NAME: _____ **STUDENT #:** _____

SS marking scheme

BIO 1140 Introduction to Cell Biology
MIDTERM #2, March 24, 2014 SUPPLEMENTAL
Dr. D.A Johnson
Total points on this exam is 32 pts

YOU HAVE ONE HOUR TO COMPLETE THIS EXAM

Instructions:

1. Make sure that you have a complete test package. You should have a set of multiple choice questions with a written-answer questionnaire, and a Scantron. Both components must be returned at the end of the midterm.
2. Fill in the Scantron with your name, student number and course code **BIO 1140SS**

Answer the following 14 multiple choice questions **on the Scantron sheet** provided. Choose only one answer from among the choices. (14 marks)

1. DNA binding proteins often can read the sequence of nucleotides along the DNA without having to separate the chains. How do they do this?
   a. The conformations of the phosphate groups reflect the DNA sequence.
   b. The DNA binding proteins often contain domains that fit into the DNA grooves.
   c. The conformations of the deoxyribose sugars reflect the DNA sequence.
   d. The conformations of the ribose sugars reflect the DNA sequence.

2. The two strands of a DNA double helix are said to be antiparallel. This means that
   a. the 5' end of one strand is directly paired with the 5' end of the other strand.
   b. since the double helix twists, it is not perfectly parallel.
   c. one strand has a negative charge and the other strand has a positive charge.
   d. the 5' end of one strand is directly paired with the 3' end of the other strand.
   e. all viral RNA.

3. Why is the DNA of interphase chromosomes very dispersed?
   a. to protect the DNA
   b. to allow replication to occur
   c. to allow transcription to occur
   d. to allow ribosome translocation to the cytoplasm
   e. b and c

4. Since a DNA polymerase cannot synthesize DNA without a primer, some molecule other than DNA must be laid down as a primer to start replication. What molecule is laid down as a primer and which end of that molecule must be free and thus available to attach to new nucleotides?
   a. carbohydrates, free 5' end
   b. RNA, free 3' end
   c. carbohydrate, free 3' end
   d. RNA, free 5' end
   e. protein, free 3' end

5. What happens if histone H1 is selectively extracted from compacted chromatin (30 nm fibers)?
   a. 30-nm fibers uncoil to form a thinner, more extended beaded filament.
   b. 30-nm fibers coil to form a thicker, less extended cylindrical filament.
   c. 30-nm fibers completely disassemble to their component nucleotides.
   d. 30-nm fibers break into small fragments.
   e. 30-nm fibers break up into large fragments.

6. When histone H1 has been removed from chromatin prior to being prepared for electron microscopy, what phrase below describes what investigators see in the resultant electron micrographs?
   a. a coiled coil
   b. beads on a string
   c. a hollow tube
   d. a windmill
   e. a sunburst

7. During the chromatin remodelling that accompanies gene expression, acetylation
   a. adds an acetyl group (CH_3CO) to the cyotsine nucleotides of DNA.
   b. adds an acetyl group (CH_3CH_2) to the DNA of a promoter sequence.
   c. adds an acetyl group (CH_3CO) to the histone protecting the transcription unit of a gene.
   d. adds an acetyl group (CH_3CO) to the histone protecting the promoter region of a gene.

8. Chromatin remodelling
   a. is subject to well-characterized stages of regulation by the cell.
   b. blocks access to genes that should not be expressed in a particular cell.
   c. is unaffected by alterations to the DNA sequences of a cell.
   d. results in specific patterns of gene expression.
   e. all of the above

9. What word below most accurately describes transposable elements?
   a. stable
   b. offspring
   c. helpers
   d. genetic parasite
   e. genetic symbionts

10. The greatest similarities among codons specifying the same amino acid occur _____.
   a. in the first two nucleotides of the triplet
   b. in the last two nucleotides of the triplet
   c. in the first and third nucleotides of the triplet
   d. in the third nucleotide of the triplet
   e. in the middle nucleotide of the triplet

11. What is the most common mechanism for repairing damage to DNA?
    a. direct repair of the damage
    b. selective excision of the damaged section and use of the complementary strand to replace excised portion
    c. simple removal of damaged portion without replacement
    d. simplistic repair of the damage
    e. altruistic repair of the damage

12. What is the explanation for the wide discrepancies in genome sizes from species to species?
    a. More advanced organisms have more DNA.
    b. Genomes have an extremely variable number of repeated DNA sequences that do not code for proteins.
    c. Some organisms have multiple repeats of each gene.
    d. More advanced organisms have more genes.
    e. More advanced organisms have more centromeric DNA.

