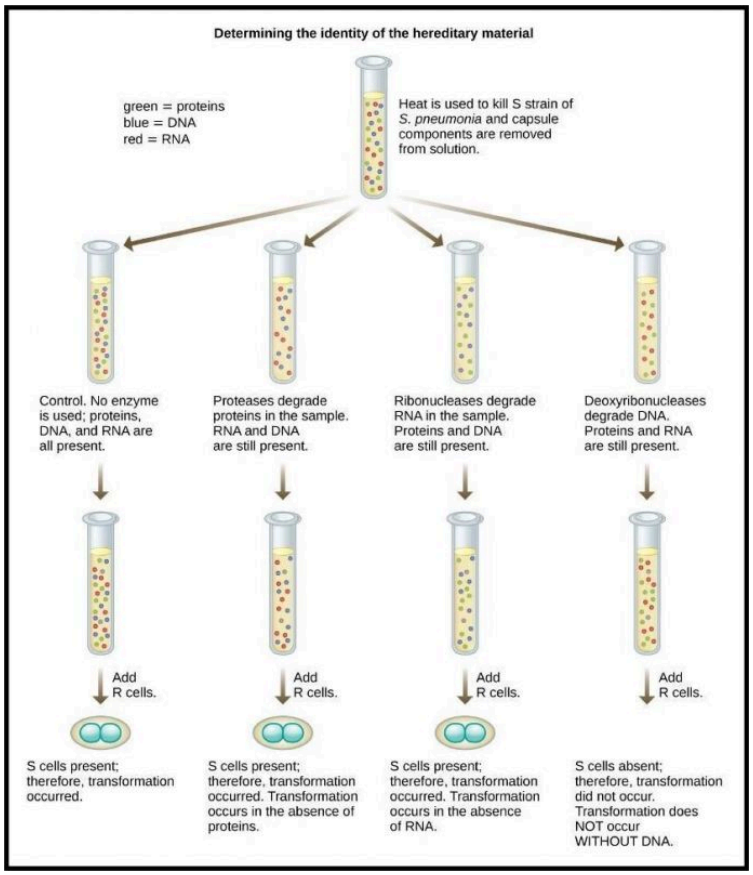


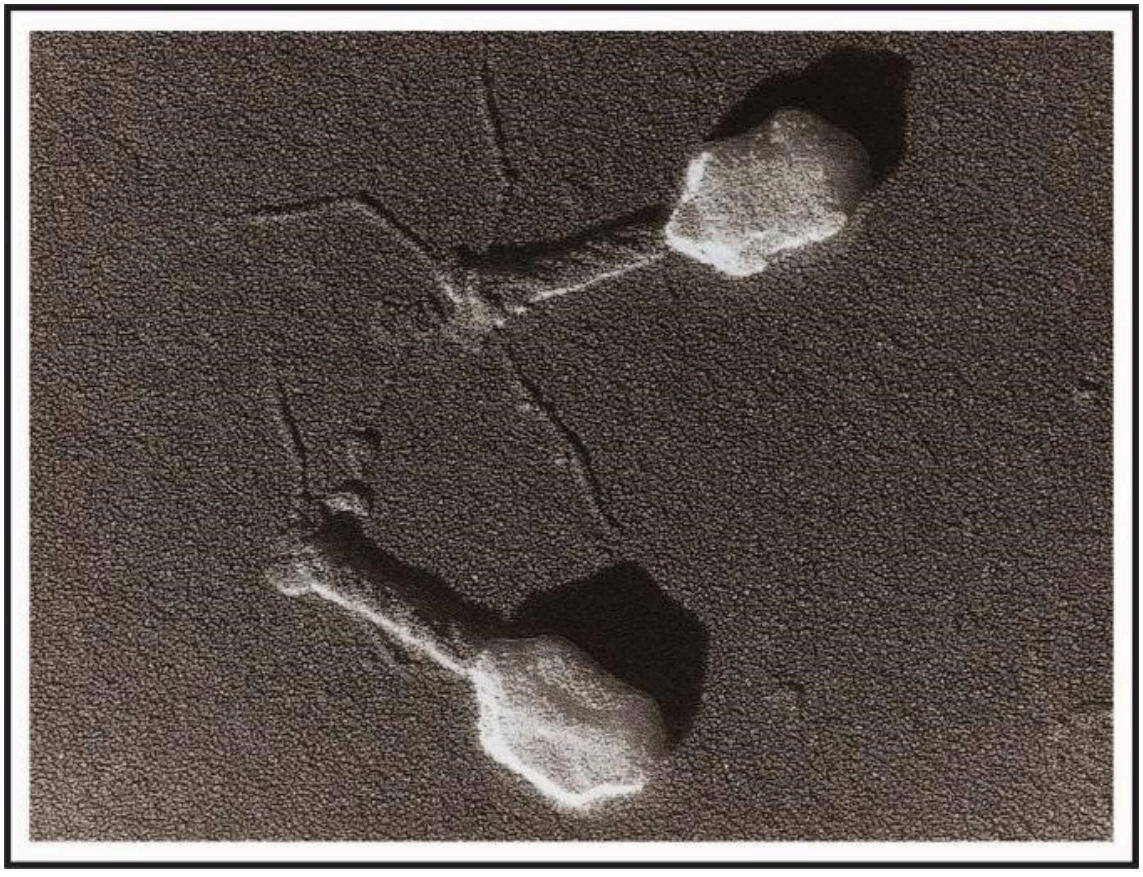
Figure 5.2 ***Avery, McCarty, MacLeod Experiment ---*** *image used from OpenStax (access for free at https://openstax.org/books/biology-2e/pages/1-introduction)*

Key Questions

- Describe the Avery, McCarty, and MacLeod experiment.
- What was the key finding of the experiment?

Bacteriophage T2

To confirm the results from Avery, McCarty, and MacLeod, Alfred Hershey and Martha Chase examined **T2 bacteriophage.** T2 bacteriophage is a type of virus that infects the bacterium *Escherichia coli* (see **figure 5.3**). T2 bacteriophages contain two molecular components: DNA and protein. The DNA of the bacteriophage is encased within a bacteriophage head structure made of protein. T2 bacteriophage also contains other protein structures, including a tube-like sheath, tail fibers, and a base plate. During the bacteriophage life cycle, T2 bacteriophage acts like a hypodermic needle, injecting the bacteriophage genetic material into a host *E. coli* cell. The genetic material of the bacteriophage then reprograms the host *E. coli* cell to shut off many host cell functions and instead produce progeny T2 bacteriophages. Hershey and Chase were interested in determining which of the two bacteriophage T2 components, DNA or protein, was responsible for producing progeny bacteriophage particles. In essence, Hershey and Chase were asking whether DNA or protein is the genetic material of bacteriophage T2.



