

8.3: Secondary structure and replication of DNA

Learning Objectives

- Understand the double helix model and the replication process of DNA.

Secondary structure of DNA

Double helix model of DNA

It was observed from experimental data that although the composition of DNA varies from specie to specie, the amount of adenine (A) is always equal to the amount of thymine (T), and the amount of guanine (G) is always equal to the amount of cytosine (C). In 1953, Watson and Crick proposed a model of DNA with the help of Franklin's X-ray analysis. The Model, illustrated in Figure 8.3.1, is:

- a DNA molecule is made up of two strands wound around each other like a spiral stair ladder,
- the two strands run antiparallel, i.e., one from a 5' to 3' and the other from a 3' to 5' direction,
- each strand has a backbone of alternating deoxyribose and phosphate, groups like the rails of the stair ladder, and
- the two strands are connected at each nucleotide through hydrogen bonds between nitrogen bases: adenine associated with thymine of the second strand, and guanine connected with cytosine of the second strand, or vice versa, like a closed zip.

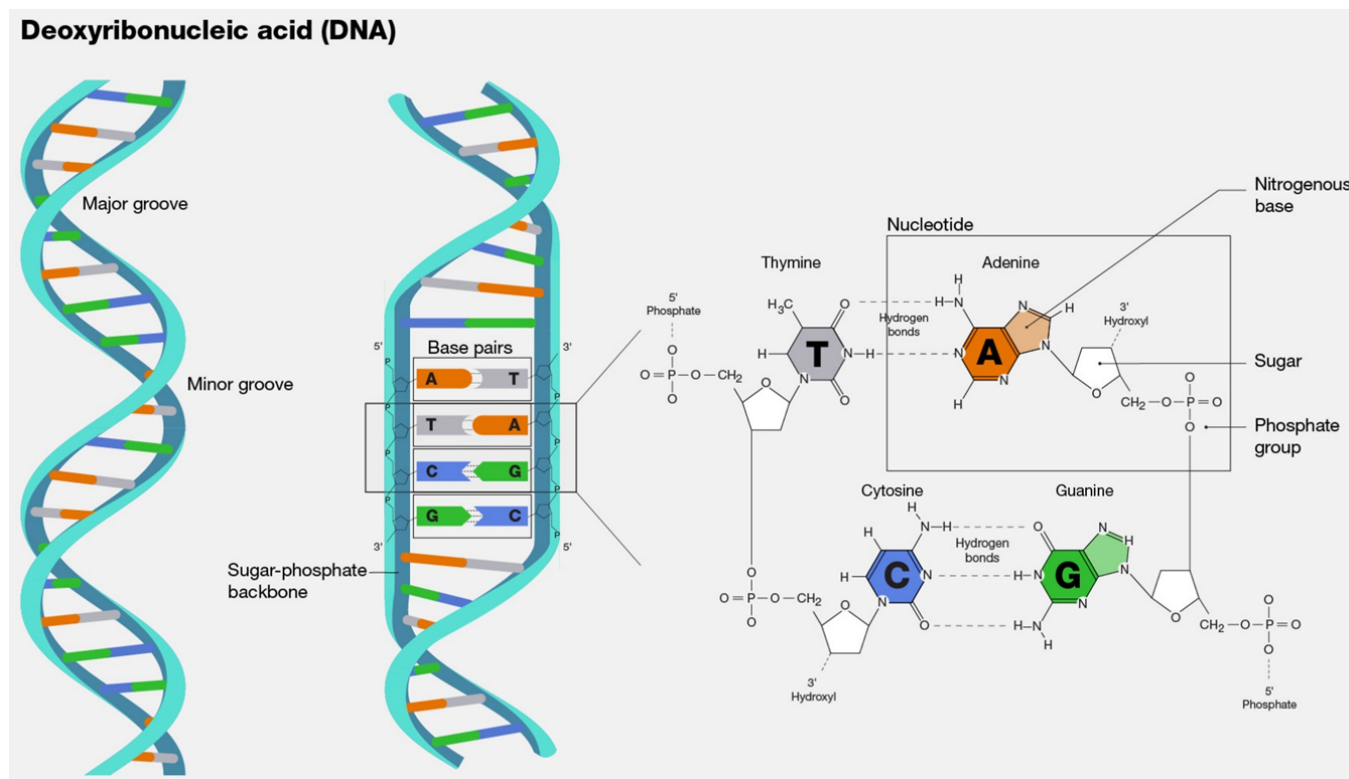


Figure 8.3.1: Double helix model of DNA (left), a section showing an overlay of alternating deoxyribose and phosphate backbone making the railing; adenine (A) paired with thymine (T) or guanine (G) paired with cytosine (C) making the steps of the double helix (middle); and a subsection enlarged to show the skeletal structure with T bonded with A by two hydrogen bonds and C connected with G by three hydrogen bonds (right). (Copyright; [National Human Genome Research Institute](#), Public domain)

