Chapter 17

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- Protein Synthesis is Split into Two Steps:
    1. Transcription − Synthesis of RNA using DNA as a template (occurs in the nucleus)
    2. Translation − Actual synthesis of a polypeptide using mRNA (occurs in the cytoplasm, specifically the ribosome)
- "Central Dogma" − Flow of genetic information in a cell
- DNA → RNA → protein → trait
- RNA − Ribose sugar, uracil instead of thymine, single stranded, and comes in three forms: mRNA, tRNA, and rRNA
- RNA Polymerase separates 2 strands and adds nucleotides (does not need primer or helicase, like DNA)
- Promoter Region − A binding site before the beginning of the gene
    1. The TATA box binding site is a repeating AT sequence
    2. Binding site for RNA polymerase and transcription factors
    3. Transcription factors (suite of DNA-binding proteins) bind to promoter region, and turn on or off transcription, which triggers the binding of RNA polymerase to DNA
- RNA bases are matched to DNA bases on one of the DNA strands, goes in the 5' to 3' direction
- Transcription Process
    1. Initiation − Transcription factors mediate the binding of RNA polymerase to an initiation sequence (TAT box)

2. Elongation − RNA polymerase continues unwinding DNA and adding nucleotides to the 3' end
3. Termination − RNA polymerase reaches a (codon) terminator sequence, such as UGA, UAA, or UAG

- Post-transcriptional processing

1. Need to protect mRNA from enzymes on its trips from nucleus to cytoplasm
2. Enzymes in cytoplasm attack mRNA
3. Protect ends of the molecule
4. Add 5' GTP cap
5. Add poly-A tail (50-250+ A nucleotides)
6. Longer tail, mRNA lasts longer, producing more protein
7. Eukaryotic genes are not continuous, split into segments
8. RNA splicing
   (a) Exons − the real gene
      i. Expressed/coding DNA
   (b) Introns − the junk
      i. In between sequence

- Splicing must be accurate! A single base added or lost throws off the reading frame
- RNA Splicing Enzymes (snRNPs)

1. Small nuclear RNA
2. Proteins

- Spliceosome

1. Several snRNPs
2. Recognize splice site sequence
   (a) Cut and paste gene

- Alternative Splicing

1. A single gene can code for more than one protein
   (a) Certain introns may be included or exons excluded
   (b) Allows humans to have a large diversity of proteins

- DNA transcribes to mRNA, which is translated into proteins, which can code for traits

- Translation − From nucleic acid language to amino acid language
    1. mRNA codes for proteins in triplets called codons
    2. The Codons
        (a) Code for all life
        (b) Support theory for a common origin of all life
        (c) Code is redundant (several codons for each amino acid)
        (d) Third base is called a "wobble"
        (e) Start Codon
            i. AUG − Methionine
        (f) Stop Codons
            i. UGA, UAA, UAG
        (g) tRNA uses anti-codons, attached to an amino acid, to compliment codons
            i. tRNA transfers amino acids from cytoplasm to ribosome − Very by anticodons and amino acid attached to end
    3. Ribosomes − Facilitate coupling of tRNA anticodon to mRNA codon
        (a) Structure − Made of ribosomal RNA (rRNA) & proteins, and 2 subunits (large and small), which makes it functional only when the two units are attached
        (b) A site (aminoacyl-tRNA site) − holds tRNA carrying next amino acid to be added to the chain
        (c) P site (peptidyl-tRNA site) − holds tRNA carrying growing polypeptide chain
        (d) E site (exit site) − empty tRNA leaves ribosome from exit site

- Building a polypeptide
    1. Initiation − brings together mRNA, ribosome subunits, initiator tRNA
    2. Elongation − adding amino acids based on codon sequence
    3. Termination − end codon

- Transcription and translation are simultaneous in prokaryotes
    1. DNA is in cytoplasm
    2. No mRNA editing
    3. Ribosomes read mRNA as it is being transcribed

- Prokaryotes vs Eukaryotes − Time and physical separation between the processes (eukaryotes take about one hour to go from DNA to protein), and has no RNA processing

- Mutations

1. Point Mutations (Single base change)
   (a) Silent Mutation − No amino acid change due to redundancy in code
   (b) Missense Mutation − Change amino acid
   (c) Nonsense Mutation − Changes to stop codon
2. Frameshift Mutations (Shift the reading frame)
   (a) Insertions − Adding bases
   (b) Deletions − Losing bases

- If mutations occur in gametes, it affects the next generation, bot not in somatic cells
- Sickle Cell Anemia − Single point mutation

1. Primarily Africans
   (a) Recessive inheritance pattern
   (b) Strikes 1 out of 400 African Americans
   (c) The sixth amino acid, which is supposed to be Glu and is hydrophilic, is mutated into Val, which is hydrophobic

- Cystic Fibrosis − Deletion frameshift mutation

1. Recessive
2. Normal allele codes for a membrane protein that transports Cl^- across cell membrane
   (a) Defective of absent channels
   (b) Thicker and stickier mucus oats around cells
   (c) Mucus build-up in various areas
3. CTT is deleted from the sequence