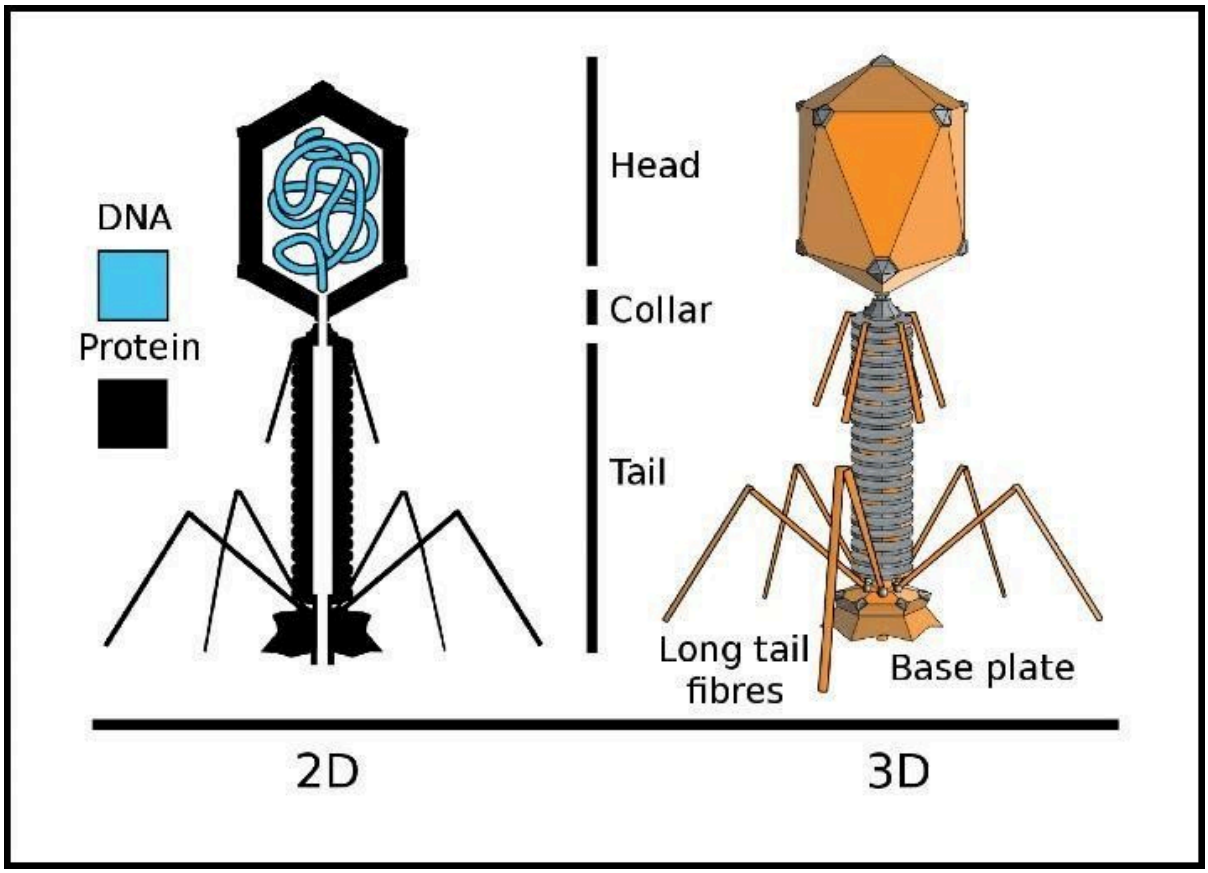


Figure 5.3 ***A) Typical Bacteriophage.*** *The bacteriophage was imaged in a scanning electron microscope.* ***---*** *licensed under CC BY 4.0* ***B) Bacteriophage Structure ---*** *Tevenphage by Adenosine licensed under CC BY-SA 2.5*

The Hershey-Chase Experiment

The Hershey and Chase experiment relied on two important experimental details:

- A kitchen blender can separate the bacteriophage components that remain attached to the surface of the host bacterial cell from the bacteriophage components that are injected into the cytoplasm of the *E. coli* cell.
- Bacteriophage proteins can be distinguished from bacteriophage DNA using radioactive labeling. Bacteriophage proteins were radiolabeled with ^{35}S (a radioactive isotope of sulfur) and the bacteriophage DNA was radiolabeled with ^{32}P (a radioactive isotope of phosphorus). Note that sulfur is found in proteins and not in DNA; phosphorus is a component of DNA and is not found in proteins. Thus, Hershey and Chase could determine whether DNA or protein is the bacteriophage T2 genetic material by determining whether ^{35}S or ^{32}P is injected into the host *E. coli* cell during a bacteriophage infection.

The Hershey and Chase experiment was done as follows (see **figure 5.4**):

1. In one experiment, bacteriophage T2 proteins were radiolabeled with ^{35}S. In another experiment, bacteriophage T2 DNA was radiolabeled with ^{32}P.
2. The radiolabeled bacteriophages were mixed in two separate reactions with *E. coli* cells to allow bacteriophage infections to occur.
3. After bacteriohage T2 injected its genetic material, the reactions were subjected to blending. During blending, the bacteriophage components that remained on the surfaces of the *E. coli* cells were released.
4. The infected *E. coli* were collected in a centrifuge. The empty bacteriophage components (phage head, tail, tail fibers) remain in the supernatant (liquid) after centrifugation. The *E. coli* cells and the bacteriophage genetic material are found in a pellet at the bottom of the centrifuge tube.
5. The amount of radioactivity in the supernatant and pellet was calculated.