13. Which of the following reasons explains why a single-stranded DNA circle cannot serve as a DNA polymerase template?
    a. DNA polymerase cannot initiate DNA strand formation.
    b. DNA polymerase can only add nucleotides to the 3'-hydroxyl end of an existing strand.
    c. DNA polymerase can only add nucleotides to the 5'-hydroxyl end of an existing strand.
    d. DNA polymerase requires a primer.
    e. a, b and d

14. The greatest variability among codons specifying the same amino acid occur _____.
    a. in the first two nucleotides of the triplet
    b. in the last two nucleotides of the triplet
    c. in the first and third nucleotides of the triplet
    d. in the third nucleotide of the triplet
    e. in the middle nucleotide of the triplet

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WRITTEN-ANSWER QUESTIONNAIRE SS
ONLY RESPONSES WRITTEN WITHIN THE BOXES WILL BE MARKED.

Answer 3 questions. Each is worth 4 marks.

1. How was transformation used to determine that DNA was the genetic information?
2. What theme links chromatin structure, transcription, histones and DNA modification?
3. Explain the role of primase and DNA polymerase in leading and lagging strand DNA synthesis.
4. What is the Wobble hypothesis and what is the molecular explanation for it.

Everyone must answer this question. It is worth 6 marks.

In the original model for a genome there were genes coding for proteins with non-coding DNA between them. But the genome is much more complex that we thought. Discuss this statement while drawing examples and inspiration from this Figure.
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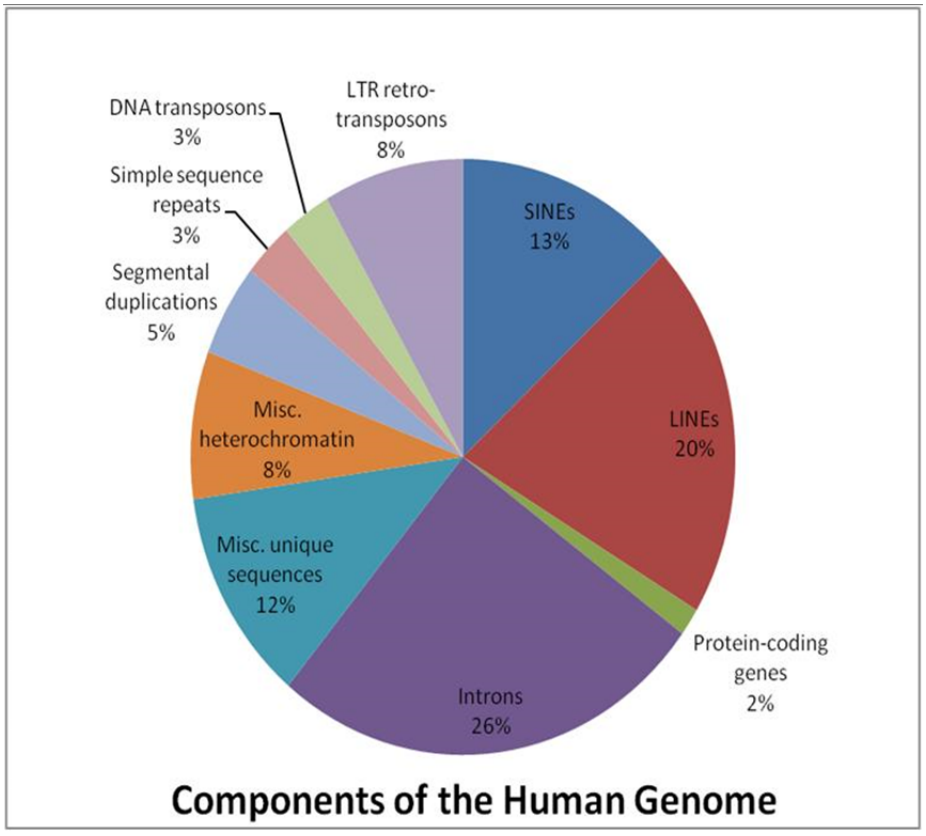

How was transformation used to determine that DNA was the genetic information?

