

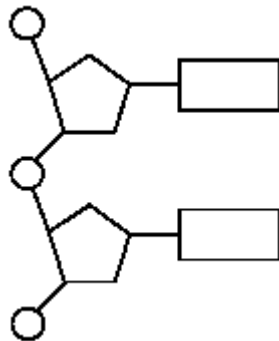
## Outline

### Chapter 11—DNA: The Carrier of Genetic Information

- I. Mutations
  - A) Any change of DNA
- II. The **Structure of DNA** allows it to carry Information and to be Faithfully Duplicated
  - A) DNA has sugar (deoxyribose), phosphate group, nitrogenous bases (four)

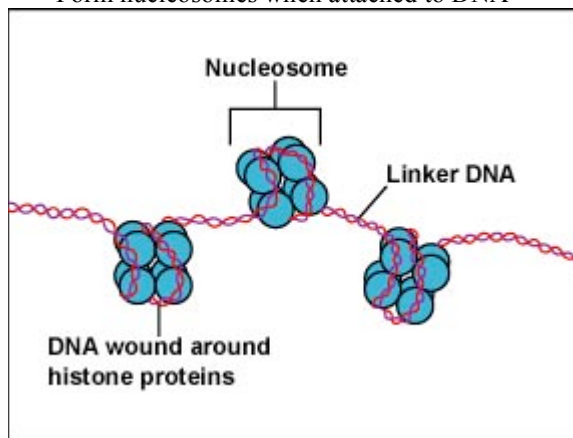


- 1. Nucleotide
  - a. DNA building block
  - b. Nitrogenous Bases
    - i. Purines = double ringed structures—Adenine and Guanine
    - ii. Pyrimidines = single ringed structures—Thymine and Cytosine
    - iii. Pyrimidines hydrogen bond to purines to create the rungs of the DNA ladder
      - 1. Chargaff's Rule
        - i) In a DNA strand there is an equal amount of purines and pyrimidines
        - ii) Adenine always bonds with Thymine; Cytosine always bonds with Guanine
  - c. Sugar to base bond = covalent bond
  - d. Base to Base bond = hydrogen bond
  - e. 3 nucleotides in a row = codon
  - f. DNA can contain large amounts of info because of its ability to contain so many nucleotides
  - g. 2-D DNA model



- h. 3' doesn't have extra phosphate, while the 5' side of the sugar phosphate backbone does have an extra phosphate attached
          - i. phosphodiester linkage
            - i. Covalent linkage between two nucleotides in a strand of DNA or RNA
            - ii. Includes a phosphate group bonded to the sugars of two adjacent nucleotides
  - B) Each DNA molecule is composed of two polynucleotide chains that associate as a double helix
    - 1. The two chains are antiparallel (meaning they run in opposite directions)
- III. DNA Replication is Semiconservative
    - A) Suggests each complementary strand of DNA can serve as a templet for a new strand of DNA
      - 1. Results = 2 identical double helixes
        - a. Each has one old (the templet) and one new strand
    - B) The Process
      - 1. DNA strands must be unwound during replication
        - a. DNA helicase (enzyme)

- i. Opens DNA – snips hydrogen bonds in between bases
      - ii. The separated strands want to coil up
    - b. Helix-destabilizing proteins prevent reformation of double helix until the strands are copied
    - c. Topoisomerases snips little sections of DNA and eventually rejoins them to prevent tangling
  - 2. DNA synthesis always proceeds in a 5' → 3' direction
    - a. DNA polymerase
      - i. Links together new nucleotides
      - ii. Can ONLY add nucleotides to the 3' end
      - iii. Uses energy (triphosphate: ATP)
  - 3. DNA synthesis requires an RNA primer
    - a. DNA polymerase can only add to an existing strand
    - b. RNA primer = short piece of RNA that gets laid down
    - c. Pg. 253 Figure 1-10
      - i. RNA primer is later degraded and space is filled with DNA
      - ii. Replication fork is always moving
      - iii. Bubble is always getting bigger
      - iv. The replication usually begins in the middle of the DNA (origin of replication)
  - 4. DNA replication is discontinuous in one strand and continuous in the other
    - a. Replication begins at specific sites on DNA called origins of replication
    - b. In eukaryotic chromosomes, replication is initiated at many points
    - c. Leading strand
      - i. Forms smoothly and continuously
      - ii. Always moves toward replication fork
    - d. Lagging strand
      - i. Always grows away from replication fork
    - e. DNA is formed in chunks called Okazaki fragments
      - i. DNA ligase joins them
  - 5. Most DNA synthesis is bidirectional
    - a. Two replication forks
    - b. Typically, many replication bubbles on one strand of DNA
    - c. Makes it more efficient
    - d. Telomeres tell DNA to stop replicating
- C) DNA is Packaged in a Highly Organized Way in Chromosomes
- 1. Chromosomes
    - a. Made up of protein and DNA
    - b. Histones
      - i. Protein in chromosome
      - ii. Positively charged and can associate with DNA, which is negatively charged because of phosphate
      - iii. Form nucleosomes when attached to DNA