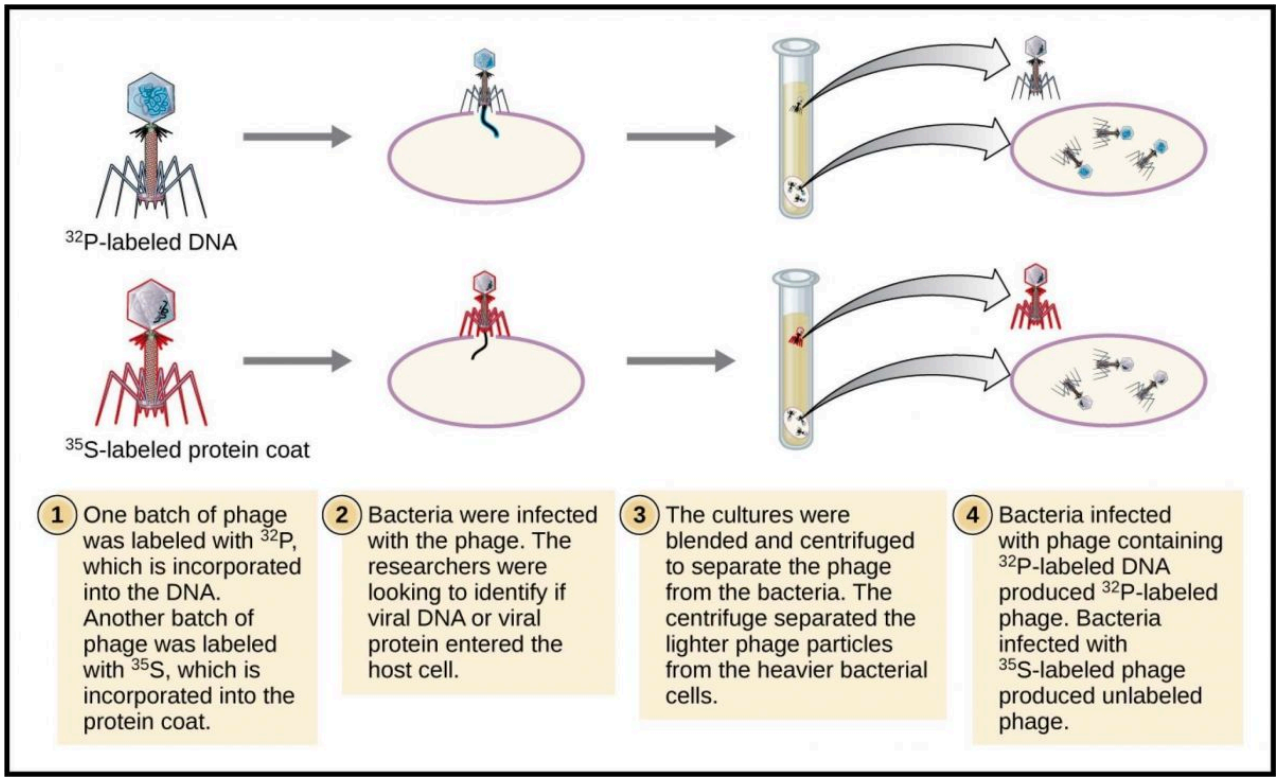


Figure 5.4 ***Hershey - Chase Experiment ---*** *image used from OpenStax (access for free at https://openstax.org/books/biology-2e/pages/1-introduction)*

Blending removed most of the ^{35}S from the *E. coli* cells in the pellet. Thus, proteins are not injected into *E. coli* to direct the formation of progeny T2 bacteriophages. In contrast, most of the ^{32}P was found in the host *E. coli* cells in the pellet after blending and centrifugation, indicating that DNA is injected into host *E. coli* cells. Note that after the completion of the bacteriophage life cycle, the progeny bacteriophages also contained ^{32}P; the progeny bacteriophages contained little ^{35}S. Thus, the ^{32}P labeled DNA is heritable. The Hershey and Chase experiment showed that DNA serves as the genetic material for bacteriophage T2. The work of Avery, McCarty, and MacLeod combined with the results of the Hershey-Chase experiment provided compelling evidence that DNA is the genetic material of viruses and bacteria.

Key Questions

- Describe the Hershey-Chase experiment.
- What was the key finding of the experiment?

DNA is the Genetic Material of Eukaryotes

Eukaryotic cells are not as easy to work with in the lab as bacteria and bacteriophages. As a result, it was easier to determine that DNA is the genetic material of bacteria and bacteriophages than eukaryotic cells. Evidence that DNA is the genetic material of eukaryotes relied on the combination of both indirect evidence and direct evidence.

Several lines of indirect evidence suggest that DNA is the genetic material of eukaryotic cells. Scientists reasoned that the genetic material of eukaryotes should be found within chromosomes because chromosomes are copied and distributed to daughter cells during mitosis and meiosis. Chromosomes contain both proteins and DNA; however, the DNA component is found exclusively in chromosomes (protein is found in the cell cytoplasm as well). In addition, a

diploid cell, which contains twice as many chromosomes as a haploid cell, also contains roughly twice as much DNA as a haploid cell. No such correlation was observed when the protein content of haploid and diploid cells was compared. Finally, **ultraviolet light (UV light)** causes mutations that affect the phenotype of a cell. The wavelength of UV light that produces the highest frequency of mutations corresponds to the wavelength of UV light that is absorbed most strongly by DNA. On the other hand, the wavelength of UV light absorbed most strongly by proteins does not alter phenotpye.

Recombinant DNA technology provided direct evidence that DNA is the genetic material of eukaryotic cells. In this technique, a DNA sequence from a eukaryotic cell is isolated and then introduced into a bacterial cell. This eukaryotic DNA sequence can then be transcribed by the bacterial cell to make a messenger RNA (mRNA); the mRNA is then translated by bacterial ribosomes to make a protein. The resulting protein often changes the phenotype of the bacterial cell. Moreover, the introduced eukaryotic DNA sequence is passed on to the progeny bacterial cells during bacterial cell division. As an example, recombinant DNA technology allowed scientists to insert the human insulin gene into bacteria. These bacterial cells then produce the human insulin protein (change in phenotype) and transfer the human insulin gene to daughter cells after cell division (inherited). The fact that introduced eukaryotic gene can result in protein production, can alter the phenotype of a bacterial cell, and can be passed to progeny bacterial cells provided strong evidence that DNA is the genetic material of eukaryotes.

Key Questions

- What are the three lines of indirect evidence that DNA is the genetic material of eukaryotes?
- What direct evidence shows that DNA is the genetic material of eukaryotes?

