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Course/Section _____

Date _____

Professor/TA _____



Activity 17.1 Modeling transcription and translation: What processes produce RNA from DNA and protein from mRNA?

Create a model of the processes of transcription and translation. Your model should be a dynamic (working or active) representation of the events that occur first in transcription in the nucleus and then in translation in the cytoplasm.

For the purposes of this activity, assume there are *no introns* in the mRNA transcript.

When developing and explaining your model, be sure to include definitions or descriptions of the following terms and structures:

gene

DNA

nucleotides: A, T, G, and C versus A, U, G, and C

RNA modification(s) after transcription

mRNA

RNA polymerase

poly(A) tail

5' cap

translation

protein synthesis

ribosome (large versus small subunit)

A, P, and E sites

tRNA

rRNA

start codon (methionine)

aminoacyl-tRNA synthetase

amino acids (see Figure 17.4, page 329, in *Biology*, 8th edition)

peptidyl transferase

polypeptide

codons

stop codons

anticodons

initiation

elongation

termination

polypeptide

Building the Model

- Use chalk on a tabletop or a marker on a large sheet of paper to draw a cell's plasma membrane and nuclear membrane. The nucleus should have a diameter of about 12 inches.
- Draw a DNA molecule in the nucleus that contains the following DNA sequence:
Template strand 3' TAC TTT AAA GCG ATT 5'
Nontemplate strand 5' ATG AAA TTT CGC TAA 3'
- Use playdough or cutout pieces of paper to represent the various enzymes, ribosome subunits, amino acids, and other components.
- Use the pieces you assembled to build a dynamic (claymation-type) model of the processes of transcription and translation.
- When you feel you have developed a good working model, use it to explain the processes of transcription and translation to another student or to your instructor.

Use your model of transcription and translation to answer the questions.

1. How would you need to modify your model to include intron removal? Your explanation should contain definitions or descriptions of the following terms and structures:
pre-mRNA exons
RNA splicing spliceosome
introns
2. If 20% of the DNA in a guinea pig cell is adenine, what percentage is cytosine? Explain your answer.

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3. A number of different types of RNA exist in prokaryotic and eukaryotic cells. List the three main types of RNA involved in transcription and translation. Answer the questions to complete the chart.

a. Type of RNA	b. Where is it produced?	c. Where and how does it function in cells?

4. Given your understanding of transcription and translation, fill in the blanks below and indicate the 5' and 3' ends of each nucleotide sequence. Again, assume no RNA processing occurs.

Nontemplate strand of DNA: 5' ATGTATGCCAATGCA 3'

Template strand of DNA: ___' T _____'

mRNA: ___' A ___ U _____'

Anticodons on complementary tRNA: ___' ___/___/___/___/___/___'



5. Scientists struggled to understand how four bases could code for 20 different amino acids. If one base coded for one amino acid, the cell could produce only four different kinds of amino acids (4^1). If two bases coded for each amino acid, there would be four possible choices (of nucleotides) for the first base and four possible choices for the second base. This would produce 4^2 or 16 possible amino acids.

- a. What is the maximum number of *three-letter codons* that can be produced using only four different nucleotide bases in DNA?
- b. How many different codons could be produced if the codons were four bases long?

Mathematical logic indicates that at least three bases must code for each amino acid. This led scientists to ask:

- How can we determine whether this is true?
- Which combinations of bases code for each of the amino acids?

To answer these questions, scientists manufactured different artificial mRNA strands. When placed in appropriate conditions, the strands could be used to produce polypeptides.

Assume a scientist makes three artificial mRNA strands:

- (x) 5' AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 3'
- (y) 5' AAACCCAAACCCAAACCCAAACCCAAA 3'
- (z) 5' AUAUAUAUAUAUAUAUAUAUAUAU 3'

When he analyzes the polypeptides produced, he finds that:

x produces a polypeptide composed entirely of lysine.

y produces a polypeptide that is 50% phenylalanine and 50% proline.

z produces a polypeptide that is 50% isoleucine and 50% tyrosine.

- c. Do these results support the three-bases-per-codon or the four-bases-per-codon hypothesis? Explain.

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- d. The type of experiment just described was used to discover the mRNA nucleotide codons for each of the 20 amino acids. If you were doing these experiments, what sequences would you try next? Explain your logic.

6. Now that the complete genetic code has been determined, you can use the strand of DNA shown here and the codon chart in Figure 17.4 (page 329) in *Biology*, 8th edition to answer the next questions.

Original template strand of DNA: 3' TAC GCA AGC AAT ACC GAC GAA 5'

- a. If this DNA strand produces an mRNA, how does the sequence of the mRNA read from 5' to 3'?
- b. For what sequence of amino acids does this mRNA code? (Assume it does not contain introns.)

- c. The chart below lists five point mutations that may occur in the original strand of DNA. What happens to the amino acid sequence or protein produced as a result of each mutation? (Note: Position 1 refers to the first base at the 3' end of the transcribed strand. The last base in the DNA strand, at the 5' end, is at position 21.)

Original template strand: 3' TAC GCA AGC AAT ACC GAC GAA 5'

Mutation	Effect on amino acid sequence
i. Substitution of T for G at position 8.	
ii. Addition of T between positions 8 and 9.	
iii. Deletion of C at position 15.	
iv. Substitution of T for C at position 18.	
v. Deletion of C at position 18.	
vi. Which of the mutations produces the greatest change in the amino acid sequence of the polypeptide coded for by this 21-base-pair gene?	

7. Sickle-cell disease is caused by a single base substitution in the gene for the beta subunit of hemoglobin. This base substitution changes one of the amino acids in the hemoglobin molecule from glutamic acid to valine. Look up the structures of glutamic acid (glu) and valine (val) on page 79 of *Biology*, 8th edition. What kinds of changes in protein structure might result from this substitution? Explain.

8. Why do dentists and physicians cover patients with lead aprons when they take mouth or other X-rays?

17.1 Test Your Understanding

During DNA replication, which of the following would you expect to be true? Explain your answers.

- T/F 1. More ligase would be associated with the lagging strand than with the leading strand.
- T/F 2. More primase would be associated with the lagging strand than with the leading strand.
- T/F 3. More helicase would be associated with the lagging strand than with the leading strand.
- T/F 4. DNA ligase links the 3' end of one Okazaki fragment to the 5' end of another Okazaki fragment in the lagging strand.
- T/F 5. In the lagging strand, the enzyme DNA polymerase III that produces the next Okazaki fragment also removes the short segment of primer RNA on the previous Okazaki fragment.
6. You obtain a sample of double-stranded DNA and transcribe mRNA from this DNA. You then analyze the base composition of each of the two DNA strands and the one mRNA strand, and get the following results. The numbers indicate the percentage of each base in the strand:

	A	G	C	T	U
strand 1	40.1	28.9	9.9	0.0	21.1
strand 2	21.5	9.5	29.9	39.1	0.0
strand 3	40.0	29.0	9.7	21.3	0.0

- a. Which of these strands must be the mRNA? Explain.
- b. Which one is the template strand for the mRNA? Explain.