The logic of complementary base pairing

Two strands of DNA are complementary to each other as adenine (A) always faces thymine (T), and guanine (G) meets cytosine (C) in the other strand. The AT and GC are called complementary base pairs. The logic of this complementing is the following:

- Purines, i.e., adenine (A) and guanine (G), are larger, and pyrimidines, i.e., cytosine (C) and thymine (T), are smaller. So, a purine in one strand pairs with a pyrimidine in the other strand to keep a nearly uniform gap between the two strands.

- Adenine (A) makes two hydrogen bonds with thymine (T), and guanine (G) makes three hydrogen bonds with cytosine (C) in the other strand. The other possible combinations of purine and pyrimidine are unstable: A can have no hydrogen bond with C, and G can have only one with T.

The base pairing, i.e., AT and GC, complements the two strands. The multiple hydrogen bonding between each nucleotide of DNA holds the two strands together like a closed zip.

Replication of DNA

When a cell divides into two, each daughter cell needs a complete set of genetic information from the parent cell. The genetic information is in the form of the sequence of nucleotides in the DNA.

DNA replication is the process by which the DNA is copied in a cell at the time of cell division.

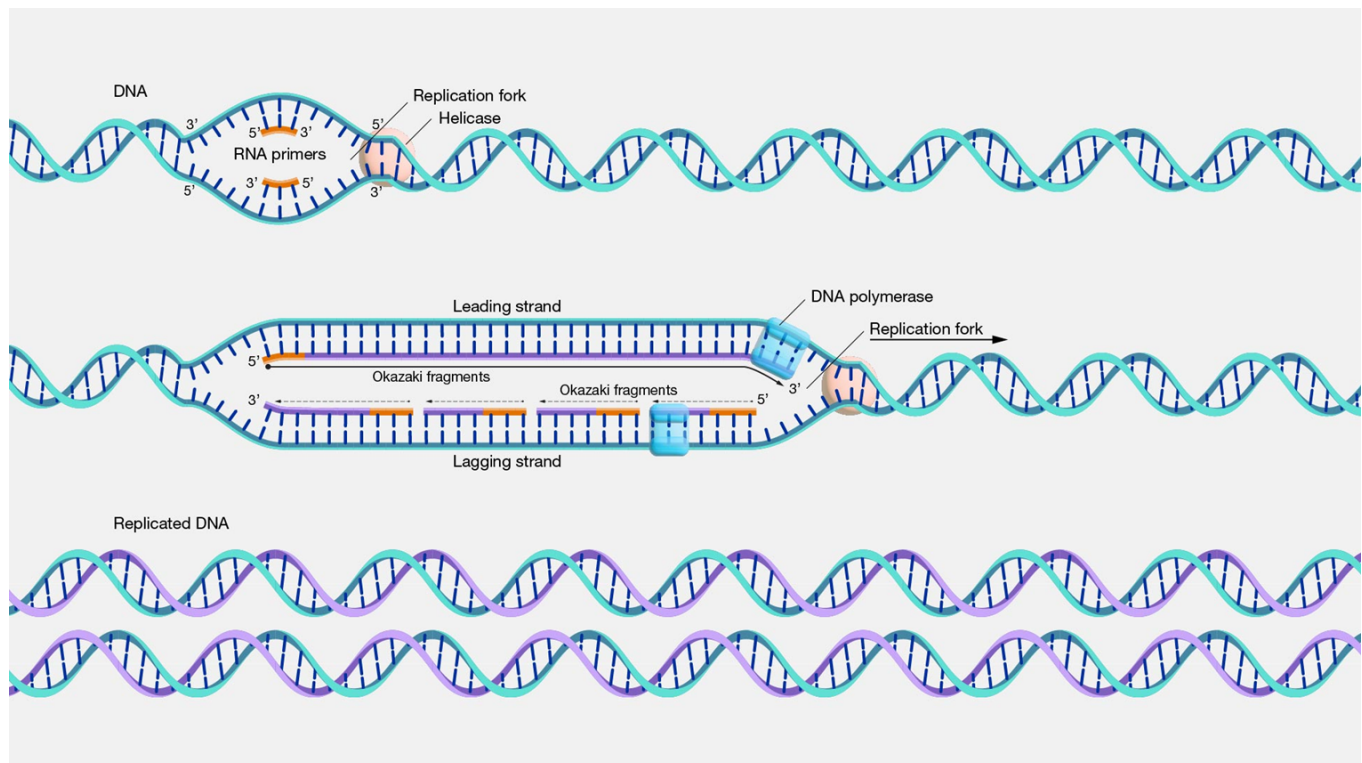


Figure 8.3.2: Illustration of DNA replication: Unzipping the double helix by enzyme helicase at the replication fork and initiation of the synthesis by RNA primers which are removed and replaced with DNA at the end (top), Continuous DNA strand synthesis in the leading strand and synthesis in fragments in the lagging strand from 5' to 3' directions (middle), and replicated DNA carrying one strand (blue) from the parent DNA and its complementary strand (purple) synthesized during the replication process. (Copyright; [National Human Genome Research Institute](#), Public domain)