B. The Structure of DNA and RNA

Overview of Nucleic Acid Structure

Nucleic acid molecules (DNA and RNA) have four levels of structural complexity (see **figure 5.5**):

- **Nucleotide**. Nucleotides are the basic subunits (the building blocks) of nucleic acid molecules.
- **Nucleic acid strand**. A nucleic acid strand is a chain of nucleotides covalently linked together via **phosphodiester** bonds.
- **Double helix**. Two nucleic acid strands of either DNA or RNA can hydrogen bond together to form a double helix structure.
- **Chromosomes**. DNA molecules associate with NAP proteins or histone proteins to form prokaryotic and eukaryotic chromosomes. We discussed the structures of prokaryotic and eukaryotic chromosomes in Part 2.

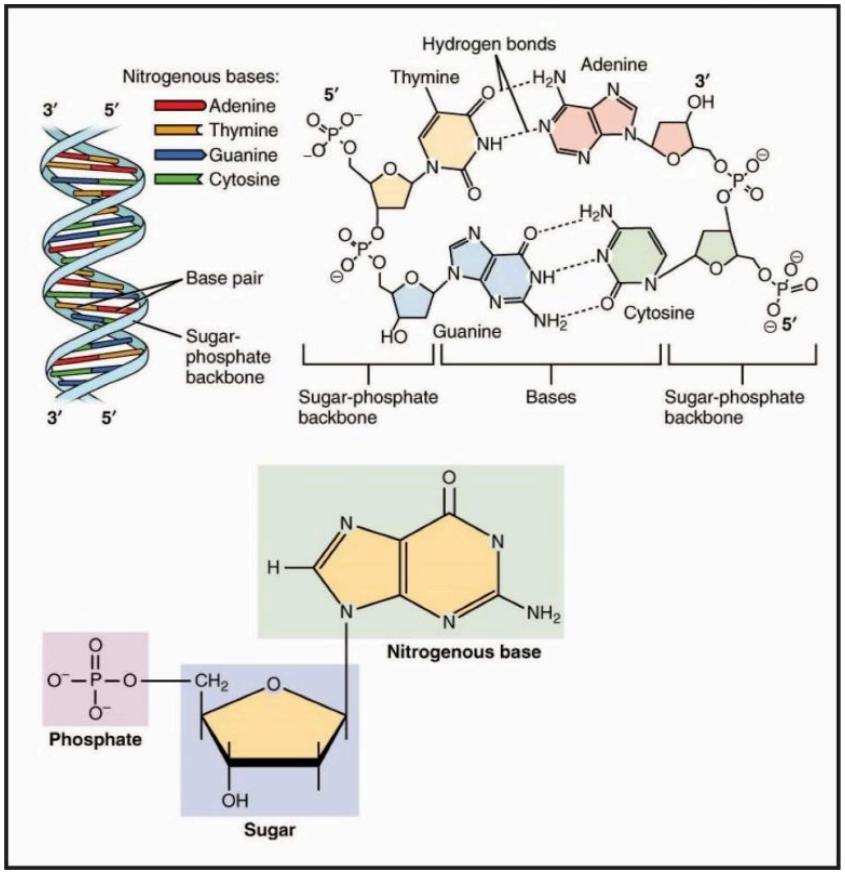


Figure 5.5 ***Overview of DNA Structure.*** *The basic subunits of DNA and RNA are nucleotides (bottom). Two nucleic acid strands can interact through hydrogen bonding (upper right). The general structure of a DNA double helix (upper left). This image is from OpenStax (access for free at* https://openstax.org/books/biology-2e/pages/1-introduction*)*

Nucleotides

A nucleotide is composed of the following molecular components (see **figure 5.6**):

- **One, two, or three phosphate groups**. When the cell synthesizes DNA and RNA strands, the nucleotides used as substrates contain three phosphate groups. However, When a nucleotide is incorporated into a DNA or RNA strand, two of the phosphate groups are released.
- **A pentose sugar**. In DNA, the pentose sugar is **deoxyribose**; in RNA, the pentose sugar is **ribose**. Deoxyribose and ribose are distinguished by the chemical groups attached to the carbon atoms within the pentose sugar. Specifically, the carbon atoms within both deoxyribose and ribose are numbered 1' (one-prime) to 5' (five prime) (**see figure 5.6**). The nitrogenous base (see below) in both deoxyribose and ribose is attached to 1' carbon. The 2' carbon in deoxyribose is attached to two hydrogen atoms, the 2' carbon in ribose is attached to a hydroxyl group and a hydrogen atom. As a result, one of the fundamental differences between a DNA nucleotide and an RNA nucleotide is the chemical group attached to the 2' carbon. The 3' carbon in both deoxyribose and ribose is attached to a hydroxyl group. It is important to note that the hydroxyl group attached to the 3' carbon plays a critical role in DNA and RNA synthesis (see Parts 6 and 9). The 4' carbon in both deoxyribose and ribose is involved in maintaining the integrity of the pentose ring structure. The 5' carbon in both deoxyribose and ribose is attached to a phosphate group. This phosphate group also plays an important role in DNA and RNA synthesis (see Parts 6 and 9).
- **A nitrogenous base**. There are two types of nitrogenous bases found in DNA and RNA nucleotides (see figure 5.6):
  - **Pyrimidines**. The pyrimidine nitrogenous bases consist of a single carbon/nitrogen ring structure. The pyrimidine bases are **cytosine (C)**, **thymine (T)**, and **uracil (U)**. T is found only in DNA; U is found only in RNA. C is found in both DNA and RNA.
  - **Purines**. The purine nitrogenous bases consist of a double carbon/nitrogen ring structure. The purines bases include **adenine (A)** and **guanine (G)**. A and G are found in both DNA and RNA.

The nucleotide substrates used to build DNA and RNA are called **deoxynucleoside triphosphates (dNTPs)** and **nucleoside triphosphates (NTPs)**, respectively. In the dNTP/NTP nomenclature "N" is the specific name of the nitrogenous base (A,U,C,G, and T); TP refers to triphosphate. For example, dTTP contains deoxyribose as the pentose sugar; deoxyribose is attached to thymine (1' carbon) with three phosphate groups attached to the 5' carbon. GTP contains ribose as the pentose sugar; ribose is attached to guanine (1' carbon) with three phosphate groups attached to the 5' carbon.

Key Questions

- What are the functions of the 1', 2', 3', 4' and 5' carbons in deoxyribose and ribose?
- How are purines and pyrimidines different?
- Which purines and pyrimidines are found in DNA?
- Which purines and pyrimidines are found in RNA?
- What is meant by "dNTP" and "NTP"?

