

Chapter 16

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- DNA vs Protein

1. DNA consists of pairs of Adenine, Thymine, Cytosine, and Guanine ($C \leftrightarrow G$, $A \leftrightarrow T$), and a phosphate backbone.
2. Contains four structures: primary, secondary, tertiary, and quaternary.
3. Primary source of genetic information
 - (a) RNA can be used in some cases
4. Eukaryotic Cells – Multiple linear chromosomes, found in nucleus
5. Prokaryotic Cells – Circular chromosomes, found in cytosol
6. Plasmids – Separate extra piece of circular DNA

- Chargaff's Rules

1. Varies from species to species
2. All four bases not in equal quantity
3. In humans, base pairs are usually about:
 - (a) $A \approx 30.9\%$
 - (b) $T \approx 29.4\%$
 - (c) $G \approx 19.9\%$
 - (d) $C \approx 19.8\%$

- DNA Structure:

1. Monomers: Nucleotides
2. Nucleotide structure:
 - (a) Phosphate
 - (b) Sugar (deoxyribose)
 - (c) Nitrogenous Base

- i. Adenine, guanine, thymine, cytosine
- Nitrogenous Base and Pairing in DNA
 - 1. Purines:
 - (a) Adenine
 - (b) Guanine
 - 2. Pyrimidines
 - (a) Thymine
 - (b) Cytosine
 - 3. Pairing
 - (a) A:T
 - i. 2 Hydrogen Bonds
 - (b) C:G
 - i. 3 Hydrogen Bonds
- Structure is a double helix
- Anti-parallel strands
 - 1. Nucleotides in DNA backbone are bonded from phosphate to sugar between 3' & 5' carbons
 - (a) DNA molecule has a 'direction'
 - (b) Complementary strand runs in opposite direction
 - (c) Direction is in the 5' direction
- Bonding in DNA
 - 1. Phosphate backbone uses covalent bonds (strong)
 - 2. Base pairs use hydrogen bonds (weak)
- DNA Packing
 - 1. DNA double helix wraps around histones (“beads on a string”)
 - 2. This wrapped “wire” wraps around again
 - 3. This creates a chromosome
- DNA Replication
 - 1. Is semi-conservative
 - 2. Base pairing allows each strand to serve as a template for a new strand

3. New strand is 1/2 parent template and 1/2 new DNA
4. Step One: Replication
 - (a) DNA is unwinded through use of the helicase enzyme
 - (b) Replication fork is made
 - (c) Helicase breaks the hydrogen bonds between two strand separating them
 - (d) Free nucleotides are present in the nucleus
 - (e) There is always a leading and a lagging strand
 - (f) DNA Polymerase creates complementary base pair
 - (g) DNA Polymerase moves towards 3' end
 - (h) Leading Strand:
 - i. RNA Primer is formed from RNA nucleotides, and bonds to start strand
 - ii. DNA Polymerase lays down the nucleotides in 5' to 3' direction of new DNA strand
 - iii. Can only add nucleotides to 3' end of a growing DNA strand
 - (i) Lagging Strand:
 - i. Runs in opposite direction of leading strand
 - ii. RNA Primer is joined to the parent strand by RNA Primase
 - iii. DNA Polymerase then works in the 5' to 3' direction, while laying down nucleotides forming Okazaki Fragments
 - iv. RNA Primer is removed from the fragments and replaced with DNA nucleotides
 - v. DNA Ligase attaches the fragment backbones to each other
- DNA is edited and proofread
 1. Many forms of Polymerase cut and remove abnormal bases, proofread and correct typos, and repairs mismatched bases
 2. Reduces error rate to 1 in 10 billion