The process begins when an enzyme helicase catalyzes breaking hydrogen bonds, causing the DNA double helix to unzip, as illustrated by simulation in Figure 8.3.2 and explained in a video from [yourgenome](#). Each strand acts as a template for the synthesis of a new strand. As the complementary nucleotides come together, DNA polymerase joins the nucleotide by forming phosphodiester linkages from a 5' to 3' direction, as simulated in Figure 8.3.3. The leading strand is one strand of the initial DNA that unzips in a 3' to 5' direction. The leading strand's complementary strand is continually synthesized from the 5' to 3' direction. The other strand of the initial DNA that unzips in a 5' to 3' direction is called the lagging strand. The complementary strand of the lagging strand is synthesized in portions from 5' to 3' direction, called Okazaki fragments. An enzyme, called DNA ligase joins the fragments by forming phosphodiester linkages between them. This way, almost perfect copies of the entire DNA are synthesized. At this time, the cell can divide, and each daughter cell receives a replica of the parent DNA, which in many cases is identical to the DNA of the parent cell. The complementary base pairing in DNA ensures the correct placement of the nucleotides in the new DNA strands.

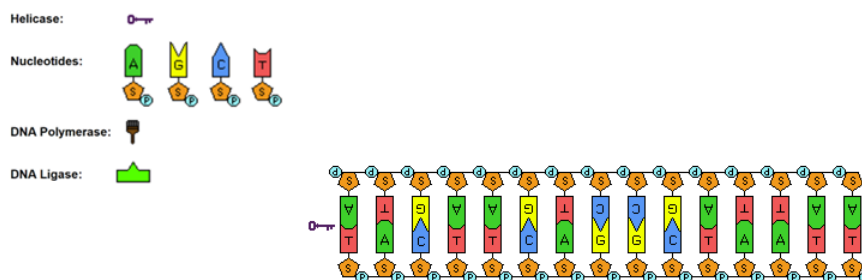
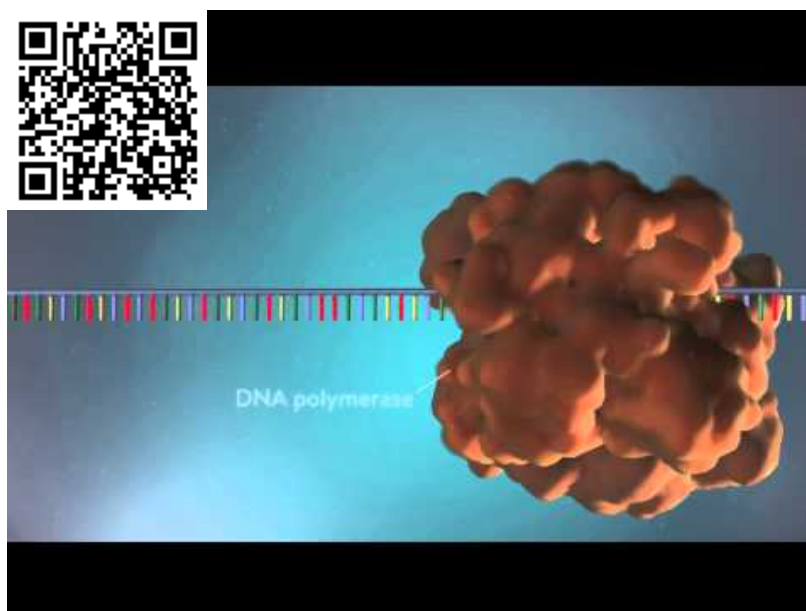


Figure 8.3.3: Simulation illustrating the DNA replication process. (Copyright: Steven Kuensting, CC BY-SA 4.0, via Wikimedia Commons)



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