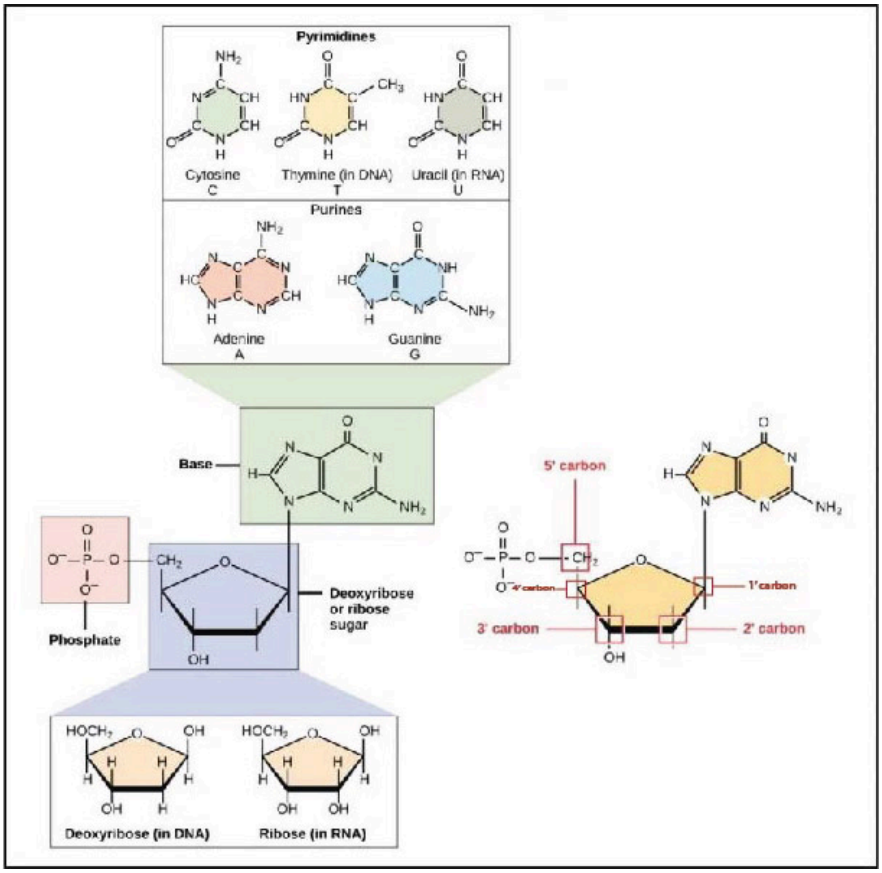


Figure 5.6 ***Nucleotide Structure*** *--- image used from OpenStax (access for free at* https://openstax.org/books/biology-2e/pages/1-introduction*)*

Nucleic Acid Strands

Nucleotides are covalently linked to form a nucleic acid **strand** (see **figure 5.7**). Specifically, the sugars of two adjacent nucleotides are linked together by **phosphodiester bonds** to form the **backbone** of the nucleic acid strand. The phosphate groups in the backbone give the nucleic acid strand a negative electrical charge.

A strand of DNA or RNA has **directionality** or **polarity**. The formation of phosphodiester bonds between nucleotides produces a nucleic acid strand in which the 5′ carbon of the nucleotide at one end of the strand contains a free phosphate group (the **5′ end** of the strand). The 3′ carbon of the nucleotide at the other end of the nucleic acid strand (the **3′ end** of the strand) is attached to a free hydroxyl group.

Each nucleic acid strand has a particular sequence of nitrogenous bases. The sequence of these nitrogenous bases on a single nucleic acid strand is written from the free 5′ end to the free 3′ end, for example 5′-TTGCAGG-3′. The sequence of the nitrogenous bases allows nucleic acid molecules to carry genetic information.

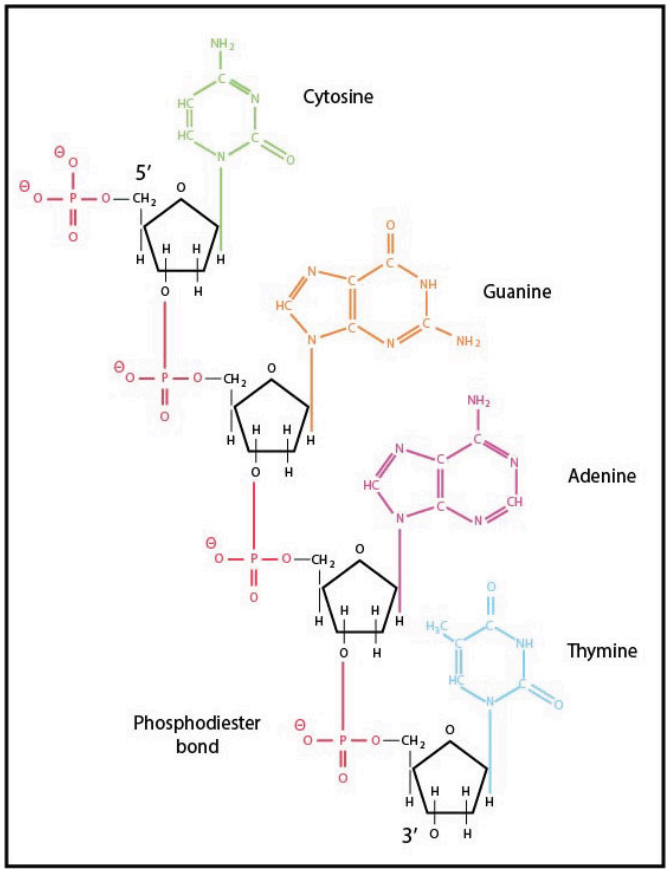


Figure 5.7 ***Structure of a DNA Strand.*** *The sequence of this nucleic acid strand is 5′-CGAT-3′. --- Image created by SL*

Key Questions

- How are adjacent nucleotides linked within a nucleic acid strand?
- How do you know which end of the nucleic acid strand is the 5′ end and which end is the 3′ end?

