Genetics (BIL-250)
Review Questions #1

(2-1) What is the historical basis for concluding that the heritable material is composed of DNA or RNA and not protein?

(2-1) Illustrate the phosphodiester bond, and explain why we speak about DNA 5' to 3'.

(2-2) How does the strength of base pairing differ between A, C, G, and T, and why?

(2-3) Illustrate a DNA double helix. Label the bases and sugar-phosphate backbone.

(2-4) How does RNA differ from DNA?

(2-1) What is the relationship between cellular DNA content and the structural or organizational complexity of the organism?

(2-2) Arrange the following in increasing order of eukaryotic chromosome condensation, beginning with the simplest level of organization (1) and ending with the most complex level of organization (6).

_____ Chromatin fiber

_____ Metaphase chromosome

_____ DNA double helix

_____ Extended section of looped domains on chromosome

_____ "Beads-on-a-string" form of chromatin

_____ Condensed section of chromosome

(2-3) How does the DNA of prokaryotes and eukaryotes differ?

(3-1) Draw a DNA replication fork and identify and label the locations of the following major components: (1) 5' and 3' ends of each strand, (2) leading strand, (3) lagging strand, (4) single-stranded binding proteins, (5) DNA polymerase, (6)Okazaki fragments, (7) RNA primer, (8) DNA helicase, (9) DNA ligase, (10) primase.

(3-2) How did the Meselson-Stahl experiment demonstrate that DNA replication is semiconservative and not conservative?

(4-2) Discuss problems and limitations of the "One gene – one enzyme hypothesis" and how it can be better formulated.

(4-3) Explain one example of how mutations in either the α- or β-hemoglobins can produce an altered phenotype that may be adaptive to a particular geographic region.

(5-1) Distinguish between leader sequence, trailer sequence, coding sequence, intron, spacer sequence, nontranscribed spacer sequence, external transcribed spacer sequence, and internal transcribed sequence.

(5-2) Briefly summarize the post-transcriptional modifications and processing events that take place on the primary transcripts of eukaryotic rRNA and protein-coding genes.

(5-3) What major difference concerning the timing of transcription and translation exists between prokaryotes and eukaryotes?

(6-1) Why is degeneracy of the genetic code important for maintaining protein structure and function?

(6-2) What are the 4 main types of amino acids? How many amino acids are there total? How many stop codons exist?

(6-3) Illustrate a peptide bond? Label the N- and C- termini.

(6-4) What distinguishes primary, secondary, tertiary, and quaternary protein structure?

(6-5) What is a framewhift mutation? Why may they be deleterious?

(6-6) What is the wobble in the genetic code?

(6-7) How does tRNA become aminoacylated?

(6-8) Illustrate the site of protein synthesis on the ribosome? Label the P, A, and E sites and indicate the position of the growing peptide before and after elongation.

(7-1) How did Lamarck's and Darwin's concepts of adaptation and inheritance differ?

(7-2) How was Salvador Luria's and Max Delbrück's 1943 experiment with *E. coli* used to test alternative hypotheses about environmental induction of adaptive mutations?

(7-3) Identify and distinguish: transition, transversion, insertion, deletion, indel, missense mutation, nonsense muation, neutral mutation, silent mutation, and frameshift mutation:

(7-4) How might a tRNA gene act as an intergenic suppressor mutation? What other factors involving protein translation might need to be compensated for?

(7-5) What are the differences between base analogs, base modifying agents, and intercalating

agents?

(7-6) What are the important DNA repair mechanisms that exist?