- **Griffith's experiment:** The original transformation experiments established that a heat-killed bacterial extract (or lysate) could change a non-lethal bacterium (rough) into a lethal bacterium (smooth) (1 mark)
    - **If students confuse bacteria with virus, deduct 0.5 marks**
- 0.5 marks for enzyme/function + 0.5 marks for conclusion on transformation
    - A protease that breaks down protein did not affect transformation (1 mark)
    - An RNAse that degrades RNA did not affect transformation (1 mark)
    - Only DNA degradation (or DNAse treatment) led to the loss of the transforming principle (1 mark)

The Hershey & Chase experiment is not acceptable.

What theme links chromatin structure, transcription, histones and DNA modification?

- The theme is the histone code (1.0).
- The histone code is hypothesized to be a code consisting of covalent histone modifications (1.0).
- The type and number of modifications **(e.g. Me, Ac, P)** on the histones in the octomer and DNA (1.0)
    - influence chromatin structure and gene expression (**transcription/heterochromatin/euchromatin also acceptable, as long as they relate it somehow to gene expression**) (1.0).

Explain the role of primase and DNA polymerase in leading and lagging strand DNA synthesis

- Primase is an RNApol that makes **RNA** primers **(the idea of RNApol OR RNA primers need to be there, if not, deduct 0.25 marks)**(0.5). On the leading strand one primer is made (0.5).
- On the lagging strand primers are needed for each Okazaki fragment **(can be referred to as multiple primers)** (or periodically or continually) **Can also accept: as result of DNApol with multiple primers** (1.0)
- DNApol are synthesize DNA continuously in leading synthesis (1.0)
- and fill in the gaps (or repair **or discontinuous replication)** created during lagging strand synthesis (1.0)

What is the Wobble hypothesis and what is the molecular explanation for it.
(1 mark per statement)

- The genetic code is redundant **OR** degenerate (1.0)
- More than one codon can be recognized by a single tRNA (1.0).
- The "Wobble Hypothesis" states that the 1st position on the anticodon can form hydrogen bonds (or recognize) several bases in the degenerate 3rd position of the codon (1.0)
- by non-standard (**OR** they could give an example to illustrate such as G-U or I-U or I-C or I-A) that are stabilized by proteins (1.0) **(if proteins not mentioned, deduct 0.5 marks)**
- **prevent ways to mutate (if this statement is made, they must make the link to degeneracy and can only be awarded 0.5 marks)**

In the original model for a genome there were genes coding for proteins with non-coding DNA between them. But the genome is much more complex that we thought. Discuss this statement while drawing examples and inspiration from this Figure.
Note: This Figure illustrates several examples and there are many ways of describing them. You have to be adept. Each is worth 2.0 where 1.0 is given for a description and 1.0 for the link to the genome.

i. Introns **&** exons: in the original model they did not exist which in your DNA genes are mostly inton (26%) and only 2% exon;
ii. in the original model there were no transposable elements that moved via a DNA intermediate while in you DNA 3% of the genome is "DNA transposon";
iii. in the original model there were no transposable elements that moved via an RNA intermediate while a large percent of your genome is retroposon. **(both cut or copy mechanism are acceptable)**
    a. There are three types: LTR retroposons, SINES: Short INterspersed Elements and LINES: Long INterspersed Elements. THEY ONLY NEED TO DESCRIBE AND DEFINE ONE.
iv. in the original model there were no simple sequence repeats such or duplications but in you DNA we time small tandem repeats or VNTRs and larger duplicated regions that may contain genes.

Notes:
Mark only first two answers.
Students must refer back to the original model in every answer, if they do not deduct 0.5 marks
0.5 marks for every element mentioned from figure
Misc. repeats: are large repeats (centromeres, telomeres) are acceptable but they must talk about the sequences, NOT how these relate to structure.