Determining the Structure of the Double Helix

James Watson and Francis Crick were awarded the Nobel Prize in 1962 for determining the structure of DNA; however, their work was built upon the contributions of other noteworthy scientists (see **figure 5.8**). For example, in the early 1950s, Linus Pauling, who won two Nobel Prizes himself, demonstrated that ball-and-stick models could describe the locations of individual atoms within biological molecules. Pauling is known for using ball-and-stick models to describe the secondary structures found within proteins. Watson and Crick mimicked Pauling's approach by building a ball-and-stick model of the DNA double helix.

The structure of the DNA double helix could not have been determined without the **X-ray diffraction** technique. X-ray diffraction involves subjecting a substance, such as DNA, to X-rays. When the X-rays pass through the DNA, the atoms within the DNA diffract the X-rays to produce a unique pattern on photographic film. This pattern can be interpreted using mathematics to determine the location of every atom within DNA. Rosalind Franklin and Maurice Wilkins used X-ray diffraction to determine that DNA has a helical structure and a diameter of 2 nanometers (2 nm), suggestive of two nucleic acid strands.

Moreover, Erwin Chargaff isolated DNA from many different organisms (bacteria, yeast, chickens, and humans) and then studied the nitrogenous base composition of this isolated DNA. Chargaff found that the total percentage of adenine (A) within any DNA molecule was nearly identical to the total percentage of thymine (T). Likewise, the percentage of cytosine (C) was nearly identical to the total percentage of guanine (G). These relationships are known as **Chargaff's rule**.

Watson and Crick used the observations/approaches of Pauling, Franklin, Wilkins, and Chargaff to build a ball-and-stick DNA model with the following features:

- The phosphate-sugar backbones of the two nucleic acid strands are on the outside of the DNA molecule.
- The nitrogenous bases are on the inside of the DNA molecule.
- The two nucleic acid strands are antiparallel (see below).
- Adenine forms two hydrogen bonds with thymine within the center of the DNA molecule; guanine forms three hydrogen bonds with cytosine. These hydrogen bonding interactions between nitrogenous bases are called **base pairing**.

Watson and Crick also proposed a mechanism by which the DNA double helix could be copied prior to cell division (**semi-conservative replication**). We will examine the process of semi-conservative replication in Part 6.

Key Questions

- What was the contribution of Pauling, Franklin and Wilkins, and Chargaff to the DNA story?
- Describe Watson and Crick's model of the DNA double helix.

The DNA Double Helix

Watson and Crick showed that the two phosphate-sugar backbones within DNA are found on the outside of the DNA molecule, directly exposed to water within the cell (see **figure 5.9**). Also, hydrogen bonds are formed between pairs of nitrogenous bases, called **base pairs (bp)**, located in the interior of the double-helix. Adenine always forms two hydrogen bonds with thymine, and guanine always forms three hydrogen bonds with cytosine. This relationship between nitrogenous bases is called the **AT/GC rule** or **Chargaff's rule**. Thus, the nitrogenous bases in one strand of DNA are **complementary** to the nitrogenous bases in the other DNA strand. Because of these hydrogen bonding interactions, DNA sequences with a higher proportion of GC base pairs are more stable than DNA molecules that are rich in AT base pairs. Additionally, there are 10 base pairs per complete turn of the DNA double helix. Every turn is 3.4 nm in length, meaning that each base pair within the DNA double helix is separated by 0.34 nm. The DNA double helix is 2 nm wide.

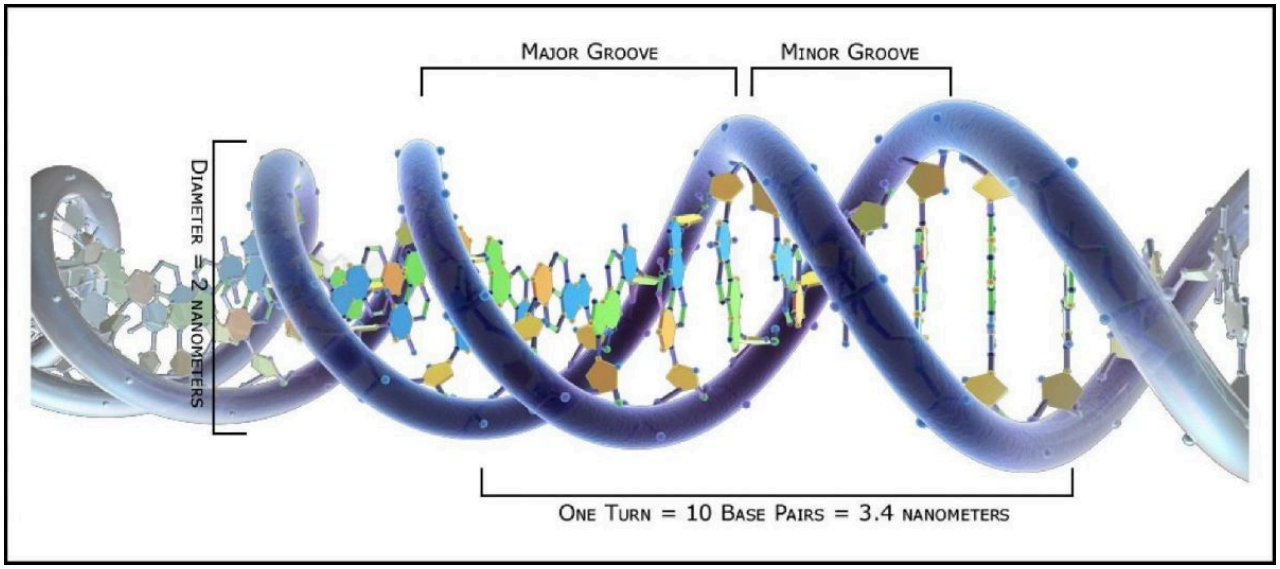


Figure 5.9 ***DNA Double Helix Structure.*** *The backbones of each DNA strand are represented by blue ribbons. [3D Science DNA Structure](#) by [3DScience.com](#) used under license [CC BY 2.5](#)*

The two nucleic acid strands of DNA are **antiparallel (**see **figure 5.10)**. One DNA strand starts with the free 5' phosphate group at the top of the DNA strand and ends with the free 3' hydroxyl group at the bottom. The other DNA strand runs in the opposite direction; the free 5' phosphate group is at the bottom end of the DNA strand, the free 3' hydroxyl group is at the top.

You can predict the sequence of one strand of DNA if you know the sequence of the other DNA strand. For example, if one DNA strand is 5'-GCCATG-3', then the opposite DNA strand is 3'-CGGTAC-5'. As a result, the two DNA strands are said to be **complementary** (see **figure 5.10**).