- c. Nucleosome

- i. Part of chromatin, the complex of nucleic acids and protein that makes up the chromosome
  - ii. Wound up part can NOT be read
  - iii. Unwind when new protein needs to be made in S phase of Interphase
  - iv. Nucleosomes are held in place (around histone) by scaffolding proteins
  - v. DNA is packed tightly to save room
  - vi. Loosely coiled DNA is called euchromatin (active state)
  - vii. Tightly coiled DNA is called heterochromatin (inactive state/not being read)
  - viii. Telomeres = ends of DNA
    1. no genetic information
    2. telomerase = makes DNA physically longer
- IV. Only a small proportion of the DNA in the nucleus constitutes genes and that the majority of DNA consists of repetitive sequences

## Chapter 12—RNA and Protein Synthesis: The Expression of Genetic Information

### DNA and RNA

- I. Structure
  - A. DNA
    1. Double-stranded
    2. Deoxyribose sugar-phosphate backbone
    3. Adenine, Thymine, Guanine, Cytosine
  - B. RNA
    1. Single-stranded
    2. Ribose sugar-phosphate backbone
    3. Adenine, Uracil, Guanine, Cytosine
- II. RNA Synthesis – steps
  - A. RNA Polymerase attaches to promoter sequence on DNA strand
  - B. DNA Helicase unwinds the DNA helix
  - C. RNA Polymerase proceeds in the 3' → 5' direction on DNA, adding a complementary RNA base for every DNA base
  - D. Transcription is complete when the RNA polymerase hits a stop codon.

2.6.3 Describe the genetic code in terms of codons composed of triplets of bases.

2.6.4 Explain the process of translation, leading to peptide linkage formation.

Include the roles of messenger RNA (mRNA), transfer RNA (tRNA), codons, anticodons and ribosomes.

A **codon** is a triplet of mRNA nucleotides. The 64 possible codons collectively constitute a universal genetic code in which each codon specifies an amino acid in a polypeptide, or a signal to either start or terminate polypeptide synthesis.

During **translation**, a polypeptide chain specified by the mRNA is synthesized.

1. Each **triplet** (three-base sequence) in the mRNA constitutes a codon, which specifies one amino acid in the polypeptide chain, or a stop or start signal.
2. Translation requires tRNAs and complex cell machinery, including ribosomes.

The genetic code is defined at the mRNA level. There are 61 codons that code for amino acids, plus three codons that serve as stop signals.

- The start signal for all proteins is the codon **AUG**, which also specifies amino acid **methionine**.
- The genetic code is read from mRNA as a series of nonoverlapping triplets that specify a single sequence of amino acids.
- The genetic code is said to be degenerate because it is redundant; that is, some amino acids are specified by more than one codon.

- The genetic code is virtually universal, strongly suggesting that all organisms are descended from a common ancestor. Only a few minor exceptions to the standard code.

RNA is translated to form a polypeptide

Transfer RNAs (tRNAs) are critical parts of decoding machinery because they act as “adapters” that provide a connection between amino acids and nucleic acids. Each tRNA can:

- Link with a specific amino acid
- Recognize the appropriate mRNA codon for that particular amino acid, since it has the **anticodon**.

**Anticodon** - A sequence of three nucleotides in transfer RNA that is complementary to, and combines with, the three nucleotide codon on messenger RNA, thus helping to specify the addition of a particular amino acid to the end of a growing polypeptide.

Translation requires that:

- Each tRNA anticodon be hydrogen bonded to the complementary mRNA codon
- The amino acids carried by the tRNAs be linked together in the order specified by the order of codons in the mRNA.

The last bullet, is possible because of ribosomes, **rRNAs**

- **Ribosomes** attach to one end of the mRNA and travel along it, thereby allowing the tRNAs to attach sequentially to the codons of mRNA.

So that everything fits into place, to form a polypeptide.

Terms:

**Messenger RNA** - RNA that specifies the amino acid sequence of a protein; transcribed from DNA

**Ribosomes** - Organelles that are part of the protein synthesis machinery of both prokaryotic and eukaryotic cells; consist of a larger and smaller subunit, each composed of ribosomal RNA (rRNA) and ribosomal proteins.

**Transfer RNA (tRNA)** - RNA molecules that bind to specific amino acids and serve as adapter molecules in protein synthesis. The tRNA anticodons bind to complementary mRNA codons.

**Translation** - The conversion of information provided by mRNA into a specific sequence of amino acids in a polypeptide chain; process also requires transfer RNA and ribosomes.

2.6.5 Define the terms degenerate and universal as they relate to the genetic code

*Degenerate* (we called this *redundant*)– having more than one triplet to code for one amino acid. Certain amino acids are specified by more than one codon. Only methionine and tryptophan have single triplet codes. All other amino acids have 2-6 codons that code for one amino acid.

*Universal* – found in all living organisms. The same nucleotides code for the same amino acids nearly every organism. Suggests that this code evolved very early in the history of life.

2.6.6 Explain the relationship between one gene and one polypeptide

One gene codes for one polypeptide. One protein will contain multiple polypeptides. Remember that the sequence of amino acids in a polypeptide determine the shape of the protein which determines the function of the protein.