Honors Biology – Unit 4 – Chapter 10
"MOLECULAR BIOLOGY OF THE GENE"

1. DNA → RNA → PROTEIN → TRAIT

2. structure of deoxyribonucleic acid (DNA), Chargaff's rules

3. DNA replication: goal and location

4. "semi-conservative" DNA replication

    - helicase, replication fork, DNA polymerase, 5' end, 3' end, DNA ligase

5. transcription: goal and location

6. RNA processing: 5' cap, 3' tail, splicing

    - Introns IN the trash! Exons are EXpressed!

7. translation: goal and location

8. translation: mRNA, tRNA, rRNA, ribosomes, codons, anti-codons

9. genetic code chart

10. point mutation (substitution) vs. frame-shift mutation (addition or deletion)

Honors Biology – Chapter 10 Word Roots
"MOLECULAR BIOLOGY OF THE GENE"

anti- = opposite (*anti-codon:* a specific sequence of three nucleotides on a tRNA molecule that is complementary to a particular codon triplet on an mRNA molecule)

capsa- = a box (*capsid:* the protein shell that encloses the viral genome)

exo- = out, outside, without (*exon:* in eukaryotes, the coding portion of a gene)

-genesis = origin, birth (*mutagenesis:* the creation of a mutation)

helic- = a spiral (*double helix:* The form of native DNA, composed of two adjacent polynucleotide strands wound into a spiral shape)

intro- = within (*intron:* a non-coding, intervening sequence within a eukaryotic gene) in eukaryotes, a non-expressed [non-coding] portion of a gene that is excised from the RNA transcript)

liga- = bound or tied (*DNA ligase:* an enzyme that catalyzes the covalent bonding of adjacent DNA nucleotides)

lyso- = loosen (*lysogenic cycle:* a type of bacteriophage replication cycle in which the viral genome is incorporated into the bacterial host chromosome as a prophage)

lyto- = loosen (*lytic cycle:* a type of viral replication cycle resulting in the release of new viruses by lysis [breaking open] of the host cell)

muta- = change (*mutation:* a change in the nucleotide sequence of DNA); **-gen** = producing (*mutagen:* a physical or chemical agent that causes mutations; *mutagenesis:* the creation of a mutation)

-phage = to eat (*bacteriophage:* a virus that infects bacteria)

poly- = many (*polynucleotide:* a molecule composed of many nucleotide monomers, covalently bonded together)

pro- = before (*promoter:* a sequence of DNA that provides the binding site for RNA polymerase during transcription); **-phage** = to eat (*prophage:* phage DNA that has inserted by genetic recombination into the DNA of a prokaryotic chromosome)

retro- = backward (*retrovirus:* an RNA virus that reproduces by reverse-transcribing its RNA into DNA and then inserting the DNA into a cellular chromosome)

Honors Biology – Chapter 10 Word Roots
"MOLECULAR BIOLOGY OF THE GENE"

semi- = half (*semi-conservative model:* type of DNA replication in which the replicated double helix consists of one old strand, derived or "conserved" from the parent molecule, and one newly made strand)

trans- = across (*transduction:* the transfer of DNA from one cell to another via a bacteriophage; *transformation:* a phenomenon in which external DNA is assimilated by a cell; *translation:* the process in which an amino acid sequence is produced by reading an RNA transcript); **-script** = write (*transcription:* the synthesis of RNA on a DNA template)

virul- = poisonous (*viroid*: a plant pathogen composed of molecules of naked, circular RNA several hundred nucleotides long; *virus:* an infectious agent that requires a host cell for reproduction)

PROPERTY OF:

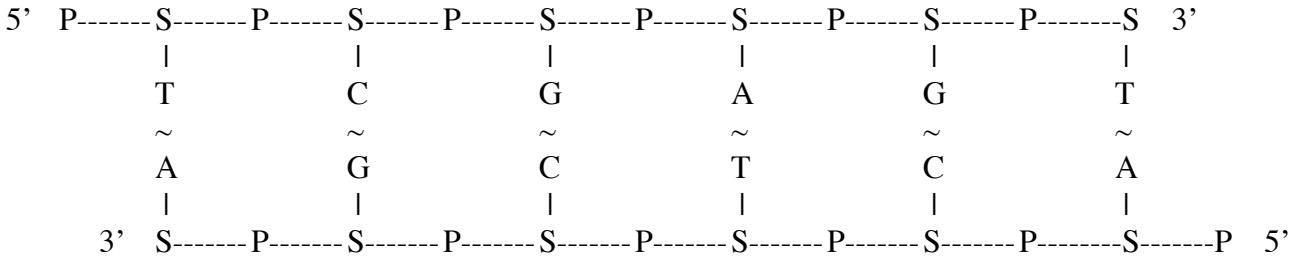
HONORS BIOLOGY – UNIT 4 – CHAPTER 10 NOTES