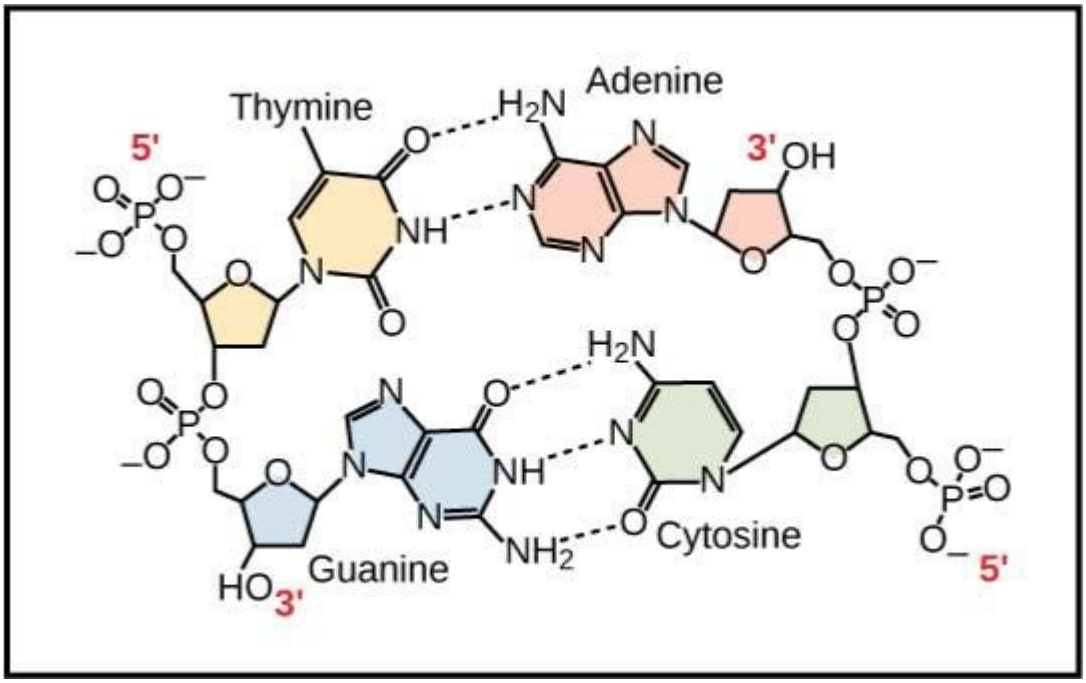


Figure 5.10 ***Complementary Base Pairs*** *--- Image used from OpenStax (access for free at [https://openstax.org/books/biology-2e/pages/1-introduction](#))*

Key Questions

- What is the distance between adjacent base pairs within DNA?
- How many base pairs are found per helical turn in DNA?
- How does DNA strand polarity relate to the antiparallel structure of DNA?

Other Features of DNA

The backbone of the DNA double helix is right-handed, meaning that the backbone turns in the clockwise direction as you look down the axis of the DNA molecule. Within the central part of the double helix, the nitrogenous bases form hydrogen bonds (A with T; G with C). The base pairs themselves are flat (planar) and stack on top of each other, much like the stairs of a spiral staircase. On the outside of the DNA double helix, there are **major** and **minor** grooves where the nitrogenous bases are directly exposed (see **figure 5.9** above). Proteins that bind to specific base pair sequences within the DNA double-helix interact mainly with the major groove and to a lesser extent with the minor groove. These proteins bind to the DNA double helix to control DNA replication and transcription.

Key Questions

- How do DNA-binding proteins recognize the nitrogenous bases in DNA?

Alternative Forms of DNA

The structure of the DNA double helix detailed above is the standard form of DNA **(B DNA)**. B DNA is the predominant form of DNA that is found in aqueous environments, including living cells. Interestingly, there are at least two alternative forms of DNA, called **A DNA** and **Z DNA** (see **figure 5.11**).

The A form of DNA is produced in the laboratory under high salt (low water) conditions. The A DNA structure is more compact than B DNA, has 11 base pairs (bp) per turn of the helix, and is 2.3 nm wide. Like B DNA, A DNA is a right-handed double helix; however, while the base pairs are perpendicular to the axis of the double helix in B DNA, the base pairs in A DNA are tilted relative to the axis of the molecule.

The Z form of DNA is a left-handed double helix, having a more extended structure. Z DNA has 12 base pairs per turn of the helix, and is only 1.8 nm wide. Z DNA is favored over B DNA when cytosine bases are modified by the addition of **methyl** ($-CH_3$) chemical groups. The functional significance of Z DNA is unknown; however, Z DNA may form in certain circumstances within living cells. Scientists speculate that Z DNA formation near a particular gene may influence whether the gene can be activated by transcription to produce an RNA molecule.

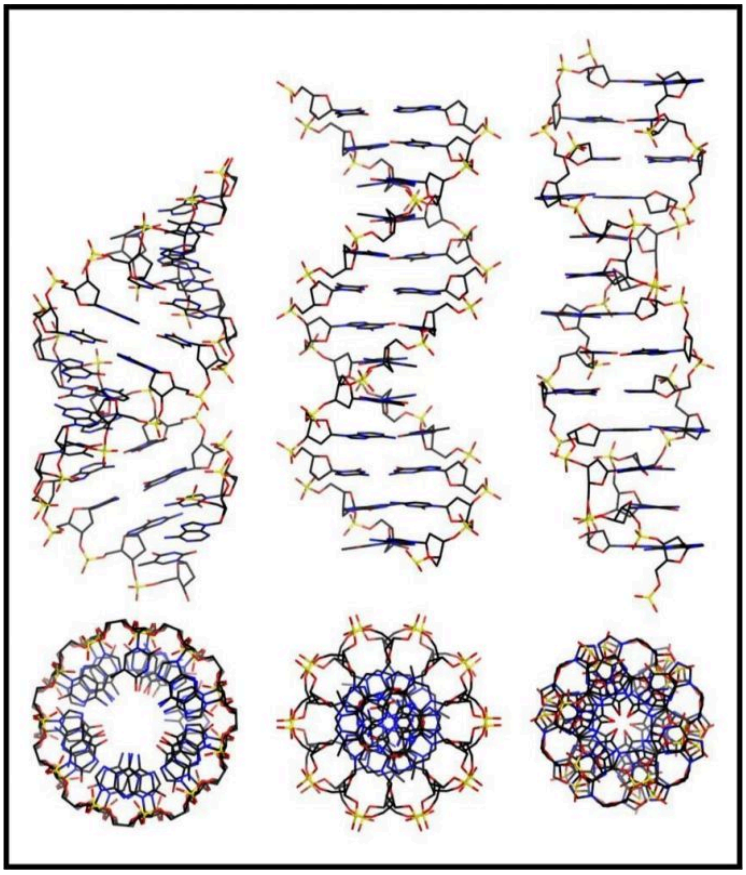


Figure 5.11 ***Left) A-DNA, Middle) B-DNA, Right) Z-DNA*** *---* *DnaConformations by Mauroesguerroto licensed under CC BY-SA 4.0*

Key Questions

- How do A-DNA, B-DNA, and Z-DNA differ from one another?

RNA Structure

Nucleic acid strands composed of RNA nucleotides have a similar structure as DNA strands. For example, RNA strands have a backbone composed of negatively charged phosphate groups, adjacent nucleotides within an RNA strand are linked by phosphodiester bonds, and the RNA strand has polarity (5' and 3' ends). However, RNA differs from DNA in that RNA molecules contain the pentose sugar ribose, RNA molecules are often single-stranded, and RNA strands are much shorter than DNA strands.

Since many RNA molecules are single-stranded, there is the possibility that nitrogenous bases in one part of an RNA molecule can form base pairs via hydrogen bonding with nitrogenous bases in another part of the same RNA molecule. These base pairing interactions form short regions of double-stranded RNA. One important RNA structure formed in this way is a **stem-loop (hairpin loop)**. For example, **transfer RNA (tRNA)** molecules, which play a critical role in the translation process (see Part 11), are noteworthy because each tRNA molecule contains three stem-loop structures (see **figure 5.12**).

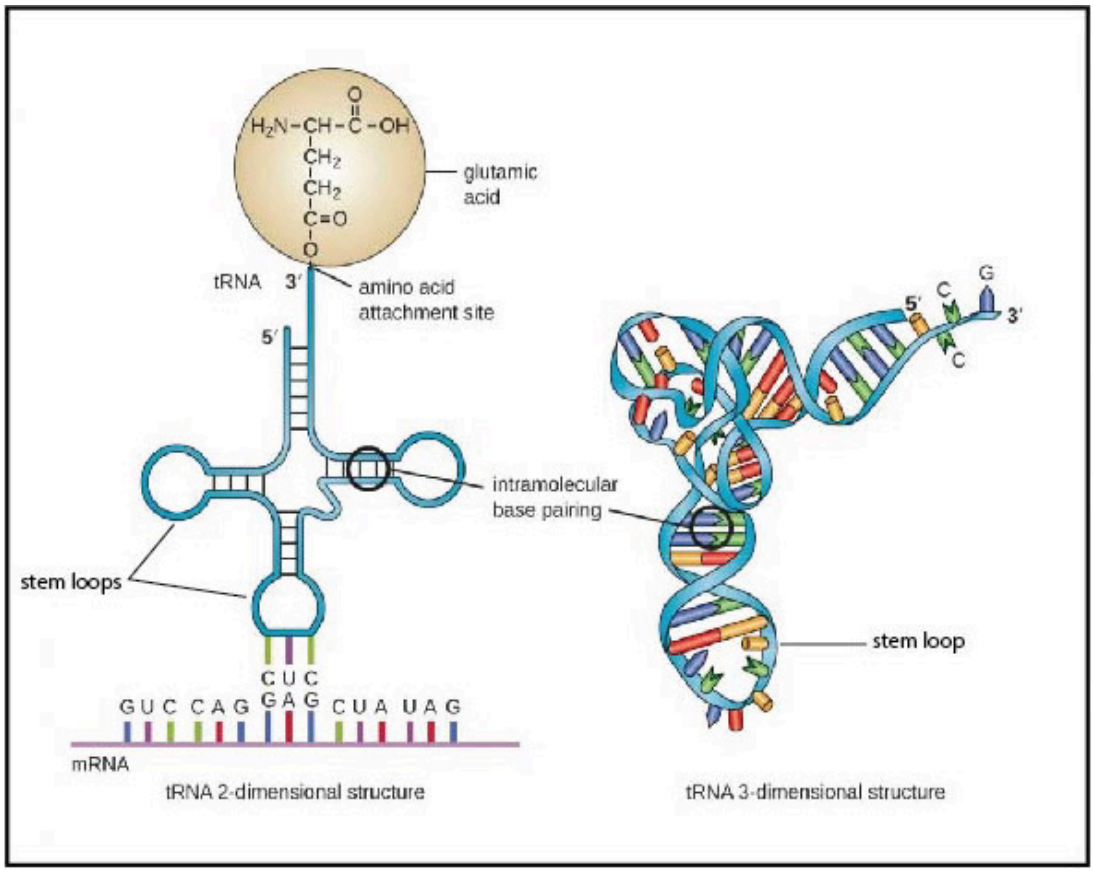


Figure 5.12 ***tRNA Structure*** *--- Image used from OpenStax (access for free at* https://openstax.org/books/biology-2e/pages/1-introduction*)*

Key Questions

- What are the structural differences between DNA and RNA?

Review Questions

Fill in the Blank:

1. In the Griffith experiment, the _____ strain of bacteria kills the mouse.
2. The bacterium _____ was used in the Hershey-Chase experiment, while the bacterium _____ was examined in the Frederick Griffith experiment.
3. Avery, McCarty, and MacLeod found that the enzyme _____ destroyed the transforming principle in bacteria, whereas the enzymes _____ and _____ did not.
4. The _____ experiment showed that DNA is the genetic material of bacteriophage T2.
5. In eukaryotes, a _____ cell has twice the amount of DNA as a _____ cell, but both cells have similar amounts of protein.
6. Each base pair within the DNA double helix is separated by _____ nanometers (nm).
7. The two purines found in RNA are _____ and _____.
8. The pentose sugar in dCTP is _____, while the pentose sugar in ATP is _____.
9. Proteins bind to DNA primarily at the _____ groove.
10. The _____ form of DNA exists in aqueous environments while the _____ form of DNA exists when cytosines are methylated.
11. The _____ experiment is sometimes called the “blender experiment”.