MOLECULAR BIOLOGY OF THE GENE

Evidence of DNA
- Frederick Griffith: Transformation of Bacteria experiment
- Alred Hershey & Marth Chase: Bacteriophage experiment

Structure of DNA
- deoxyribonucleic acid
- 2 "complementary" strands that form a double helix (spiral)
- made up of 4 nucleotides: A, T, C, G
    - A = adenine
    - T = thymine
    - C = cytosine
    - G = guanine
- 3 parts to each nucleotide:
    1. sugar (called deoxyribose)
    2. phosphate group (abbreviated as a P with a circle around it)
    3. nitrogenous base (A, T, C, and G)
- the sugars and phosphates alternate to form a "backbone"
- the nitrogenous bases face inward
- complementary nitrogenous bases are held together by weak hydrogen bonds (H-bonds)
- Chargaff's Rules for base-pairing: A and T bind together, G and C bind together (they fit together using a lock and key fit)
- 5' end of the DNA = phosphate group
- 3' end of the DNA = sugar group

EXAMPLE OF A COMPLEMENTARY STRAND OF DNA:



DNA Replication

- GOAL: to produce an identical copy of the DNA
  LOCATION: nucleus
- Semi-Conservative Replication = Each of the original strands serves as a template for making a new complementary strand. Each daughter molecule contains one of the original parent strands as well as one new daughter strand.
- Helicase is the enzyme that melts (cuts) the H-bonds between the strands of DNA. This produces the "replication fork".
- The replication fork is the fork-like opening between the two strands.
- DNA polymerase is the enzyme that adds the complementary nucleotides (bases) one at a time. This follows Chargaff's base=pairing rules (A with T, C with G).
- DNA is ONLY built from 5' → 3'. This means it ONLY be "read" from 3' → 5'.
- The leading strand is made all in one piece. The lagging strand is made in fragments.
- Ligase is the enzyme that connects the fragments of the lagging strand. They are joined together with covalent bonds.

Mutations

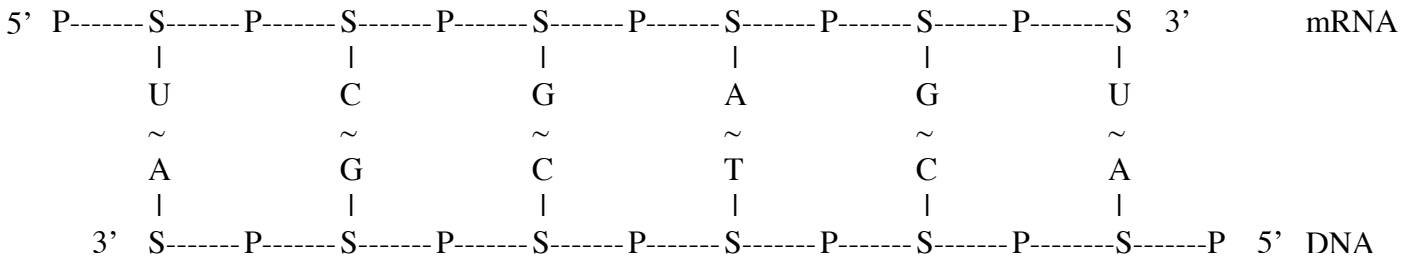
- A mutation is any change or mistake in the DNA.
- 1. deletion mutation = nucleotides are deleted
  EX: GGTACTCAACGT becomes
  GGTAACGT (the ACTC sequence was deleted)
- 2. duplication mutation = extra nucleotides are added
  EX: GGTACTCAACGT becomes
  GGTACGTACTCAACGT (the GTAC sequence was duplicated)
- 3. inversion mutation = a sequence of nucleotides is flipped
  EX: GGTACTCAACGT becomes
  GGTACTGCAACT (the CAACG sequence was inverted to GCAAC)
- 4. translocation mutation = a sequence of nucleotides is moved to a different location
  EX: GGTACTCAACGT becomes
  GGTACGACTCAT (the ACG near the end was moved near the middle)

Structure of RNA

- ribonucleic acid
- made of 1 strand of nucleic acids
- made up of 4 nucleotides: A, U, C, G
  - A = adenine
  - U = uracil
  - C = cytosine
  - G = guanine
- 3 parts to each nucleotide:
  1. sugar (called ribose)
  2. phosphate group (abbreviated as a P with a circle around it)
  3. nitrogenous base (A, U, C, and G)
- the sugars and phosphates alternate to form a "backbone"
- RNA is built off of a DNA template. (This process is called transcription.)
- Chargoff's Rules for base-pairing between DNA and RNA:
  - an A in DNA becomes a U in RNA
  - a T in DNA becomes an A in RNA
  - a G in DNA becomes a C in RNA
  - a C in DNA becomes a G in RNA

  (they fit together using a lock and key fit)

EXAMPLE OF DNA FORMING A COMPLEMENTARY STRAND OF mRNA:



Transcription

- GOAL: to produce a copy of mRNA that is complementary to the strand of DNA
  LOCATION: nucleus
- RNA polymerase is the enzyme that has two functions in transcription:
  1. melts (cuts) the H-bonds in the DNA to free up the strands
  2. adds the complementary nucleotides (bases) one at a time
     This follows Chargoff's base=pairing rules (A → U, T → A, G → C, C → G).
- RNA is <u>ONLY</u> built from 5' → 3'. The DNA can <u>ONLY</u> be "read" from 3' → 5'.

Post-Transcription Processing

- Three things happen to the mRNA after transcription, but before translation:
  1. 5' protective cap (protects the "front" of the mRNA from enzymatic breakdown)
  2. 3' poly-A tail (protects the "end" of the mRNA from enzymatic breakdown)
  3. The introns are removed, leaving behind just the exons.
     (mRNA sequences that do not need to be converted into proteins are removed)
     HINT: Introns go <u>IN</u> the trash. Exons are <u>EX</u>pressed.

Three Types of RNA

1. mRNA = messenger RNA
   used by a ribosome to convert a DNA sequence into a protein (amino acid sequence)
2. tRNA = transfer RNA
   used to bring the amino acids to the ribosomes
3. rRNA = ribosomal RNA
   found in a ribosome (makes up the physical structure of a ribosome)

Translation (Protein Synthesis)

- GOAL: to produce a protein based on a sequence of mRNA
  LOCATION: ribosomes

1. Large and small subunits of a ribosome join together.
   The strand of mRNA is sandwiched in between them.
2. The first 3 letters (bases) of the mRNA are "read" by the ribosome.
   NOTE: Every three bases is called a CODON.
3. The appropriate tRNA brings the correct amino acid according to the genetic code chart.
   The 3 bases at the bottom of the tRNA must be complementary to the codon. These 3 bases at the bottom of the tRNA is called an ANTI-CODON. The codon and anti-codon must make a lock and key fit, according to Chargoff's Rules (A with U and C with G).
4. Translation begins with the start codon (AUG).
   Translation ends with the stop codon (UAA, UAG, or UGA).
5. Translation produces the primary structure of a protein. The protein must then be folded to produce the secondary, tertiary, and quaternary structures.

Diagram of Translation

Alanine	Serine	Serine	Valine	← amino acids
\	\	\	\	
tRNA	tRNA	tRNA	tRNA	← tRNA molecules
C G C	U C G	A G U	C A U	← anti-codons
| | |	| | |	| | |	| | |	
G C G	A G C	U C A	G U A	← codons
mRNA	mRNA	mRNA	mRNA	← mRNA molecules

DNA and mRNA Mutations

- A mutation is any change or mistake in the DNA.
- 1. point mutation = nucleotides are replaced by other nucleotides
     EX: GGTACTCAACGT becomes
     GGTACTCACCGT (an A became a C)
- 2. frame-shift mutation = nucleotides are either added or deleted
     EX: GGTACTCAACGT becomes
     GGTACTGCAACGT (a G was added near the middle)
     EX: GGTACTCAACGT becomes
     GGTCTCAACGT (an A was deleted near the beginning)
- Frame-shift mutations are generally much more harmful because they change the "reading frame" for the ribosome. A point mutation typically only changes 1 amino acid. A frame-shift mutation typically changes all of the amino acids that are after the addition or the deletion.